PHENOTYPIC AND GENETIC DIVERSITY IN THE FOXTAIL MILLET

(*Setaria italica* (L.) P. Beauv.) CORE COLLECTION

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Abstract

Abstract

Title	**:**	**Phenotypic and genetic diversity in the foxtail millet (S*etaria italica* (L.) P. Beauv.) core collection**
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Foxtail millet core collection consisting of 155 accessions was evaluated at three environments for 12 qualitative and 13 quantitative traits to study the phenotypic diversity and to identify trait specific accessions. Foxtail millet core collection was also molecularly profiled using 84 SSR markers to study molecular genetic diversity, population structure and to identify SSR markers associated with the agronomic traits.

In REML analysis variance due to genotypes (σ^2_g) and genotype × environment (σ^2_{ge}) were significant for all the 13 quantitative traits. On the basis of phenotypic dissimilarity between pair of accessions, ten pairs of most diverse accessions were identified for breeding program for the developing high yielding cultivars with a broad genetic base and for the development of mapping populations. On the basis of pooled BLUPs (Best Linear Unbiased Predictors) of three environments, we have identified trait specific accessions for economically important traits such as yield and its traits contributing to yield (15 accessions for each trait). These accessions could be used in recombination breeding to develop cultivars with desirable combination of traits.

The SSR markers detected a total of 1,356 alleles with an average of 16.14 alleles per locus. Of these, 368 were rare alleles; 906 common alleles; and 82 the most frequent alleles. Sixty one unique alleles which were specific to a particular accession and useful for germplasm identification were also detected. The genetic diversity of foxtail millet in this study was

correlated well with racial classification and the race *indica* showed greater genetic distance from the *maxima* and *moharia*. Ten pairs of genetically most diverse accessions were identified. Large molecular variation observed in core collection could be utilized effectively for selection of diverse parents for breeding cultivars and development of mapping populations. Mantel test showed significant correlation between phenotypic and molecular dissimilarity matrix.

The STRUCTURE analysis provided the evidence for the presence of four subpopulations. The mixed linear model (MLM) was used and the number of significant marker trait association was 130 in E1, 69 in E2 and 106 in E3 at $P \leq 0.05$, whereas only 49 in E1, 23 in E2 and 61 in E3 were found to be highly significant MTAs at $P \leq 0.01$. In pooled BLUPs of three environments, a total of 108 MTAs were detected at $P \leq 0.05$. Of these 18 SSR markers showed 37 significant associations at $P \leq 0.01$ with yield and yield contributing traits. Fifteen MTAs, that occurred in all three environments and overall in pooled data were identified as stable. Our research provided a first report of association study for yield and yield contributing traits in foxtail millet using SSR markers. The results from this research also demonstrated the use of core collection as association mapping panel to disclose marker-trait associations in foxtail millet for yield traits that could lead to effective utilization of *ex-situ* conserved genetic resources.

ABBREVIATIONS

AFLP	Amplified Fragment Length Polymorphism
AMOVA	Analysis of Molecular Variance
BLUPs	Best Linear Unbiased Predictors
bp	base pair
cm	Centimeter
CTAB	Cetyl Trimethyl Ammonium Bromide
DNA	Deoxyribo Nucleic Acid
dNTP	deoxy Nucleotide Tri-Phosphate
EDTA	Ethylene Diamine Tetra Acetic acid
EST-SSR	Expressed Sequence Tag-SSR
g	Gram
GCV	genotypic coefficient of variation
GD	genetic distance
H’	Shannon and Weaver diversity index
h^2_b	Heritability in the broad sense
HCL	hydrochloric acid
ICRISAT	International Crop Research Institute for the Semi-Arid Tropics
Kg ha^{-1}	Kilogram per hectare

LD	linkage disequilibrium
M	Molar
MCMC	Markov Chain Monte Carlo
mg	milligram
$MgCl_2$	Magnesium chloride
ml	millilitre
mm	millimetre
mM	millimolar
MTAs	Marker Trait Associations
NaCl	Sodium chloride
ng	nanogram
PCA	Principal Component Analyses
PCoA	Principle Coordinate Analysis
PCR	Polymerase Chain Reaction
PCs	Principal Components
PCV	Phenotypic Coefficient of Variation
PIC	Polymorphic Information Content
pmole	Picomole
QTL	Quantitative Trait Loci
RAPD	Randomly Amplified Polymorphic DNA
REML	Residual Maximum Likelihood

RFLP	Restriction Fragment Length Polymorphism
RNA	Ribonucleic acid
RNase	Ribonuclease
rpm	revolutions per minute
SE	Standard Srrors
SNP	Single-Nucleotide Polymorphism
σ_p	Phenotypic standard deviation
SSR	Simple Sequence Repeat
TASSEL	Trait Analysis by aSSociation, Evolution and Linkage
TBE	Tris Borate EDTA
TE	Tris EDTA
UPGMA	Unweighed Pair Group Method based on Arithmatic Average
UV	Ultraviolet
V	volt
µg	microgram
µl	microlitre
$\sigma^2 g$	Genotypic variance
σ^2_{ge}	Variance due to genotype x environment interaction
$\sigma^2 p$	phenotypic variance
%	per cent
°C	degree Celsius

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(M.VETRIVENTHAN)

CONTENTS

LIST OF TABLES

LIST OF PLATES

LIST OF FIGURES

LIST OF APPENDIX

Introduction

CHAPTER I

INTRODUCTION

The genus *Setaria* belongs to the tribe *Paniceae,* subfamily *Panicoideae* and family *Poaceae* in the grass family. There are about 125 species widely distributed in warm and temperate parts of the world. It contains crop, wild and weed species with different breeding systems, life cycles and ploidy levels (Benabdelmona *et al.,* 2001). Foxtail millet (*Setaria italica* (L.) P. Beauv.) is an autogamous, diploid (2n = 18), C_4 panicoid crop species of the grass family *Poaceae* with a relatively small genome size of ~515 Mb (Li and Brutnell, 2011). The most recent archaeological evidence demonstrated that, the foxtail millet is the most ancient crop as its domestication in China dates back to 8,700 years ago (Lu *et al*., 2009). According to Vavilov (1926), the principal center of diversity for foxtail millet is East Asia, including China and Japan. Several hypotheses concerning the origin and domestication of foxtail millet have been proposed (Vavilov, 1926; de Wet *et al*., 1979; Kawase and Sakamoto, 1987). A multiple domestication hypothesis (de Wet *et al*., 1979; Li *et al.,* 1995) is widely accepted. Li *et al.* (1995) suggested a multiple domestication hypothesis with three centers, *i.e.*, China, Europe and Afghanistan-Lebanon.

Taxonomically, foxtail millet consist two subspecies, *S. italica* subsp. *italica* and subsp. *viridis*. The geographical origin of foxtail millet based on cytological studies indicated that wild ancestor of foxtail millet is *S. viridis* (Kihara and Kishimoto, 1942; Li *et al*., 1945). Based on the comparative morphology of the foxtail millet accessions, Prasada Rao *et al*. (1987) have recognized three races of foxtail millet: (1) race *moharia* from Europe, southeast Asia, Afghanistan and Pakistan; (2) race *maxima*, common in eastern China, Georgia (Eurasia), Japan, Korea, Nepal and Northern India; and (3) race *indica,* found in the remaining parts of the India and Sri Lanka. A new system of classification recognizing four races, *i.e., maxima*, *moharia*, *indica* and *nana*, of foxtail millet was proposed by Li *et al.* (1995). However, at ICRISAT the classification recognizing three races (Prasad Rao, 1986) is followed.

Foxtail millet is an important grain crop in temperate, subtropical, tropical Asia and in parts of southern Europe. China, India and Japan are the major foxtail millet growing countries in the world. With the rapid development of maize and other crops, foxtail millet has gradually

become a minor crop in the last 80 years but it is still widely cultivated in Asia, Europe, North America, Australia and North Africa as grain food or forage (Austin, 2006). At present, in India the crop is cultivated on a very limited area of around 0.5 million hectares in sporadic patches in the states of Andhra Pradesh, Karnataka, Tamil Nadu, Maharastra, Rajasthan, Madhya Pradesh, Uttar Pradesh and North Eastern states with annual production of 0.29 million tones and productivity of 600 Kg ha^{-1}. In Tamil Nadu, it is grown an average area of about 3,000 ha (Nirmalakumari *et al.,* 2005) covering western zone especially, in Coimbatore, Madurai, Dindigul, Erode, Salem and Tirunelveli (Senthil *et al.*, 2005).

The foxtail millet grain is (per 100g) rich in protein (11.2g) and iron (2.8mg) as compared to rice (7.9 g protein and 1.8 mg Fe) and rich in fat 4.0g per 100g which is superior to rice and wheat (http://www.fao.org/docrep/t0818e/T0818E0a.htm). The foxtail millet bran constituted 9.39 per cent crude oil, 12.48 per cent crude protein and 51.69 per cent crude fiber (Liang *et al*., 2010). In the raw foxtail millet, Coulibaly and Chen (2011) reported presence of vitamins B1, B2, B6, C and E, 0.393, 0.142, 0.724, 0.120 and 0.176 mg/100g, respectively. Foxtail millet grain may be cooked and eaten like rice, either entire or broken; flour used for making porridge and puddings. Foxtail millet has low glycemic index (GI), used for preparation of low GI biscuits and burfi, a sweet product and it is an ideal food for people suffering from diabetes (Thathola *et al.,* 2010; Anju and Sarita, 2010). It is also used as bird feed for feeding cage birds and by-product of the foxtail millet is used as animal feed extensively in China (En *et al.,* 2008).

In view of the several merits, this crop deserves increased attention in research. At present, the genebank at ICRISAT, Patancheru, India holds 1,542 foxtail millet germplasm accessions from 26 countries which provide great opportunity for its utilization in research. These accessions need to be evaluated in multi-environmental trails to identify suitable parental material for use in breeding programmes. However, better access to and use of the genetic resources in collections have become important issues and continue to grow in number and size around the world. Many plant germplasm collections now face major problems of size and organization. The large size and heterogeneous structure of collections have hindered efforts to increase the use of germplasm in crop improvement. Recognizing this, Frankel, 1984 proposed a core collection approach, which can be used to overcome this problem efficiently. A core collection consists of a limited set of accessions (about 10%) derived from an existing

germplasm collection, chosen to represent the genetic spectrum in the whole collection (Brown, 1995).

After the concept of the core collection was proposed, there is a growing interest in the development of core collections in several germplasm collections [rice (Yan *et al.,* 2007), pearl millet (Bhattacharjee *et al.,* 2007; Upadhyaya *et al.,* 2009b), sorghum (Prasada Rao and Ramanatha Rao, 1995; Grenier *et al.,* 2001), finger millet (Upadhyaya *et al.* (2010b), prosomillet (Upadhyaya *et al.,* 2011c), barnyard millet (Upadhyaya *et al.,* 2011e), chickpea (Hannan *et al.,* 1994; Upadhyaya *et al.,* 2001a), groundnut (Holbrook *et al.,* 1993; Upadhyaya *et al.,* 2001b and 2003; Dwivedi *et al.,* 2008), pigeonpea (Reddy *et al*., 2005) etc.,] using various types of traits and sampling techniques.

Foxtail millet has received little research attention in the past years and continued to be a neglected and underutilized crop (Upadhyaya *et al*., 2008a). This is due to the poor seedling establishment, need for hand weeding and lack of breeding effort for improvement are major reasons for its reduced use (Ahanchede *et al*., 2004). It is incorrect to consider foxtail millet as a low yielding crop, the actual problem being that growing conditions in many areas are poor (Jiaju, 1986) beside lack of improved cultivar. Hence, the greater use of diverse germplasm in breeding and improved crop management is suggested to improve the productivity of this crop. There is a wide genetic diversity available in foxtail millet and characterizing these resources is a prerequisite for the genetic improvement. To enhance utilization of this diversity in research, Upadhyaya *et al.* (2008a) established core collection in foxtail millet (155 accessions) using the taxonomic and qualitative traits data from the entire collection (1474 accessions) of foxtail millet conserved at ICRISAT genebank. In view of the limited resources available especially for a low priority crop such as foxtail millet, the core collection will provide a good working collection that can be extensively characterized for all economically important traits (Upadhyaya *et al*., 2008a).

Once the core accessions are selected, the next logical step is to understand the level of genetic diversity in the core collection and identification of sources for traits of economic importance including resistance to biotic and abiotic stresses, yield and related traits for further use in breeding. Various types of data have been used to analyse the phenotypic and genetic diversity in core collection including taxonomical, morphological, agronomical and molecular

markers. Multi environmental evaluation and characterization of core collection for morphological and agronomical traits will help to identify suitable trait specific accessions for use in breeding high yield cultivars with a broad genetic base. Now germplasm characterization based on molecular markers has gained importance due to the speed and quality of data generated. But, it is unrealistic to subject an entire collection to molecular and biochemical analysis (Gepts, 1995) because of large size of collections conserved in genebanks. However, molecular characterization of core collection due to reduced size is possible, would help in revealing the population structure and in assessing the genetic diversity at DNA level with limited resources (Upadhyaya *et al.,* 2008a).

Several DNA-based molecular markers are available for genetic diversity analysis for most of the crops. The core collection accessions have been characterized initially using DNA markers such as isoenzyme markers, RAPD, AFLP (Skroch *et al.,* 1998; Ghislain *et al.,* 1999; Liu *et al*., 2002; Fu *et al.,* 2005). However, the SSR markers are now the markers of choice in most areas of molecular genetics as they are highly polymorphic even between closely related lines, require low amount of DNA, can be easily automated for high throughput screening, can be exchanged between laboratories and are highly transferable between populations. Microsatellite (SSR) markers were utilized in apple (*Malus* spp.) (Hokanson *et al.,* 1998), common beans (*Phaseolus vulgaris* L.) (Blair *et al.,* 2009) core collections, chickpea compost collection (Upadhyaya *et al.,* 2008b) and US peanut mini core collection (Kottapalli *et al.,* 2007) to reveal genetic diversity.

The phenotypic variation of many complex traits of agricultural or evolutionary importance is influenced by multiple quantitative trait loci (QTL), their interaction, the environment and the interaction between QTL and environment (Zhu *et al*., 2008). Therefore identification of QTL based on only conventional phenotypic evaluation is not possible (Collard, *et al*., 2005). Linkage analysis and association mapping are two most commonly used tools for dissecting complex traits for identification of QTL. Association mapping is an alternative approach to linkage analysis which identifies quantitative trait loci (QTL) by examining the marker-trait associations that can be attributed to the strength of linkage disequilibrium between markers and functional polymorphisms across a set of diverse germplasm (Zhu *et al*., 2008). As a new alternative to linkage analysis, association mapping

offers three advantages, (i) increased mapping resolution, (ii) reduced research time, and (iii) greater allele number (Yu and Buckler, 2006).

Presence of population structure within an association mapping population can be an obstacle to the application of association mapping as it often generates spurious genotype-phenotype associations (Yu and Buclker, 2006). To account for population structure in association mapping, two major statistical methods, genome control (Devlin and Roeder, 1999; Zheng *et al.,* 2005) and structured association (Pritchard *et al.,* 2000b) available. Recently, Yu *et al.* (2006) developed mixed-liner model (MLM) approach to perform association analysis, accounting for both population structure (Q) and relative kinship (K), which can be performed with TASSEL software (Bradbury *et al.,* 2007). It is one of the most common methods of association analysis in plants, and has been successfully applied in several crops (Neumann *et al.,* 2011; Borbra *et al.,* 2010; Murrary *et al.,* 2009; Wen *et al.,* 2009; Malosetti *et al*., 2007; Yu and Buckler, 2006; Breseghello and Sorrells, 2006). Currently, SSRs and SNPs are two main types of molecular markers used to evaluate genetic diversity, population structure and familial kinship in association panels. SSR markers have been used for a study of population structure in maize (Remington *et al.,* 2001), rice (Garris *et al.,* 2003) and wild diploid alfalfa (Şakiroğlu *et al.,* 2010) and LD based association studies in rice (Borbra *et al.,* 2010; Jin *et al.,* 2010; Wen *et al.,* 2010; Agrama *et al.,* 2007), wheat (Reif *et al*., 2011) and maize (Yang *et al.*, 2010b).

However, knowledge of genetic diversity and linkage disequilibrium (LD) is very limited in foxtail millet and its wild ancestor, green foxtail millet. Such information helps to understand the domestication process and allow further research in these species, including association mapping and identification of agricultural significant genes (Wang *et al*., 2010) for further improvement. Until now, association mapping using the existing natural variation present in the germplasm for the detection of marker trait associations (MTAs) has not been reported in foxtail millet, and QTL reported by the earlier studies (Doust *et al.,* 2004, 2005; Doust and Kellogg, 2006) were identified through linkage mapping approach based on RFLP genotyping of mapping population. To date, there were no reports on QTL and MTAs in foxtail millet using SSR marker because of limited number of SSRs markers reported in this crop. Therefore, there is a need for the identifying genomic regions association with yield and yield contributing traits in foxtail millet. To achieve this, multi-environmental characterization and genotyping of core collection by molecular markers is required. This would also help in

identification of genetically diverse trait specific accessions for breeding improved cultivars. With this view, the present study was undertaken with the following objectives:

1. To assess the phenotypic diversity in foxtail millet core collection using morpho-agronomic traits from multi environment evaluations.
2. To identify the trait-specific sources for yield and its related traits in foxtail millet core collection.
3. Identification of polymorphic SSR markers for foxtail millet.
4. To assess genetic diversity and population structure in the foxtail millet core collection using SSR markers.
5. To identify SSR markers associated with important traits including yield using association mapping in foxtail millet.

CHAPTER II

REVIEW OF LITERATURE

Small millets are gaining importance because of their nutritional values and adaptability to drought and varied soil and environmental conditions. They have many nutritious and medicinal functions. Realizing the nutraceutical values of small millets, they are now considered as "nutri-cereals". Foxtail millet (Setaria italica (L.) P. Beauv.) is also known as italian foxtail, german millet, hey millet, chinese millet, hungarian millet, kangni, navane, tenai, korra and rela. It is one among the small millets which is still used as staple food in China and India.

2.1 ORIGIN, EVOLUTION AND DISTRIBUTION

Foxtail millet is one of the world's most important and ancient domesticated crops and its domestication in China dates back to 8,700 years ago (Lu et al., 2009). The geographical origin of foxtail millet based on cytological studies indicated that S. italica was first domesticated in an area ranging from Afghanistan to India. Afterwards, it dispersed both eastward and westward from there (Kawase and Sakamoto, 1987). According to Vavilov (1926), the principal center of diversity for foxtail millet is East Asia, including China and Japan. Several hypotheses concerning the origin and domestication of foxtail millet have been proposed (Vavilov, 1926; de Wet et al., 1979; Kawase and Sakamoto, 1987). A multiple domestication hypothesis (de Wet et al., 1979; Li et al., 1995) is widely accepted. Li et al. (1995) suggested a multiple domestication hypothesis with three centers, i.e., China, Europe and Afghanistan-Lebanon.

2.2 TAXONOMY

Cultivated foxtail millet was recognized by Linnaeus (1753) as Panicum italicum. Variants within the species were later recognized as P. germanicum Mill. and P. glomeratum (Mansfeld, 1952) and transferred to Setaria and combined into S. italica (foxtail millet) by Beauvois (1812), who also transferred the weedy P. viride L. (green foxtail) to Setaria. Foxtail millet and the weedy green foxtail are morphologically and genetically allied. Foxtail millet

also crosses naturally (de Wet et al., 1979) and experimentally with green foxtail (Li et al., 1945) to produce fertile hybrids (Prasada Rao et al., 1986) and both have same number of chromosome (2n=18). Phylogenetic analysis using chloroplast and nuclear genes show foxtail and green millet as close relatives (Giussani et al., 2001; Doust et al., 2007), which support the hypothesis that foxtail millet is a domesticated version of green millet (Li et al., 1944, 1945; de Wet and Harlan, 1975; Wang et al., 1995).

Foxtail millet is an autogamous diploid (2n=18) C4 panicoid crop species of the grass family Poaceae, with cross pollination averaging about 4 per cent (Li et al., 1935). The inflorescence is a spike with short side branches bearing spikelets and bristles. Each spikelet consists of a pair of glumes that embrace two minute flowers; the lower one sterile and the upper one is bisexual, with three stamens and a long oval smooth ovary with two long styles, which terminate in a brush like stigma (Hector, 1936). One to three bristles develop at the base of each spikelet (Vinall, 1924). Anthesis in foxtail millet generally takes place near midnight and in the morning but varies significantly with environment (Malm and Rachie, 1971).

2.2.1 Racial classification of cultivated foxtail millet

Initially, foxtail millet was differentiated into ssp. moharium to include cultivars with numerous culms and small, cylindrical inflorescences and ssp. *maxima* to include cultivars with one or a few culms and large inflorescences (Dekaprelevich and Kasparian, 1928). Later, Körnicke and Werner, 1885 divided the foxtail millet into two cultivar complexes on the basis of inflorescence structure. Cultivars with large, pendulous inflorescences were included in group *maxima*, and those with smaller, erect inflorescences, in group *moharia*. Prasada Rao et al. (1986) added another race, i.e., *indica* along with *maxima*, *moharia* races. A new system of classification recognizing four races, i.e., *maxima*, *moharia*, *indica* and *nana*, of foxtail millet was proposed by Li et al. (1995). They described the plants which resembles the wild green millet (S. viridis), and are very short and slender, with many tillers, very short panicles with poor yield performance and early maturity as a separate race nana. At present, foxtail millet accessions present in ICRISAT genebank were classified based on three races as proposed by Prasada Rao et al. (1986) and described below (Figure 1).

2.2.1.1 Race '*moharia*'

Cultivars of race *moharia* often resemble members of wild ssp. viridis in phenotype, except that they have lost the ability of natural seed dispersal. Plants are 25 to 100 cm tall, with 5 to 52 (average 8.6) tillers per plant. Tillers are usually branched to produce a well developed terminal inflorescence and several, smaller lateral inflorescences. Terminal inflorescences are erect or nodding at maturity and 5 to 20 cm long. Panicle branches are short and compactly arranged on the primary axis. Bristles are well developed or more rarely shorter than the spikelets. Race *moharia* is cultivated in southeastern Europe, southwestern Russia, Afghanistan and Pakistan. Cultivars from Afghanistan have small inflorescence with unusually large grains (Prasada Rao et al., 1986). This race is represented by 243 accessions (16.49%) in the ICRISAT genebank (Upadhyaya et al., 2008a). The race *moharia* comprises three subraces viz., *glabra*, *aristata* and *fusiformis*.

2.2.1.2 Race '*maxima*'

The race *maxima* is extensively variable. It is characterized by spikelets closely arrange on elongated lateral branches, giving the inflorescence a lobed appearance. Plants are 45 to 100 cm tall with 1 to 8 (average 1.6) unbranched tillers, each bearing a terminal inflorescence. Gritzenko (1960) recognized two types of inflorescence. Plants from China, Japan and Korea are tall, with large, pendulous inflorescences of 12-30 cm long and well developed bristles. Plants with smaller, essentially erect inflorescences occurring in northwestern China and Mongolia commonly have short bristles and often have the panicle branches tightly packed along the primary axis. The race *maxima* was introduced into the United State, where it is grown as bird feed. It also occurs in Nepal and Assam (Prasada Rao et al., 1986). In the collection at the ICRISAT genebank, the race *maxima* is represented by 235 accessions (15.94%) (Upadhyaya et al., 2008a). The race *maxima* comprises three subraces viz., *compacta*, *spongiosa* and *assamense*.

2.2.1.3 Race '*indica*'

The race *indica* was probably derived from a combination of *moharia* cultivars from southwestern Asia and *maxima* cultivars from China. It is intermediate in culm number (average 6.6) and inflorescence size between races *moharia* and *maxima* and cultivated in southern Asia (Prasada Rao et al., 1986). The germplasm collection in ICRISAT genebank is

dominated by this race and represented by 996 accessions (67.57%) (Upadhyaya et al., 2008a). The race *indica* comprises four subraces, namely *erecta*, *glabra*, *nana* and *profusa*.

2.3 FOXTAIL MILLET GENE POOL

Observations drawn from interspecific hybridization and hybrid pollen fertility suggest that the genus Setaria is organized into three gene pools. The primary gene pool is composed of diploid species (2n=2x=18) S. italica and its putative wild ancestor S. viridis (Harlan and de Wet, 1971). A secondary gene pool contains S. adhaerans (2n=2x=18) and the two allotetraploids S. verticillata and S. faberii (2n=4x=36) (Li et al., 1942; Benabdelmouna et al., 2001). The tertiary gene pool contains S. glauca (or S. pumila, 4x to 8x) in addition to many other wild species (Zangré et al., 1992).

2.4 IMPORTANCE OF FOXTAIL MILLET

Today, the only well-known human food among Old World species is S. italica, however, other species like S. intermedia, S. liebmannii, S. macrostachya, S. pallidifusca, S. palmifolia, S. parviflora, S. pumila, S. sphacelata, S. verticillata and S. viridis were also used in Europe, Africa, and Asia. It is an important grain crop in temperate, subtropical, tropical Asia and in parts of southern Europe. China, India and Japan are the chief foxtail millet growing countries in the world. China ranks first in foxtail millet production in the world and it is grown across the entire country, but the principle growing region is within the latitude of 32° to 48°N, and longitude of 108°E to 130°E (Jiaju, 1986). With the rapid development of maize and other crops, foxtail millet has gradually become a minor crop in the last 80 years. However, it is still widely cultivated in Asia, Europe, North America, Australia and North Africa as grain food or forage, remains an essential food for home consumption in India, China, Korea and Japan (Austin, 2006). It is not correct to consider foxtail millet as a low yielding crop, the actual problem being that growing conditions in many areas are poor and grown as rainfed beside lack of improved cultivars. The yield level of 1,500-2,250 Kg ha-1 has been reported from China (Jiaju, 1986).

At present in India, the crop is cultivated on a very limited area of around 5 lakhs hectares in sporadic patches in the states of Andhra Pradesh, Karnataka, Tamil Nadu, Maharastra, Rajasthan, Madhya Pradesh, Uttar Pradesh and North eastern states with annual production of 0.29 lakhs tones and productivity of 600 Kg ha-1. In Tamil Nadu it is grown over

an area of around 3000 hectares (Nirmalakumari et al., 2005). The foxtail millet is grown in Tamil Nadu as rainfed crop, covering western zone especially, in Coimbatore, Madurai, Dindigul, Erode, Salem and Tirunelveli (Senthil et al., 2005). In India, several millet based cropping systems were followed ('Sara and Baranaja' in Himalaya Gharwal, 'Pannendu pantalu' in the Zaheerabad region of Andhra Pradesh, 'Ragi pairu' in Tamil Nadu) and in those places, foxtail millet were cultivated along with other millets (Srinivas, 2008).

The foxtail millet grain (per 100g) is rich in protein (11.2g) and iron (2.8mg) as compared to rice (7.9g protein and 1.8mg Fe) and rich in fat 4.0g which is superior to rice (2.7g), wheat (2.0g) and sorghum (3.1g) (http://www.fao.org/docrep/t0818e/T0818E0a.htm). The foxtail millet bran constituted 9.39 per cent crude oil, 12.48 per cent crude protein and 51.69 per cent crude fiber (Liang et al., 2010). In the raw foxtail millet, Coulibaly and Chen (2011) reported the presence of vitamins B1, B2, B6, C and E, 0.393, 0.142, 0.724, 0.120 and 0.176 mg/100g, respectively. During germination, they also noticed slight decrease of vitamin B1 and increase in other vitamins.

Foxtail millet grain may be cooked and eaten like rice, either whole or broken. Its flour is used for making porridge and puddings. It is currently used in various dishes mixed with rice, baked goods, weaving food, and brewing industry (Kim et al., 2009). Foxtail millet has low glycemic index (GI), used for preparation of low GI biscuits and burfi, a sweet product (Thathola et al., 2010; Anju and Sarita, 2010). The grains also make an ideal food for people suffering from diabetes (Thathola et al., 2010; Anju and Sarita, 2010) and gastric problem as well used to treat chickenpox (Ramprasad, 2005).

Because of the minuteness of flowers, delicate process of anthesis and its variation with the environment, the time of anthesis, hybridization of foxtail millet is challenging but it can be done as described by Siles et al. (2001). Foxtail millet varieties are remarkably drought and salt tolerant and further breeding for these characteristics can increase the usefulness of foxtail millet in semi-arid and marginal lands (Li and Wu, 1996; Dekker, 2003). Foxtail millet will also be useful as an experimental crop to investigate many aspects of plant architecture, genome evolution, physiology in the bioenergy grasses (Doust et al., 2009) and for the study of C4 photosynthesis, artificial selection, abiotic stress tolerance and biomass production in the Panicoid grasses (Li and Brutnell, 2011). The difficulty of making crosses, lack of efficient

crossing techniques and lack of proper utilization of existing genetic resources have resulted in a limited number of genetic studies and consequently, little or no genetic improvement of foxtail millet had been realized in this crop.

In view of the several merits and limited research undertaken for its yield improvement, this crop deserves increased attention in research. The genebank at ICRISAT, Patancheru, India holds 1,542 foxtail millet germplasm accessions from 26 countries which provide great opportunity for its utilization in research. Upadhyaya et al. (2008a) developed core collection for its effective utilization in crop improvement. In view of the limited resources available for agricultural research in developing countries, especially for low priority crops such as foxtail millet, the core collection will provide a good working collection that can be extensively characterized for all economically important traits including the reaction to various stress factors and for nutritional traits, such as protein, ß carotene, iron and zinc contents (Upadhyaya et al., 2008a). The molecular characterization of core collection would help in revealing the population structure and in assessing the genetic diversity at DNA level with minimal resources.

2.5 IMPORTANCE OF GERMPLASM COLLECTION AND ITS UTILIZATION

The germplasm represent the sum total of hereditary materials, i.e., all the alleles of various genes, present in a crop species and its wild relatives which includes landraces, advanced breeding lines, popular cultivars, wild and weedy relatives. The genes required for crop improvement are present in different lines, varieties, strains or populations of the crop species and their wild relatives. However, extensive germplasm collections of various crops and their wild relatives continued to be grown in number and size. The present status of germplasm collections held at ICRISAT genebank as on 01.05.2011 is 1,19,739 accessions from 144 countries which include 1,17,032 cultivated and 2,707 wild species of ICRISAT mandate crops. The collection includes 37,949 accessions of sorghum, 22,211 accessions of pearl millet, 20,267 accessions of chickpea, 13,632 accessions of pigeonpea, 15,445 accessions of groundnut and 10,235 accessions of small millets.

Increasing size of germplasm collections have hindered efforts to increase the use of germplasm which leads to low use in crop improvement. A large number of germplasm lines are distributed by the genebank for use in crop improvement programs. ICRISAT genebank

distributed more than 7,00,000 samples of accessions to scientists in India and 143 other countries. Of the germplasm supplied by the genebank, a very small proportion has been used in crop improvement programs. For example, at ICRISAT, between 1986 and 2008, a total of 10,331 advanced groundnut breeding lines (ICGV #) were developed from thousands of crosses involving 1,270 unique parents out of these only 171 were germplasm lines, including 10 wild out of 15,445 accessions (Upadhyaya et al., 2010a). This is mainly due to lack of information on traits of important to breeders that shows high environment effect and genotype × environment interaction and require replicated multilocation evaluation to identify parents for its use in breeding program. Hence, it is appropriate to have a small sample of a few hundred germplasm lines, which represent the entire diversity present in the crop species, with multi-environmental evaluation data, which would greatly encourage the breeders to utilize more germplasm lines in to their breeding program (Upadhyaya et al., 2010a). To overcome the limited use and enhance the utilization of germplasm resources, the concept of core collection was proposed by Frankle (1984).

2.5.1 Core collection

Germplasm collection is a means of preserving the genetic diversity of a cultivated species before that diversity is lost as a result of implementing high input crop monoculture systems (Yan et al., 2007). The management and use of germplasm collections could be enhanced if a small sample of a few hundred germplasm lines, which represent the entire diversity present in the crop species, were selected (Upadhyaya et al., 2010a). Frankle (1984) proposed a 'core collection' which would represent, "With a minimum of repetitiveness, the genetic diversity of a crop species and its relatives". A core collection consists of a limited set of accessions (about 10%) derived from an existing germplasm collection, chosen to represent the genetic spectrum in the whole collection. Core collection should include as much as possible of its genetic diversity and the entries in the core are chosen primarily to be representative (Brown, 1995). The core collections were set up to preserve the genetic diversity of cultivated species. The accessions excluded from the core would be retained as the reserve collection (Brown, 1989).

After the concept of the core collection was proposed, there is a growing interest in the development of core collections using different sampling strategies. Due to reduced size, the

core collections can be evaluated extensively and more economically for important traits. Following this approach, core collections have been constituted in several crops species (Table 1). Again, the germplasm collections held by most of the International Agricultural Research Centers genebanks are very large in size. For example, the IRRI genebank holds more than 1,08,000 rice accessions; hence the size of core collection will be about 11,000 accession (~ 10%) which again restrict its proper evaluation and use by breeders (Upadhyaya et al.,2010a). To overcome this, Upadhyaya and Ortiz (2001) developed the concept of mini core (10% of core or 1% of entire collection) collection. The minicore collections have been developed in several crops (Table 1) at ICRISAT and elsewhere following Upadhyaya and Ortiz (2001). Once the core and mini core are developed, it is possible to evaluate the germplasm extensively and more economically for important traits with limited resources and time.

2.5.2 Foxtail millet germplasm conserved at different institutions

Germplasm provides basic raw materials for any crop improvement programs and provide valuable genes for various biotic, abiotic stress and yield contributing characters. Institute of Crop Germplasm Resources, Chinese Academy of Agricultural Sciences, China (26,233 accessions) and National Bureau of Plant Genetic Resources, India (4,392 accessions) maintaining major germplasm collections of foxtail millet. At present, ICRISAT holds 1,542 accessions of foxtail millet. Some of the national and international organizations/genebanks conserving foxtail millet accessions were presented in Table 2. For effective utilization of existing genetic resources in research, it is necessary to develop core collection representing genetic diversity of the entire collection for its use in crop improvement program.

2.5.3 Core collection in foxtail millet

In general, grain yield levels of foxtail millet are low and increased use of diverse germplasm in breeding is suggested to improve the productivity of this crop. Foxtail millet has received little research attention in the past years and continues to be a neglected and underutilized crop (Upadhyaya et al., 2008a). This is mainly due to poor seedling establishment, need for hand weeding and lack of breeding effort for improvement (Ahanchede et al., 2004) beside lack of improved cultivars. There is a wide genetic diversity available in foxtail millet and systematic characterization and evaluation of germplasm is necessary to utilize the potential of preserved germplasm by the breeders for their crop improvement

program. To enhance utilization of foxtail millet germplasm in research, Upadhyaya et al. (2008a) developed core collection of foxtail millet (155 accessions) using the data on taxonomic and qualitative traits. Initially, they classified the germplasm accessions into three taxonomic races (*indica*: 996 accessions, *maxima*: 235 accessions and *moharia*: 243). The principal coordinate analysis (PCoA) was performed on 12 qualitative traits for each of the biological races separately. Clustering using scores of first five PCoAs by Ward (1963) resulted into 29 clusters. From each cluster, 10 per cent or at least one accession was included in the core collection resulting in selection of 155 accessions, which is 10.51 per cent of the entire collection. The data on geographic origin, qualitative as well as quantitative traits were used for the validation of the core collection. This core collection has value in crop improvement programs due to reduced size. It can be evaluated extensively (replicated, multiplications) to identify of diverse trait specific accessions with more precision.

2.6 GENETIC DIVERSITY STUDIES IN FOXTAIL MILLET

Study of genetic diversity is the process by which variation among individuals or groups of individuals or populations is analyzed by a specific method or a combination of methods. Analysis of genetic relationships in crop species is an important component of crop improvement program, since it provides information about genetic diversity of the crop species which is a basic tool for crop improvement. Accurate assessment of the levels and patterns of genetic diversity is invaluable in crop breeding which facilitate reliable classification of accessions and identification of subsets of core accessions with possible utility for specific breeding purpose (Mohammadi and Prasanna, 2003). Various types of data have been used to analyze the genetic diversity in crops, including pedigree, morphological, biochemical obtained by analysis of isoenzymes, seed proteins and molecular marker data. Since each method provides different types of information, the choice of method depends on the need of the researchers.

In foxtail millet various types of data have been used to analysis genetic diversity; morphological (Li et al., 1995 and 1996; Murugan and Nirmalakumari, 2006; Nirmalakumari and Vetriventhan, 2010), biochemical data obtained by analysis of isoenzymes (Jusuf and Pernes, 1985) and molecular marker data (Schontz and Rether, 1998 and 1999; Fugunaga et al., 2002; Fugunaga and Kato, 2002; Van et al., 2008; Jia et al., 2009). Each of these has its own

advantages and disadvantages for measuring genetic diversity. The major advantage of biochemical and molecular marker data is their genotypic nature and can reflect direct changes at the DNA sequence level. It is unrealistic to subject the entire collection to molecular and biochemical analysis (Gepts, 1995) unless simple methods are found.

2.6.1 PHENOTYPIC DIVERSITY

A core collection is a subset of accessions from the entire collection that capture most of the available diversity (Brown, 1989), can be evaluated extensively due to its reduced size and the information derived from it could be used as guide for most efficient utilization of the entire collection. A core collection was extensively evaluated for agronomical and morphological traits in many crops chickpea (Kashiwagi et al., 2005;Pande et al., 2006), groundnut (Upadhyaya et al., 2009a; Upadhyaya et al., 2006a), finger millet (Upadhyaya et al., 2011a) and Spanish Barley (Silver et al., 2010) to identified trait specific accessions for biotic and abiotic stresses and for agronomic traits. Phenotypic characterization is also useful for identification of QTL for various economic traits using molecular marker traits association studies.

Various methods have been used to study the phenotypic diversity in earlier studies. The important findings relevant to the phenotypic diversity study in foxtail millet are reviewed under the following headings.

1. Genetic divergence
2. Studies on range of variation and variability parameters
3. Correlation studies and path analysis

2.6.1.1 Genetic divergence

The genetic divergence in the foxtail millet genotypes were estimated through Mahalanobis'D2 analysis in various reports (Nagarajan and Prasad, 1980; Sheriff and Shivashankar, 1992; Maloo and Bhattacharjee, 1997; Selvarani and Gomathinayagam, 2000a, Murugan and Nirmalakumari, 2006). The number of genotypes used in their studies ranged from 40 to 225 and the genotypes were grouped into 4 to 33 clusters. In these studies, the characters such as number of branches, days to maturity, test weight, seed yield per plant, grain yield, straw yield and harvest index contributed more towards divergence. These studies

concluded that, the geographical distribution was not related to genetic diversity. The cluster analysis of foxtail millet (2,907 genotypes, Li et al., 1995; 741 genotypes, Nirmalakumari and Vetriventhan, 2010) using morphological and agronomic descriptors and reported the existence of high levels of variation for all the characters.

The Shannon-Weaver diversity index (H') was used to estimate the phenotypic diversity in foxtail millet by Li et al. (1996) and Upadhyaya et al. (2008a). Li et al. (1996) reported the diversity indices for leaf colour of seedling, starch composition and 1000 grain weight showed significant differences among regions, and Upadhyaya et al. (2008a) reported presence of the highest H' for plant height, flag leaf blade width, flag leaf sheath length, peduncle length and panicle exertion in entire set when compared to other traits of foxtail millet germplasm conserved at ICRISAT and in core collection.

Upadhyaya et al. (2008a) conducted a hierarchical cluster analysis (Ward, 1963) using the scores of the first five principal coordinates (PCos) and the accessions were grouped in to 29 clusters. From each clusters, 10 per cent of the accessions were selected to constitute a core collection 155 accessions in foxtail millet.

Ochiai et al. (1994) studied morphological variation of landraces collected from northern Pakistan and recognized three groups, i.e., the Chitral, the Baltistan and the Dir groups. Ochiai (1996) conducted an experiment and reported the four patterns of tiller development in foxtail millet, Type I, Type II, Type III and Type IV.

2.6.1.2 Studies on range of variation and variability parameters

Range is a crude measure of variability and it provides a spread of variability for a particular character. Presence of wide range of variation in foxtail millet was reported in various studies (Reddy et al. 2006; Upadhyaya et al. 2008a; Nirmalakumari and Vetriventhan, 2010) for various morphological and agronomical traits.

The relative values of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) give an idea about the magnitude of variability present in the population. Heritability is a quantitative measure which provides information about the correspondence between genotypic variance and phenotypic variance, i.e., the ratio of variance due to hereditary differences ($\sigma 2g$) to the total phenotypic variance ($\sigma 2p$) and expressed as

percent. Since heritability is also influenced by environment, the information on heritability alone may not help in pin pointing characters enforcing selection. The heritability estimates in along with the predicted genetic gain will be more reliable (Johnson et al., 1955) for formulating suitable breeding methods. Heritability gives the information on the magnitude of inheritance of quantitative traits, while genetic advance will be helpful in formulating suitable selection procedures. The earlier studies on phenotypic and genotypic coefficients of variation, heritability and genetic advance as per cent in foxtail millet are reviewed in Table 3.

2.6.1.3 Studies on correlation and path analysis

The knowledge of differences in economically important plant characters and their correlation with each other would be of great help in correct selection of parents and in planning of breeding programme. Correlation coefficient is a statistical measure, which is used to find out the strength and direction of relationship between two or more variables. It measures the mutual relationship between two or more variables. In plant breeding, correlation analysis provides information about yield components and thus helps in the selection of superior genotypes from diverse genetic populations. Earlier studies about correlation in foxtail millet are presented in Table 4.

The concept of path analysis was originally developed by Wright in 1921, but this technique was first used for plant selection by Dewey and Lu, 1959. Path coefficient analysis is simply a standardized partial regression coefficient, which splits the correlation coefficient into the measures of direct and indirect effect of a set of yield attributing characters on grain yield. So, it helps in determining yield attributing characters. Studies on the extent of direct and indirect influence of different yield attributing characters on grain yield reported by several earlier workers are presented in Table 5.

2.6.2 IDENTIFICATION OF TRAIT SPECIFIC SOURCES

The use of genetic resources in the breeding programs have been mainly as sources of resistance to pests and diseases (Knauft and Gorbet, 1989), or as sources of male sterility, short stature or any such character with simple inheritance. There have been fewer efforts for identifying germplasm lines for increasing yield potential than for pest resistance and nutritional quality (Halward and Wynne, 1991). Because such traits are highly influenced by environment and require multi-environment testing to accurately characterize them (Upadhyaya

et al., 2010a). Thus, identification of promising resources for the environment sensitive quantitative characters is a difficult task.

However, with the use of core and mini core collections of chickpea (Upadhyaya and Ortiz, 2001), sources for high grain yield (Upadhyaya et al., 2007a), tolerance to drought (Kashiwagi et al., 2005), disease (Pande et al., 2006), early maturity, seed size and grain yield (Upadhyaya et al., 2007a). Similarly, in groundnut using core and minicore collection, the new sources for tolerance to drought (Upadhyaya, 2005) and low temperature at germination (Upadhyaya et al 2009a), and for early-maturity (Upadhyaya et al., 2006a), were identified. Upadhyaya et al. (2005) identified 15 fastigiata, 20 vulgaris, and 25 hypogaea type groundnut accessions for pod yield and its components by multi-location evaluation of groundnut core collection for Asia region. Silver et al. (2010) screened the Spanish Barley Core Collection for resistance to powdery mildew, scald, leaf rust, net blotch, barley yellow dwarf virus (BYDV) and barley mild mosaic virus (BaMMV). Foxtail millet core collection was evaluated and neck blast resistant foxtail millet accessions were identified (ICRISAT Archival Report, 2009). Upadhyaya et al. (2011a) evaluated finger millet core collection for grain nutrients and identified accessions rich in Fe, Zn, Ca and protein. Hence, multi-environmental evaluation/characterization of foxtail millet core collection and identification of trait specific sources for different yield contributing traits will provides new sources for future breeding program in foxtail millet. The accessions from the reserve collection (remaining part of the entire collection) can also be examined selectively for additional sources of useful traits from the same cluster from which the accessions in the core collection have been identified (Upadhyaya et al., 2008a).

2.6.3 MOLECULAR DIVERSITY

There are three major types of genetic markers (morphological, biochemical, and DNA (or) molecular markers) used to study the genetic diversity in crops. The major disadvantages of morphological and biochemical markers are that they may be limited in number and influenced by environmental factors and the developmental stage of the plant (Winter and Kahl, 1995). DNA markers are the most widely used type of marker mainly due to their abundance. They arise from different classes of DNA mutations such as substitution mutations (point mutations), rearrangements (insertions or deletions) or errors in replication of tandemly

repeated DNA (Paterson, 1996). These markers are selectively neutral because they are usually located in non-coding regions of DNA. Unlike morphological and biochemical markers, DNA markers are practically unlimited in number and are not affected by environmental factors and/or the developmental stage of the plant (Winter and Kahl, 1995).

A comprehensive study of the molecular genetic variation present in germplasm would be useful for determining whether morphologically based taxonomic classifications reflect patterns of genomic differentiation. It would also provide information on the population structure, allelic richness, and diversity parameters of germplasm to help breeders use genetic resources for cultivar development more effectively. Now germplasm characterization based on molecular markers has gained importance due to the speed and quality of data generated. But, it is unrealistic to subject an entire collection to molecular and biochemical analysis (Gepts, 1995) because of large size of collections conserved in genebanks. However, molecular characterization of the core collection is possible due to reduced size, would help in revealing the population structure and in assessing the genetic diversity at DNA level with limited resources and time (Upadhyaya et al., 2008a).

Several DNA-based molecular markers are available for genetic diversity analysis for most of all the crops. The core collection accessions were characterized initially using DNA markers such as RAPD in common bean (Phaseolus vulgaris L.) (Skroch et al., 1998) and potato (Solanum tuberosum L.) (Ghislain et al., 1999), isoenzyme markers in Wild barley (Hordeum vulgare ssp. spontaneum) (Liu et al., 2002) and AFLP markers in oats (Fu et al., 2005).

2.6.3.1 Microsatellite (or) Simple Sequence Repeats (SSR)

The SSR markers are now the markers of choice in most areas of molecular genetics as they are highly polymorphic even between closely related lines, require low amount of DNA, can be easily automated for high throughput genotyping, can be exchanged between laboratories and are highly transferable between populations. The SSR markers are co-dominant markers and good for studies of population genetics and mapping. The SSR markers were used to study the genetic diversity of Japanese barley cultivars (Turuspekov et al., 2001), wheat (Stepien et al., 2007), chickpea (Cicer arietinum L.) (Upadhyaya et al., 2008b) and genus Arachis (Koppolu et al., 2010). Microsatellite (SSR) markers were also utilized to reveal

genetic diversity in apple (Malus spp.) (Hokanson et al., 1998), common beans (Phaseolus vulgaris L.) (Blair et al., 2009) core collections, US peanut mini core collection (Kottapalli et al., 2007) and rice core and minicore collection (Agrama et al., 2009; Zhang 2011).

The SSR markers have been used for a study of population structure in maize (Remington et al., 2001), rice (Garris et al., 2003) and wild diploid alfalfa (Şakiroğlu et al., 2010) and linkage disequilibrium (LD) based association studies in rice (Agrama et al., 2007, Borbra et al., 2010, Jin et al., 2010, Wen et al., 2009), wheat (Reif et al., 2011), maize (Yang et al., 2010b), sorghum (Shehzad et al., 2009), common bean (Blair et al., 2009), soybean (Jun et al., 2008) and rape (Brassica napus L.) (Rezaeizad et al., 2011).

2.6.3.2 Foxtail millet linkage map and comparative studies

At present in foxtail millet, two complete genetic maps were created using RFLP markers (Devos et al., 1998; Wang et al., 1998) which provides foundation for genetic analysis. The first comprehensive genetic map of foxtail millet genome was reported by Wang et al. (1998) using RFLP markers. Two maps were constructed, first one based on an intraspecific cross (Longgu25 x Pagoda flower green, two cultivars of S.italica) and other based on S.italica (cv.B100) x S. viridis (acc.A10) interspecific cross. Nine linkage groups were obtained, corresponding to the nine chromosomes of the species (S. italica and S. viridis are 2n=2x=18). Linkage groups were assigned to chromosomes using trisomic millet lines. They compared the intraspecific map to an interspecific map, constructed in a S. italica x S. viridis cross. Both the order of the markers and the genetic distances between the loci were highly conserved. The second genetic map was generated by intervarietal cross within foxtail millet by Devos et al. (1998) by adding additional rice probes in addition to 160 RFLP probes (Wang et al., 1998) to investigate the synteny of foxtail millet with rice, giving a map containing 257 loci and spanning 1050 cM. Due to the limiting number of RFLP markers and inconvenience of operation, other marker systems are needed. The simple sequence repeats, which are distributed widely and throughout plant genomes, are valuable genetic markers because of their high polymorphism and simple operation procedure (Jia et al., 2009). Recently, Jia et al. (2009) developed foxtail millet SSR linkage map by integrating 81 newly developed SSR markers with 20 RFLP anchored markers. Devos et al. (1998, 2000) performed comparative genomic

research among foxtail millet, rice and pearl millet and they found the close relationships of the gramineous crops.

2.6.3.2 Studies on genetic diversity and molecular characterization in foxtail millet

The relatively small genome size, IC genome size=490Mb (Doust et al., 2009), and diploid nature of foxtail millet made it a suitable organism for genetic and molecular studies. However, as the crop is considered as minor cereal of only regional importance, genetic studies have lagged behind those of other staple cereals (Wang et al., 1998). Understanding of genetic relationship between foxtail millet and other species of the Setaria complex can help us for successful parent selection and hybridization, as well as to organize germplasm, identify cultivars and ensure sampling from broad range of genetic variability (Benabdelmouna et al., 2001). A lot of molecular studies focused on geographical variation of foxtail millet and studied the evolutionary relationships between foxtail millet and its wild relative green millet using isozymes (Jusuf and Pernes, 1985; Wang et al. 1995), RAPD (Li et al., 1998; Schontz and Rether, 1999,), RFLP (Fukunaga et al., 2002; Fukunaga and Kato, 2002), AFLP (Le Thierry d'Ennequin et al., 2000) and SNPs (Van et al., 2008). They reported that, the genetic groups in their analysis were closed related to the geographical origin of the different genotypes used in their studies and green foxtail presents a larger diversity than foxtail millet.

Wang et al. (2010) surveyed DNA sequence for nine loci across 50 accessions of cultivated foxtail millet and 34 of its wild progenitor to study the nucleotide variation in foxtail millet to reveal the pattern of genetic diversity within and between foxtail millet and green millet. They found that, the diversity of wild green millet was much higher than the domesticated foxtail millet. On an average, the cultivars lost 55 per cent of the diversity harbored by the wild progenitor during the domestication process and domesticated foxtail millet shared almost 75 per cent of its polymorphism with green foxtail.

Until now, the only sources of SSR markers available for foxtail millet are from Jia et al. (2007, 2009). Jia et al. (2007) developed EST-SSR markers in foxtail millet and reported the transferability of those in other Gramineae species. Jia et al. (2009) developed 269 SSR primer pairs from two genomic libraries enriched for (GA)n and (CA)n of foxtail millet. To detect the polymorphism of newly developed SSR markers, Jia et al. (2009) selected 37 primer pairs randomly and were used to amplify DNA of 40 diverse foxtail millet accessions. Totally 228

alleles were detected, with an average of 6.16 alleles per locus with polymorphic information content value for each locus ranged from 0.413 to 0.847, with an average of 0.697. Unweighted Pair Group Method analysis (UPGMA) revealed that the 40 foxtail millet cultivars grouped into five clusters in which the landraces grouping was largely consistent with ecotypes while the breeding varieties from different provinces in China tended to be grouped together. Also they found positive correlation between PIC and number of alleles and between PIC and number of repeat units. Yang et al., (2010a) studied the genetic variation of 20 foxtail millet cultivars by 60 pair of SSR primers and 20 cultivars were divided into four groups in which landraces were divided into three groups and showed higher genetic variation than that of improved cultivars.

Both EST-SSR (Jia et al., 2007) and SSR markers developed by Jia et al. (2009) provides platform for further genetic diversity, population structure and identification of genomic regions associated with trait of interest.

2.5 POPULATION STRUCTURE AND ASSOCIATION MAPPING

Foxtail millet is one of the most ancient domesticated crops. It is becoming a model system for studying biofuel crops and comparative genomics among the grasses (Wang et al., 2010). It is more tractable experimental model because of its small diploid genome (1C=490Mb) and inbreeding nature as compared to large genomes of the outbreeding species like pearl millet (diploid, IC=2,352Mb), napiergrass (tetraploid, IC=2,254Mb) and switchgrass (tetraploid, 1C=1,372-1,666Mb, octaploid IC=2,352-3,136Mb) (Doust et al., 2009).

The phenotypic variation of many complex traits of agriculturally importance is influenced by multiple quantitative trait loci (QTL), their interaction, the environment and the interaction between QTL and environment (Holland, 2007). Linkage analysis and association mapping are the two most commonly used tools for dissecting complex traits (Zhu et al., 2008). Among these two methods, association mapping is based on historical recombination and natural genetic diversity of the different population which lead to a higher mapping resolution (Zhu et al., 2008). Association mapping based on linkage disequilibrium (LD) provides a powerful tool for dissecting quantitative traits in plants (Yu and Buckler, 2006; Zhu et al., 2008) leads to most effective utilization of ex situ conserved natural genetic diversity of worldwide crop germplasm resources (Abdurakhmmonov and Abdukarimov, 2008). Association mapping also provides an additional possibility of analyzing several traits

simultaneously (Borba et al., 2010). Furthermore, precision of association analysis increased by including data collected over years of experimental analysis with genotypes of breeding programs. A natural mapping population for association analysis must be comprised of diverse individuals that can be derived from wild relatives, core collection of germplasm or subsets of breeding germplasm and elite germplasm (Breseghello and Sorrells, 2006).

One of the sources of false positives in association mapping is population structure, which is a division of the population into distinct subgroups related by kinship often generates spurious genotype-phenotype associations (Yu and Buckler, 2006; Zhu et al., 2008). Initially, structured association (Pritchard et al., 2000a; Thornsberry et al., 2001) was used and it was first implemented in TASSEL (Trait Analysis by aSSociation, Evolution and Linkage) to reduce the risk of false positives arising from population structure. Recently, a unified mixed model method was developed which improves on the previous method by integrating population structure (Q) and family relatedness (K) within population showed to be superior (Yu et al., 2006) to Q model (Bradbury et al. 2007). The Q + K methods was implemented in TASSEL as a mixed liner model (MLM) function, accounting for both population structure (Q) and relative kinship (K) (Bradbury et al. 2007). It is the most common method of association analysis in plants and has been successfully applied in rice (Agrama et al., 2007; Wen et al., 2009; Borba et al., 2010), wheat (Breseghello and Sorrells, 2006; Liu et al., 2010; Neumann et al., 2011), sorghum (Murrary et al., 2009), Arabidopsis (Zhao et al., 2007) and potato (Malosetti et al., 2007).

A thorough understanding of genetic diversity, population structure and familial relatedness in a given association panel is necessary for successful association studies. Currently, SSRs and SNPs are two main types of molecular markers used to evaluate genetic diversity, population structure and familial kinship of association panels (Yang et al., 2010b). The SSR markers mostly used in previous studies to dissect population structure in maize (Remington et al., 2001), rice (Garris et al., 2003), wild diploid alfalfa (Şakiroğlu et al., 2010) and several other crops. Association of phenotypic traits with microsatellite alleles has been found to be practical in several crops species like rice (Agrama et al., 2007, Wen et al., 2009; Borbra et al., 2010, Jin et al., 2010), wheat (Reif et al., 2011), maize (Yang et al., 2010b), sorghum (Shehzad et al., 2007), common bean (Blair et al., 2009), soybean (Jun et al., 2008) and rape (Brassica napus L.) (Rezaeizad et al., 2011).

In order to detect more alleles, germplasm selected should include all genetic variation of a species theoretically because diverse germplasm include more extensive recombination in the history and allow high level of resolution (Wang et al., 2008). The species for which a core collection has been established, the core would be the idea material for association mapping (Whitt and Buckler, 2003). Association mapping based on core collection of germplasm provides a valuable alternative to gene mapping approach based on bi-parental populations (Wen et al., 2009) due to its reduced size and represents the entire collections of that species. The core collection was effectively used to study population structure and association mapping in rice (Brobra et al., 2010), common bean (Blair et al., 2009) and demonstrated the usefulness for identification of markers associated with phenotypic variation [marker trait associations (MTAs)]. Wang et al. (2008) analyzed the population structure and linkage disequilibrium (LD) of mini-core set of maize inbred lines. Association mapping with diverse germplasm or wild populations can identify new superior alleles that were not captured by breeding practices and support introgression of these alleles into elite breeding germplasm (Kumar et al., 2011).

However, knowledge on the level of genetic diversity and linkage disequilibrium (LD) is very limited in foxtail millet and its wild ancestor, green foxtail. Such information would help to understand the domestication process of cultivated species and will allow further research in these species, including association mapping and identification of agriculturally significantly genes involved in domestication (Wang et al., 2010). Until now, association mapping using the existing natural variation present in the germplasm for the detection of MTAs has not been reported in foxtail millet, and QTL reported by the earlier studies (Doust et al., 2004, 2005; Doust and Kellogg, 2006) were identified through linkage mapping approach based on RFLP genotyping of mapping population. To date, there were no MTAs reports available in foxtail millet using SSR marker because of limited number of SSRs markers reported in this crop. Therefore, there is a need for development SSR markers and the identification genomic region association with yield and yield contributing traits in foxtail millet.

Figure 1. Foxtail millet racial classification (according to Prasada Rao et al., 1986)

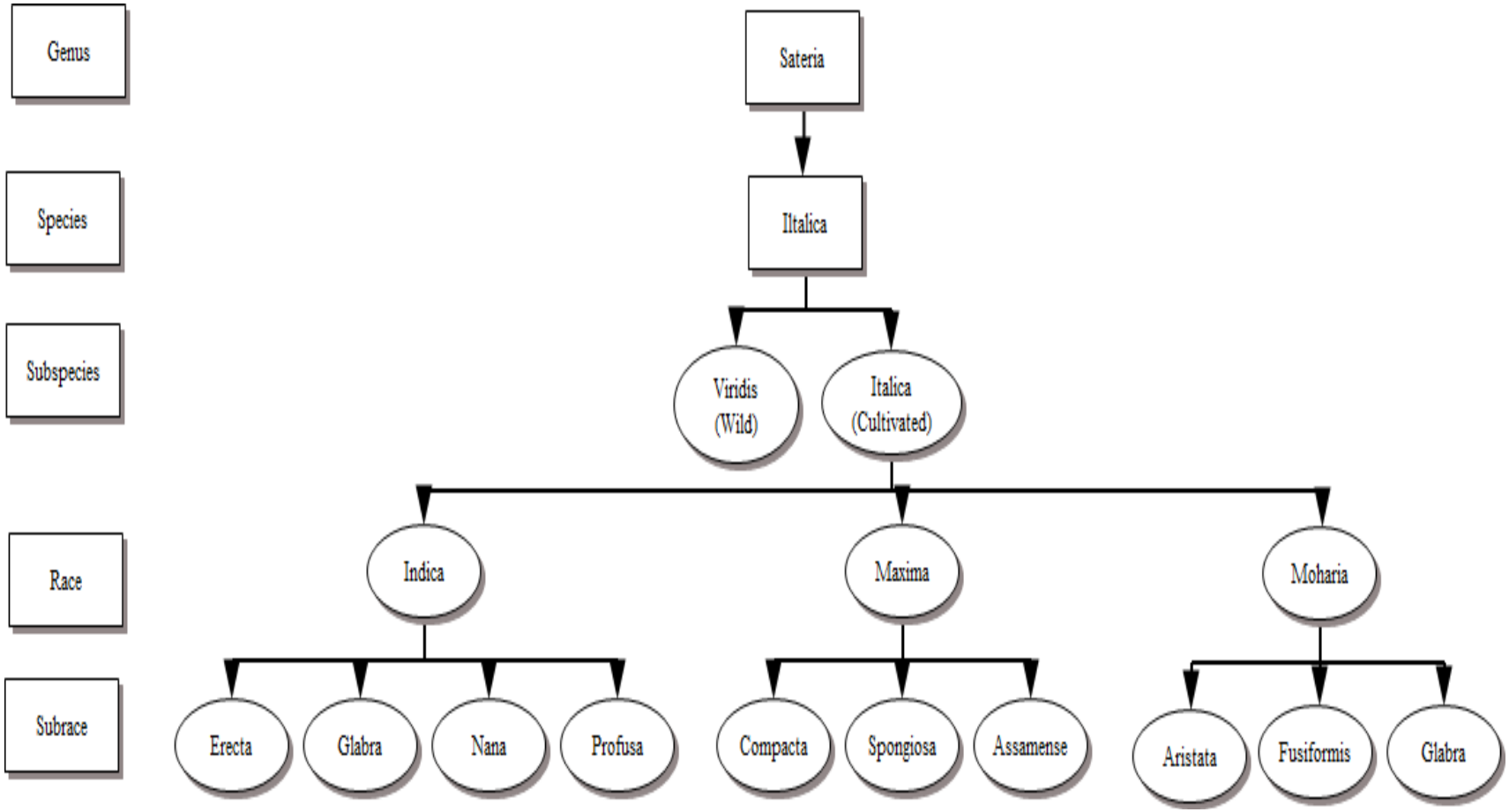


Table 1. Core and minicore collections for different crops

Crop	Number of accessions used	Number of traits involved	Number of Accessions in core	References
Rice	18,412	14	1790	Yan *et al.* (2007)
	4,310	50 phenotypic traits and 36 SSRs	932	Zhang et al. (2011)
Pearl millet	16,063	11	1,600	Bhattacharjee *et al.*(2007)
Pearl millet (Augmented)	20,766	12	2,094	Upadhyaya *et al.* (2009b)
Sorghum	33,100	7	3,475	Prasada Rao and Ramanatha Rao (1995)
	22,473	20	2,247	Grenier *et al.* (2001)
Chickpea	3350		505	Hannan *et al.* (1994)
	16,991	13	19,56	Upadhyaya *et al.* (2001a)
Groundnut	7,432		831	Holbrook *et al.* (1993)
		15	504 (Asian core)	Upadhyaya *et al.* (2001b)
	14,310	14	1704	Upadhyaya *et al.* (2003)
			77 (Valencia core)	Dwivedi *et al.* (2008)
Pigeonpea	12,153	14	1290	Reddy *et al.* (2005)

Finger millet	5,940	14	622	Upadhyaya *et al.* (2006b)
Foxtail millet	1,474	23	155	Upadhyaya *et al.* (2008a)
Safflower	5522	12	570	Dwivedi *et al.* (2005)
Sesame	4251	14	453	Xiurong *et al.* (2000)
Saccharum spontaneum	342	11	75	Tai and Miller (2001)
Minicore collection				
Rice	1794	26 phenotypic traits and 70 molecular markers	217	Agrama *et al.* (2009)
Chickpea	1956	22	211	Upadhyaya and Ortiz (2001)
Groundnut	1704	31	184	Upadhyaya *et al.* (2001b)
	831	16	112	Holbrook and Dong (2005)
Pigeonpea	1290	33	146	Upadhyaya *et al.* (2006c)
Sorghum	2,247	21	242	Upadhyaya *et al.* (2009c)
Pearl millet	2,094	18	238	Upadhyaya *et al.* (2011b)
Finger millet	5940	14	80	Upadhyaya *et al.* (2010b)
Foxtail millet	1474	23	35	Upadhyaya *et al.* (2011d)

Table 2. List of National and International organization/institutions conserving foxtail millet germplasm

Institute/Genebank	Country	No. of accessions
Australian Tropical Crops & Forages Genetic Resources Centre	Australia	336
Plant Genetic Resources Centre, BARI	Bangladesh	515
Institute of Crop Germplasm Resources, Chinese Academy of Agricultural Sciences	China	26233
Biologie Végétale Appliquée, Institut Louis Pasteur	France	850
Laboratoire des Ressources Génétiques et Amélioration des Plantes Tropicales, ORSTOM	France	3500
AICRP on Small Millets	India	2512
International Crop Research Institute for the Semi-Arid Tropics (ICRISAT)	India	1542
National Bureau of Plant Genetic Resources	India	4392
Ramaiha Genebank, Plant Genetic Resources, Tamil Nadu Agricultural University, Coimbatore	India	774
Regional Station Akola, NBPGR	India	349
Department of Genetic Resources I, National Institute of Agrobiological Sciences	Japan	2531
Plant Germplasm Institute, Faculty of Agriculture, Kyoto University	Japan	274
National Genebank of Kenya, Crop Plant Genetic Resources Centre - Muguga	Kenya	786
Estación de Iguala, Instituto Nacional de Investigaciones Agrícolas	Mexico	350
North Central Regional Plant Introduction Station, USDA-ARS, NCRPIS	United States of America	1010

Table 3. The earlier studies on phenotypic and genotypic coefficients of variation and heritability in foxtail millet

Trait	PCV	GCV	H^2	GA (% of mean)	Authors
Days to 50 per cent flowering	Moderate	Moderate	High	Moderate	Nirmalakumari and Vetriventhan (2010); Basheeruddin and Sahib (2004)
	Low	Low	High	High	Nirmalakumari *et al.* (2008)
	Low	Low	Medium	Low	Lakshmanan and Guggari (2001)
	Low	Low	High	Low	Selvarani and Gomathinayagam (2000b)
	-	-	High	Low	Islam *et al*. (1990)
	Low	Low	High	Moderate	Reddy and Jhansilakshmi (1991a)
	High	High	High	Moderate	Cill and Randhawa (1975)
Plant height	Moderate	Moderate	High	High	Nirmalakumari and Vetriventhan (2010); Basheeruddin and Sahib (2004); Selvarani and Gomathinayagam (2000b); Reddy and Jhansilakshmi (1991a)
	Low	Low	High	Moderate	Lakshmanan and Guggari (2001)
	-	-	High	High	Islam *et al.* (1990)
	High	High	High	Moderate	Cill and Randhawa (1975)
Basal tiller number	High	High	High	High	Nirmalakumari and Vetriventhan (2010); Nirmalakumari *et al.* (2008); Reddy and Jhansilakshmi (1991a); Cill and Randhawa (1975)
	-	-	High	High	Islam *et al*. (1990)
Flag leaf blade length	Moderate	Moderate	High	High	Nirmalakumari *et al*. (2008)
Flag leaf blade width	Moderate	Moderate	High	High	Nirmalakumari *et al.* (2008)
Peduncle length	High	High	High	High	Nirmalakumari *et al*. (2008)
Panicle exertion	High	Moderate	High	High	Nirmalakumari *et al.* (2008)
Inflorescence length	Moderate	Moderate	Medium	High	Reddy and Jhansilakshmi (1991a)
	Moderate	Moderate	High	High	Nirmalakumari and Vetriventhan (2010); Nirmalakumari

					et al. (2008); Lakshmanan and Guggari (2001)
	Moderate	Low	Medium	Low	Cill and Randhawa (1975)
	-	-	High	High	Islam *et al*. (1990)
Inflorescence width	Low	Low	Medium	Moderate	Cill and Randhawa (1975)
Weight of five panicles	Moderate	High	High	High	Reddy and Jhansilakshmi (1991a)
Grain Yield	Moderate	High	Medium	High	Reddy and Jhansilakshmi (1991a)
	High	High	High	High	Nirmalakumari and Vetriventhan (2010); Selvarani and Gomathinayagam (2000b)
	Moderate	Moderate	High	High	Nirmalakumari *et al.* (2008); Lakshmanan and Guggari (2001)
	-	-	High	High	Islam *et al*. (1990)
	High	High	Medium		Basheeruddin and Sahib (2004); Cill and Randhawa (1975)

Table 4. The earlier studies about correlation on different yield and yield contributing traits in foxtail millet

Traits	Positive correlation with	Negative correlation with	References
Days to 50 per cent flowering	Days to maturity, plant height, inflorescence length and grain yield	-	Nirmalakumari and Vetriventhan (2010)
	Plant height, flag leaf length, flag leaf blade width, flag leaf sheath length, peduncle length, inflorescence length, inflorescence width and weight of five panicles	Basal tillers, panicle exertion	Upadhyaya *et al*. (2008a)
	Plant height and fodder yield	-	Basheeruddin and Sahib (2004)
	Days to maturity, plant height and fodder yield	-	Santhakumar (1999)
	Days to maturity	-	Chidambaram and Palanisamy (1995)
	Days to maturity and plant height	Grain yield/plant, harvest index and basal tillers	Reddy and JhansiLakshmi (1991b)
	Plant height, days to maturity and tiller number	-	Islam *et al.* (1990)
	Days to maturity, plant height, ear length, ear girth and 1000-grain weight	Tiller number and grain yield	Cill and Randhawa (1975)
Plant height	Days to flowering, days to maturity, Inflorescence length and grain yield	-	Nirmalakumari and Vetriventhan (2010)
	Days to flowering, flag leaf blade length, flag leaf blade width, flag leaf sheath length, peduncle length, inflorescence length, inflorescence width and weight of five panicles	Panicle exertion	Upadhyaya *et al.* (2008a)
	Grain yield	-	Channappagoudar *et al*. (2008);

Traits	Positive correlation with	Negative correlation with	References
			Murugan and Nirmalakumari (2006)
	Days to 50 per cent flowering, days to maturity and fodder yield	-	Basheeruddin and Sahib (2004)
	Inflorescence length, fodder yield and grain yield	-	Santhakumar (1999)
	Total dry matter production, straw yield, harvest index and root weight	-	Chidambaram and Palanisamy (1995)
	Days to flowering, days to maturity and inflorescence length	Basal tillers	Reddy and JhansiLakshmi (1991b)
	-	Effective tillers, days to maturity and inflorescence length	Reddy and JhansiLakshmi (1991a)
	Days to flowering and Inflorescence length	1000 grain weight	Islam *et al*. (1990)
	Panicle length, days to maturity, yield/plant	-	Islam *et al*. (1989)
	Ear length, Ear girth, 1000 grain weight and days to flowering	Grain yield, tiller number	Cill and Randhawa (1975)
Basal tillers	Effective tillers and grain yield	-	Nirmalakumari and Vetriventhan (2010)
	-	Days to flowering, plant height, flag leaf blade length, flag leaf blade width, flag leaf sheath length, peduncle length, inflorescence length,	Upadhyaya *et al*. (2008a)

Traits	Positive correlation with	Negative correlation with	References
		inflorescence width and weight of five panicles	
	Grain yield		Channappagoudar *et al.* (2008)
	Days to flowering, days to maturity, 1000 grain weight and grain yield	-	Islam *et al.* (1990)
	Grain yield per plant	Days to flowering, inflorescence length, bristle length and weight of main ear	Reddy and JhansiLakshmi (1991b)
	Days to maturity	-	Islam *et al.* (1989)
	Effective tillers, grain yield	panicle length	Navale and Harinarayana (1987)
	Grain yield	Plant height, days to flowering, ear length, ear girth, 1000 grain weight and yield	Cill and Randhawa (1975)
Flag leaf blade length	Days to flowering, plant height, flag leaf blade width, flag leaf sheath length, peduncle length, inflorescence length, inflorescence width and weight of five panicles	Basal tillers number	Upadhyaya *et al*. (2008a)
Flag leaf blade width	Days to flowering, plant height, flag leaf blade length, flag leaf sheath length, peduncle length, inflorescence length, inflorescence width and weight of five panicles	Basal tillers number	Upadhyaya *et al*. (2008a)
Flag leaf sheath length	Days to flowering, plant height, flag leaf blade length, flag leaf blade width, peduncle length, inflorescence length, inflorescence width and weight of five panicles	Basal tillers number and panicle exertion	Upadhyaya *et al*. (2008a)

Traits	Positive correlation with	Negative correlation with	References
Peduncle length	Days to flowering, plant height, flag leaf blade length, flag leaf blade width, flag leaf sheath length, panicle exertion, inflorescence width and weight of five panicles	Basal tillers number	Upadhyaya *et al*. (2008a)
Panicle exertion	Peduncle length	Days to flowering, plant height, flag leaf sheath length, inflorescence length, inflorescence width and weight of 5 panicles	Upadhyaya *et al*. (2008a)
Inflorescence length	Days to flowering, days to maturity, plant height and grain yield	Effective tillers	Nirmalakumari and Vetriventhan (2010)
	Days to flowering, plant height, flag leaf blade length, flag leaf blade width, flag leaf sheath length, peduncle length, inflorescence width and weight of five panicles	Basal tillers number, panicle exertion	Upadhyaya *et al*. (2008a)
	Grain yield	-	Murugan and Nirmalakumari (2006)
	Grain yield, fodder yield and plant height	-	Santhakumar (1999)
	Weight of main ear and plant height	Basal tillers,	Reddy and JhansiLakshmi (1991b)
	Weight of main ear and flag leaf area	Plant height and effective tillers	Reddy and JhansiLakshmi (1991a)
	Plant height, days to maturity, 1000 grain weight and grain yield	-	Islam *et al.* (1990)
	Plant height, days to maturity and yield/plant	-	Islam *et al.* (1989)
	Ear girth, 1000 grain weight, days to flowering and	Tiller number	Cill and Randhawa (1975)

Traits	Positive correlation with	Negative correlation with	References
	plant height		
Inflorescence width	Days to flowering, plant height, flag leaf blade length, flag leaf blade width, flag leaf sheath length, peduncle length, inflorescence width and weight of five panicles	Basal tillers number	Upadhyaya *et al*. (2008a)
	Days to flowering, plant height, 1000 grain weight and grain yield	Tiller number	Cill and Randhawa (1975)
Weight of main ear	Days to flowering, plant height, flag leaf blade length, flag leaf blade width, flag leaf sheath length, peduncle length, inflorescence width and weight of five panicles	Basal tillers number and panicle exertion	Upadhyaya *et al*. (2008a)
	Grain yield	-	Murugan and Nirmalakumari (2006)
	Grain yield per plant and inflorescence length	Basal tillers	Reddy and JhansiLakshmi (1991b)
	Grain yield per plant, inflorescence length	-	Reddy and JhansiLakshmi (1991a)
	Grain yield, total dry matter production, straw yield	-	Chidambaram and Palanisamy (1995)

Table 5. The earlier studies related to path coefficients analysis in foxtail millet

Authors	Contribution
Dezfouli and Mehrani (2010)	The number of tillers, stem diameter and days to 50 per cent flowering were positive and directly affected seed yield, while spike length effected seed yield negatively (-0.323). The number of seeds per spike, number of leaves and number of tillers as well as days to 50 per cent flowering had positive direct effect on fodder yield.
Nirmalakumari and Vetriventhan (2010)	The direct effect of days to 50 per cent flowering on grain yield was positive and negligible and number of productive tillers on grain yield was positive and high. Panicle length showed moderate positive direct effect on grain yield. Greater yield advantage could be achieved by using germplasm with more productive tillers, medium panicle length and medium duration.
Murugan and Nirmalakumari (2006)	Correlation and path coefficient analysis revealed that straw yield per plant and harvest index were the major determining characters for grain yield among foxtail millet genotypes.
Maloo and Philip (2001)	The maximum direct effects of biological yield and harvest index on seed yield and other characters like weight of panicles, seed yield per panicle, flag leaf area, 1000 seed weight, seed protein content, seed oil content and days to flowering showed positive direct contribution in atleast one crop season. Weight of panicle and seed yield per panicle showed positive and high direct effect in only one environment. Plant height, panicle length, flag leaf area and 1000 seed weight had low or negative
Santhakumar (1999)	Direct effect of plant height and panicle length was low and fodder yield was recorded moderate direct effect on grain yield.
Rathod *et al.* (1996)	Total tillers, productive tillers per plant, harvest index and biological yield were the most important yield components influencing yield, having significant positive effects at the genotypic and phenotypic levels.
Reddy and Jhansilakshmi (1991b)	Direct effect of plant height, inflorescence length and bristle length were high positive direct effect on grain yield whereas harvest index and biological yield had very high positive direct effect.
Reddy and Jhansilakshmi (1991a)	Path coefficient analysis indicated higher direct contribution (effects) of harvest index and biological yield towards grain yield. Plant height, inflorescence length was found to have high direct effect whereas weight of main ear showed high negative effect towards grain yield. Harvest index and biological yield could be relied on in improving grain yield potential in foxtail millet.

CHAPTER III

MATERIALS AND METHODS

The ICRISAT genebank, Patancheru, India holds 1,542 foxtail millet germplasm accessions from 26 countries. To utilize this diversity in research, a core collection in foxtail millet (155 accessions) (Upadhyaya *et al.,* 2008a) representing diversity of entire collection was established using data on taxonomic and 12 qualitative traits. The present study was undertaken to assess the phenotypic and genetic diversity of this foxtail millet core collection and to determine marker trait association for yield and related traits using SSR markers.

3.1 PHENOTYPIC DIVERSITY

3.1.1 Materials

The genetic materials used in this study were 155 accessions of foxtail millet core collection (Upadhyaya *et al.,* 2008a) and four controls (ISe 375, ISe 376, ISe 1468 and ISe 1541). Core collection consisted of 102 accessions from race *indica* (65.8%), 24 accessions from race *maxima* (15.5%) and 29 accessions from race *moharia* (18.7%). The information on origin and racial classification of accessions is presented in Table 6a and 6b.

The foxtail millet core collection was evaluated during the 2009/10 *Rabi*/*Summer* at Coimbatore (E1) and Madurai (E2) and the 2010 rainy season at ICRISAT (E3), Patancheru, thus constituting three environments. Weather details of the three locations are given in Table 7. The experiments were planted on red soils (alfisols) in all three environments. The sowing was done on ridges which were 75 cm apart. Each accession occupied a single row of 4m length, with a plant-to-plant spacing of 10cm. Fertilizer was applied at the rate of 20 kg N_2 and 50 kg P_2O_5 ha^{-1} as basal dose and 45 kg N_2 ha^{-1} as top dressing. Irrigation and hand weeding were given on need basis.

3.1.2 Methods

3.1.2.1 Characters studied

The data on 12 qualitative (Table 8) and 13 quantitative traits (Table 9) were recorded based on the descriptors of *Setaria italica* and *S. pumila* (IBPGR, 1985). The data on all qualitative traits [plant pigmentation (PP), leaf colour (LFCL), growth habit (GH), culm

branching (CB), bristle length (BL), panicle lobing (PL), inflorescence compactness (INFC), lobe compactness (LC), grain colour (GRC), plant lodging (PL), leaf senescence (SENE) and overall plant aspect (PAS)], and days to 50 per cent flowering (DF) and plot yield were recorded on plot basis. The data on basal tiller number (BT) and single plant yield (SPY) were recorded on five representative plants in the plot. The remaining nine quantitative traits *viz.,* plant height (PLHT), flag leaf blade length (FLBL), flag leaf blade width (FLBW), flag leaf sheath length (FLSL), peduncle length (PEDL), panicle exertion (PEX), inflorescence length (INFL), inflorescence width (INFW), and weight of five panicles (W5P) were recorded on the main culms of the five representative plants in a plot. Average values of these five plants were computed and mean values used for statistical analysis. The measure of plot yield was converted into grain yield Kg ha^{-1}.

3.2 STATISTICAL ANALYSIS

In all the three environments, the experiment was conducted in the alpha-design (Paterson and Williams, 1976) with three replications. The details of the statistical analysis performed are described below.

3.2.1 Residual Maximum Likelihood (REML) method

The data on quantitative traits were analyzed for each environment separately using Residual Maximum Likelihood (REML) (Patterson and Thompson, 1971) in GenStat 12th edition (http://www.genstat.co.uk) considering genotypes as random. Pooled analysis of the data from all three environments was performed considering genotype as random and environment as fixed. Significance of environments was tested using Wald statistic. Variance components due to genotypes (σ^2_g), genotype x environment (σ^2_{ge}) and standard errors (SE) were estimated for individual and pooled analysis. Best linear unbiased predictors (BLUPs) (Schonfeld and Werner, 1986) were obtained for all the quantitative traits for each accession for individual environment and pooled analysis. Mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and broad sense heritability of all the quantitative traits were calculated using GenStat version 12 for each environment separately and for pooled data.

3.2.1.1 Phenotypic and genotypic co-efficient of variation (PCV and GCV)

For each character, PCV and GCV were computed based on the methods given by Burton (1952).

$$PCV = \frac{\sqrt{Phenotypic\ variance}}{mean} \times 100$$

$$GCV = \frac{\sqrt{Genotypic\ variance}}{mean} \times 100$$

The coefficients of variation were categorized as suggested by Sivasubramanian and Madhavamenon (1973)

Percent variability	Category
< 10 %	Low
11 – 20 %	Moderate
>20 %	High

3.2.1.2 Heritability

Heritability in the broad sense (h^2_b) was calculated according to Lush (1940).

$$h^2_b = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

σ^2_p = phenotypic variance

σ^2_g = genotypic variance

The heritability values were categorized as follows:

Heritability in per cent	Category
< 30	Low
31 – 61	Medium
> 61	High

3.2.1.3 Genetic advance

It is a measure of genetic gain under selection. Genetic advance is defined as the difference between the mean genotypic value of the selected lines and the mean genotypic value of the parental population. It was derived according to the method of Johnson *et al.* (1955) for each character separately for all three environments and for pooled data.

$$\text{Genetic advance (GA)} = \frac{\sigma^2_g}{\sigma_p} \times k$$

Where,

σ^2_g = Genotypic variance,

σ_p = Phenotypic standard deviation and

k = Selection differential at a particular level of selection intensity (5%) which takes into account the mean phenotypic value of the selected families (Falconer, 1967).

Genetic advance was expressed as percentage of mean by using the formula suggested by Johnson *et al.* (1955).

$$\text{Genetic advance as percentage of mean} = \frac{Genetic\ advance}{Mean} \times 100$$

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

Low	: less than 10%
Moderate	: 10-20 %
High	: More than 20 %

3.2.2 Comparison of mean and variance

Best Linear Unbiased Predictors (BLUPs) were determined for each accession for all quantitative traits for individual environment and for pooled data. Mean, range and variances of the entire core collection and three basic races for all quantitative traits in individual environment and pooled data were estimated. Mean of races and environments were compared using Newman-Keuls test (Newman, 1939; Keuls, 1952) and the homogeneity of variances among the

races was tested using Levene's (Levene, 1960) procedure using the software SAS/STAT2® 9.2 (SAS Institute Inc.2009).

3.2.3 Correlation and path coefficient analyses

Phenotypic correlations between yield and its component traits and among themselves for individual environment and pooled data were estimated to determine the significant association between the agronomic traits using the software GenStat version 12. Only those correlations which are greater than 0.500 or smaller than -0.500 were considered as useful as at least 25 per cent of the variation in one trait is predicted by the other (Upadhyaya *et al*., 2010c). Path coefficient analysis for individual environment and pooled data were carried out as suggested by Dewey and Lu (1959) by keeping yield as dependent variable and other yield attributing characters as independent variables using GenStat version 12. The direct and indirect effects were classified based on the scale given by Lenka and Misra (1973).

Value of direct or indirect effects	Rate or scale
More than 1.00	Very high
0.30 to 0.99	High
0.20 to 0.29	Moderate
0.10 to 0.19	Low
0.00 to 0.09	Negligible

3.2.4 Principal Component Analysis (PCA)

Principal component analyses (PCA) based on 13 quantitative traits for individual environment and pooled data as well as three races within environment and pooled data were performed to find out the relative importance of different traits in capturing the variation in core collection. The observations for each trait were standardized by subtracting mean from each observation and subsequently dividing by its standard deviation. This resulted in standardized values for each trait with average 0 and standard deviation of 1. The standardized values were used to perform PCA using GenStat version 12. A hierarchical cluster analysis for individual environment separately and for pooled data was performed using scores of the first three principal components (PCs) following Ward (1963).

3.2.5 **Shannon-Weaver Diversity Indices**

Shannon and Weaver diversity index (H′) (Shannon and Weaver, 1949) was used as a measure of phenotypic diversity for each trait. A low H′ indicates extremely unbalance frequency classes for an individual traits and a lack of genetic diversity. The index was estimated based on 12 qualitative and 13 quantitative traits for individual environment and for pooled data as well as three races within environment and pooled data using GenStat version 12.

3.2.6 Phenotypic dissimilarity matrix

Gower's (1971) dissimilarity matrix was calculated using 12 qualitative and 13 quantitative traits for individual environment separately and for pooled data using GenStat version 12. Most dissimilar and least dissimilar accessions were identified in foxtail millet core collection based on dissimilarity matrix.

3.2.7 Selection of trait specific accessions

On the basis BLUPs of pooled data of three environments, the best 15 accessions were selected for different economic important yield related traits and their agronomic desirability was compared with the control cultivars.

3.3 MOLECULAR DIVERSITY

3.3.1 Genomic DNA isolation

The foxtail millet core collection and four control cultivars were planted in the 3rd week of October 2009 in glass house at ICRISAT, Patancheru, India and DNA was extracted from the single representative seedling of each accession by using a high-throughput mini-DNA extraction method (Mace *et al.,* 2003) as described below:

Reagents required

1. 3% CTAB (Cetyl Trimethyl Ammonium Bromide) buffer having 10mM Tris, 1.4M NaCl, 20mM EDTA and 3% CTAB. The pH was adjusted to 8.0 using HCL. Just before use, mercaptoethanol (0.17%) was added.
2. Chloroform-isoamyl alcohol mixture (24:1) stored in the dark at room temperature
3. Ice-cold isopropanol

4. RNase-A (10 mg/ml) dissolved in solution containing 10mM Tris (pH 7.5) and 15mM NaCl stored at –20°C; working stocks were stored at 4°C
5. Phenol:chloroform-iso-amyl alcohol mixture (25:24:1)
6. 3 M sodium acetate (pH 5.2)
7. Ethanol (absolute and 70)
8. $T_1E_{0.1}$ buffer (10mM Tris and 1mM EDTA)
9. $T_{10}E_1$ buffer (0.5M Tris and 0.05M EDTA)

High-throughput mini- DNA extraction

(i) Sample preparation

1. Steel balls (4-mm in diameter and 3 numbers per extraction tube) (Spex CertiPrep, USA), pre-chilled at –20ºC for about 30 minutes, were put into the 12 × 8-well extraction tubes with strip caps (Marsh Biomarket, USA), which were kept on ice.
2. The CTAB buffer was pre-heated in 65°C water bath before start of DNA extraction.
3. Leaf samples (Final weight of 20-30mg) were cut into pieces (1mm in length). These cut leaves were transferred to the extraction tubes, which were fitted into a 96-tube box.

(ii) Grinding and extraction

4. A volume of 450µl of pre-heated CTAB buffer was added to each extraction tube containing a leaf sample.
5. Leaf tissues were disrupted to release DNA into the buffer solution using a Sigma GenoGrinder™ (Spex CertiPrep, USA) at 500 strokes/minute for 5 minutes.
6. Grinding of leaf tissues was repeated until the color of the buffer solution became pale green and the cut leaf bits were sufficiently macerated.
7. After grinding, the tube box was fixed in a locking device and incubated at 65ºC in a water bath for 20 minutes with occasional shaking.

(iii) Solvent extraction

8. A volume of 450µl of chloroform-isoamyl alcohol mixture (24:1) was added to each tube and the samples were centrifuged at 6200 rpm for 10 minutes (Sigma centrifuge model 4K15C with Qiagen rotor model NR09100: 2 × 1120 g SW).

9. After centrifugation the aqueous layer (approximately 300 µl) was transferred to a fresh strip tube (Marsh Biomarket).

(iv) Initial DNA precipitation

10. To the tube containing aqueous layer, 0.7 volumes (approximately 210µl) of cold isopropanol (kept at –20ºC) was added. The solutions were carefully mixed and the tubes were kept at –20ºC for 10 minutes.

11. The samples were centrifuged at 6200rpm for 15 minutes.

12. The supernatant was decanted under a fume-hood and pellets were allowed to air dry (minimum 20 minutes).

(v) RNase-A treatment

13. In order to remove co-isolated RNA, 200µl of low salt TE buffer ($T_1E_{0.1}$) and 3µl of RNase-A (stock 10mg/µl) were added to each tube containing dry pellet and mixed properly.

14. The solution was incubated at 37ºC for 30 minutes.

(vi) Solvent extraction

15. After incubation, 200µl of phenol-chloroform-isoamyl alcohol mixture (25:24:1) was added to each tube, carefully mixed and centrifuged at 5000 rpm for 10 minutes.

16. The aqueous layer was transferred to fresh tubes and chloroform-isoamylalcohol (24:1) mixture was added to each tube, carefully mixed and centrifuged at 5000rpm for 10 minutes. The aqueous layer was transferred to fresh tubes.

(vii) DNA precipitation

17. To the tubes containing aqueous layer, 15µl (approximately $1/10^{th}$ volume) of 3M sodium acetate (pH 5.2) and 300µl (2 volume) of absolute ethanol (kept at –20ºC) were added and the tubes were subsequently placed in a freezer (–20ºC) for 5 minutes.

18. Following incubation, the box containing tubes was centrifuged at 6200rpm for 15 minutes.

(viii) Ethanol wash

19. After centrifugation, supernatant was carefully decanted from each tube having ensured that the pellets remained inside the tubes and 200µl of 70 per cent ethanol was added to the tubes followed by centrifugation at 5000 rpm for 5 minutes.

(ix) Final re-suspension

20. Pellets were obtained by carefully decanting the supernatant from each tube and then allowed to air dry for one hour.

21. Completely dried pellets were re-suspended in 100µl of $T_{10}E_1$ buffer and incubated overnight at room temperature to allow them to dissolve completely.

22. Dissolved DNA samples were stored in 4ºC.

3.3.2 DNA quantification and quality check

The quality and quantity of DNA were checked by agarose gel electrophoresis as described below.

Reagents required were:

1. Agarose

2. 1X TBE buffer

For 10X TBE buffer, 109g of Tris and 55g of boric acid were dissolved one by one in 800 ml distilled water; then 40ml of 0.5M EDTA (pH 8.0) was added. The volume was made up to 1 liter with distilled water and sterilized by autoclaving. This was stored at 4°C. To prepare working solution (1X), the stock solution was diluted 10 times.

3. Ethidium bromide (10 mg/ml)

A quantity of 100 mg ethidium bromide was dissolved in 10 ml of distilled water. The vessel containing this solution was wrapped in aluminium foil and stored at 4°C.

4. Orange loading dye

0.5 M EDTA (pH 8.0)	10ml

5 M NaCl	1ml
Glycerol	50ml
Distilled water	39ml

Orange dye powder (Orange G, Gurr Certistain®) was added till the color became sufficiently dark.

Procedure

A quantity of 0.8g of agarose was added to 100ml of 1X TBE buffer and the slurry was heated using microwave oven until the agarose was completely dissolved. After cooling the solution to about 60°C, 5µl of ethidium bromide solution was added and the resulting mixture was poured into the gel-casting tray for solidification. Before the gel solidified, an acrylic comb of desired well number was placed on the agarose solution to form wells for loading samples. Each well was loaded with 5µl of sample aliquot having 3µl distilled water, 1µl Orange dye and 1µl of DNA sample. The DNA samples of known concentration (lambda DNA of 50ng/µl, 100ng/µl and 200ng/µl) were also loaded on to the gel to estimate the DNA concentration of the experimental samples. The gel was run at 70V for 20 minutes. After completing the electrophoresis run, DNA on the gel was visualized under UV light and photographed. If the DNA was observed as a clear and intact band, the quality was considered good, whereas a smear of DNA indicated poor quality. The band intensity was compared with lambda DNA to know the approximate quantity of DNA.

3.3.3 SSR genotyping

At the time of starting the investigation, there were no SSR markers publically available in foxtail millet except few EST-SSR (Jia *et al.,* 2007). Initially, four foxtail millet EST-SSRs (Jia et al., 2007), 31 pearl millet (Thudi *et al.,* 2010) and 24 finger millet (Dida *et al.,* 2007) genomic SSR markers were used. Later, a set of 80 SSR markers located across nine chromosomes of foxtail millet were selected based on the foxtail millet linkage map reported by Jia et al. (2009). The forward primers of all these 139 SSR markers were synthesized by adding M13-forward primer sequence (5'CACGACGTTGTAAAACGAC3') at the 5'end of each primer. All these 139 markers were tested for amplification using a set of eight phenotypically most diverse accessions (ISe 31, ISe 746, ISe 748, ISe 827, ISe 995, ISe 1037, ISe 1129 and ISe

1227) (Table 10) in the core collection for optimizing PCR conditions and concentration of the reaction mix, and to check the polymorphism. Finally, three foxtail millet EST-SSRs, twelve finger millet SSRs, four pearl millet SSRs and all 80 foxtail millet SSRs were identified as polymorphic on the eight diverse accessions (Table 11 and Table 12). Thus, a total of 99 SSR markers were used for genotyping entire foxtail millet core collection.

Table 10. Details of most diverse accessions with race, sub-race and country of origin

S.No	Diverse accessions	Race	Sub race	Origin	Species	Sub Species
1	ISe 31	*indica*	*nana*	India	*italica*	*italica*
2	ISe 746	*indica*	*nana*	India	*italica*	*italica*
3	ISe 748	*indica*	*glabra*	India	*italica*	*italica*
4	ISe 827	*maxima*	*compacta*	China	*italica*	*italica*
5	ISe 995	*indica*	*nana*	India	*italica*	*italica*
6	ISe 1037	*moharia*	*aristata*	Lebanon	*italica*	*italica*
7	ISe 1129	*maxima*	*compacta*	Syria	*italica*	*italica*
8	ISe 1227	*moharia*	*glabra*	Russia and CISs	*italica*	*italica*

Genomic DNA of all the genotypes were diluted to 5ng/µl and used as template for amplification of SSR markers. The PCR reactions were performed in 5µl volume consisting of 1µl of 5ng DNA template, 0.5µl of 2mM dNTPs, 0.2µl of 25 mM $MgCl_2$, 0.5 µl of primer containing 1:5:5 ratio of 2 pmole/µl M13 tailed forward primer, 2 pmole/µl reverse primer and 2 pmole/µl of M13-Forward primer labeled with either 6-Fam or Vic or Ned or Pet (Applied Biosystems), 0.5µl of 10X PCR buffer and 0.15 U of *Taq* DNA polymerase (SibEnzymes Ltd, Russia). PCR amplifications are performed on ABI thermal cycler (GeneAmp, PCR system 9700, PE Applied biosystems) using a common touchdown PCR amplification profile for the series of markers. A touch down PCR amplification profile with 94^{o}C for 3 min of initial denaturation cycle, followed by first 10 cycles of 94^{o}C for 15 seconds, 61°C for 30 sec and 72°C for 30 sec, with 1°C decrease in temperature per cycle, then 40 cycles of 94°C for 15 sec with constant annealing temperature (54°C) and 72°C for 30 sec, followed by a final extension at 72°C for 20 min. The PCR products were tested for amplification on 1.2 per cent agarose (Plate 5A).

3.3.4 Capillary electrophoresis

i. Sample preparation

A set of 25 PCR multiplex sets were constructed based on the allele size range estimates and the type of forward primer label of the markers. Each set consisted of four SSR markers with different labels and allele size. For post PCR multiplexing, 1µl PCR product of each of 6-FAM, VIC, NED and PET-labeled products were pooled (according to above mentioned criteria) and mixed with 7 µl of Hi-Di formamide (Applied Biosystems, USA), 0.2 µl of the LIZ-500 size standard (Applied Biosystems, USA) and 2.8 µl of distilled water. The pooled PCR amplicons were denatured 5 minutes at 95°C and cooled immediately on ice and size-separated by capillary electrophoresis using an ABI Prism 3730 DNA analyzer (Applied Biosystems Inc.).

ii. SSR fragment analysis

Raw data produced from ABI 3730*xl* Genetic Analyser was analysed using Genemapper® software version 4.0 (Applied Biosystems, USA) and fragment size was scored in base pairs (bp) based on the relative migration of the internal size standard (Plate 5B).

3.3.5 Molecular data analysis

The fragment sizes for all markers were used to analysis basic statistics using PowerMarker version 3.25 (Liu and Muse, 2005), including the polymorphic information content (PIC), allelic richness as determined by total number of the detected alleles and number of alleles per locus, gene diversity and occurrence of unique, rare, common, most frequent alleles and heterozygosity (%).

3.3.5.1 Polymorphic Information Content (PIC)

The polymorphic information content (PIC) was estimated as below (Botstein *et al.* 1980).

$$\widehat{PIC}_l = 1 - \sum_{u=1}^{k} \tilde{p}_{lu}{}^2 - \sum_{u=1}^{k-1} \sum_{v=u+1}^{k} 2\tilde{p}_{lu}^2 \tilde{p}_{lv}^2$$

3.3.5.2 Gene diversity

Gene diversity often referred to as expected heterozygosity, is defined as the probability that two randomly chosen alleles from the population are different. An unbiased estimator of gene diversity at the l^{th} locus is

$$\hat{D}_l = (1 - \sum_{u=1}^{k} \tilde{p}_{lu}{}^2)/(1 - \frac{1+f}{n}),$$

3.3.5.3 Heterozygosity

Heterozygosity is simply the proportion of heterozygous individuals in the population. At a single locus and it was estimated as

$$\hat{H}_l = 1 - \sum_{u=1}^{k} \tilde{P}_{luu}$$

3.3.5.4 Allele and genotype frequencies

The sample allele frequencies are calculated as $\tilde{p}_u = n_u/(2n)$, with the variance estimated as

$$\mathrm{var}(\tilde{p}_u) \hat{=} \frac{1}{2n}(\tilde{p}_u + \tilde{P}_{uu} - 2\tilde{p}_u^2)$$

Where

where $\hat{=}$ means "estimated by".
The sample genotype frequencies $\tilde{P}_{uv}$ are calculated as n_{uv}/n. Both the $\tilde{p}_u$s and $\tilde{P}_{uv}$s are unbiased maximum likelihood estimates (MLEs) of the population frequencies. Confidence intervals for allele and genotype frequencies are formed by resampling individuals from the data set.

3.3.5.5 Unique, rare and common alleles

Unique alleles are those that are present in one accession or in one group of accessions but absent in other accessions or group of accessions. Rare alleles are those whose frequency is ≤ 1 per cent in the investigated materials. Common alleles are those occurring between 1-20 per cent in the investigated materials while those occurring >20 per cent was classified as most frequent alleles (Upadhyaya *et al*., 2008b).

3.3.5.6 Clustering

Unweighted neighbor-joining tree was constructed based on the simple matching dissimilarity matrix of 84 SSR markers genotyped across the foxtail millet core collection along with four controls as implemented in DARwin 5.0.156 programme (Perrier and Jacquemoud-Collet, 2006).

3.3.5.7 Principle Coordinate Analysis (PCoA)

The PCoA of the foxtail millet core collection accessions was performed based on Nei (1973) distance matrix using GENALEX 6.41 (Peakall and Smouse, 2006).

3.3.5.8 Pairwise *Fst* and Nei's genetic distance

Pairwise comparison on the basis of the values of F_{st} could be interpreted as standardized population distance between two populations. Pairwise *Fst* and genetic distance among the three races were calculated using GENALEX 6.41 (Peakal and Smouse, 2006).

3.3.5.9 Analysis of Molecular Variance

Analysis of Molecular Variance (AMOVA) was performed to partition molecular variance within and among races and populations identified by the cluster analysis based on 999 permutation using the software GENALEX 6.41(Peakall and Smouse, 2006)

3.3.5.10 Correlation coefficients

The Pearson correlations among number of repeat unit, number of alleles per locus, major allele frequency, gene diversity and PIC for 84 SSR markers were estimated.

3.3.5.11. Mantel test

The Mantel test (Mantel, 1967) was employed to calculate matrix correlation coefficients and to simulate a probability distribution for the comparison based on 9999 permutation to better understand the relationships between phenotypic and molecular dissimilarity. These analyses were performed using the software package Mantel (version 2.0) (Liedloff, 1999).

3.4 POPULATION STRUCTURE ANALYSIS

A set of 72 SSR markers located across nine linkage group of foxtail millet were used to dissect the population structure in foxtail millet core collection. In order to infer the population structure of the foxtail millet core collection without considering the pre-existing race and sub-race classification or geographical information, the analysis were performed using the software package STRUCTURE 2.3.2. The program STRUCTURE implements a model based clustering method for inferring population structure using genotype data consisting of unlinked markers to identify *k* clusters to which the program then assigns each individual genotype. The method was introduced by Pritchard *et al.* (2000) and extended by Falush *et al.* (2003, 2007). To determine most appropriate *k* value, burn-in Markov Chain Monte Carlo (MCMC) replication was set to 10,000 and data were collected over 100,000 MCMC replications in each run. Five independent runs were performed setting the number of population (*k*) from 2 to 10 using a model allowing for no admixture and correlated allele frequencies. The basis of this kind of clustering method is the allocation of individual genotypes to *k* clusters in such a way that Hardy-Weinberg equilibrium and linkage equilibrium are valid within clusters, whereas these kinds of equilibrium are absent between clusters. The *k* value was determined by LnP(D) in STRUCTURE output and an *ad hoc* statistic Δk based on the rate of change in LnP(D) between successive *k* (Evanno *et al.,* 2005). The final subpopulation were determined based on rate of change in *LnP(D)* between successive *k,* stability of grouping patter across five run and germplasm information about the material under study.

An analysis of molecular variance (AMOVA) was performed using the software GENALEX 6.41 (Peakall and Smouse, 2006) to evaluate population differentiation among the four subpopulations. Furthermore, genetic distances among these four subpopulations were calculated as Nei's genetic distance and pairwise *Fst.* Principal Coordinate Analysis (PCoA) and unweighted neighbor-joining phylogenetic analysis was conducted to further assess the population subdivisions.

3.5. LINKAGE DISEQUILIBRIUM (LD)

The genome-wide linkage disequilibrium (LD) between all pairs of SSR alleles were analyzed using the software TASSEL. LD was estimated by weighted average of squared allele-frequency correlations (r^2) between pairs of SSR loci. The significance of pairwise LD among all

possible SSR loci was evaluated using TASSEL with the rapid permutation test in 10,000 shuffles. The LD values between all pairs of SSR loci were plotted as triangle LD plots using TASSEL to estimate the general view of genome wide LD patterns.

3.6. ASSOCIATION MAPPING

Association of SSR marker genotypes with trait of interest was tested using the mixed liner model (MLM) method as described by Yu *et al.* (2006) using TASSEL 2.1. This method simultaneously takes into account multiple levels of both gross level population structure (Q) and finer scale relative kinship (K). The statistical model can be described in Henderson's notations (Henderson, 1975) as follows:

$$\mathbf{y} = \mathbf{X\beta} + \mathbf{Zu} + \mathbf{e}$$

Where,

y = the vector of observations

ß = unknown vector containing fixed effects including genetic marker and population structure (**Q**)

u = unknown vector of random additive genetic effects from multiple background QTL for individuals or lines

X and **Z** = the know design matrices

E = unobserved vector of random residuals.

Each of the marker allele is fit as a separate class with heterozygotes fits as additional marker classes. The resulting marker effect is not decomposed into additive and dominance effects but simply tested for overall significance. The **u** and **e** vectors are assumed to be normally distributed with null mean and variance of

$$\mathrm{Var}\begin{pmatrix}\mathbf{u}\\ \mathbf{e}\end{pmatrix} = \begin{pmatrix}\mathbf{G} & \mathbf{0}\\ \mathbf{0} & \mathbf{R}\end{pmatrix}$$

Where $G=\sigma_a^2 K$ with σ_a^2 as the unknown additive genetic variance and K as the kinship matrix.

The population structure analysis was conducted by running STRUCTURE and the population structure matrix (Q) was constructed at *K*=4. The kinship-matrix was calculated using TASSEL considering all mapped markers. In the MLM approach, the option to calculate the heritability separately for each marker was used. The EM method was chosen and the MLM

parameters were left at the default setting from TASSEL. The EM method uses an expectation-maximization algorithm to derive a REML estimate of the variance components. The BLUPs were determined for each accession for all quantitative traits for individual environment and pooled data were used for the association analysis for phenotypic data input. Marker trait association analysis was performed for three environments separately and for pooled data. The SSR markers associated with trait of interest were identified based on *P* value of marker, which determines whether a QTL is associated with the marker. The R^2 (marker) indicating the fraction of the total variance explained by the marker. Only those makers which having $P \leq 0.05$ were selected as significant markers associated with the trait of interest.

Table 6a. List of 155 accessions present in foxtail millet core collection and four control cultivars along with information on race, sub-race and origin

No	Entry	Race	Sub-race	Origin	*Species*	*Sub Species*
1	ISe 2	*indica*	*nana*	India	*italica*	*italica*
2	ISe 18	*indica*	*nana*	India	*italica*	*italica*
3	ISe 31	*indica*	*nana*	India	*italica*	*italica*
4	ISe 49	*indica*	*nana*	India	*italica*	*italica*
5	ISe 90	*indica*	*nana*	India	*italica*	*italica*
6	ISe 96	*indica*	*nana*	India	*italica*	*italica*
7	ISe 132	*indica*	*nana*	India	*italica*	*italica*
8	ISe 144	*indica*	*nana*	India	*italica*	*italica*
9	ISe 156	*indica*	*nana*	India	*italica*	*italica*
10	ISe 160	*indica*	*nana*	India	*italica*	*italica*
11	ISe 179	*indica*	*nana*	India	*italica*	*italica*
12	ISe 195	*indica*	*glabra*	India	*italica*	*italica*
13	ISe 200	*indica*	*nana*	India	*italica*	*italica*
14	ISe 237	*indica*	*nana*	India	*italica*	*italica*
15	ISe 238	*indica*	*nana*	India	*italica*	*italica*
16	ISe 254	*indica*	*nana*	India	*italica*	*italica*
17	ISe 267	*indica*	*nana*	India	*italica*	*italica*
18	ISe 289	*indica*	*profusa*	India	*italica*	*italica*
19	ISe 302	*indica*	*nana*	India	*italica*	*italica*
20	ISe 362	*indica*	*nana*	India	*italica*	*italica*
21	ISe 364	*indica*	*nana*	India	*italica*	*italica*
22	ISe 375	*maxima*	*assamense*	India	*italica*	*italica*
23	ISe 388	*indica*	*nana*	India	*italica*	*italica*
24	ISe 398	*indica*	*nana*	India	*italica*	*italica*
25	ISe 403	*moharia*	*aristata*	India	*italica*	*italica*
26	ISe 458	*moharia*	*aristata*	USA	*italica*	*italica*
27	ISe 480	*indica*	*nana*	China	*italica*	*italica*
28	ISe 507	*indica*	*nana*	Kenya	*italica*	*italica*
29	ISe 525	*indica*	*nana*	USA	*italica*	*italica*
30	ISe 663	*indica*	*nana*	Switzerland	*italica*	*italica*
31	ISe 710	*indica*	*nana*	India	*italica*	*italica*
32	ISe 717	*indica*	*nana*	Pakistan	*italica*	*italica*
33	ISe 719	*moharia*	*aristata*	Pakistan	*italica*	*italica*
34	ISe 735	*moharia*	*aristata*	Pakistan	*italica*	*italica*
35	ISe 745	*indica*	*nana*	India	*italica*	*italica*
36	ISe 746	*indica*	*nana*	India	*italica*	*italica*
37	ISe 748	*indica*	*glabra*	India	*italica*	*italica*
38	ISe 751	*indica*	*glabra*	India	*italica*	*italica*
39	ISe 758	*indica*	*glabra*	India	*italica*	*italica*
40	ISe 769	*moharia*	*aristata*	India	*italica*	*italica*

No	Entry	Race	Sub-race	Origin	*Species*	*Sub Species*
41	ISe 771	*indica*	*nana*	India	*italica*	*italica*
42	ISe 783	*indica*	*nana*	India	*italica*	*italica*
43	ISe 785	*indica*	*nana*	India	*italica*	*italica*
44	ISe 792	*indica*	*nana*	India	*italica*	*italica*
45	ISe 795	*indica*	*nana*	India	*italica*	*italica*
46	ISe 796	*indica*	*nana*	India	*italica*	*italica*
47	ISe 813	*indica*	*nana*	India	*italica*	*italica*
48	ISe 827	*maxima*	*compacta*	China	*italica*	*italica*
49	ISe 828	*indica*	*nana*	China	*italica*	*italica*
50	ISe 838	*indica*	*nana*	India	*italica*	*italica*
51	ISe 840	*indica*	*nana*	India	*italica*	*italica*
52	ISe 842	*indica*	*profusa*	India	*italica*	*italica*
53	ISe 846	*indica*	*nana*	India	*italica*	*italica*
54	ISe 869	*indica*	*nana*	India	*italica*	*italica*
55	ISe 900	*indica*	*glabra*	India	*italica*	*italica*
56	ISe 907	*indica*	*nana*	India	*italica*	*italica*
57	ISe 909	*indica*	*nana*	India	*italica*	*italica*
58	ISe 914	*indica*	*nana*	India	*italica*	*italica*
59	ISe 931	*indica*	*nana*	India	*italica*	*italica*
60	ISe 936	*indica*	*nana*	India	*italica*	*italica*
61	ISe 946	*indica*	*nana*	India	*italica*	*italica*
62	ISe 956	*indica*	*nana*	India	*italica*	*italica*
63	ISe 963	*indica*	*nana*	India	*italica*	*italica*
64	ISe 969	*indica*	*nana*	India	*italica*	*italica*
65	ISe 983	*indica*	*nana*	India	*italica*	*italica*
66	ISe 985	*indica*	*nana*	India	*italica*	*italica*
67	ISe 995	*indica*	*nana*	India	*italica*	*italica*
68	ISe 999	*indica*	*nana*	India	*italica*	*italica*
69	ISe 1000	*indica*	*nana*	India	*italica*	*italica*
70	ISe 1009	*moharia*	*aristata*	Lebanon	*italica*	*italica*
71	ISe 1026	*moharia*	*aristata*	Lebanon	*italica*	*italica*
72	ISe 1037	*moharia*	*aristata*	Lebanon	*italica*	*italica*
73	ISe 1059	*maxima*	*spongiosa*	India	*italica*	*italica*
74	ISe 1067	*maxima*	*compacta*	Syria	*italica*	*italica*
75	ISe 1118	*moharia*	*glabra*	Syria	*italica*	*italica*
76	ISe 1119	*moharia*	*glabra*	Syria	*italica*	*italica*
77	ISe 1129	*maxima*	*compacta*	Syria	*italica*	*italica*
78	ISe 1134	*indica*	*nana*	Syria	*italica*	*italica*
79	ISe 1136	*indica*	*nana*	Syria	*italica*	*italica*
80	ISe 1137	*indica*	*nana*	Syria	*italica*	*italica*
81	ISe 1151	*moharia*	*glabra*	Syria	*italica*	*italica*
82	ISe 1161	*moharia*	*glabra*	Syria	*italica*	*italica*
83	ISe 1162	*moharia*	*aristata*	Syria	*italica*	*italica*

No	Entry	Race	Sub-race	Origin	*Species*	*Sub Species*
84	ISe 1163	*moharia*	*aristata*	Syria	*italica*	*italica*
85	ISe 1177	*indica*	*nana*	Syria	*italica*	*italica*
86	ISe 1181	*maxima*	*compacta*	China	*italica*	*italica*
87	ISe 1187	*maxima*	*compacta*	China	*italica*	*italica*
88	ISe 1201	*maxima*	*compacta*	China	*italica*	*italica*
89	ISe 1204	*maxima*	*compacta*	Russia and CIS	*italica*	*italica*
90	ISe 1209	*moharia*	*fusiformis*	Russia and CIS	*italica*	*italica*
91	ISe 1227	*moharia*	*glabra*	Russia and CIS	*italica*	*italica*
92	ISe 1234	*moharia*	*glabra*	Russia and CIS	*italica*	*italica*
93	ISe 1251	*maxima*	*compacta*	Russia and CIS	*italica*	*italica*
94	ISe 1254	*moharia*	*glabra*	Russia and CIS	*italica*	*italica*
95	ISe 1258	*maxima*	*compacta*	Russia and CIS	*italica*	*italica*
96	ISe 1269	*indica*	*nana*	South Africa	*italica*	*italica*
97	ISe 1286	*moharia*	*glabra*	Turkey	*italica*	*italica*
98	ISe 1299	*moharia*	*glabra*	Iran	*italica*	*italica*
99	ISe 1302	*moharia*	*aristata*	Afghanistan	*italica*	*italica*
100	ISe 1305	*moharia*	*glabra*	Spain	*italica*	*italica*
101	ISe 1312	*moharia*	*glabra*	Unknown	*italica*	*italica*
102	ISe 1320	*moharia*	*glabra*	USA	*italica*	*italica*
103	ISe 1332	*moharia*	*glabra*	Afghanistan	*italica*	*italica*
104	ISe 1335	*moharia*	*glabra*	Hungary	*italica*	*italica*
105	ISe 1338	*maxima*	*compacta*	Turkey	*italica*	*italica*
106	ISe 1354	*indica*	*nana*	India	*italica*	*italica*
107	ISe 1387	*indica*	*glabra*	Sri Lanka	*italica*	*italica*
108	ISe 1400	*indica*	*nana*	India	*italica*	*italica*
109	ISe 1402	*indica*	*nana*	India	*italica*	*italica*
110	ISe 1406	*indica*	*nana*	India	*italica*	*italica*
111	ISe 1408	*indica*	*nana*	India	*italica*	*italica*
112	ISe 1419	*indica*	*glabra*	India	*italica*	*italica*
113	ISe 1454	*indica*	*glabra*	India	*italica*	*italica*
114	ISe 1458	*indica*	*glabra*	India	*italica*	*italica*
115	ISe 1460	*indica*	*glabra*	India	*italica*	*italica*
116	ISe 1474	*indica*	*glabra*	United Kingdom	*italica*	*italica*
117	ISe 1511	*indica*	*nana*	India	*italica*	*italica*
118	ISe 1547	*maxima*	*compacta*	Korea	*italica*	*italica*
119	ISe 1563	*maxima*	*compacta*	Korea	*italica*	*italica*
120	ISe 1575	*maxima*	*compacta*	Korea	*italica*	*italica*
121	ISe 1581	*maxima*	*compacta*	Korea	*italica*	*italica*
122	ISe 1593	*maxima*	*compacta*	Korea	*italica*	*italica*
123	ISe 1597	*indica*	*glabra*	India	*italica*	*italica*
124	ISe 1605	*indica*	*nana*	India	*italica*	*italica*
125	ISe 1610	*indica*	*glabra*	Malawi	*italica*	*italica*
126	ISe 1629	*indica*	*nana*	India	*italica*	*italica*

No	Entry	Race	Sub-race	Origin	*Species*	*Sub Species*
127	ISe 1638	*moharia*	*glabra*	Taiwan	*italica*	*italica*
128	ISe 1647	*maxima*	*compacta*	Taiwan	*italica*	*italica*
129	ISe 1655	*indica*	*glabra*	Taiwan	*italica*	*italica*
130	ISe 1664	*indica*	*nana*	India	*italica*	*italica*
131	ISe 1666	*maxima*	*spongiosa*	India	*italica*	*italica*
132	ISe 1674	*moharia*	*glabra*	India	*italica*	*italica*
133	ISe 1685	*indica*	*profusa*	India	*italica*	*italica*
134	ISe 1687	*maxima*	*spongiosa*	India	*italica*	*italica*
135	ISe 1704	*indica*	*nana*	India	*italica*	*italica*
136	ISe 1725	*maxima*	*compacta*	Nepal	*italica*	*italica*
137	ISe 1736	*maxima*	*compacta*	Nepal	*italica*	*italica*
138	ISe 1745	*indica*	*nana*	Myanmar	*italica*	*italica*
139	ISe 1762	*indica*	*nana*	India	*italica*	*italica*
140	ISe 1767	*indica*	*glabra*	India	*italica*	*italica*
141	ISe 1773	*indica*	*nana*	India	*italica*	*italica*
142	ISe 1780	*indica*	*nana*	India	*italica*	*italica*
143	ISe 1789	*indica*	*glabra*	India	*italica*	*italica*
144	ISe 1805	*indica*	*nana*	India	*italica*	*italica*
145	ISe 1806	*indica*	*glabra*	India	*italica*	*italica*
146	ISe 1808	*indica*	*nana*	India	*italica*	*italica*
147	ISe 1820	*indica*	*erecta*	India	*italica*	*italica*
148	ISe 1846	*indica*	*nana*	India	*italica*	*italica*
149	ISe 1851	*indica*	*nana*	India	*italica*	*italica*
150	ISe 1858	*indica*	*nana*	India	*italica*	*italica*
151	ISe 1859	*indica*	*nana*	India	*italica*	*italica*
152	ISe 1881	*indica*	*nana*	India	*italica*	*italica*
153	ISe 1888	*indica*	*nana*	Ethiopia	*italica*	*italica*
154	ISe 1892	*indica*	*profusa*	USA	*italica*	*italica*
155	ISe 1900	*indica*	*nana*	USA	*italica*	*italica*
Checks						
156	ISe375	*maxima*	*assamense*	India	*italica*	*italica*
157	ISe376	*maxima*	*assamense*	India	*italica*	*italica*
158	ISe1468	*indica*	*glabra*	India	*italica*	*italica*
159	ISe1541	*maxima*	*spongiosa*	India	*italica*	*italica*

Table 6b. Geographic distribution of foxtail millet core collection accessions

S.No	Country	Total No. of accessions	Indica				Maxima			Moharia		
			Erecta	Glabra	Nana	Profusa	Assamense	Compacta	Spongiosa	Aristata	Fusiformis	Glabra
1	Afghanistan	2								2		
2	China	6			1			5				
3	Ethiopia	1			1							
4	Hungary	1										1
5	India	93	2	11	68	3	1	2	3	2		1
6	Iran	1										1
7	Kenya	1			1							
8	Korea,	5						5				
9	Lebanon	3								3		
10	Malawi	1		1								
11	Myanmar	1		1								
12	Nepal	2						2				
13	Pakistan	3			1					2		
14	Russia and CIS	7						3			1	3
15	South Africa	1			1							
16	Spain	1										1
17	Sri Lanka	1		1								
18	Switzerland	1			1							
19	Syria	12			4			1		1		6
20	Taiwan	3		1				1				1
21	Turkey	2						1				1
22	United Kingdom	1		1								
23	USA	5			3					1		1
24	Unknown	1		1								
	Total	155	2	17	81	3	1	20	3	11	1	16

Table 7. Weather details of three environments during crop period were foxtail millet core collection was evaluated

Environment	Location	Season / Year	Temperature (°C)	Rainfall (mm)	Altitude	Latitude	Longitude
E1	Department of Millets, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India	*Rabi*/Summer 2009/10	12-42	700	426	11.01°N	76.95°E
E2	Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Madurai, Tamil Nadu, India	*Rabi*/Summer 2009/10	18-40	850	101	9.92°N	78.12°E
E3	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Andhra Pradesh, India	Rainy season, 2010	20-30	953	545	17.53°N	78.27°E

Table 8. List of qualitative characters studied in foxtail millet core collection

S.No	Qualitative traits	Description	Parameters
1	Plant pigmentation (Plate 1A)	Color of the plant recorded at flowering stage	1 Not Pigmented (green) 2 Pigmented 3 Deep purple
2	Leaf colour	Leaf color at dough stage	1 Green 2 Pigmented 3 Yellow
3	Growth habit	Growth habit recorded at dough stage	1 Erect 2 Erect geniculate 3 Decumbent 4 Prostrate
4	Culm branching (Plate 1B)	Culm branches (nodal tillers) at maturity	1 High 2 Medium 3 Low
5	Bristle length (Plate 2A)	Bristle length at maturity	1 Long 2 Medium 3 Short
6	Panicle lobing (Plate 2B)	Lobing of panicle at maturity	1 Non Lobed 2 Medium Lobed 3 Dense Lobed
7	Inflorescence compactness (Plate 3A)	Shape of inflorescence at maturity	1 Loose 2 Medium 3 Compact
8	Lobe compactness (Plate 3B)	Lobe compactness at maturity	1 Loose 2 Medium 3 Compact
9	Grain colour (Plate 4)	Grain color at maturity	1 Yellow 2 Red 3 Light grey 4 Dark Grey 5 Black 6 Brown 7 Black and White
10	Plant lodging	Lodging at maturity	1. No Lodging 2. Slightly Lodging 3. Medium Lodging 4. Mostly Lodging 5. Completely Lodging
11	Leaf senescence	Death of leaves and	1. Leaves completely green at

S.No	Qualitative traits	Description	Parameters
		Sstalk at grain maturity	maturity 2. Leaves almost green at maturity 3. Leaves moderately green at maturity 4. Leaves almost dry at maturity 5. Leaves completely dry at maturity
12	Overall plant aspect	Overall agronomical desirability of the accession as observed visually	1. Very Good 2. Good 3. Average 4. Poor 5. Very poor

Table 9. List of quantitative characters studied in foxtail millet core collection

S.No	Quantitative traits	Description
1	Days to 50 per cent flowering	Counted as days from sowing to 50 per cent of plants in flower
2	Plant height (cm)	Measured from ground level to tip of inflorescence at dough stage
3	Basal tiller number	Number of tillers at ground level or from the basal nodes
4	Flag leaf blade length (mm)	Measured from ligule to tip of flag leaf
5	Flag leaf blade width (mm)	Measured at widest point of flag leaf
6	Flag leaf sheath length (mm)	Measured from node to ligule of flag leaf at flowering stage
7	Peduncle length (mm)	Measured from top most node to base of the inflorescence
8	Panicle exsertion (mm)	Measured from the exposed point of the peduncle from the leaf sheath up to base of the inflorescence at dough stage
9	Inflorescence length (mm)	Measured from lowest branch to tip of last branch of inflorescence
10	Inflorescence width (mm)	Inflorescence measured in its natural position at widest part
11	Weight of five panicles (g)	Weight of 5 panicles after harvesting
12	Single plant yield (g)	Average yield of five representative plants
13	Grain yield (Kg/ha^{-1})	Grain yield recorded as Kg/ha

Table 11. Details of 80 foxtail millet SSR markers with chromosome location, repeat motif, forward and reverse primer sequences

S. No	Name of SSR marker	Chromosome location	Repeat motif	Forward Primer	Reverse Primer
1	b165	1	(CT)36	GCTTTGGTTTGGTTTGGTTGG	CCATTAGTCTCTGCCCTTGTT
2	p21	1	(GT)13(GC)9	CGGAGGCCATAGGGATAGAC	CCGACAGGTACTCCAAGGTG
3	p3	1	(GT)34	GCAGAAAGCATGCCGTAGTC	GCTTGGAGTCCACATGGATAG
4	b260	1	(GA)24	GAAGAGAGAAGCAGCGTTC	AAACCACACTTGCCCTGA
5	b126	1	(CT)18(CA)28	TCGCTCCTTATTAGCTTACCACA	ATGATTTGCATTTGCTTTGC
6	p8	1	(AC)26	CGATCGAATGATCGATGAAC	CCCTTTGTCCGATCACGTC
7	p50	1	(AC)30	GGGGATACACCGAGATAGAGG	CCCCACATACCAGCAGTTG
8	b110	1	(CA)15(GA)8	CGGCACTAACCGAAGGAAC	ATACGGAGGTGGCAGCA
9	p16	1	(AC)16	TTTCTCCCTCTCTCGATTCC	AAATTGGCGTGCTAACAACC
10	p88	1	(AC)5(GT)22	CAAGCCACCCAGTCTAGAGG	TTCATCAGAACTGCGCAAAC
11	p33	1	(AC)24	CTCCAACCTCACCACTCCAC	CATGCCTCCTCGTCTCCTC
12	b112	1	(CA)16(TA)6	CCACCCATTTCAGGTTCTGC	TTGTGGTCAGATTAGGTTGGTC
13	b227	1	(GA)26	TGATCTGGCAGAACGAACA	CAATTCCTGGACCAATATGC
14	b153	1	(GT)30	ACCCAACACATTCTCCTGAA	TGCTATCAAAATAGTGCTAGAAT
15	p58	1	(AC)19	CCTGAGCTCATCCACACAAC	CAGCCTGGAGGAAAGGAATAG
16	p92	1	(TG)12	TGGAATTGGAACCCTTTCG	GCCATGCAAACAGTACCATC
17	p87	1	(GA)21	ACCTTTGACAAACGAGACACG	GTTCGACTTGCATTGACTGG
18	b242	2	(GA)37	CACTACCACTGTTCCAGATCG	CAGGGACCTTGCTTGCATAC
19	b115	2	(CA)18	GGTAGCGACGGATCTACAGC	GCTAGCAAATGCTGTCATGG
20	b233	2	(GA)41	GCCACGCACACCAACTT	CTCCCGCAGAACACGCA
21	p56	2	(CA)24	GATGTGTACGGGTTGCATTG	TGGGTTTCAGGGCTCTCTC

S. No	Name of SSR marker	Chromosome location	Repeat motif	Forward Primer	Reverse Primer
22	p80	2	(CA)26(GA)17	GCCGTTGGATTTGATTATGG	TGTGGTTAGTTTATGTGGCTTG
23	b151	2	(GT)15	TCATCTAGGTAGGCACCAAC	TTGCTTTCTCTGTTATATGCGT
24	b163	3	(CT)23	CTCGGAAGCTCAGATTCTCC	CACTTCCTGCAGCTCTCACA
25	b186	3	(GA)40	CCCGTATAAATGTCATCATCCC	GCACCTGGCTTCCCTTT
26	p61	3	(CA)17	CATCCGCGTCATCTGAATC	ACCTGCTGCTATCCATCACC
27	p9	3	(GT)26	AGGCTGAAGTGAGCAAGCAG	TGCCGTACCTCCCAGTTTAG
28	p85	3	(CA)26	GAATTAGGCCGATGCACAAC	ATCCTAACTGCATGGCAAGG
29	p98	3	(GT)13	ATTCATCAGTAGCACAGC	TGGAACTAAGAACAGGAAAC
30	b225	3	(GA)28	ACCAAGAACTGCCTGCAC	TGCTTAGAACCCACTTGATCG
31	b226	3	(GA)10	TACCTCCCGTTCCGTTTTGT	CGCATTGATGGCTTACAGTT
32	b109	4	(CT)33	TGTAGAGTGGCTAGGACCAT	GTTTCTTCCATCATGCCTTCTT
33	p2	4	(GT)33	GCCGAAACCCTTGTCTCTAC	CGCCACCAGCAACAATATC
34	b255	4	(GA)30	ACCAAGAACTGCCTGCAC	TGCTTAGAACCCACTTGATCG
35	p34	4	(GT)17	GAGTCTCTTCCCCGTCTCTG	TTTGCCAAGCCTTCATAACC
36	P100	4	(CA)20	AGTTGACACCACACATAACAA	AGAATACTCCTACCTGCCAC
37	p42	4	(AC)15	GCGACTTTCCCCTTCCAATC	TTCCTTTTGTTGGCTTCTCC
38	b236	4	(CT)45	TCTGGACCAGCATTCTGTCTT	GGTAACTCTGCTTGGACGAG
39	b247	4	(GA)26	GATTGCTCTCTCACACACACG	GCCCGATGGCTGCTAGT
40	b129	5	(CA)24	CACACTCTTCTCCCCTTTTCC	ACGGTAACGGAGGATGGCTA
41	b188	5	(CT)21	AGCTGGTGGCCTTGTGTG	GGGAGAAGTTTTGGAGCGTA
42	p75	5	(CA)30	ATGCCATGGGAATTTGAACC	GTTTGATGCAGGACGAGAGG
43	b125	5	(CT)19(CA)13(CACG)11	GCCATGAAACAGGTACAAAAGG	GCATCCCCTTAATTTGTCAATG
44	b177	5	(GA)56	GCACCTTTCTCCTTGTTCCTG	TGTTACTCTCTCTCAACTTGCAG
45	b196	5	(CT)7	AATGTTTGCTTGCTACTTTGAG	CGTTTGTGTGGCAGATTGG

S. No	Name of SSR marker	Chromosome location	Repeat motif	Forward Primer	Reverse Primer
46	b111	5	(GT)18(GA)23	AGGATGGTTTGTGTAGCCTG	TTAGTAGTTATGTGTATCGCCG
47	p17x	5	(AC)10…(AC)9	CGGACACCTGAAAGACGAA	GTCACTTGTTGTTGTTGCG
48	b223	5	(GA)34	GGCATTAACTACATTGACAGTGG	AAAACCAACAGTTCCCTCGT
49	p48	5	(CA)20	AGACCTATCTTGTAAGAGCACACA	CGTACGTCTAATTCCGCATACT
50	b234	6	(CT)26	GCCGCAACGAACAACCG	CCTGTCCCTATCCCTGTCG
51	p10	6	(GT)21	CAATCACATCCGAGCATTTC	CACCCACCGTGTTGATCTG
52	b190	6	(GA)25	GAAATTTCACAAGTGTTGGTG	TGATCGGAGCAGAGTGTTGA
53	b159	6	(CT)24	GCCAGTCCGAGATGGTTAAG	AGCTCTAGCAGTTGGGGACA
54	b200	7	(GA)24	CATCGATCTCAACCTGTCCTT	ATGAGCCGTCATGTCACAAA
55	b107	7	(CT)25	AGAACGAGGTGGTGTGTGG	GGGTCTCACGCTCTCATCA
56	p59	7	(AC)22	TAATTTTGTGGCGTGGGATG	GCACTGGTTTTGTTGAATGG
57	b124	7	(CA)13	GCTTGTGCACGGGATGCACC	CAAGGCTTATGCCTGCGTCAAC
58	b142	7	(CA)29(TA)4	TGGTAAAACTCCCATATTGAGC	GCCCCATCCTTGATAACAGA
59	b202	7	(CA)14	AGAGCCCACGTCAAACC	AAACTGGACTAGAAGAAGCATAG
60	b123	7	(AC)19	GGTGTTCTCCTGTGTGC	AGAGTTATTTCCAGCATTAGTG
61	b185	8	(CT)30	GCACGTGTGACTTTCCACAT	GTGAATGGCACACGAAACTG
62	p6	8	(GT)14	AAGGATGGAATTTGCCACTG	TTTCGACGATTTGCTTCAAC
63	b258	8	(CA)9(GA)35	GGGCCAATAATGGTTGCATA	TTGCACATCCAAATCTTTCC
64	b269	9	(GA)45	GTGCGTGCCTCCCTTTA	CCAGATGCTTCCACGGT
65	p44	9	(CA)22	TTCCCGGAACAGACAAGAAC	GCGTTGGAAGCCATGGAG
66	b265	9	(GA)28	AATAATGGAGAGGCAGCATCC	CGAATCAAGGTGTGCGTG
67	p4	9	(GT)28	CGCTAGCTGTAGCAGCCTTC	ATTCGCAGCAGCTGAAACTC
68	b246	9	(GA)29	CACGCACGTAGTATTGCTAT	GTTCTGGGCTTCTGGCTG
69	b251	9	(GA)22	ACTCGAGATCTGCTCAAACC	TGGCTTTTGTTTTATGACTCAC

S. No	Name of SSR marker	Chromosome location	Repeat motif	Forward Primer	Reverse Primer
70	b187	9	(CT)36	TTGGACAAATGACGCTATGC	CTGCATCAAATCAGGACCAC
71	b217	9	(GA)29	TGCAGCAGCTAGGGAGG	CCGAATGCACGGTGATGA
72	p38	9	(GT)22	GTCGTCCCACGTATGAAACC	TGATTTCACCTACCGATTTGC
73	b166	9	(CT)24	CGCCCATACTACCCAACAG	ACCTCACCTTCCACTCCTC
74	p91	9	(GT)23	AGCTGTGCTCCTCTGATCTTG	TAACGTGGGGATGCACTAGC
75	m2	9	(CT)10	ATCGGAAAGCAGCGCAC	TCGTTCCTCCACCACTGC
76	b174	9	(GA)30	TTTCGGGTAAGAATTGAGATGG	GGTAGCAAGGTGACAAAGTT
77	b105	9	(CT)39(AC)6	ACTTGCATTGGTCGCCTTTA	ACGCGCATTCAATCAGACTA
78	b171	9	(CT)26	CACCACCACCCCGTTATATT	GGAGGAAGTTTGGAGGGAAG
79	p20	9	(CA)33(GA)11	GTGCCCGCTTAGCTTTAATC	ATGCACGTGGGACCCATAC
80	p41	9	(GT)25	CGTGCGTTATGTGATCCTAGC	ACGTTTGCCTCTGCTTCTTG

Table 10. Details of SSR Markers selected from related species along with repeat motif, forward and reverse sequence

S.No	Marker name	Chromosome location	Map Id	Position (cM)	Repeat Motif	Forward_Primer	Reverse_Primer
1	P13 (EST-SSR)	None	None	None	(CA)6	GGAGAGATTCCGGGCTCTAGT	ACGGTTCCGACATTTTAACG
2	P2 (EST-SSR)	None	None	None	(CT)5	CCAACACGCAATCGCAGAA	AGGCAGTGGGTTTGAGCAT
3	P5 (EST-SSR)	None	None	None	(CAT)5	TTGCCTTGAGCTCTTTGATG	GCTGATACTGATATGTCTGATGAGGA
4	ICMM02C05	None	None	None	(TGT)12	GATGGAAGCCTGAGCTTTTG	GTTTTCGAGTCCGAAGGTAG
5	ICMM02C24	None	None	None	(TG)4n(TC)6	TCTTTTCCAACCATGTGCAA	AACGTGTACCAACCTTTTC T
6	ICMM02D07	None	None	None	(ACC)5	AACAACCCAAACCACAAGCTCAC	C ACTCGAACACCAAACCCAACAA
7	ICMM02D15B	None	None	None	(CA)5	AACGGAAGGGTAAGGCAGTT	TTGACGGAAT AACGGAAGG
8	UGEP102	10	Finger millet genetic map	3.7	(TG)17	ATGCAGCCTTTGTCATCTCC	GATGCCTTCCTTCCCTTCTC
9	UGEP11	5Ab	Finger millet genetic map	63.5	(CT)12	CCTCGAGTGGGGATCCAG	AAGACGCTGGTGGAAATAGC
10	UGEP12	8B	Finger millet genetic map	50.8	(CT)22	ATCCCCACCTACGAGATGC	TCAAAGTGATGCGTCAGGTC
11	UGEP15	3A	Finger millet genetic map	6.5	(CT)22	AAGGCAATCTCGAATGCAAC	AAGCCATGGATCCTTCCTTC
12	UGEP26	5B	Finger millet genetic map	121.1	(CGG)7	ATGGGGTTAGGGTTCGAGTC	TGTCCCTCACTCGTCTCCTC
13	UGEP3	3A,3B	Finger millet genetic map	A(75.8),B(64)	(CA)7N12(GA)15	CCACGAGGCCATACTGAATAG	GATGGCCACTAGGGATGTTG
14	UGEP56	9A	Finger millet genetic map	7.4	(GT)12	CTCCGATACAGGCGTAAAGG	ACCATAATAGGGCCGCTTG
15	UGEP77	4B	Finger millet genetic map	4.8	(CT)19	TTCGCGCGAAATATAGGC	CTCGTAAGCACCCACCTTTC
16	UGEP8	3B	Finger millet genetic map		(GA)13	ATTTCCGCCATCACTCCAC	AGACGCAAATGGGTAAATGTC
17	UGEP81	6B	Finger millet genetic map	2.9	(GT)12	AAGGGCCATACCAACACTCC	CACTCGAGAACCGACCTTTG
18	UGEP90	6B	Finger millet genetic map	23.3	(CT)11/(CT)8	GGCCTTTGCAGTCATGTGAG	CGACTCCAGGTGTTGTTGG
19	UGPE53	2A	Finger millet genetic map	6.6	(AG)26	TGCCACAACTGTCAACAAAAG	CCTCGATGGCCATTATCAAG

CHAPTER IV

EXPERIMENTAL RESULTS

The foxtail millet core collection (Upadhyaya *et al*., 2008a) developed at ICRISAT genebank consisted of 155 accessions from 23 countries and one accession with unknown origin. The core accessions along with four controls (ISe 375, ISe 376, ISe 1468 and ISe 1541) were evaluated in three environments [Coimbatore (E1), Madurai (E2) and ICRISAT, Patancheru (E3)]. The accessions were characterized for 12 qualitative and 13 quantitative traits. They were also genotyped using 99 SSR markers. Thus, the current study was formulated to understand the morphological and genetic diversity and population structure in the foxtail millet core collection and to identify the marker trait association through association mapping using SSR markers. The results of the investigation are presented below.

4.1. QUALITATIVE TRAITS

4.1.1 FREQUENCY DISTRIBUTION

The frequency distributions of different phenotypic classes of the 12 qualitative traits revealed large variation for each trait. The results for each trait are described below briefly and presented in Table 13 and Appendix 1.

4.1.1.1 Plant Pigmentation

Depending on plant colour, the pigmentation was recorded as green, pigmented (light purple) and deep purple. Of the 155 accessions of core collection, 126 accessions (81.3%) were green, 26 accessions (16.8%) pigmented and 3 accessions (1.9%) deep purple. Green pigmentation was predominant in all the races (87.3% in *indica*, 66.7% in *maxima* and 72.4% in *moharia*). The pigmented accessions in *indica*, *maxima* and *moharia* were 10.8, 29.2 and 27.6 per cent, respectively. Two accessions in *indica* and one accession in *moharia* had deep purple plant colour.

4.1.1.2 Leaf colour

Leaf colour was recorded in three classes: green, pigmented and yellow. In the entire core collection, 84.5 per cent (131 accessions) were green, 9.0 per cent (14 accessions) yellow and 6.5 per cent (10 accessions) pigmented. Within the individual races, the maximum

proportion was of green colored leaves, 83.3 in *indica*, 87.5 in *maxima* and 86.2 per cent in *moharia*. The other two classes were <20 per cent in these races.

4.1.1.3 Growth habit

Of the four classes (erect, erect geniculate, decumbent and prostrate), erect growth habit was predominant (95.5%) in core collection as well in different races (98.0% in *indica*, 93.1% in *moharia* and 87.5% in *maxima*). 'Decumbent' was absent in all three races whereas 'prostrate' was absent in *indica* and *moharia.* Two accessions each in *indica*, *maxima* and *moharia* were 'erect geniculate'.

4.1.1.4 Culm branching

Culm branching was recorded as high, medium and low. In the entire core collection, 41.9 per cent (65 accessions) had high culm branching, 34.8 per cent (54 accessions) medium culm branching and the remaining 23.2 per cent (36 accessions) low culm branching. Race wise high culm branching was predominant in *moharia* (72.4%), low culm branching in *maxima* (75.0%) and medium culm branching in *indica* (44.1%).

4.1.1.5 Bristle length

It was recorded in three classes: long, medium and short. Long bristles were predominant in the core collection (62 accessions, 40.0%) and in race *indica* (51 accessions, 50.0%). Short bristles were predominant in *maxima* (19 accessions, 79.2%) and 51.7 per cent (15 accessions) of the accessions in *moharia* had medium bristle length.

4.1.1.6 Panicle lobing

Of the three classes (non lobed, medium lobed and dense lobed), dense lobed 53.6 per cent (83 accessions) was the most frequent in entire core collection as well in *indica* (58.8%) and *maxima* (83.3%) races. In the case of *moharia*, non lobed accessions were predominant (69.0%).

4.1.1.7 Inflorescence compactness

Inflorescence compactness was classified into three classes (loose, medium and compact) of which, compact (119 accessions, 76.8%) inflorescence was the most prevalent in the entire core collection and as well as in all three races (95.8% in *maxima*, 86.2% in *moharia* and 69.6% in *indica*). The medium and loose inflorescence compactness classes in entire core collection were 19.4 and 3.9 per cent, respectively.

4.1.1.8 Lobe compactness

Observation on lobe compactness was recorded as loose, medium and compact. The compact lobe was the most prevalent in the entire core collection (91.0%) as well in *maxima* (95.8%), *indica* (91.2%) and *moharia* (86.2%). Loose lobe compactness was absent in *maxima* and *moharia*.

4.1.1.9 Grain color

Four classes (yellow, red, black, and black and white) out of seven classes known were present in the core collection. Yellow grain color was the most common in the entire core collection (91.6%) as well as in all three races (93.1% in *moharia,* 91.7% in *maxima*, and 91.2% in *indica*). The grain colors black was present in *indica* (1 accession) and *maxima* (1 accession) and black and white was present only in *indica* (2 black and white accessions). Six accessions in *indica* were red out of nine accessions in entire core collection (remaining one was in *maxima* and two in *moharia*)

4.1.1.10 Lodging

Of the five classes (non lodging, slightly lodging, medium lodging, mostly lodging and completely lodging), 77 accessions (49.7%) were non lodging followed by slightly lodging (57 accessions, 36.8%), medium lodging (20 accessions, 12.9%) and mostly lodging (1 accession, 0.7%). Completely lodging was absent in the core collection. Among three races, non lodging was the most prevalent in *maxima* (62.5%) followed by *indica* (50.0%) and *moharia* (37.9%). The class completely lodging was absent in all the three races and mostly lodging were absent in race *indica* and *moharia*.

4.1.1.11 Leaf senescence

This trait was recorded at maturity in five classes: leaves completely green, leaves almost green, leaves moderately green, leaves almost dry and leaves completely dry. In the entire core collection, leaves almost green (47.1%) was the most common class represented by 73 accessions followed by leaves moderately green (43 accessions, 27.7%) and leaves completely green (24 accessions, 15.5%). A large proportion of the accessions of race *indica* (59 accessions, 57.8%) predominated by leaves almost green. In *maxima,* 41.7 per cent of the accessions (10 accessions) were classified as leaves completely green whereas 34.5 per cent of accessions (10 accessions) from *moharia* were classified as leaves moderately green at maturity.

4.1.1.12 Overall plant aspect

Overall plant aspect was classified into five classes (very good, good, average, poor and very poor), of which good (43.2%) and average (34.2%) plant scores were the most prevalent in the core collection. The *indica* was predominated with good (55 accessions, 53.9%) followed by average plant score (39 accessions, 38.2%). A large percentage of accessions belonging to *maxima* had good (10 accessions, 41.7%) and poor (7 accessions, 29.7%) plant scores and *moharia* had 51.7 per cent poor and 34.5 per cent average plant scores.

4.1.2. SHANNON WEAVER DIVERSITY INDICES

The Shannon-Weaver diversity indices (H′) were estimated for 12 qualitative traits in the core collection and for each race to compare H′ values in foxtail millet core collection (Table 14). Leaf senescence (0.46), bristle length (0.45) and culm branching (0.45) in *indica*, over all plant aspects (0.59) and leaf senescence (0.58) in *maxima,* and leaf senescence (0.60) and plant lodging (0.52) in *moharia* had the highest H′.

The accessions from *moharia* had the slightly higher pooled H′ (0.32±0.048) across the traits followed by *indica* (0.30±0.041) and *maxima* (0.30±0.049). Among the qualitative traits, leaf senescence (0.55) and over all plant aspects (0.55) had the highest H′ followed by culm branching (0.47), bristle length (0.47) and plant lodging (0.44) in the entire core collection. Growth habit (0.09) and grain colour (0.15) had the low H′ index in the entire core collection.

4.2 QUANTITATIVE TRAITS

The data on 13 quantitative traits in individual environment separately and for pooled data were analyzed to estimate variance components due to genotype (σ^2_g) and genotype × environments (σ^2_{ge}), to compare mean and variance, to estimate phenotypic diversity, Shannon-Weaver diversity index (H′) and principle component analysis (PCA). The results of various analyses are presented below.

4.2.1. VARIANCE COMPONENTS

The Residual Maximum Likelihood (REML) analysis of individual environment indicated that the σ^2_g for all the traits studied were significant in all three environments (Table 15). Pooled analysis of the data from three environments was performed considering genotype as random and environment as fixed. In pooled analysis, both σ^2_g and σ^2_{ge} interaction were significant for all the traits. Wald's statistics was significant for all the traits except flag leaf

sheath length indicating that the three environments were adequate to differentiate the core collection genotypes.

4.2.2. VARIABILITY STUDIES

The data on quantitative characters were analyzed using REML in GenStat version 12 and Best Linear Unbiased Predictors (BLUPs) (Schonfeld and Werner, 1986) were obtained for each accession in individual environment separately and for pooled data. The range, mean, phenotypic variance (σ^2_p), genotypic variance (σ^2_g), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and broad sense heritability (h^2_b) of all the quantitative traits were calculated for each environment separately and for pooled data.

The estimates on PCV (%), GCV (%), heritability (h^2_b) and genetic advance as per cent of mean are given in Table 16 and Figure 4. The value of PCV obtained with respect to various quantitative traits ranged from 16.50 to 60.56 in E1, 14.56 to 64.94 in E2, 12.73 to 48.21 in E3 and 12.08 to 53.51 in pooled, where as values of GCV ranged from 16.06 to 60.20 in E1, 14.25 to 64.64 in E2, 12.40 to 47.03 in E3 and 10.48 to 50.71 in pooled. The lowest and the highest value PCV and GCV were noted for peduncle length and weight of five panicles, respectively in all the environments and for pooled data. High PCV was observed for all the characters except peduncle length (16.50) in E1, peduncle length (14.56), flag leaf sheath length (18.11) and flag leaf blade width (18.65) in E2, peduncle length (12.73) and flag leaf sheath length (18.08) in E3, and peduncle length (12.08), flag leaf sheath length (17.28), panicle exertion (17.71) and flag leaf blade width (19.81) in pooled data, which showed moderate PCV. The same trend was observed for GCV estimates also. All the traits exhibited narrow differences between PCV and GCV in all three environments and pooled data.

The estimates of broad sense heritability ($h^2_{b,}$ %) in foxtail millet core collection ranged from 89.02 (flag leaf sheath length) to 99.56 (days to 50% flowering) in E1, 93.08 (flag leaf blade width) to 99.71 (days to 50% flowering) in E2, 89.99 (flag leaf blade width) to 99.95 (days to 50% flowering) in E3 and 75.28 (peduncle length) to 96.33 (days to 50% flowering) in pooled. High heritability estimates for all the traits were observed in all three environments as well as pooled.

The estimate of genetic advance as per cent of mean was high for all the characters in all three environments and pooled data except peduncle length in pooled data (18.73%), which was expressed moderated genetic advance as per cent of mean.

4.2.3 RANGE AND MEAN PERFORMANCE

Mean and range were calculated for each trait in individual environment separately as well as pooled and for races within and between individual environments and pooled. Mean of different traits were tested using the Newman-Keuls procedure to compare the mean performance three environments and races. The range, mean and comparison of mean (Newman's Keuls test) are presented in Table 17, 18, and 19a and 19b, respectively. Mean performance of each accession for 13 quantitative traits in E1, E2, E3 and pooled data are present in Appendix 2, 3, 4 and 5, respectively. Frequency distribution of quantitative traits across three environments showed the similar trend (Figure 5). The estimates of mean and range were presented below.

4.2.3.1 Days to 50 per cent flowering (Days)

The widest range of days to 50 per cent flowering was observed in all the three environments (31.1-102.8 days in E1, 31.1-102.9 days in E2, and 32.7-103.6 days in E3) and in pooled data (31.8-103.1 days). Among the races, *indica* showed the wide range of variation (36.4-102.8 days in E1, 37.4-102.9 days in E2 and 41.7-103.6 days in E3) followed by *maxima* (31.1-76.9 days in E1, 31.1-79.3 days in E2 and 33.3-61.3 days in E3) and *moharia* (35.6-65.0 days in E1, 35.4-53.7 days in E2 and 32.9-56.0 days in E3) (Table 17).

The mean days to 50 per cent flowering was similar in all three environments (53.7±0.76 days in E1, 52.5±0.64 days in E2 and 53±0.24 days in E3) and pooled (53.1±0.51 days) and did not differ significantly from each other (Table 18). However, mean days to 50 per cent flowering of three races within each environment differed significantly. The mean days to 50 per cent flowering was maximum in *indica* (57.2 in E1, 56.0 in E2, 57.3 in E3 and 56.5 in pooled data) and *maxima* was intermediate between *indica* and *moharia* in all three environments and pooled (Table 19a). The mean days to 50 per cent flowering of the individual races between environment (*indica*, *maxima* and *moharia*) not differ significantly (Table 19b).

4.2.3.2 Plant height (cm)

A wide range for plant height was observed in foxtail millet core collection (Plate 6A) and the maximum range was observed in E1 (28.1-162.0cm) followed by E2 (35.6-137.0cm) and E3 (37.7-138.8cm). Among the races, *maxima* had the maximum range of plant height in all three environments (28.1-143.1cm in E1, 36.5-127.5cm in E2 and 39.63-122.7cm in E3).

The mean plant height was 100.3±4.45 in E1, 94.2±2.38 in E2, 94.7±4.52 in E3 and 96.4±2.99 in pooled, and it did not differ significantly between environments (Table 18). However, mean plant height of three races differed significantly with each other in all three environments and in pooled data. Plants of *indica* accessions were tallest whereas *maxima* were intermediate between *indica* and *moharia* in all three environments and pooled data (Table 19a). The mean plant height for the race *indica* in E1 significantly differed E2, E3 whereas *maxima* and *moharia* did not show significant difference between environments (Table 19b).

4.2.3.3 Basal tiller number

Maximum range of basal tiller number was observed in E1 (1.1 to 8.9) compared to E2 (1.1-6.2) and E3 (1-5.1). In pooled data, it ranged from 1.1 to 5.9. Among the races, *moharia* in E2 (1.1-6.2) and E3 (1.0-5.1), and *indica* E1 (1.4-8.9) showed the maximum range of basal tillers (Table 17).

The mean basal tiller number was higher in E1 (4.2±0.29) followed by to E2 (3.3±0.25) and E3 (2.8±0.05) with an overall mean of 3.5±0.15 in pooled data and basal tiller number differ significantly in each environment (Table 18). The mean basal tiller number was low in *maxima* (2.5 in E1, 2.0 in E2, 1.5 in E3 and 2.1 in pooled) and significantly differed from *indica* and *moharia* in all three environments (Table 19a). Mean basal tiller number of the race *indica* significantly differed in each environment whereas E1 significantly differed from E2 and E3 for *maxima,* and *moharia* (Table 19b).

4.2.3.4 Flag leaf blade length (mm)

In the core collection, a wide range was observed for flag leaf blade length and it was the highest in E1 (64.4-440.1mm) followed by E2 (69.1-436.8mm) and E3 (119.0-468.0mm). Among the races, *indica* had the maximum range of flag leaf blade length in all three environments (134.0-440.1mm in E1, 123.8-436.8mm in E2 and 176.0-468.0mm in E3) (Table 17).

The mean flag leaf blade length was high in E3 (275.8±14.13mm) followed by E1 (250.1±9.11mm) and E2 (229.7±6.37mm) and significantly differed in each environment (Table 18). Mean flag leaf blade length of the three races significantly differed from each other in E1 and E3 whereas in E2, *indica* significantly differed from *maxima* and *moharia*. In all three environments and pooled, the race *indica* was the highest mean flag leaf blade length (281.9mm in E1, 254.7mm in E2, 304.5mm in E3 and 280.0mm in pooled) and *maxima* were intermediate

between *indica* and *moharia* (Table 19a). The mean flag leaf blade length of *indica* and *maxima* significantly differed in each environment whereas the race *moharia* did not differ significantly in each environment (Table 19b).

4.2.3.5 Flag leaf blade width (mm)

The range flag leaf blade width was the highest in E1 (6.8 to 31.5mm) followed by E3 (9.0-27.9mm) and E2 (9.5-27.9mm). The race *maxima* in E1 (7.8-30.6mm) and E3 (13.4-27.9mm) and in pooled data (11.5-27.2mm), *indica* in E2 (11.1-27.9mm) showed the maximum range of variation for mean flag leaf blade width (Table 17).

The E1 (19.0±0.91mm) and E3 (18.6±1.21mm) had the maximum mean flag leaf blade width and both of these environments were differed significantly from E2 (16.4±0.78mm) (Table 18). The mean flag leaf blade width of the race *moharia* significantly differed from *indica* and *maxima* in all three environments as well as in pooled and there was no significant difference between *indica* and *maxima*. The highest mean flag leaf blade width was observed in *maxima* (21.4mm in E1, 17.4mm in E2, 20.1mm in E3 and 19.9mm in pooled) and *indica* was intermediate between *maxima* and *moharia* (Table 19a). The mean flag leaf blade width of the *indica* in E2 (16.9mm) significantly differed from E1 (19.9mm) and E3 (19.4mm). No significant difference was observed between environments for the race *maxima* and *moharia* (Table 19b).

4.2.3.6 Flag leaf sheath length (mm)

The E1 had the maximum range of flag leaf sheath length (52.0-191.2mm) followed by E2 (48.5-181.2mm) and E3 (50.9-179.1mm). In pooled BLUPs of three environments, flag leaf sheath length ranged from 47.4-175.3mm. Among the races, *maxima* showed the highest range of variation (52.0-181.1mm in E1, 48.5-172.4mm in E2 and 50.9-155.7mm in E3) compared to *indica* and *moharia* in all three environments (Table 17).

The mean flag leaf sheath length was slightly higher in E3 (135.0±6.34mm) than E1 (133.4±9.40mm) and E2 (131.8±4.03mm) however, it did not differ significantly (Table 18). Among the races, *indica* had the maximum mean flag leaf sheath length in all three environments (143.9mm in E1, 140.9mm in E2 and 145.0mm in E3) and pooled (143.4mm), and *maxima* was intermediate between *indica* and *moharia*. All the three races differ significantly with each other in all three environments (Table 19a). However, individually mean flag leaf sheath length of

indica, *maxima* and *moharia* races was not significantly different in three environments (Table 19b).

4.2.3.7 Peduncle length (mm)

Peduncle length ranged from 160.3 to 423.2mm in E1, 196.9 to 416.0mm in E2 and 189.3 to 409.8mm in E3. The race *maxima* in E1 (178.6-423.2mm) and E3 (189.3-409.2mm), *indica* in E2 (203.9-416.0mm) had the maximum range of peduncle length (Table 17).

Mean peduncle length was the slightly higher in E2 (309.4±9.02mm) than E3 (300.8±8.33mm) and E1 (297.9±11.00mm), it did not differ from each environment (Table 18). Among the races, mean peduncle length of *indica* and *maxima* were significantly differed from *moharia* in all three environments as well in pooled data. The race *indica* had the highest mean peduncle length in E1 (306.5mm) and E2 (319.3mm) and *maxima* was intermediate between *indica* and *moharia* (Table 19a). Mean peduncle length of the race *indica* in E2 significantly differed from E1 and E3 whereas the race *maxima* and *moharia* did not differ in each environment (Table 19b).

4.2.3.8 Panicle exertion (mm)

The range of panicle exertion was the maximum in E1 (99.7 to 300.2mm) followed by E3 (86.7-284.2mm) and E2 (97.6-259.6mm). In pooled of three environments, panicle exertion ranged from 107.4 to 279.0mm. The race *maxima* had wide range of variation for panicle exertion in E1 (101.9-300.2mm) and E3 (123.7-284.2mm) where as in E2, *indica* showed maximum range from 100.2 to 259.6mm (Table 17).

The E2 had the highest mean panicle exertion (182.3±6.90mm) and significantly differed from E1 (169.4±6.80mm) and E3 (165.7±3.33mm) (Table 18). The E1, E2 did not differ significantly for mean panicle exertion between three races whereas the race *indica* significantly differ from *maxima* and *moharia* in E3. The highest mean panicle exertion was observed for the race *maxima* in all environments (184.7 in E1, 187.3 in E2 and 180.8 in E3) and pooled data (183.5mm) compared to *indica* and *moharia* (Table 19a). The mean panicle exertion for the race *indica* significantly differed in each environment, whereas the race *maxima* and *moharia* did not differ significantly between environments (Table 19b).

4.2.3.9 Inflorescence length (mm)

A wide range of inflorescence length was observed in foxtail millet core collection (Plate 6B). The maximum range of inflorescence length was observed in E1 (26.0 to 281.8mm) followed by E3 (33.0-286.6mm) and E2 (38.0-250.0mm). The race *indica* showed the maximum range of variation for inflorescence length in all the environments (43.3-281.8mm in E1, 67.1-250.6mm in E2 and 115.8-286.6mm in E3) and pooled (91.1-257mm) (Table 17).

The mean inflorescence length was the maximum in E1 (149.5±8.61mm) and E3 (147.0±5.56mm) and significantly differed from E2 (121.8±3.87mm) (Table 18). The mean inflorescence length of the three races significantly differed from each other in all three environments and in pooled data. The race *indica* had the highest mean inflorescence length whereas the race *maxima* was intermediate between *indica* and *moharia* (Table 19a). The mean inflorescence length of the race *indica* in E1 and E3 significantly differed from E2 and no significant difference was found for the race *maxima* and *moharia* between three environments (Table 19b).

4.2.3.10 Inflorescence width (mm)

The range of inflorescence width was maximum in E1 (6.6-31.5mm) followed by E3 (7.0-26.9mm) and E2 (9.6-24.8mm). Among the races, *indica* had maximum range of inflorescence width in all three environments (10.2-31.5mm in E1, 10.1-24.8mm in E2 and 10.4-26.9mm in E3) and pooled (11.0-26.0mm) (Table 17).

The mean inflorescence width was maximum in E1 (16.9±0.650mm) and significantly differed from E2 (15.9±0.91mm) and E3 (14.8±0.68mm) (Table 18). Among the races, the race *indica* and *maxima* did not differ significantly and both these races differ significantly from *moharia* in all three environments (Table 19a). The mean inflorescence width of the race *indica* in E2 significantly differed from E1 and E3. However, the race *maxima* and *moharia* did not differ significantly between environments for this trait (Table 19b).

4.2.3.11 Weight of five panicles (g)

The maximum range of variation for weight of five panicles was observed in E2 (2.5 to 72.9g) followed by E1 (2.3-70.6g) and E3 (3.5-46.9g). The race *maxima* observed a wide range of variation (2.6-67.2g in E1, 3.2-72.9g in E2, 4.2-44.2g in E3 and 3.8-58.4g in pooled) in all three environments and pooled followed by *indica* and *moharia* (Table 17).

In E1, mean weight of five panicles was the maximum (25.6±1.74g) followed by E3 (22.2±2.35g) and E2 (22.0±1.42g), however, it did not differ significantly between environments (Table 18). Among three races within the environments, *moharia* significantly differed from *indica* and *maxima*, and *indica* and *maxima* not differed significantly in all three environments and pooled data. The race *maxima* in E1 (29.9g) and E2 (27.0g), *indica* in E3 (25.3g) had the highest mean weight of five panicles (Table 19a). The mean weight of five panicles of the race *indica* in E2 and E3 significantly differed from E1 and the race *maxima* and *moharia* did not differ significantly between environments (Table 19b).

4.2.3.12 Single plant yield (g)

The range of single plant yield was the maximum in E1 (3.0-59.0g) followed by E2 (3.1-55.5g) and E3 (2.3-22.6g). Among the races, *indica* showed wide range of single plant yield in all the environments (4.9-59.0g in E1, 4.2-55.5g in E2 and 3.5-22.6g in E3) and pooled (7.8-43.1g) (Table 17).

The mean single plant yield was the highest in E1 (23.9±2.18g) followed by 19.4±1.65g in E2 and 11.2±1.07g in E3, it differ significantly in each environment. The mean single plant yield of *indica* was high in all three environments (28.1g in E1, 22.7g in E2, 13.1g in E3 and 21.4g in pooled) and race *maxima* was intermediate between *indica* and *moharia*. The three races differ significantly with each other for mean single plant yield of in all three environments as well in pooled data (Table 19a). The mean single plant yield of the race *indica* significantly differed in each environment, however the race *maxima* in E3 significantly differed from E1 and E2, and the race *moharia* in E1 significantly differed from E2, E3 (Table 19b).

4.2.3.13 Grain yield per plot (Kg ha^{-1})

Grain yield per plot (Kg ha^{-1}) ranged from 172.0 to 3,290.0 Kg ha^{-1} in E1, which was the highest followed by E2 (150.0-2662.0 Kg ha^{-1}) and E3 (143.0-1,460.5kg ha^{-1}). In pooled, it ranged from 196.0 to 2240.0 Kg ha^{-1}. Among the races, *indica* in E1 (516-3290 Kg ha^{-1}) and E3 (168.0-1460.0 Kg ha^{-1}), and *maxima* in E2 (200.0-2662.0 Kg ha^{-1}) and pooled (211.0-2013.0 Kg ha^{-1}) showed the highest range of grain yield per plot (Kg ha^{-1}) (Table 17).

The mean grain yield per plot (Kg ha^{-1}) was the maximum for E1 (1612.4±121.10 Kg ha^{-1}) followed by E2 (1219.0±101.40 Kg ha^{-1}) and E3 (741.9±67.63 Kg ha^{-1}), and it significantly

differed in each environment. In pooled, the mean grain yield per plot (Kg ha^{-1}) was 1181.8±58.70 Kg ha^{-1} (Table 18). The race *indica*, *maxima* and *moharia* significantly differed from each other in E1 and E2, whereas *maxima* and *moharia* significantly differ from *indica* in E3 (Table 19a). The mean grain yield per plot (Kg ha^{-1}) [1] of the race *indica* and *moharia* significantly differed between environments, whereas the race *maxima* in E3 significantly differed from E1 and E3 (Table 19b).

4.2.4 VARIANCES

Variances of 13 quantitative traits were calculated in individual environment separately and in pooled data for entire core collection and three basic races. The homogeneity of variances of three races and environments were tested using Levene's test.

Variances were homogenous between environments for only four traits *viz*., days to 50 per cent flowering, flag leaf blade length, flag leaf sheath length and panicle exertion out of 13 quantitative traits studied between environments. The remaining nine traits *viz.*, plant height, basal tillers number, flag leaf blade width, peduncle length, inflorescence length, inflorescence width, weight of five panicles, single plant yield and grain yield per plot (Kg ha^{-1}) were heterogeneous (Table 20a).

Variances was homogenous between three races for days to 50 per cent flowering and single plant yield in E1, days to 50 per cent flowering, basal tillers number, flag leaf blade length, flag leaf blade width, peduncle length, panicle exertion, inflorescence length, inflorescence width and single plant yield in E2, days to 50 per cent flowering, flag leaf blade width, flag leaf sheath length, inflorescence length, inflorescence width, single plant yield and grain yield per plot (Kg ha^{-1}) in E3. In pooled, variances were homogenous for days to 50 per cent flowering, flag leaf blade width, inflorescence width and single plant yield (Table 20b).

Homogeneity of variance was also tested for individual race wise between environments. The traits like days to 50 per cent flowering, flag leaf blade length, flag leaf blade width, inflorescence length for the race *indica*, days to 50 per cent flowering, plant height, flag leaf blade length, flag leaf sheath length, peduncle length and panicle exertion were homogenous for the race *maxima*. All the quantitative traits except basal tillers number, flag leaf blade length and flag leaf blade width were homogenous between environments for the race *moharia* (Table 20c).

4.2.5 CORRELATION COEFFICIENTS

Phenotypic correlations based on BLUPs of all the three environments separately and for pooled data were calculated between 13 quantitative traits. In total, 64 correlations were significant in E1, 60 in E2, 70 in E3 and 65 in pooled data out of 78 correlations in each environment. In the present study, only those correlations which are greater than 0.500 or smaller than -0.500 were considered as useful as at least 25 per cent of the variation in one trait is predicted by the other (Upadhyaya *et al*., 2010c). In total, 35 useful correlations were observed in E1, 28 in E2, 36 in E3 and 40 in pooled (Table 22).

4.2.5.1 Correlation between grain yield and other component traits

Nine out of 12 traits, days to 50 per cent flowering, plant height, flag leaf blade length, flag leaf blade width, flag leaf sheath length, inflorescence length, inflorescence width, weight of five panicles and single plant yield showed significant positive correlation with grain yield per plot (Kg ha^{-1}) in all three environments and overall in the pooled data. Basal tillers in two environments (E1, E3 and pooled data), and peduncle length in E2 and pooled data showed significant positive correlation with grain yield per plot (Kg ha^{-1}). Panicle exertion was the only trait which showed significant negative correlation with grain yield per plot (Kg ha^{-1}) in E1 (-0.228), E3 (-0.197) and in pooled (-0.191) (Table 21).

Grain yield per plot (Kg ha^{-1}) had useful positive correlation with plant height in E1 (0.651), E2 (0.578) and pooled (0.678), flag leaf blade length in E1 (0.567), E3 (0.505) and pooled (0.627), flag leaf sheath length in pooled (0.548), inflorescence length in E1 (0.513), E2 (0.504) and pooled (0.582) and weight of five panicles in E2 (0.514) and pooled (0.514). Single plant yield showed useful positive correlation in all three environments and pooled (0.952 in E1, 0.932 in E2, 0.716 in E3 and 0.899 in pooled) (Table 22).

4.2.5.2 Inter correlation among the yield component traits

It could be observed on pursuing Table 21 that most of the characters had positive inter correlation with each other.

4.2.5.2.1 Days to 50 per cent flowering (Days)

Days to 50 per cent flowering had highly significant positive correlations with plant height, flag leaf blade length, flag leaf blade width, flag leaf sheath length, inflorescence length, inflorescence width, weight of five panicles and single plant yield in all three environments and

pooled. Basal tiller number and peduncle length had significant positive correlation in E1 and panicle exertion was highly significant negative correlation with days to 50 per cent flowering in all three environments and pooled data (Table 21).

Days to 50 per cent flowering showed useful positive correlations with plant height (0.676 in E1, 0.571 in E2, 0.725 in E3 and 0.716 in pooled), flag leaf blade length (0.730 in E1, 0.703 in E2, 0.699 in E3 and 0.796 in pooled), flag leaf blade width (0.592 in E1, 0.581 in E2, 0.617 in E3 and 0.674 in pooled), inflorescence length (0.719 in E1, 0.673 in E2, 0.707 in E3 and 0.776 in pooled) and weight of five panicles (0.547 in E1, 0.544 in E2, 0.537 in E3 and 0.597 in pooled) in all three environments and pooled whereas flag leaf sheath length in E3 (0.549) and pooled (0.520) and inflorescence width in E1 (0.626), E3 (0.570) and pooled (0.630) observed useful correlation with days to 50 per cent flowering (Table 22).

4.4.5.2.2 Plant height (cm)

The correlation analysis revealed that, plant height showed highly significant positive correlations with flag leaf blade length, flag leaf blade width, flag leaf sheath length, peduncle length, inflorescence length, inflorescence width, weight of five panicles and single plant yield in all three environments and pooled. Basal tiller number had significant positive correlation in E1 (0.251) and E2 (0.182), and significant negative correlation in E3 (-0.177). Panicle exertion observed significant negative correlation in E3 (-0.143) (Table 21).

Plant height showed useful positive correlations with flag leaf blade length (0.894 in E1, 0.761 in E2, 0.847 in E3 and 0.855 in pooled), flag leaf blade width (0.632 in E1, 0.517 in E2, 0.705 in E3 and 0.662 in pooled), flag leaf sheath length (0.759 in E1, 0.700 in E2, 0.816 in E3 and 0.786 in pooled), inflorescence length (0.880 in E1, 0.775 in E2, 0.853 in E3 and 0.861 in pooled), inflorescence width (0.660 in E1 0.514 in E2, 0.636 in E3, 0.608 in pooled), weight of five panicles (0.591 in E1, 0.553 in E2, 0.722 in E3 and 0.678 in pooled) and single plant yield (0.651 in E1, 0.536 in E2, 0.637 in E3 and 0.698 in pooled) were found to be positive significant correlation with days to 50 per cent flowering (Table 22).

4.2.5.2.3 Basal tiller number

Basal tillers number showed significant positive correlation with flag leaf blade length (0.165), flag leaf sheath length (0.245), inflorescence length (0.195), and single plant yield (0.238) in E1. Flag leaf blade length (0.204) and flag leaf sheath length (0.148) had significant positive correlations with basal tiller number in E2. Flag leaf blade width (-0.213 in E1, -0.190 in

E2, -0.464 in E3 and -0.369 in pooled) and weight of five panicles (-0.177 in E1, -0.176 in E2, -0.419 in E3 and -0.344 in pooled) had significant negative correlations in all three environments and pooled. Peduncle length (-0.235), panicle exertion (-0.191) and inflorescence length (-0.195) in E3, inflorescence width in E2 (-0.157), E3 (-0.425) and pooled (-0.345) also had significant negative correlation with basal tiller number (Table 21). There was no useful correlation of basal tiller number with other traits.

4.2.5.2.4 Flag leaf blade length (mm)

Flag leaf blade length had highly significant positive correlation with flag leaf blade width, flag leaf sheath length, peduncle length, inflorescence length, inflorescence width, weight of five panicles and single plant yield in all three environments and pooled. Panicle exertion had negative correlation in E3 (-0.241) and pooled (-0.143) with flag leaf blade length (Table 21).

Flag leaf blade length had useful positive correlation with flag leaf blade width (0.747 in E1, 0.621 in E2, 0.724 in E3 and 0.728 in pooled), flag leaf sheath length (0.740 in E1, 0.616 in E2, 0.734 in E3 and 0.692 in pooled) and inflorescence length (0.903 in E1, 0.780 in E2, 0.833 in E3 and 0.864 in pooled) in all three environments and pooled, whereas inflorescence width in E1 (0.714), E3 (0.652) and pooled (0.676), weight of five panicles in E1 (0.644), E3 (0.670) and pooled (0.628) and single plant yield in E1 (0.589) , E3 (0.628 and pooled (0.616) showed useful positive correlation with flag leaf blade length (Table 22).

4.2.5.2.5 Flag leaf blade width (mm)

Flag leaf blade width had highly significant positive correlation with flag leaf sheath length, peduncle length, inflorescence length, inflorescence width, weight of five panicles and single plant yield in all three environments and pooled. Panicle exertion showed negative significant correlation with flag leaf blade width in E3 (-0.168) (Table 21).

Useful positive correlation of flag leaf width was observed with inflorescence length (0.726 in E1, 0.636 in E2, 0.681 in E3 and 0.709 in pooled) and weight of five panicles (0.674 in E1, 0.513 in E2, 0.721 in E3 and 0.755 in pooled) in all three environments and pooled, whereas flag leaf sheath length in E1 (0.570), E3 (0.571) and pooled (0.517) and inflorescence width in E1 (0.770), E3 (0.771) and pooled (0.746) had useful positive correlation with flag leaf blade width (Table 22).

4.2.5.2.6 Flag leaf sheath length (mm)

Flag leaf sheath length showed highly significant positive correlation with peduncle length, inflorescence length, inflorescence width, weight of five panicles and single plant yield in all the environments and pooled (Table 21).

Highly significant positive useful correlation of flag leaf sheath length was observed with peduncle length (0.654 in E1, 502 in E2 and E3 and 0.549 in pooled) and inflorescence length (0.731 in E1, 0.620 in E2, 0.776 in E3 and 0.694 in pooled) in all the environments and pooled, whereas weight of five panicles in E3 (0.559) and pooled (0.500) and single plant yield in E3 (0.567) and pooled (0.535) (Table 22) showed useful correlation with flag leaf sheath length

4.2.5.2.7 Peduncle length (mm)

The trait peduncle length had significant positive correlation with panicle exertion and inflorescence length in all the environments and pooled. Weight of five panicles in E3 (0.214) and pooled (0.245) and single plant yield in E2 (0.155), E3 (0.141) and pooled (0.189) showed significant positive correlation with peduncle length (Table 21). Peduncle length had positive useful correlation only with panicle exertion (0.748 in E1, 0.756 in E2, 0.797 in E3 and 0.716 in pooled) in all three environments and pooled data (Table 22).

4.2.5.2.8 Panicle exertion (mm)

Panicle exertion had significant negative correlation with inflorescence length in E3 (-0.241) and pooled (-0.172), inflorescence width in E3 (-0.266) and pooled (-0.197), weight of five panicles in E3 (-0.145) and single plant yield in E1 (-0.213), E3 (-0.234) and pooled (-0.197) (Table 21). Panicle exertion did not show useful correlation of panicle exertion with other traits.

4.2.5.2.9 Inflorescence length (mm)

Highly significant and positive correlation was observed between inflorescence length with inflorescence width, weight of five panicles and single plant yield (Table 21). Weight of five panicles (0.594 in E1, 0.532 in E2, 0.667 in E3 and 0.664 in pooled) and single plant yield (0.533 in E1, 0.504 in E2, 0.573 in E3 and 0.621 in pooled) had positive useful correlation with inflorescence length in all the environments and pooled, whereas inflorescence width showed useful correlation in E1 (0.709), E3 (0.531) and pooled (0.646) (Table 22).

4.2.5.2.10 Inflorescence width (mm)

Inflorescence width had highly significant positive correlation with weight of five panicles and single plant yield in all three environments (Table 21). Useful positive correlation of inflorescence width was observed with weight of five panicles in all the environments (0.787 in E1, 0.580 in E2 and 0.726 in E3) and pooled (0.842) (Table 22).

4.2.5.2.11 Weight of five panicles (g)

Weight of five panicles had highly significant positive and useful correlation with single plant yield in all the environments (0.518 in E1, 0.529 in E2 and 0.500 in E3) and pooled (0.570) (Table 21 and 22).

4.2.5.2.12 Single plant yield (g)

The trait single plant yield had highly significant positive and useful correlation with grain yield per plot (Kg ha^{-1}) in all the environments (0.952 in E1, 0.932 in E2 and 0.726 in E3) and pooled (0.899) (Table 21 and 22).

4.2.6 PATH COEFFICIENT ANALYSIS

The direct effect of single plant yield on grain yield per plot (Kg ha^{-1}) (Table 23) was positive and high in all the environments and pooled (0.891 in E1, 0.911 in E2, 0.61 in E3 and 0.929 in pooled) whereas the direct effect of plant height in pooled (0.216), flag leaf blade length in E3 (0.275), peduncle length in pooled (0.264) and weight of five panicles in E3 (0.239) were positive and moderate. Peduncle length in E3 (2.837) shown very high positive effect on grain yield per plot (Kg ha^{-1}). Plant height (-0.216), inflorescence length (-0.271) and inflorescence width (-0.276) in E3 showed negative and moderate direct effect whereas flag leaf sheath length (-1.441) and panicle exertion (-2.552) in E3 showed negative and high direct effect on grain yield per plot (Kg ha^{-1}).

The indirect effects of days to 50 per cent flowering (0.384 in E1, 0.386 in E2, 0.329 in E3 and 0.438 in pooled), plant height (0.567 in E1, 0.503 in E2, 0.427 in E3 and 0.640 in pooled), flag leaf blade length (0.511 in E1, 0.390 in E2, 0.425 in E3 and 0.570 in pooled), flag leaf blade width (0.330 in E1, 0.313 in E2, 0.311 in E3 and 0.417 in pooled), flag leaf sheath length (0.378 in E1, 0.387 in E2, 0.388 in E3 and 0.515 in pooled), inflorescence length (0.463 in E1, 0.472 in E2, 0.386 in E3 and 0.564 in pooled), inflorescence width (0.389 in E1, 0.362 in E2, 0.243 in E3 and 0.441 in pooled) and weight of five panicles (0.453 in E1, 0.492 in E2, 0.339 in E3 and 0.534 in pooled) through single plant yield were positive and high.

The residual variance was low in all the three environments (0.115 in E1, 0.085 in E2 and 0.348 in E3) and pooled (0.071) (Table 23).

4.2.7. DIVERSITY ANALYSIS

4.2.7.1. Shannon Weaver Diversity Indices

The Shannon-Weaver diversity indices (H′) were calculated to compare diversity index (H′) values among 13 quantitative traits and three races of foxtail millet core collection (Table 24).

Flag leaf blade width, flag leaf sheath length, peduncle length in all three environments and pooled along with plant height, inflorescence width in E1, panicle exertion and inflorescence length in E2, panicle exertion, inflorescence length, inflorescence width, weight of five panicle, single plant yield and grain yield per plot (Kg ha^{-1}) in E3, and panicle exertion and inflorescence width in pooled had the maximum H′ value.

For the race *indica*, flag leaf sheath length, peduncle length, panicle exertion in all three environments and pooled along with basal tiller number, grain yield per plot (Kg ha^{-1}) in E1, basal tiller number and inflorescence width in E2, single plant yield, weight of five panicles and grain yield per plot (Kg ha^{-1}) in E3, and plant height and grain yield per plot (Kg ha^{-1}) in pooled had the maximum H′.

Peduncle length, plant height in all three environments and pooled, flag leaf blade length and flag leaf sheath length in two out of three environments and pooled had the maximum H' values for the race *maxima*, whereas the quantitative traits like basal tillers, flag leaf sheath length, peduncle length, panicle exertion had the maximum H′ in all three environments and pooled for the race *moharia*.

All three environments had the similar mean H′ values across the traits (0.59±0.006 in E1, 0.57±0.008 in E2 and 0.58±0.007 in E3). Among the races, *indica* showed the highest pooled H′ across the traits (0.587±0.009 in E1, 0.60±0.009 in E2, 0.59±0.019 in E3 and 0.59±0.013 in pooled data across the environments) and the race *moharia* showed the low pooled H′ across the traits (0.49±0.019 in E1, 0.47±0.028 in E2, 0.50±0.018 in E3 and 0.47±.019 in pooled data across the environments) in all three environments as well as pooled.

4.2.7.2 Phenotypic diversity matrix

Gower's (1971) dissimilarity matrix was calculated using 12 qualitative and 13 quantitative traits for individual environment separately and for pooled data in the foxtail millet core collection. The mean diversity was 0.255 in E1 and E2, 0.250 in E3 and 0.253 in pooled. Frequency distribution of phenotypic dissimilarity index between pair of accessions is presented in Figure 6. The maximum phenotypic diversity was observed between ISe 1687 and ISe 1254 in E1 (0.635), E2 (0.608) and pooled data of three environments (0.640) and between ISe 1597 and ISe 1312 in E3 (0.595). The minimum phenotypic diversity observed between ISe 999 and ISe 869 in E1 (0.006), ISe 1820 and ISe 909 in E2 (0.006) and pooled data of three environments (0.003) and between ISe 846 and ISe 663 in E3 (0.001) (Table 25).

Based on the diversity index ten pairs of most diverse accessions were identified in each environment separately and in pooled data of three environments (Table 26). Most of the pair of accessions which expressed the most diverse in pooled data was also found in individual environment as well. The ten pairs of accessions, ISe 1687-ISe 1254, ISe 1597-ISe 1312, ISe 1687-ISe 1201, ISe 1881-ISe 1312, ISe 1597-ISe 1320, ISe 1687-ISe 1129, ISe 1687-ISe 1312, ISe 1685-ISe 827, ISe 1286-ISe 1059, and ISe 1687-ISe 1118 were the most diverse pair accessions identified in foxtail millet core collection based on pooled data of three environments.

4.2.7.3 Principal Component Analysis (PCA)

The PCA on the mean values of the entire core collection and races was performed which provided a reduced dimension model that could indicate measured differences among the accessions and races.

4.2.7.3.1 PCA based on environments

The purpose of the analysis is to obtain a small number of linear combinations of the 13 quantitative traits which account for most of the variability in the data. The results revealed the importance of the first three PCs in discriminating the foxtail millet core collection in individual environment and pooled, since first three PCs had eigen values greater than or equal to 1.0 (Table 27). The percentage of total variance explained by the first three PCs was 78.6 in E1, 71.6 in E2, 83.1 in E3 and 82.1 in pooled.

The PC1 was the most important component and accounted for more variation in all the three environments and pooled (51.3 in E1, 46.8 in E2, 54.3 in E3 and 55.1 in pooled). The eigen values of PC1 were 6.67, 6.08, 7.06 and 7.16 in E1, E2, E3 and pooled, respectively.

The PC1 separates accessions based on flag leaf blade length (0.362), plant height (0.356), inflorescence length (0.352), inflorescence width (0.307), days to 50 per cent flowering (0.305) and flag leaf sheath length (0.288) in E1, plant height (0.359), inflorescence length (0.353), flag leaf blade length (0.346), days to 50 per cent flowering (0.306), flag leaf blade width (0.298) and grain yield per plot (Kg ha^{-1}) (0.298) in E2, plant height (0.356), flag leaf blade length (0.347), inflorescence length (0.346), flag leaf blade width (0.319), flag leaf sheath length (0.318), weight of five panicles (0.315) and days to 50 per cent flowering (0.300) in E3. In pooled, PC1 separates the accessions based on plant height (0.353), flag leaf blade length (0.348), inflorescence length (0.346), flag leaf blade width (0.310), weight of five panicle (0.304), flag leaf sheath length (0.301) and days to 50 per cent flowering (0.301) in pooled. The PCA reduced the original 13 characters to10 in each in E1, E3 and pooled and 9 in E2.

Considering PCA analysis for all the three environments, days to 50 per cent flowering, plant height, basal tiller number, flag leaf blade length, flag leaf blade width, peduncle length, panicle exertion and inflorescence length occurred in all three environments in the first three PCs, indicating their importance for characterization of foxtail millet germplasm accessions.

The scatter plot of first two PCs and colour coding of genotypes on the basis of races based on pooled mean of three environments and 13 quantitative traits are shown in Figure 7, where axis PC1 explained 55.09 per cent and PC2 explained 14.61 per cent of the total variation. The accessions from *indica* (red) and *moharia* (blue) clearly separated whereas few accessions from *maxima* (green) were found mixed along with *moharia* and *indica* group.

4.2.7.3.2 PCA based on races

The results revealed the importance of the first three PCs in the races, since first three PCs had eigen values greater than or equal to 1.0. The percentage of total variation explained by the first three PCs in race *indica* were 66.7, 61.5, 73.5 and 70.8 in E1, E2, E3 and pooled, respectively, which were less as compared to variation explained in *maxima* and *moharia* (89.2 in E1, 82.5 in E2, 83.2 in E3 and 89.9 in pooled for *maxima* and 82.5 in E1, 74.9 in E2, 85.9 in E3 and 87.1 in pooled for *moharia*) (Table 28, 29, 30 and 31). The eigen value of PC1 was 4.51 in E1, 4.11 in E2, 5.34 in E3 and 5.06 in pooled for the race *indica* whereas 8.10, 7.13, 7.37 and 8.09 in E1, E2, E3 and pooled, respectively for *maxima* and 7.55 in E1, 6.30 in E2, 7.86 in E3 and 8.01 in pooled for the race *moharia.*

Considering PCA analysis for races between environments, the traits like flag leaf blade length, flag leaf blade width, peduncle length and grain yield per plot (Kg ha^{-1}) were occurred in the first three PCs in all three environments and pooled for the race *indica*. The traits like days to 50 per cent flowering, plant height, flag leaf blade length, peduncle length, panicle exertion, weight of five panicles and single plant yield in *maxima,* and plant height, flag leaf blade length, flag leaf blade width, panicle exertion, inflorescence length and weight of five panicles were occurred in the first three PCs in all three environments and pooled for the race *moharia.*

4.2.7.4 Clustering

The hierarchical cluster analysis (Ward, 1963) of individual environment and pooled was conducted using the scores of first three PCs accounting 78.6, 71.6, 83.1 and 82.6 per cent of total variance in E1, E2, E3 and pooled, respectively. The clustering pattern in all the three environments and pooled were fairly consistence with three biological races.

In E1, cluster analysis delineated the 159 accessions (155 accessions from core collection and 4 controls) into two clusters namely *A* and *B* at linkage distance 80 (Figure 8). The cluster *A* was divided into sub-clusters *AI* and *AII* and was dominated with accessions from *maxima* and *moharia*, respectively. Out of 17 accessions in the sub-cluster *AI*, the race *maxima* dominated with 11 accessions along with 5 accessions from *moharia* and 1 accession from *indica*. The sub-cluster *AII* was predominated by *moharia* with 17 accessions along with 3 *maxima* and 1 *indica*. Similarly, cluster *B* was divided into two sub-clusters namely *BI* and *BII* at linkage distance 60. The sub-cluster BI was represented by the mixture of both *indica* (13 accessions) and *maxima* (10 accessions). Out of 103 accessions from *indica*, 88 accessions were grouped together in sub-cluster *BII* along with 7 *moharia* and 3 *maxima*.

At linkage distance 60, the accessions are grouped into two clusters namely *A* and *B* in E2 (Figure 9). The cluster *A* represented by the mixture of *moharia* with 25 accessions and *maxima* with 10 accessions out of 39 accessions in this cluster. The cluster *B* was subdivided into two sub-clusters, *BI* and *BII* at linkage distance 40. The sub-cluster *BI* dominated with *indica* containing 10 accessions along with 3 accessions from *maxima*. The sub-cluster *BII* was the largest cluster which contained predominantly the race *indica* (89 accessions) compared to *maxima* (12 accessions) and *moharia* (4 accessions).

In E3, the accessions were grouped into cluster *A* and cluster *B* (Figure 10) at linkage distance 80. The cluster A consisted of 37 accessions of which *moharia* dominated with 25

accessions compared to *maxima* (7 accessions) and *indica* (5 accessions). The cluster *B* was subdivided into two sub-clusters, *BI* and BII. The sub-cluster *BI* was represented by mixture of accessions from *indica* (29 accessions) and *maxima* (19 accessions) along with 2 *moharia* out of 50 accessions in this sub-cluster. In the sub-cluster *BII*, 69 accessions from *indica* grouped together and dominated in this sub-cluster along with 2 accessions from *moharia* and one accession from *indica*.

The hierarchical cluster analysis using the method of Ward (1963) on the first three PCs estimated from the pooled mean of three environments accounting 82.55 per cent of total variation. The foxtail millet core collection accessions were grouped into two clusters namely cluster *A* and cluster *B* at linkage distance 60 (Figure 11). The cluster *A* was dominated by the race *moharia* with 26 accessions out of 29 accessions present in the core collection along with 11 *maxima* and 4 *indica*. The cluster *B* was subdivided in to two sub-clusters namely *BI* and *BII*. The sub-cluster *BI* comprised of 52 accessions of which 34 *indica*, 16 *maxima* and 2 *moharia*. Accessions from *maxima* mixed with *moharia* (in cluster A, 11 accessions) and *indica* (in sub-cluster *BI*, 16 accessions). The sub-cluster *BII* was dominated by *indica* with 65 accessions out of 66 accessions in this cluster (1 *moharia*).

4.3. IDENTIFICATION OF TRAIT SPECIFIC SOURCES

In the present study, a wide range of variability was available in foxtail millet core collection for yield and its component traits. The trait specific accessions were identified based on pooled BLUPs of three environments and compared with mean of four control cultivars ± LSD. Most of the accessions selected as trait specific sources appeared in top 15 ranks in all the three environments or atleast in two out of three environments.

4.3.1 Sources for early flowering

Performance of 15 each for early maturing accessions in foxtail millet core collection is given in the Table 32a. The accessions which flowered significantly early were ISe 1201, ISe 1312, ISe 1320, ISe 1234, ISe 1563, ISe 827, ISe 1335, ISe 1151, ISe 1258, ISe 1286, ISe 1254, ISe 1655, ISe 1181, ISe 1161 and ISe 1638 (range from 31.8 to 39.4 days to 50% flowering). These accessions had mean days to 50 per cent flowering of 37.1 days ranged from 31.8 to 34.5 days. All selected accessions were significantly earlier than control cultivars.

4.3.2 Sources for tallness

Plant height showed significant positive correlation with grain yield per plot (Kg ha^{-1}). The 15 accessions with tall plants were: ISe 1736, ISe 1881, ISe 1687, ISe 1597, ISe 999, ISe 983, ISe 1511, ISe 717, ISe 751, ISe 1474, ISe 748, ISe 1059, ISe 1419, ISe 769 and ISe 1387 in increasing order of plant height from 121.1 to 140.4 cm. All the selected accessions were significantly taller than the control cultivars mean + LSD (114.6) (Table 32b).

4.3.3 Sources for maximum basal tiller number

The accessions namely ISe 1846, ISe 286, ISe 1299, ISe 914, ISe 748, ISe 1305, ISe 362, ISe 1664, ISe 1269, ISe 999, ISe 710, ISe 1009, ISe 1408, ISe 1129 and ISe 1162 were selected as the sources for more basal tiller number. The mean of the selected accessions (5.2) was 43 per cent more than the mean of the control cultivars (2.2). All the selected accessions had significantly more basal tillers than control cultivars mean + LSD (2.7) (Table 32c).

4.3.4 Sources for maximum flag leaf blade length (mm)

The accessions namely ISe 717, ISe 1666, ISe 983, ISe 1059, ISe 2, ISe 144, ISe 1511, ISe 132, ISe 1687, ISe 748, ISe 1419, ISe 769, ISe 1387, ISe 1597 and ISe 751 were selected as the sources for maximum flag leaf blade length. These accessions had mean flag leaf blade length of 345.6mm ranged from 308.9 to 425.3mm which was on average 15 per cent higher than the mean of the control cultivars (300.5) (Table 32d).

4.3.5 Sources for maximum flag leaf width (mm)

The accessions namely ISe 144, ISe 375, ISe 1745, ISe 1251, ISe 1059, ISe 1575, ISe 900, ISe 1685, ISe 1687, ISe 751, ISe 748, ISe 1597, ISe 1593, ISe 1387 and ISe 769 were the selected as the sources for maximum flag leaf blade width. Flag leaf width of the selected accessions ranged from 21.9 to 27.2mm with the mean of 24.6mm, which was higher than the mean of the control cultivars (22.3mm) (Table 32e).

4.3.7 Sources for maximum inflorescence length (mm)

The sources for maximum inflorescence length are ISe 1059, ISe 1881, ISe 1511, ISe 1687, ISe 717, ISe 1725, ISe 1454, ISe 769, ISe 1387, ISe 1419, ISe 751, ISe 1685, ISe 748 and ISe 1597. All the 15 accessions had significantly higher inflorescence length than the control cultivars mean + LSD (151.6mm). The mean of selected accessions (219.3mm) was above 60 per cent higher than the mean of the control cultivars (137.6mm) (Table 32f).

4.3.8 Sources for maximum inflorescence width (mm)

ISe 1251, ISe 1454, ISe 1059, ISe 1610, ISe 751, ISe 983, ISe 748, ISe 18, ISe 769, ISe 1387, ISe 1687, ISe 1597, ISe 375, ISe 1419 and ISe 1685 were selected as the best 15 accessions for maximum inflorescence width (Table 32g).

4.3.9 Sources for maximum weight of 5 panicles (g)

The accessions namely ISe 302, ISe 132, ISe 1419, ISe 1511, ISe 1736, ISe 1474, ISe 748, ISe 1685, ISe 1685, ISe 1687, ISe 769, ISe 1251, ISe 1597, ISe 375, ISe 1454 and ISe 1666 were selected as the sources for maximum weight of five panicles (Table 32h).

4.3.10 Sources for maximum single plant yield (g)

Single plant yield had highly positive and significant correlation with grain yield per plot (Kg ha^{-1}) in all the environments and pooled. The top most 15 accessions produced the maximum single plant yield are ISe 1767 ISe 1000, ISe 388, ISe 1059, ISe 238, ISe 1846, ISe 1685, ISe 1597, ISe 1406, ISe 1888, ISe 364, ISe 1474, ISe 956, ISe 1687 and ISe 1881. The mean single plant yield of selected accessions (34.4g) was higher than the control cultivars mean (30.3g) (Table 32i).

4.3.11 Sources for higher grain yield (Kg ha^{-1})

The genotypes namely ISe 1805, ISe 1780, ISe 1408, ISe 1000, ISe 1685, ISe 1736, ISe 388, ISe 1767, ISe 1474, ISe 1687, ISe 1846, ISe 956, ISe 364, ISe 1881 and ISe 1888 produced the maximum grain yield per plot (Kg ha^{-1})[1] and were selected as the potential sources for high grain yield per plot (Kg ha^{-1})[1]. The mean grain yield per plot (Kg ha^{-1})of the selected accessions (2021 Kg ha^{-1}) was higher than the control cultivars mean (1927 Kg ha^{-1}) (Table 32j).

4.4 MOLECULAR DIVERSITY IN FOXTAIL MILLET CORE COLLECTION

Initially, 139 markers were used to check polymorphism across eight phenotypically most diverse accessions in foxtail millet core collection. Of these, 99 SSR markers including 80 SSR foxtail millet genomic SSRs, three unmapped foxtail millet EST-SSRs, 12 finger millet and four pearl millet genomic SSRs markers were used to genotyping the entire core collection accessions. Finally, 84 SSR markers (72 foxtail millet SSRs, 3 foxtail millet EST-SSRs, 5 finger millet SSRs and 4 pearl millet SSRs) produced clear, scorable and polymorphic marker profiles and were therefore used for the further analysis.

4.4.1 Allelic richness and genetic diversity in foxtail millet core collection

The 84 SSR markers detected a total of 1,356 alleles in 155 accessions of foxtail millet core collection (Table 33 and 34). The number of alleles per locus ranged from 4 (b196 and p56) to 35 (b171) with an average 16.14 alleles per locus. The marker b171 (35 alleles) detected the highest number of alleles followed by p4 (31 alleles), b109 (30 alleles), b260 (29 alleles) and p236 and b174 (28 alleles). Distribution of number of alleles per locus among 84 SSR markers in the same order as in linkage groups (Jia *et al.,* 2009) is presented in Figure 12. The polymorphic information content (PIC) values ranged from 0.06 (b196) to 0.95 (b260) with an average of 0.70. Out of 84 markers, 69 markers were highly polymorphic with PIC values were more than 0.50 and 89 per cent of markers were PIC value more than 0.30. Gene diversity varied from 0.06 (b196) to 0.95 (b260), with an average of 0.72. Seventy one out of 84 SSRs showed high gene diversity (> 0.50) and only 13 SSR markers showed a gene diversity of <0.50.

Of the three foxtail millet EST-SSRs, P13 showed the highest number of alleles (13 alleles) with gene diversity of 0.83, heterozygosity of 0.11 and PIC value of 0.81. Three (UGEP3, UGEP81 and UGEP56) out of five finger millet SSRs had 20 alleles each. Gene diversity ranged from 0.22 (UGEP8) to 0.78 (UGEP3) and PIC values varied for 0.22 (UGEP8) to 0.77 (UGEP3). In case of four pearl millet SSR markers, ICMM02C24 detected the highest number of alleles (21 alleles) and ICMM02D07 showed the highest heterozygosity (0.56 in) in the foxtail millet core collection.

4.4.1.1 Heterozygosity

A varying range of heterozygosity was detected in the investigated materials which ranged from 0 (p33, b196, p92, b151, p56, p21, b258, p8, m2 and p98) to 0.56 (ICMMO2D07) (Table 33 and 34). Ten SSR markers detected no heterozygosity, 63 markers showed <0.10 heterozygosity and only 11 markers showed more than 0.10 heterozygosity. Of the 11 SSR markers, 3 each were in foxtail millet EST-SSRs [P5 (0.10) and P13 (0.11) and P2 (0.26)], finger millet SSRs [UGEP102 (0.10), UGEP3 (0.28) and UGEP56 (0.31)] and pearl millet SSRs [ICMMO2D15B (0.14), ICMMO2C24 (0.24) and ICMM02D07 (0.56)].

4.4.1.2 Unique, rare, common and most frequent alleles

Of the 1,356 alleles detected in the 155 accessions of core collection, 368 were rare, 906 common and 82 the most frequent alleles (Table 33 and 34, Figure 13). A total of 61 unique alleles were detected in core collection, which were present only in one accession and absent in other accessions (Table 35). The P5 and p92 had no rare alleles, whereas all the other markers

showed rare alleles which ranged from 1 (p61, b202, b196, b226, p34, p269, p56, p20, p21, b115, m2, ICMM02C05, P2 and UGEP102) to 12 (ICMM02C24 and UGEP81). Common alleles were detected for all the 84 SSR loci which varied from 1 (p91) to 24 (b109, b260 and b171). In contrast, only 63 SSR loci showed the most frequent alleles of which 19 SSRs had two and 44 SSRs had only one most frequent allele. Twenty one SSR loci did not show the most frequent alleles (Table 34).

4.4.2 Biological diversity in foxtail millet core collection

Biologically, the 155 accessions of foxtail millet core collection belonged to three races namely *indica* (102 accessions), *maxima* (24 accessions) and *moharia* (29 accessions). The 84 SSR markers detected a total of 997 (73.53%) alleles in *indica*, 784 (57.82%) in *maxima* and 844 (62.24%) in *moharia* (Table 33 and 36). Within the race *indica*, the number of alleles ranged from 2 (p33, b196, p91, p98, p56 and ICMM02C05) to 25 (b187) with a mean of 11.87. In the race *maxima*, the number of alleles per locus ranged from 2 (b196) to 19 (b109) with an average of 9.33 where in race *moharia*, the number of alleles ranged from 2 (b110, p91, p56 and m2) to 20 (b174 and b247) with an average of 10.05.

The PIC values ranged from 0.02 (p33, b196, p91and ICMM02C05) to 0.93 (b260 and b187) in *indica*, 0.08 (b196) to 0.91 (b109) in *maxima* and 0.12 (p56) to 0.94 (b174) in *moharia* with an average of 0.63 in *indica* and 0.72 in *maxima* and *moharia*. For the race *indica*, gene diversity averaged 0.65, ranging for the single markers from 0.02 (p33, b196, p91and ICMM02C05) to 0.93 (b260 and b187) whereas the accessions from the race *maxima* varied from 0.08 (b196) to 0.92 (b185, b105, b109 and b236) with an average of 0.74. In the race *moharia*, the gene diversity ranged from 0.13 (p56) to 0.94 (b171 and b174) with an average 0.74. The race *maxima* and *moharia* had the maximum mean gene diversity (0.74) and PIC (0.72) than *indica*.

4.4.2.1 Heterozygosity

The heterozygosity varied from 0 to 0.56 in the race *indica* and 12 SSR loci not detected heterozygosity. Eleven SSR loci detected >0.10 heterozygosity of which three were pearl millet markers [ICMMA02D07 (0.56), ICMM02C24 (0.24) and ICMM02D15B (0.16)], two each in finger millet SSRs [UGEP3 (0.26) and UGEP56 (0.33)] and foxtail millet EST-SSRs [P13 (0.13) and P2 (0.22)].

The heterozygosity varied from 0 to 0.39 with an average of 0.08 in the race *maxima* and 34 out of 84 SSR loci did not detected heterozygosity. Sixteen SSR loci had >0.10 per cent heterozygosity, of which three each in finger millet [UGEP56 (0.27), UGEP102 (0.25) and UGEP3 (0.39)] and pearl millet SSRs [ICMM02D15B and ICMM02C24 (0.17) and ICCM02D07 (0.38)].

The heterozygosity ranged from 0 to 0.73 with an average of 0.06 in the race *maxima*. Out of 84 SSR loci, 40 detected no heterozygosity in *moharia* and 14 had >0.10 heterozygosity. The maximum heterozygosity was observed in pear millet SSR markers, ICMM02D07 (0.73) and ICMM02C24 (0.31), finger millet SSR markers, UGEP81 (0.11), UGEP3 (0.26), UGEP56 (0.25) and foxtail millet EST-SSRs, P2 (0.34) and P5 (0.15) (Table 33 and 36).

4.4.2.2 Unique, rare, common and most frequent alleles

Of the 997 alleles detected in accessions 102 accessions of *indica*, 100 were rare, 803 common and 94 most frequent alleles (Table 33 and Figure 13). Out of 784 alleles in *maxima* (24 accessions), 688 were common and 96 most frequent alleles. In case of *moharia* (29 accessions), 760 common and 84 most frequent alleles were detected. Rare alleles were not detected in accessions in *maxima* and *moharia* and presented only in the race *indica*. A total of 44 unique alleles were detected in *indica*, 77 in *maxima* and 47 in *moharia*. List of unique alleles found in each races with accession is presented in Table 37, 38 and 39.

4.4.2.3. Genetic relationship among races

The pairwise comparison on the basis of the values of *Fst* could be interpreted as standardized population distance between two populations. The overall pairwise *Fst* in this study among the three races were 0.045. The race *maxima* showed the smallest *Fst* with *moharia* (0.032), whereas *indica* showed greatest *Fst* with *maxima* (0.053) and *moharia* (0.050). The genetic distance data agreed with the *Fst* estimates. The race *indica* showed the maximum genetic distance with *maxima* (0.273) and *moharia* (0.254) whereas the minimum genetic distance was observed between *maxima* and *moharia* (0.201).

Table 40. Pairwise estimates of Nei's genetic distance (GD) and *Fst* Values based on 84 SSR loci among three races

Populations		Nei GD	*Fst*
indica	*maxima*	0.273	0.053
indica	*moharia*	0.254	0.050
maxima	*moharia*	0.201	0.032
	Average	0.243	0.045

4.4.3 Unweighted neighbor-joining tree

The neighbor-joining tree based on simple matching dissimilarity matrix between 155 accessions of the foxtail millet core collection along with four controls using DARwin 5.0.156 programme highlighted broadly four clusters named as CI, CII, CIII and CIV (Table 41 and 42) (Figure 14).

The CI contained 87 of which 80 accessions were from the race *indica*, which was predominant in this cluster. Four *maxima* and three *moharia* were the other accessions present in this cluster. The CII consisted of 35 accessions, of these 35 accessions, *indica* dominated with accessions 22 accessions. The CIII represented by *moharia* dominated with 17 accessions out of 19 accessions present in this cluster. The ISe 1067and ISe 1338 were the other two accessions present in this cluster. The cluster CIV was represented by the race *maxima* dominated with 11 accessions out of 14 accessions. The results from the neighbor-joining phylogenetic tree corresponded well with the classification based on three biological races of foxtail millet. The clusters CI and CII were represented by accessions from *indica*, CIII and CIV dominated with accessions from *moharia* and *maxima*, respectively.

4.4.3.1 Most diverse accessions

SSR-derived data were subjected to calculate the genetic dissimilarity. This dissimilarity matrix was used to determine the level of relatedness among the accessions present in the core collection. Pair-wise estimates of dissimilarity values ranged from 0.098 to 0.956 (Table 43). Frequency distribution of dissimilarity between pair of accessions is presented in Figure 15. The

minimum dissimilarity was observed between ISe 813 and ISe 375 (0.098), and the maximum dissimilarity was observed between ISe 1320 and ISe 1162 (0.956).

Based on the dissimilarity values, five pairs of less diverse (ISe 813-ISe 375, ISe 969-ISe 931, ISe 1338-ISe 1118, ISe 909-ISe 480 and ISe 931-ISe 840) and ten pairs of most diverse accessions (ISe 1320-ISe 1162, ISe 338-ISe 1320, ISe 1773-ISe 1320, ISe 179-ISe 1320, ISe 907-ISe 1320, ISe 1808-ISe 1320, ISe 1808-ISe 1547, ISe 195-ISe 1320, ISe 946- ISe 1547 and ISe 1320-ISe 1137) were identified in foxtail millet core collection.

4.4.3.2 Allelic richness and genetic diversity

The 84 SSR markers detected a total of 845 alleles in CI, 853 in CII, 633 in CIII and 521 in CIV (Table 33 and 43). The number of alleles ranged from 1 to 24 in CI, 1 to 21 in CII, 2 to 16 in CIII and 1 to 13 in CIV with an average of 10.06, 10.15, 7.54 and 6.2 in CI to CIV, respectively. The average PIC was 0.60 in CI, 0.69 in CII, 0.68 in CIII and 0.66 in CIV. Gene diversity was slightly maximum in CII (0.71) compared to CI (0.62), CIII (0.70) and CIV (0.69). Heterozygosity was very less in all the four clusters. Three SSR markers in CI, two in CIV and one in CII were monomorphic to the respective cluster out of 84 SSR loci.

A total of 62, 53, 31 and 33 unique alleles were detected in CI, CII, CIII and CIV respectively, which was present in one accession and absent in others. The allelic composition revealed the predominance of common allele (688 in CI, 757 in CII, 531 in CIII and 390 in CIV) when compared to most frequent alleles (95, 96, 102 and 131 in CI to CIV, respectively). The rare alleles were present only in CI (62) and absent in other clusters.

4.4.4 Principal Coordinates Analysis (PCoA)

The Principal Coordinates Analysis based on Nei (1973) genetic distance was performed. The first three PCos explained 66.2 per cent of variation of which PCo1 explained 34.7 per variation and PCo2 explained 16.6 per cent of the SSR variation among the 155 accessions of foxtail millet core collection (Figure 16 and Table 44). Plotting the first two PCos and colour coding genotypes according to three biological races shows clear separation of the race *indica* (Red). The race *maxima* (Green) and *moharia* (Blue) were not clearly separated.

4.4.5 Analysis of molecular variance (AMOVA)

The distribution of molecular variance among and within the three basic races and four clusters identified by neighbor joining tree were estimated by analysis of molecular variance

(Table 45). The AMOVA revealed that seven per cent of the total genetic variance was explained by among the races while 93 per cent was among the individuals within the races. The same trend was observed when the AMOVA estimated based on four clusters identified by neighbor joining method (10 % among the clusters and 90% within the clusters).

Table 45. Analysis of molecular variance (AMOVA) based on three races and four clusters using 84 SSR markers

Source	df	SS	MS	Estimated. Variance	% of total variance
Based on races					
Among populations	2	852.67	426.34	8.22	7
Within population	152	17520.65	115.27	115.27	93
Total	154	18373.32		123.49	100
Based on four clusters					
Among Populations	3	1536.19	512.06	12.69	10
Within Population	151	16833.85	111.48	111.48	90
Total	154	18370.04		124.18	100

4.4.6 Correlations

The Pearson correlation coefficients among number of repeat unit, number of alleles per locus, gene diversity, heterozygosity and PIC using 84 SSR markers were estimated (Table 46). Number of repeat unit was highly significant and positively correlated with number of alleles per locus (0.536), gene diversity (0.514) and PIC (0.530), whereas non significant negatively correlated with heterozygosity (-0.232). Number of alleles per locus was highly significant and positively correlated with gene diversity (0.767) and PIC (0.79), and gene diversity was highly significant and positively correlated with PIC (0.998).

Table 46. Analysis of Pearson correlations among number of repeat unit, number of alleles per locus, gene diversity, heterozygosity and polymorphic information content

	No. of repeat Unit	No. of Allele	Gene diversity	Heterozygosity
No. of allele per locus	0.54**[1]			
Gene diversity	0.51**	0.77**		
Heterozygosity	-0.23	0.09	0.17	
PIC	0.53**	0.79**	0.99**	0.17

1= * and ** indicate significance at P<0.05 and <0.01 level, respectively

(Cluster I and Cluster II). Most of the accessions from the race *maxima* (Cluster III) and *moharia* (Cluster IV) grouped separately. The genetic relationship between the races was studied

based on Nei's genetic distance and $F_{st.}$ The race *indica* showed greater genetic distance with *maxima* and *moharia*, whereas less genetic distance was observed between *maxima* and *moharia*.

On the basis of PCA of 13 quantitative traits, the hierarchical clustering (Ward, 1963) analysis was performed using first three PCs of individual environment separately and for pooled. Accessions from the race *indica* were grouped into two sub-clusters *BI* and *BII*, under cluster *B*. Most of the accessions from *moharia* grouped together in cluster *A*. Accessions from *maxima* mixed with *moharia* in cluster *A* and *indica* in sub-cluster *BI*. The clustering pattern based on phenotypic data were also corresponded well with the races as like unweighted neighbor joining clusters based on 84 SSR markers.

The Mantel test (Mantel, 1967) was employed to calculate matrix correlation coefficients and to simulate a probability distribution for the comparison based on 9999 permutation for pair of matrices to better understand the relationships between phenotypic and molecular dissimilarity. Significant correlation coefficient (r=0.329) between the matrix was found. Scatter plot based on phenotypic and molecular marker dissimilarity between pair of accessions is given in Figure 17.

4.6. POPULATION STRUCTURE

Analysis of population structure using 72 SSR markers located on nine linkage group of foxtail millet provided evidence for the presence of significant population structure in the foxtail millet core collection. The *k* value was determined by *LnP(D)* in STRUCTURE output and an *ad hoc* statistic Δk based on the rate of change in *LnP(D)* between successive *k*. The final subpopulations were determined based on rate of change in *LnP(D)* between successive *k,* stability of grouping pattern across five run and germplasm information about the material under study (Figure 18 and Table 47a). Based on this information, k=4 chosen as the optimal grouping. Out of five run for k=4, the run with the highest likelihood value was selected to assign the posterior membership coefficient (Q) to each accession. A graphical bar plot was than generated with the posterior membership coefficient and presented in Figure 19.

Table 47. Average logarithm of the probability of data likelihoods (LnP(D)) of foxtail millet core collection

k	Average *Ln P(D)*	k	Average *Ln P(D)*
2	-53345.6	7	-228128
3	-49735.8	8	-363560
4	-74706.5	9	-873013
5	-354871	10	-585385
6	-193767		

Thus, the four subpopulations as inferred from the STRUCTURE analysis denoted as SP1 (Red), SP2 (Green), SP3 (Blue) and SP4 (Yellow), respectively and SP refers to subpopulation. Overall proportions of membership of the sample in each of the four subpopulations were 0.364, 0.045, 0.058 and 0.533, respectively and the maximum proportion of the accessions was found in SP4 followed by SP1 when compared to SP2 and SP3. Red colour represents the SP1 and yellow represent the SP4, are the major subpopulations along with two small subpopulations named as SP2 (green) and SP3 (blue). Subpopulation SP1 contained 59 accessions of which *moharia* dominated with 27 accessions followed by *maxima* (18 accessions) and *indica* (14 accessions) (Table 48). The SP2 consisted of five *maxima* (out of five, two are control ISe 375 and ISe 376) out of 6 accessions in this subpopulation. The remaining accessions from the race *maxima* distributed both in SP1 (18 accessions) and SP2 (5 accessions). The SP3 and SP4 were represented by the race *indica*. The SP3 consisted of seven accessions (all seven accessions from *indica*). The SP4 was the major subpopulation contained with race *indica*. Out of 87 accessions present in the SP4, 81 were from the race *indica*. The remaining 4 were from the race *maxima* and 2 *moharia*.

4.6.1 Genetic diversity of subpopulations

The 84 SSR markers detected a total of 1,150 alleles in SP1, 213 in SP2, 226 in SP3 and 840 in SP4 (Table 49). The number of alleles ranged from 3 to 30 with a mean of 13.69 in SP1. The number of alleles for the single marker in SP2 varied from 1 to 4 with an average of 2.54 alleles per locus whereas in SP3, the number of alleles ranged from 1 to 8 with an average of 2.69. In the case of SP4, the average number allele per locus was 10 which varied from 1 to 23 alleles. The PIC values ranged from 0.10 to 0.95 in SP1, 0 to 0.70 in SP2, 0 to 0.82 in SP3 and 0 to 0.93 in SP4 with an average of 0.75, 0.43, 0.37 and 0.6 in SP1 to SP4, respectively. Maximum mean PIC value was detected in SP1 and SP4 when compared to SP2 and SP3.

A total of eight SSR loci in SP2, 13 in SP3 and two in SP4 were monomorphic to the respective subpopulation. The average number of alleles per locus, gene diversity and PIC were higher in SP1 and SP4 compared to SP2 and SP3.

4.6.2 Genetic relationship among the population

Pairwise comparison on the basis of the values of F_{st} could be interpreted as standardized population distance between two populations. The pairwise F_{st} value in this study ranged from 0.054 between SP1 and SP4 to 0.282 between SP2 and SP3 with an average pairwise F_{st} of 0.143 (Table 50). The pairwise F_{st} was the highest between SP2 and SP3 (0.282) followed by between SP2 and SP4 (0.178). The genetic distance data agreed with the F_{st} estimate with the mean genetic distance of 0.532. The SP1 showed the lowest genetic distance with SP4 (0.249) and SP3 showed the lowest genetic distance with SP4 (0.249) whereas SP2 showed the greatest genetic distance with SP3 (0.977) followed by SP2 with SP4 (0.700) (Table 46).

Table 50. Pairwise estimates of Nei's genetic distance and *Fst* Values based on 84 SSR loci among the four subpopulations

Between subpopulation		*Fst*	Nei GD
SP1	SP2	0.128	0.523
SP1	SP3	0.130	0.494
SP2	SP3	0.282	0.977
SP1	SP4	0.054	0.249
SP2	SP4	0.178	0.700
SP3	SP4	0.087	0.249
	Mean	0.143	0.532

4.6.3 Analysis of molecular genetic variance (AMOVA)

The distribution of molecular genetic variation among and within the four subpopulations was estimated by analysis of molecular variance, AMOVA (Table 51). The AMOVA revealed that nine per cent of the total variance was among the subpopulations, while 91 per cent was among individuals within the subpopulations. The same trend was observed when the AMOVA estimated based on three basic races of foxtail millet (7% among populations and 93% within population) and unweighted neighbor joining phylogenetic tree (10% variation among population and 90% within population).

Table 51. Analysis of molecular variance (AMOVA) based on four subpopulations (SP1 to SP4) identified by software STRUCTURE

Source	df	SS	MS	Estimated Variance	% of vaiance
Among populations	3	1328.76	442.92	11.58	9
Within populations	151	17041.28	112.85	112.85	91
Total	154	18370.04		124.43	100

4.6.4 Assessment of population structure

In this study, principal coordinate analysis and the unweighted neighbor-joining phylogenetic analysis were conducted to further assess the population subdivisions identified using STRUCTURE.

The first three PCos explained 66.2 per cent of variation of which PCo1 explained 34.7 per variation and PCo2 explained 16.6 per cent of the SSR variation among the 155 accessions of foxtail millet core collection along with four controls (Table 44 and Figure 20). Plotting the first two PCos and colour coding genotypes according to three biological races shows clear separation of the race *indica*, most of which were present in SP4 (Figure 16). The race *maxima* and *moharia* were not clearly separated as in SP1 which was identified by STRUCTURE analysis. Plotting the first two PCos and color coding genotypes according to the four subpopulations identified using STRUCTURE shows the clear separation of four subpopulations (SP1 to SP4) with little deviations (Figure 20).

The neighbor-joining tree of 155 core accessions with four controls was constructed based on the simple matching dissimilarity matrix of 84 SSR markers genotyped across the foxtail millet core collection along with four controls. Neighbor-joining analysis grouped 159 accessions (155 core accessions and four controls) into four clusters named as C1 to CIV, respectively. The SP1 was mixed subpopulation which contained more accessions from *moharia* (27) along with *maxima* (18) and *indica* (14). Twenty six out of 37 accessions present in CII, 18 out of 19 in CIII and 12 out of 14 in CIV were from SP1. The CIII and CIV were dominated with *moharia* and *maxima* respectively. Accessions from CIII and CIV were present in SP1 which was the mixed population of *maxima* and *moharia*. Eighty one out of 87 accessions present in SP4 (represent race *indica*) and all the seven accessions present in SP3 (represent *indica*) were grouped together into CI which was dominated with race *indica* (Figure 14). Color coding of genotypes based on subpopulations identified by STRUCTURE shown in Figure 21. The SP1

(Red) and SP2 (Yellow) were the major subpopulations along with two small subpopulations named as SP2 (green) and SP3 (blue). Based on PCoA and neighbor joining tree, the subpopulation based STRUCTURE analysis fairly consistent biological races in the foxtail millet core collection at *k=4*.

4.7. ASSOCIATION ANALYSIS

A mixed liner model implemented in TASSEL 2.1 suggested by Yu *et al.* (2006) was used to conduct the association analysis and to identify the SSR markers associated with the quantitative traits in a structured foxtail millet core collection based on population structure (Q matrix) and relatedness relationship (K matrix). Each trait was represented by its mean of three replications. Association analysis was carried based on BLUPs estimated for data of three environments and pooled. The marker trait association (MTAs) detected in pooled BLUPs were considered as final and compared with the MTAs detected from individual environments separately. Details of MTAs detected in individual environments as well as pooled are presented in Table 52.

A total of 108 MTAs were found in pooled BLUPs of three environments at $P \leq 0.05$ (Table 53), whereas it varied from 62 MTAs in E2, 106 in E3 and 130 in E3 (Table 52) However, only and 37 MTAs in pooled BLUPs were found to be highly significant at $P \leq 0.01$ and it varied from 23 MTAs in E2, 49 MTAs in E1 and 61 MTAs in E3 (Table 54a to d). The number of markers associated ($P \leq 0.05$) with each trait is described below.

4.6.1 Days to 50 per cent flowering

Eight markers were associated with days to 50 per cent flowering in pooled BLUPs and distributed on chromosome 2 (b115), 3 (b225), 4 (p34), 5 (p17x), 7 (b200 and b202), 8 (b258) and 9 (b251), no MTAs was detected on chromosome 1 and chromosome 6 (Table 53). Number of MTAs was 5 in E1, 6 in E2 and 8 in E3. Of the eight MTAs detected in pooled, two were also found in atleast two out of three environments and three were present in all the three environments (Table 52).

4.6.2 Plant height

Plant height was associated with eleven markers in pooled data. Of these 11 markers, three were pearl millet SSRs (ICMM02C05, ICMM02C24 and ICMM02D15B), and the remaining 8 MTAs were distributed on chromosome 1 (p8), 3 (p98), 6 (b234), 7 (b123 and

b202), 9 (b251 and m2) and 5 (b111) (Table 53). Eleven markers in E1 and E2 and 12 in E3 were found to be significantly associated with plant height. Out of 11 MTAs detected in pooled, four were detected in all three environments and 3 MTAs present in two out of three environments (Table 52).

4.6.3 Basal tillers

Eight markers were associated significantly with basal tiller number and distributed on the chromosome 1 (p8 and p87), 2 (p56), 3 (p98), 4 (p34) and 7 (b200) and one each in foxtail millet EST-SSR (P2) and finger millet SSR (UGEP81) (Table 53). Nine significant MTAs in E1, 6 in E2 and 4 in E3 were detected. Three out of eight marker trait associations detected in pooled also found in atleast two out of three (Table 52).

4.6.4 Flag leaf blade length

Twelve markers were identified to be associated with flag leaf blade length and distributed on chromosome 1 (p8), 3 (b186 and p98), 4 (p34), 5 (b111 and p17x), 6 (b234), 7 (b200 and b202) and 9 (m2). Two pearl millet SSR markers (ICMM02C05 and ICMM02D15B) were also found to be associated with flag leaf blade length (Table 53). Fourteen MTAs were identified in E1, 5 MTAs in E2 and 8 MTAs in E3. Two out of 12 MTAs detected in pooled mean of three environments for this trait also found in all the three environments and 5 MTAs were present in two out of three environments (Table 52).

4.6.5 Flag leaf blade width

A total of six markers significantly associated with flag leaf blade width in pooled BLUPs of three environments. Of these six markers, two markers on chromosome 1 (b126 and p8) and one each in chromosome 3 (p98) and 4 (p34). One each in foxtail millet EST-SSR (P2) and pearl millet SSR (ICMM02C05) markers also found to be associated with FLBW (Table 53). Eight MTAs were detected in E1, 5 MTAs in E2 and 6 MTAs in E3. Out of six MTAs detected in pooled, three were found in two out of three environments and only one in all three environments (Table 52).

4.6.6 Flag leaf sheath length

In this study, a total of 10 markers were significantly associated with flag leaf sheath length in pooled BLUPs where as 12 in E1, 6 in E2 and 15 in E3. Ten markers were distributed as two each on chromosome 1 (p58 ad p8), 3 (b186 and p98) and 5 (b188 and p17x), and one

each on chromosome 2 (b151), 7 (b123) and 9 (m2) (Table 53). Five out of 10 MTAs detected in pooled were also found in two environments out of three and two MTAs were found in all three environments.

4.6.7 Peduncle length

Thirteen markers were identified as significantly associated with peduncle length in pooled BLUPs, of these four were distributed on chromosome 7 (b123, b200, b202 and p59), two each on chromosome 3 (b186 and p98), 9 (b166 and p91) and 1 (p8 and p87) and one each on chromosome 5 (b196) and 6 (b234) (Table 53). Of the 13 MTAs, seven were also found in two out of three environments (Table 52).

4.6.8 Panicle exertion

Panicle exertion was associated with nine markers in pooled BLUPs and distributed on chromosome 3 (b186 and b226), 5 (b196), 6 (b234), 7 (b123, b142 and b202) and 9 (b166 and p91) (Table 53). Eighteen MTAs in E1, 1 MTA in E2 and 8 MTAs in E3 were identified as significant respective environment. Six out of nine MTAs detected in pooled also found in two out of three environments evaluated.

4.6.9 Inflorescence length

A total of 8 MTAs for inflorescence length were detected in pooled and distributed on chromosome 3 (b225 and p98) and 7 (b123 and b200) and one each on chromosome 1 (b153), 4 (p34) and 9 (m2). The ICMM02D15B was also associated with this trait in pooled as well in E1 and E2. Ten MTAs in E1, 4in E2 and 12 in E3 were identified as significant MTAs in respective environment.

4.6.10 Inflorescence width

Only one marker (p98) was significantly associated with inflorescence width in pooled BLUPs which was located on chromosome 3. The marker p98 was associated with inflorescence width in pooled also found to be associated in E1 and E2. A total of 4 MTAs were detected in E1, 2 MTAs in E2 and 3 MTAs in E3.

4.6.11 Weight of five panicles

Weight of five panicles was associated with five markers in pooled BLUPs and four of these were distributed on chromosome 1 (b153 and p58), 3 (p98) and 7 (b123). The remaining one was pearl millet SSR markers (ICMM02C05). A total of six markers in each environment

were significantly associated with this weigh of five panicles. One out of 5 MTAs found in pooled BLUPs was also found in all three environments and 3 MTAs found in two out of three environments.

4.6.12 Single plant yield

A total of 12 markers were significantly associated with single plant yield in pooled BLUPs and distributed on chromosome 2 (p56), 3 ((p61 and p98), 4 (p2), 6 (b159, b190 and b234), 7 (b142 and b200) and 9 (b41). The P5 was the EST-SSR which was found to be associated with single plant yield. A total of 10 MTAs in E1, 7 MTAs in E2 and 8 MTAs in E3 were significantly associated with trait. Seven out of 12 MTAs present in pooled were also found in two out of three environments.

4.6.13 Grain yield per plot (Kg ha^{-1})

Six markers were associated significantly with grain yield per plot (Kg ha^{-1}) in pooled BLUPs and distributed as two each on chromosome 3 (p61 and p98) and 7 (b142 and b200) and one on chromosome 6 (b234). One EST-SSR was found to be associated with this trait. Six markers in E1, 8 in E2 and 5 in E3 were significantly associated with grain yield. Out of six MATs in pooled BLUPs, one MTA was found in all three environments and 2 MTAs in two out of three environments.

4.7 LINKAGE DISEQUILIBRIUM (LD)

The r^2, the square of the correlation coefficient between the two loci was used to measure LD. In a total of 155 accessions of foxtail millet core collection and 2556 pairwise comparisons (352 linked and 2204 unlinked marker pairs) of 72 mapped SSR loci, 67, 53 and 39 per cent of SSR markers pairs were significant LD at $P \leq 0.05$, $P \leq 0.01$ and $P \leq 0.001$, respectively. At the whole population level, the r^2 ranged from 0.0008 to 0.19 and 1430 pairs of loci were significant at $P \leq 0.01$. Among the inter-chromosomal pairs, r^2 ranged from 0.01 to 0.17. Scatter plot of the LD values based on the r^2 values of 155 accessions based on 72 SSR markers are shown in Figure 22, where LD values for inter-chromosomal markers are compiled in a single file at 350 cM. At Intra-chromosome level, LD was very common for distance 40 cM and likely to extend upto 170 cM. The triangle plot for pairwise LD between 72 mapped SSR marker loci in a hypothetical genome fragment, where pairwise LD values of polymorphic sites were plotted on both X and Y axis; pairwise calculations of LD (r^2) are displayed above the diagonal and below the diagonal displayed the corresponding *P*-values from rapid 1000 shuffle permutation test

(Figure 23). Each cell represents the relationship between two markers with the colour codes indicating the significance of LD. The r^2 for remaining 12 SSR markers which were not mapped on foxtail millet genome (3 foxtail millet EST-SSRs, four pearl millet SSRs and five finger millet SSRs) were also calculated. Of the 66 pairwise comparisons of 12 SSRs, 5, 1 and 4 were significant at $P<0.01$, $P<0.001$ and $P<0.0001$, respectively. Triangle pot of LD between 12 SSRs markers are presented in Figure 24. The r^2 ranged from 0.002 to 0.080.

Table 13. Frequency distribution of 12 qualitative traits in the three races and in entire core collection of foxtail millet

Characters	Classes	Indica		Maxima		Moharia		Entire core collection	
No. of accessions		102		24		29		155	
Plant Pigmentation	Not pigmented	89	(87.3)[1]	16	(66.7)	21	(72.4)	126	(81.3)
	Pigmented	11	(10.8)	7	(29.2)	8	(27.6)	26	(16.8)
	Deep purple	2	(2.0)	1	(4.3)	0	(0.0)	3	(1.9)
Leaf Colour	Green	85	(83.3)	21	(87.5)	25	(86.2)	131	(84.5)
	Pigmented	5	(4.9)	3	(12.5)	2	(6.9)	10	(6.5)
	Yellow	12	(11.8)	0	(0.0)	2	(6.9)	14	(9.0)
Growth habit	Erect	100	(98.0)	21	(87.5)	27	(93.1)	148	(95.5)
	Erect Geniculate	2	(2.0)	2	(8.3)	2	(6.9)	6	(3.9)
	Decumbent	0	(0.0)	0	(0.0)	0	(0.0)	0	(0.0)
	Prostrate	0	(0.0)	1	(4.2)	0	(0.0)	1	(0.7)
Culm branching	High	41	(40.2)	3	(12.5)	21	(72.4)	65	(41.9)
	Medium	45	(44.1)	3	(12.5)	6	(20.7)	54	(34.8)
	Low	16	(15.7)	18	(75.0)	2	(6.9)	36	(23.2)
Bristle length	Long	51	(50.0)	2	(8.3)	9	(31.0)	62	(40.0)
	Medium	33	(32.4)	3	(12.5)	15	(51.7)	51	(32.9)
	short	18	(17.7)	19	(79.2)	5	(17.2)	42	(27.1)
Panicle lobing	Non Lobed	4	(3.9)	3	(12.5)	20	(69.0)	27	(17.4)
	Medium Lobed	38	(37.3)	1	(4.2)	6	(20.7)	45	(29.0)
	Dense Lobed	60	(58.8)	20	(83.3)	3	(10.3)	83	(53.6)
Inflorescence compactness	Loose	4	(3.9)	1	(4.2)	1	(3.5)	6	(3.9)
	Medium	27	(26.5)	0	(0.0)	3	(10.3)	30	(19.4)
	Compact	71	(69.6)	23	(95.8)	25	(86.2)	119	(76.8)
Lobe compactness	Loose	1	(1.0)	0	(0.0)	0	(0.0)	1	(0.7)
	Medium	8	(7.8)	1	(4.2)	4	(13.8)	13	(8.4)
	Compact	93	(91.2)	23	(95.8)	25	(86.2)	141	(91.0)
Grain colour	Yellow	93	(91.2)	22	(91.7)	27	(93.1)	142	(91.6)
	Red	6	(5.9)	1	(4.2)	2	(6.9)	9	(5.8)
	Light Grey	0	(0.0)	0	(0.0)	0	(0.0)	0	(0.0)
	Dark Grey	0	(0.0)	0	(0.0)	0	(0.0)	0	(0.0)
	Black	1	(1.0)	1	(4.2)	0	(0.0)	2	(1.3)
	Brown	0	(0.0)	0	(0.0)	0	(0.0)	0	(0.0)
	Black and White	2	(2.0)	0	(0.0)	0	(0.0)	2	(1.3)
Lodging	Non Lodging	51	(50.0)	15	(62.5)	11	(37.9)	77	(49.7)
	Slightly Lodging	40	(39.2)	7	(29.2)	10	(34.5)	57	(36.8)
	Medium Lodging	11	(10.8)	2	(8.3)	7	(24.1)	20	(12.9)
	Mostly Lodging	0	(0.0)	0	(0.0)	1	(3.5)	1	(0.7)
	Completely Lodging	0	(0.0)	0	(0.0)	0	(0.0)	0	(0.0)
Leaf senescence	Leaves completely green at maturity	11	(10.8)	10	(41.7)	3	(10.3)	24	(15.5)
	Leaves almost green at maturity	59	(57.8)	7	(29.2)	7	(24.1)	73	(47.1)
	Leaves moderately green at maturity	29	(28.4)	4	(16.7)	10	(34.5)	43	(27.7)
	Leaves almost dry at maturity	3	(2.9)	3	(12.5)	8	(27.6)	14	(9.0)
	Leaves completely dry at maturity	0	(0.0)	0	(0.0)	1	(3.5)	1	(0.7)
Overall plant aspect	Very Good	8	(7.8)	3	(12.5)	1	(3.5)	12	(7.7)
	Good	55	(53.9)	10	(41.7)	2	(6.9)	67	(43.2)
	Average	39	(38.2)	4	(16.7)	10	(34.5)	53	(34.2)
	Poor	0	(0.0)	7	(29.2)	15	(51.7)	22	(14.2)
	Very poor	0	(0.0)	0	(0.0)	1	(3.5)	1	(0.7)

1=Numbers in parenthesis indicate percentage of accessions in each classes

Table 14. Shannon-Weaver diversity indices (H′) of 12 qualitative traits for three races and in entire core collection of foxtail millet

Qualitative traits	Indica	Maxima	Moharia	Entire core collection
Plant pigmentation	0.19	0.35	0.26	0.24
Leaf colour	0.23	0.16	0.22	0.23
Growth habits	0.04	0.19	0.11	0.09
Culm branching	0.45	0.37	0.36	0.47
Bristle length	0.45	0.33	0.44	0.47
Panicle lobing	0.35	0.26	0.36	0.43
Inflorescence compactness	0.32	0.12	0.21	0.29
Lobe compactness	0.15	0.15	0.18	0.16
Grain colour	0.18	0.07	0.11	0.15
Lodging	0.42	0.38	0.52	0.44
Leaf senescence	0.46	0.58	0.60	0.55
Overall plant aspects	0.42	0.59	0.50	0.55
Mean	0.31±0.041	0.30±0.049	0.32±0.048	0.34±0.047

Table 15. Variance components due to genotypes (σ^2g) and genotype x environment (σ^2ge) and standard errors (SE) in the foxtail millet core collection, Coimbatore (E1), Madurai (E2) during Rabi/summer 2009/10, ICRISAT (E3) during rainy season 2010 and pooled data

Environment	E1_CBE		E2_MDU		E3_ICRISAT		Pooled			
Components of variance	σ^2g	SE	σ^2g	SE	σ^2g	SE	σ^2g	SE	σ^2ge	SE
Days to 50% flowering	131.7***	14.89	141.0***	15.91	112.3***	12.81	115.6***	13.51	12.4***	1.05
Plant height (cm)	799.5***	92.25	508.6***	57.87	467.0***	55.14	492.6***	59.74	86.1***	9.10
Basal tillers	2.6***	0.30	1.5***	0.18	1.2***	0.14	1.1***	0.15	0.7***	0.06
Flag leaf blade length (mm)	5575.8***	636.80	3820.7***	434.50	4285.2***	507.50	3678.9***	450.90	872.0***	77.10
Flag leaf blade width (mm)	22.7***	2.65	8.8***	1.06	14.5***	1.83	11.2***	1.45	4.3***	0.40
Flag leaf sheath length (mm)	804.1***	101.90	551.1***	63.90	549.0***	67.30	449.1***	59.80	180.9***	19.20
Peduncle length (mm)	2268.8***	269.80	1936.1***	227.50	1378.5***	174.10	999.1***	151.60	842.1***	78.60
Panicle exertion (mm)	1228.0***	143.60	1411.2***	164.40	1080.7***	134.84	732.2***	105.00	505.1***	45.80
Inflorescence length (mm)	3462.4***	398.10	1816.6***	206.08	1984.8***	237.65	1898.0***	236.30	514.0***	47.20
Inflorescence width (mm)	30.0***	3.42	15.2***	1.81	16.8***	2.00	16.2***	2.020	4.5***	0.43
Weight of five panicles (g)	257.2***	29.29	216.4***	24.57	113.9***	13.51	148.5***	18.65	47.1***	4.02
Single plant yield (g)	172.6***	19.97	135.5***	15.56	20.9***	2.50	66.2***	9.27	43.0***	3.69
Grain yield per plot (Kg ha^{-1})	689610.0***	79283.00	489902.0***	56307.00	108756.0***	12818.00	251636.0***	35683.00	176854.0***	14909.00

*** Significant at P<0.001%

Table 16. Phenotypic and genotypic coefficients of variations (PCV and GCV), heritability (h^2_b, %) and genetic advance as per cent of mean in foxtail millet core collection evaluated at Coimbatore (E1), Madurai (E2) during Rabi/summer 2009/10 and at ICRISAT, Patancheru (E3) during rainy season 2010 and pooled

Traits	PCV (%)				GCV (%)				Heritability (h^2_b) (%)				Genetic advance as % of mean			
	E1	E2	E3	Pooled	E1	E2	E3	Pooled	E1	E2	E3	Pooled	E1	E2	E3	Pooled
Days to 50% flowering	21.31	22.53	19.95	20.56	21.26	22.50	19.94	20.18	99.56	99.71	99.95	96.33	43.70	46.28	41.09	40.79
Plant height (cm)	28.46	23.99	23.30	23.82	28.10	23.86	22.78	22.96	97.52	98.89	95.63	92.88	57.18	48.88	45.88	45.58
Basal tiller number	38.70	38.00	39.14	33.41	38.08	37.22	39.10	29.98	96.80	95.96	99.81	80.50	77.18	75.11	80.45	55.40
Flag leaf blade length (mm)	29.92	26.93	24.22	25.00	29.69	26.79	23.65	23.97	98.51	98.94	95.34	91.94	60.71	54.90	47.56	47.36
Flag leaf blade width (mm)	25.45	18.65	21.49	19.81	24.99	17.99	20.38	18.47	96.40	93.08	89.99	86.97	50.55	35.77	39.82	35.48
Flag leaf sheath length (mm)	22.58	18.11	18.08	17.28	21.31	17.84	17.40	15.92	89.02	97.05	92.57	84.91	41.41	36.20	34.48	30.22
Peduncle length (mm)	16.50	14.56	12.73	12.08	16.06	14.25	12.40	10.48	94.67	95.79	94.98	75.28	32.18	28.73	24.90	18.73
Panicle exertion (mm)	21.21	21.02	20.07	17.71	20.80	20.67	19.97	15.77	96.23	96.63	98.97	79.26	42.03	41.84	40.94	28.92
Inflorescence length (mm)	39.80	35.16	30.56	32.84	39.37	35.02	30.32	31.26	97.86	99.18	98.45	90.58	80.20	71.86	62.00	61.28
Inflorescence width (mm)	31.99	24.89	27.49	26.20	31.76	24.19	27.11	24.87	98.59	94.51	97.29	90.12	64.97	48.43	55.11	48.65
Weight of five panicles (g)	60.56	64.94	48.21	53.51	60.20	64.64	47.03	50.71	98.82	99.07	95.17	89.81	99.34	96.46	94.52	99.02
Single plant yield (g)	54.86	59.26	41.84	48.97	54.10	58.66	40.67	44.10	97.26	97.98	94.49	81.10	93.91	98.73	81.42	81.79
Grain yield per plot (Kg ha^{-1})	51.17	58.03	45.39	46.68	50.62	57.42	44.43	41.78	97.87	97.90	95.79	80.12	95.18	96.58	89.57	77.02

Table 17. Range of various quantitative traits in three races and in entire core collection of foxtail millet evaluated at Coimbatore (E1), Madurai (E2) during Rabi/summer 2009/10, ICRISAT (E3) during rainy season 2010 and pooled

Environment	E1				E2			
Traits/races	*indica*	*maxima*	*moharia*	Entire core collection	*indica*	*maxima*	*moharia*	Entire core collection
Days to 50% flowering	36.4-102.8 (66.4)[1]	31.1-76.9 (45.8)	35.6-65.0 (29.2)	31.1-102.8 (71.7)	37.4-102.9 (65.5)	31.1-79.3 (48.2)	35.4-53.7 (18.3)	31.1-102.9 (71.8)
Plant height (cm)	51.9-162.0 (110.1)	28.1-143.1 (115.0)	33.8-111.7 (77.9)	28.1-162.0 (133.9)	69.3-137.0 (67.7)	36.5-127.5 (91)	35.6-110.0 (74.4)	35.6-137.0 (101.4)
Basal tiller number	1.4-8.6 (7.5)	1.1-5.4 (4.3)	1.2-7.7 (6.5)	1.1-8.9 (7.8)	1.1-6.2 (5.1)	1.1-4.0 (2.9)	1.1-6.2 (5.1)	1.1-6.2 (5.1)
Flag leaf blade length mm)	134.0-440.1 (306.1)	66.1-342.6 (276.5)	64.4-285.8 (221.4)	64.4-440.1 (375.7)	123.8-436.8 (313.0)	73.7-280.8 (207.1)	69.1-262.3 (193.2)	69.1-436.8 (367.7)
Flag leaf blade width (mm)	11.9-31.5 (19.5)	7.8-30.6 (22.8)	6.8-24.8 (18.0)	6.8-31.5 (24.7)	11.1-27.9 (16.8)	14.2-22.9 (8.8)	9.5-17.5 (7.9)	9.5-27.9 (18.4)
Flag leaf sheath length (mm)	86.3-191.2 (104.9)	52.0-181.1 (129.1)	64.8-172.4 (107.6)	52.0-191.2 (139.20)	99.6-181.2 (81.6)	48.5-172.4 (123.9)	73.6-139.4 (65.8)	48.5-181.2 (132.7)
Peduncle length (mm)	204.2-393.5 (189.3)	178.6-423.2 (244.6)	160.3-347.8 (187.5)	160.3-423.2 (262.9)	203.9-416.0 (212.1)	196.9-0375.1 (178.2)	213.5-380.5 (167.0)	196.9-416.0 (219.1)
Panicle exertion (mm)	99.7-237.9 (138.2)	101.9-300.2 (198.3)	116.4-236.7 (120.3)	99.7-300.2 (200.5)	100.2-259.6 (159.4)	97.6-252.2 (154.6)	112.7-256.7 (144.0)	97.6-259.6 (162.0)
Inflorescence length (mm)	43.3-281.8 (238.5)	31.5-258.3 (226.8)	26.0-162.7 (136.7)	26.0-281.8 (255.8)	67.1-250.6 (183.5)	47.3-194.7 (147.4)	38.0-136.5 (98.5)	38.0-250.6 (212.6)
Inflorescence width (mm)	10.2-31.5 (21.4)	9.1-28.7 (19.6)	6.6-18.1 (11.5)	6.6-31.5 (24.9)	10.1-24.8 (14.7)	10.1-24.1 (14.0)	9.6-18.3 (8.8)	9.6-24.8 (15.2)
Weight of five panicles (g)	9.9-70.6 (60.8)	2.6-67.2 (64.6)	2.3-42.5 (40.2)	2.3-70.6 (68.4)	5.5-61.3 (55.8)	3.2-72.9 (69.7)	2.5-28.9 (26.4)	2.5-72.9 (70.3)
Single plant yield (g)	4.9-59.0 (54.1)	3.0-51.5 (48.5)	3.4-48.0 (44.6)	3.0-59.0 (56.0)	4.2-55.5 (51.3)	4.1-46.7 (42.6)	3.1-32.4 (29.4)	3.1-55.5 (52.4)
Grain yield per plot (Kg ha^{-1})	516.0-3290.0 (2774.0)	259.0-2837.0 (2578.0)	172.0-2623.0 (2451.0)	172.0-3290.0 (3118.0)	207.0-2597.0 (2390.0)	200.0-2662.0 (2462.0)	164.0-1792.0 (1628.0)	150.0-2662.0 (2512.0)

1=Numbers in parenthesis indicate difference between maximum and minimum

Table 17. Cont..

Environment	E3				POOLED			
Traits/races	*indica*	*maxima*	*moharia*	Entire core collection	*indica*	*maxima*	*moharia*	Entire core collection
Days to 50% flowering	41.7-103.6 (61.9)	33.3-61.3 (28.0)	32.7-56.0 (23.3)	32.7-103.6 (70.9)	38.5-103.1 (64.6)	31.8-89.9 (58.1)	34.7-61.9 (27.2)	31.8-103.1 (71.3)
Plant height (cm)	71.3-138.8 (67.5)	39.6-122.7 (83.1)	37.7-103.0 (65.3)	37.7-138.8 (101.1)	69.8-140.4 (70.6)	37.9-136.7 (98.8)	41.3-105.4 (64.2)	37.9-140.4 (102.5)
Basal tiller number	1.0-5.1 (4.1)	1.0-2.6 (1.6)	1.0-5.1 (4.1)	1.0-5.1 (4.1)	1.5-6.0 (4.5)	1.1-3.8 (2.8)	1.2-5.9 (4.7)	1.1-6.0 (4.9)
Flag leaf blade length mm)	176.0-468.0 (292.0)	126.0-360.6 (234.6)	119.0-310.4 (191.4)	119.0-468.0 (349.0)	177.2-425.3 (248.1)	86.6-360.4 (273.8)	95.5-275.9 (180.4)	86.6-425.3 (338.7)
Flag leaf blade width (mm)	12.0-26.2 (14.3)	13.4-27.9 (14.5)	9.0-2.3 (13.3)	9.0-27.9 (18.9)	13.6-26.8 (13.2)	11.5-27.2 (15.7)	9.5-21.2 (11.8)	9.5-27.2 (17.8)
Flag leaf sheath length (mm)	103.3-179.1 (75.8)	50.9-155.7 (104.8)	83.4-150.1 (66.7)	50.9-179.1 (128.2)	100.3-175.3 (75.0)	47.4-166.4 (119.0)	75.9-133.5 (57.6)	47.4-175.3 (127.9)
Peduncle length (mm)	235.2-409.8 (174.6)	189.3-409.2 (219.9)	209.8-409.8 (200.0)	189.3-409.8 (220.5)	226.0-365.1 (139.1)	186.8-403.9 (217.1)	217.6-361.1 (143.5)	186.8-403.9 (217.1)
Panicle exertion (mm)	86.7-235.3 (148.6)	123.7-284.2 (160.5)	120.8-275 (154.2)	86.7-284.2 (197.5)	109.7-227.9 (118.2)	107.4-279 (171.6)	127.1-247.8 (120.7)	107.4-279 (171.6)
Inflorescence length (mm)	115.8-286.6 (170.8)	57.1-202.8 (145.7)	33.0-185.1 (152.1)	33.0-286.6 (253.6)	91.1-257.1 (166.0)	46.3-212.1 (165.8)	41.1-144.5 (103.4)	41.1-257.1 (216.0)
Inflorescence width (mm)	10.4-26.9 (16.5)	10.0-23.1 (13.1)	7.0-16.3 (9.3)	7.0-26.9 (19.9)	11.0-26.0 (15)	10.6-25.4 (14.8)	8.1-16.8 (8.7)	8.1-25.9 (17.8)
Weight of five panicles (g)	9.8-46.9 (37.1)	4.2-44.2 (40.0)	3.5-28.1 (24.6)	3.5-46.9 (43.3)	9.7-54.5 (44.8)	3.8-58.4 (54.7)	2.7-32.8 (30.1)	2.7-58.4 (55.8)
Single plant yield (g)	3.5-22.6 (19.1)	3.0-15.0 (12.0)	2.3-18 15.7	2.3-22.6 (20.3)	7.8-43.1 (35.3)	4.1-38.0 (33.9)	3.3-37.0 (33.7)	3.3-43.1 (39.8)
Grain yield per plot (Kg ha^{-1})	168.0-1460.5 (1292.5)	14.0-803.4 (660.4)	166.7-1035.9 (869.2)	143.0-1460.5 (1317.5)	525.0-2240.0 (1715.0)	211.0-2013.0 (1802.0)	196.0-2084.0 (1888.0)	196.0-2240.0 (2044.0)

1=Numbers in parenthesis indicate difference between maximum and minimum

Table 18. Mean of different quantitative traits in foxtail millet core collection in three environments, Coimbatore (E1), Madurai (E2) during Rabi/summer 2009/10 and ICRISAT (E3) during rainy season 2010

Quantitative traits	Mean[1]			
	E1	E2	E3	Pooled
Days to 50% flowering	53.7±0.76a	52.5±0.64a	53.0±0.24a	53.1±0.51a
Plant height (cm)	100.3±4.45a	94.2±2.38a	94.7±4.52a	96.4±2.99a
Basal tiller number	4.2±0.29a	3.3±0.25b	2.8±0.05c	3.5±0.15b
Flag leaf blade length (mm)	250.1±9.11b	229.7±6.37c	275.8±14.13a	251.8±5.61b
Flag leaf blade width (mm)	19.0±0.91a	16.4±0.78c	18.6±1.21a	18.0±0.49b
Flag leaf sheath length (mm)	133.4±9.40a	131.8±4.03a	135.0±6.39a	133.4±4.33a
Peduncle length (mm)	297.9±11.00a	309.4±9.02 a	300.7±8.33 a	302.7±6.76a
Panicle exertion (mm)	169.4±6.80b	182.3±6.90a	165.7±3.33b	172.4±4.76b
Inflorescence length (mm)	149.5±8.61a	121.8±3.87b	14.0±5.56a	139.4±5.07a
Inflorescence width (mm)	16.9±0.65a	15.9±0.91b	14.8±0.68b	15.9±0.53b
Weight of five panicles (g)	25.6±1.74a	22.0±1.42a	22.2±2.35a	23.3±1.06a
Single plant yield (g)	23.9±2.18a	19.4±1.65b	11.2±1.07c	18.2±1.05b
Grain yield per plot (Kg ha^{-1})	1612.4±121.10a	1219.0±101.40b	741.9±67.63c	1181.8±58.70b

1= Mean of races and environments were tested following the Newman-Keuls test. Mean followed by the same letters are not significant at *P*=0.05 and mean followed by different letters are significant at *P*=0.05

Table 19a. Performance of three races for various quantitative traits in the foxtail millet core collection in three environments and pooled

Environment	Race	DF[1]	PLHT	BT	FLBL	FLBW	FLSL	PEDL	PEX	INFL	INFW	W5P	SPY	PY
E1[2]	*Indica*	57.2a[3]	114.0a	4.7a	281.9a	19.9a	143.9a	306.5a	166.6a	173.7a	18.2a	28.7a	28.1a	1896.3a
	maxima	49.5b	85.9b	2.5b	222.7b	21.4a	122.5b	305.1a	184.7a	133.4b	18.4a	29.9a	19.6b	1259.3b
	moharia	44.8c	64.1c	4.2a	160.2c	13.8b	105.4c	261.7b	166.4a	77.4c	11.3b	11.3b	12.8c	906.4c
E2	*indica*	56.0a	105.1a	3.6a	254.7a	16.9a	140.9a	319.3a	183.0a	136.9a	16.9a	25.0a	22.7a	1413.6a
	maxima	48.8b	84.5b	2.0b	186.9b	17.4a	121.8b	305.2a	187.3a	112.5b	16.2a	27.0a	16.0b	959.1b
	moharia	42.7c	64.0c	3.5a	167.2b	13.8b	108.4c	278.9b	176.4a	71.3c	12.3b	7.8b	9.2c	503.4c
E3	*indica*	57.3a	104.4a	3.0a	304.5a	19.4a	145.0a	304.8a	159.3b	166.8a	15.6a	25.3a	13.1a	890.4a
	maxima	47.3b	85.2b	1.5b	243.4b	20.1a	126.0b	305.9a	180.8a	130.9b	16.3a	24.4a	8.2b	498.2b
	moharia	41.1c	66.2c	3.3a	192.5c	14.3b	106.7c	284.7b	179.4a	86.5c	10.9b	9.0b	6.2c	379.2b
Pooled	*indica*	56.5a	107.5a	3.7a	280.0a	18.7a	143.4a	310.1a	169.6a	158.5a	16.8a	26.1a	21.4a	1402.8a
	maxima	50.2b	87.1b	2.1b	224.7b	19.9a	124.7b	306.4a	183.5a	130.8b	17.4a	27.9a	14.7b	922.9b
	moharia	43.5c	65.1c	3.7a	174.7c	13.8b	105.4c	273.6b	173.2a	79.6c	11.4b	9.5b	9.8c	618.5c

1= DF = Days to 50 per cent flowering, PLHT = Plant height (cm), BT = Basal tiller number, FLBL = Flag leaf blade length (mm), FLBW = Flag leaf blade width (mm), FLSL = Flag leaf sheath length (mm), PEDL = Peduncle length (mm), PEX = Panicle exertion (mm), INFL = Inflorescence length (mm), INFW = Inflorescence width (mm), W5P = Weight of five panicles (g), SPY = Single plant yield (g), PY = Grain yield per plot (Kg ha^{-1})

2= Coimbatore (E1), Madurai (E2) during Rabi/summer 2009/10 and ICRISAT (E3) during rainy season 2010

3= Means of races were tested following the Newman-Keuls test. Mean followed by the same letters are not significant at P=0.05 and mean followed by different letters are significant at P=0.05

Table 19b. Performance of individual races in three environments and pooled data for various quantitative traits in the foxtail millet core collection

Race	Environments	DF[1]	PLHT	BT	FLBL	FLBW	FLSL	PEDL	PEX	INFL	INFW	W5P	SPY	PY
indica	E1[2]	57.2a[3]	114.0a	4.7a	281.9b	19.9a	143.9a	306.5b	166.6b	173.7a	18.2a	28.7a	28.1a	1896.a
	E2	56.0a	105.1b	3.6b	254.7c	16.9c	140.9a	319.3a	183.0a	136.9c	16.9b	25.0b	22.7b	1413.6b
	E3	57.3a	104.4b	3.0c	304.5a	19.4a	145.0a	304.8b	159.3c	166.8a	15.6c	25.3b	13.1c	890.4c
	POOLED	56.5a	107.5b	3.7c	280.0b	18.7b	143.4a	310.1b	169.6b	158.5b	16.8b	26.1a	21.4b	1402.8b
maxima	E1	49.5a	85.9a	2.5a	222.7b	21.4a	122.5a	305.1a	184.7a	133.4a	18.4a	29.9a	19.6a	1259.3a
	E2	48.7a	83.3a	2.0b	192.6c	17.4a	121.7a	305.9a	188.1a	114.5a	16.4a	26.1a	16.5a	1002.8a
	E3	48.1a	86.9a	1.5b	250.4a	20.0a	128.2a	305.0a	177.6a	134.8a	16.3a	24.8a	8.4b	514.9b
	POOLED	50.2a	87.1a	2.1a	224.7b	19.9a	124.7a	306.4a	183.5a	130.8a	17.4a	27.9a	14.7a	922.9a
Moharia	E1	44.8a	64.1a	4.2a	160.2a	13.8a	105.4a	261.7a	166.4a	77.4a	11.3a	11.3a	12.8a	906.4a
	E2	43.5a	65.2a	3.5b	172.3a	13.8a	108.2a	277.6a	175.1a	74.4a	12.3a	8.5a	10.4b	567.0b
	E3	42.0a	66.9a	3.4b	195.8a	14.5a	105.7a	282.6a	178.2a	87.7a	11.0a	9.5a	6.6b	407.3c
	POOLED	43.5a	65.1a	3.7b	174.8a	13.8a	105.4a	273.6a	173.2a	79.6a	11.4a	9.5a	9.8b	618.5b

1= DF = Days to 50 per cent flowering, PLHT = Plant height (cm), BT = Basal tiller number, FLBL = Flag leaf blade length (mm), FLBW = Flag leaf blade width (mm), FLSL = Flag leaf sheath length (mm), PEDL = Peduncle length (mm), PEX = Panicle exertion (mm), INFL = Inflorescence length (mm), INFW = Inflorescence width (mm), W5P = Weight of five panicles (g), SPY = Single plant yield (g), PY = Grain yield per plot (Kg ha^{-1})

2= Coimbatore (E1), Madurai (E2) during Rabi/summer 2009/10 and ICRISAT (E3) during rainy season 2010

3= Means of races were tested following the Newman-Keuls test. Mean followed by the same letters are not significant at P=0.05 and mean followed by different letters are significant at P=0.05

Table 20a. Estimates of variance for various quantitative traits in foxtail millet core collection in three environments and pooled

Environment	E1[1]	E2	E3	Pooled	F-value	P>F
Days to 50% flowering[2]	129.79	138.86	113.36	118.88	0.19	0.902
Plant height (cm)	794.89	512.85	450.66	522.23	5.93	0.001**
Basal tiller number	2.46	1.43	1.23	1.24	11.31	<0.0001**
Flag leaf blade length (mm)	5528.45	3792.54	4018.59	3950.31	2.01	0.112
Flag leaf blade width (mm)	21.43	8.07	12.18	12.02	9.28	<0.0001**
Flag leaf sheath length (mm)	730.07	545.66	515.24	498.73	2.03	0.108
Peduncle length (mm)	2101.89	1826.74	1292.83	1171.32	4.88	0.002**
Panicle exertion (mm)	1141.1	1322.63	1047.84	816.91	2.25	0.081
Inflorescence length (mm)	3430.12	1823.82	2045.23	2059.82	7.05	0.000**
Inflorescence width (mm)	26.02	12.36	12.53	14.09	11.96	<0.0001**
Weight of five panicles (g)	214.78	196.26	100.41	143.64	6.06	0.001**
Single plant yield (g)	164.99	127.87	19.55	77.21	28.07	<0.0001**
Grain yield per plot (Kg ha^{-1})	661057.00	461201.00	104954.00	300755.00	49.00	<0.0001**

1=Coimbatore (E1), Madurai (E2) during Rabi/summer 2009/10 and ICRISAT (E3) during rainy season 2010

2= Homogeneity of variances were tested following Levene's test. *significant at $P \leq 0.05$; ** significant at $P \leq 0.01$

Table 20b. Estimates of variance for various quantitative traits in three races of foxtail millet core collection in three environments and pooled

Environment	Race	DF[1]	PLHT	BT	FLBL	FLBW	FLSL	PEDL	PEX	INFL	INFW	W5P	SPY	PY
E1[2]	Indica	115.10	251.93	1.63	1715.77	10.78	364.38	1393.24	831.57	1517.27	17.99	136.72	124.77	468100.90
	Maxima	137.14	1013.06	1.51	7109.94	29.09	893.57	2942.11	2428.57	4633.47	35.84	406.99	195.72	802549.36
	Moharia	42.80	408.84	3.24	5691.55	19.18	651.42	2450.25	1042.37	1843.86	8.29	92.70	89.57	371507.32
	F-value	1.04	11.85	3.32	15.43	4.12	4.13	3.49	7.98	8.59	6.03	9.98	1.79	3.73
	P>F[3]	0.355	<0.0001**	0.039*	<0.0001**	0.018*	0.018*	0.034*	0.0005**	0.0003**	0.003**	<0.0001**	0.170	0.026*
E2	Indica	131.82	178.04	1.05	2102.20	7.46	299.62	1401.15	1260.51	1271.39	9.78	131.22	309170.92	94.96
	Maxima	159.50	605.29	0.95	3502.94	5.67	933.01	2676.78	1716.77	1791.02	13.33	410.00	696497.99	179.78
	Moharia	18.43	309.96	1.52	3480.07	4.11	304.33	1461.60	1218.49	829.74	5.86	51.43	156169.29	50.44
	F-value	1.28	7.28	1.25	1.51	0.80	6.22	1.74	0.68	0.80	2.06	8.13	1.27	4.37
	P>F	0.281	0.001**	0.289	0.223	0.451	0.003**	0.179	0.510	0.452	0.130	0.000**	0.284	0.014*
E3	Indica	83.56	139.98	0.98	1342.24	6.86	201.97	806.70	720.88	892.17	9.42	52.29	10.60	63937.79
	Maxima	68.37	530.56	0.26	4622.91	14.14	508.35	1906.52	1601.60	1570.96	13.61	145.36	11.08	33834.32
	Moharia	49.05	351.06	1.11	3139.88	10.36	387.21	2428.27	1611.58	1502.03	6.09	46.22	16.46	57896.26
	F-value	0.18	10.90	5.37	8.47	1.80	2.68	5.67	3.97	1.83	0.98	7.26	1.72	1.32
	P>F	0.837	<0.0001**	0.006**	0.0003**	0.169	0.072	0.004**	0.021*	0.164	0.378	0.001**	0.178	0.271
Pooled	Indica	91.82	131.76	0.83	1254.17	6.14	191.08	711.34	630.67	890.74	9.09	74.12	48.67	171240.56
	Maxima	172.13	698.41	0.57	5231.15	14.76	712.99	1976.40	1522.88	2461.96	17.46	261.55	94.77	340577.04
	Moharia	35.68	285.97	1.40	3223.86	8.59	222.28	1167.10	833.62	1007.20	5.00	64.19	50.57	192687.97
	F-value	0.75	12.96	4.41	8.45	1.33	5.70	4.76	4.80	4.35	3.78	10.84	2.05	3.10
		0.474	<0.0001**	0.014*	0.000**	0.267	0.004**	0.001**	0.010**	0.015*	0.249	<0.0001**	0.133	0.050*

1=DF = Days to 50 per cent flowering, PLHT = Plant height (cm), BT = Basal tiller number, FLBL = Flag leaf blade length (mm), FLBW = Flag leaf blade width (mm), FLSL = Flag leaf sheath length (mm), PEDL = Peduncle length (mm), PEX = Panicle exertion (mm), INFL = Inflorescence length (mm), INFW = Inflorescence width (mm), W5P = weight of five panicles (g), SPY = Single plant yield (g), PY = Grain yield per plot (Kg ha^{-1})

2=Coimbatore (E1), Madurai (E2) during Rabi/summer 2009/10 and ICRISAT (E3) during rainy season 2010

3= Homogeneity of variances were tested following Levene's test. *significant at $P \leq 0.05$; ** significant at $P \leq 0.01$

Table 20c. Estimates of variance for various quantitative traits in three races of foxtail millet core collection in three environments and pooled

Race	Environment	DF[1]	PLHT	BT	FLBL	FLBW	FLSL	PEDL	PEX	INFL	INFW	W5P	SPY	PY
indica	E1[2]	115.10	251.93	1.63	1715.77	10.78	364.38	1393.24	831.57	1517.27	17.99	136.72	124.77	468100.90
	E2	131.82	178.04	1.05	2102.20	7.46	299.62	1401.15	1260.51	1271.39	9.78	131.22	94.96	309170.92
	E3	83.56	139.98	0.98	1342.24	6.86	201.97	806.70	720.88	892.17	9.42	52.29	10.60	63937.79
	Pooled	91.82	131.76	0.83	1254.17	6.14	191.08	711.34	630.67	890.74	9.09	74.12	48.67	171240.56
	F-value	0.48	2.63	3.84	0.91	1.69	4.39	4.12	5.58	1.81	4.72	5.60	16.54	30.88
	P>F[3]	0.698	0.050*	0.010**	0.434	0.169	0.005**	0.007**	0.001**	0.144	0.003**	0.001**	<0.0001**	<0.0001**
maxima	E1	137.14	1013.06	1.51	7109.94	29.09	893.57	2942.11	2428.57	4633.47	35.84	406.99	195.72	802549.36
	E2	141.18	538.19	0.88	3284.81	5.26	815.18	2510.30	1731.92	1608.19	12.30	367.71	166.10	647173.01
	E3	65.40	484.20	0.25	4608.92	12.39	477.93	1694.46	1524.01	1618.09	11.98	129.67	10.28	35861.43
	Pooled	172.13	698.41	0.57	5231.15	14.76	712.99	1976.40	1522.88	2461.96	17.46	261.55	94.77	340577.04
	F-value	0.940	1.790	3.700	2.000	3.250	0.410	0.520	0.650	5.580	6.140	2.720	5.770	8.810
	P>F	0.43	0.15	0.010**	0.12	0.03*	0.75	0.67	0.59	0.000**	0.000**	0.050*	0.00**	<0.0001**
Moharia	E1	42.80	408.84	3.24	5691.55	19.18	651.42	2450.25	1042.37	1843.86	8.29	92.70	89.57	371507.32
	E2	31.91	329.78	1.51	3705.76	4.24	288.06	1514.74	1221.03	916.26	5.34	68.36	94.37	275751.61
	E3	56.20	382.19	1.08	3297.27	10.16	422.84	2392.58	1478.89	1511.32	5.83	49.26	18.34	76693.22
	Pooled	35.68	285.97	1.40	3223.86	8.59	222.28	1167.10	833.62	1007.20	5.00	64.19	50.57	192687.97
	F-value	0.71	0.41	4.74	2.80	3.58	2.66	1.73	0.82	2.18	0.71	0.44	0.98	1.42
	P>F	0.551	0.749	0.004**	0.043*	0.016*	0.051	0.166	0.485	0.095	0.547	0.727	0.403	0.241

1=DF = Days to 50 per cent flowering, PLHT = Plant height (cm), BT = Basal tiller number, FLBL = Flag leaf blade length (mm), FLBW = Flag leaf blade width (mm), FLSL = Flag leaf sheath length (mm), PEDL = Peduncle length (mm), PEX = Panicle exertion (mm), INFL = Inflorescence length (mm), INFW = Inflorescence width (mm), W5P = weight of five panicles (g), SPY = Single plant yield (g), PY = Grain yield per plot (Kg ha^{-1})

2=Coimbatore (E1), Madurai (E2) during Rabi/summer 2009/10 and ICRISAT (E3) during rainy season 2010

3= Homogeneity of variances were tested following Levene's test. *significant at $P \leq 0.05$; ** significant at $P \leq 0.01$

Table 21. Phenotypic correlation coefficients between 13 characters in foxtail millet core collection in three environments, *Rabi*/summer 2009-10 at Coimbatore (E1) and Madurai (E2) and the Rainy season 2010 in ICRISAT (E3), Patancheru, India and pooled

	Environment	DF[1]	PLHT	BT	FLBL	FLBW	FLSL	PEDL	PEX	INFL	INFW	W5P	SPY
PLHT	E1	0.676***[2]											
	E2	0.571***											
	E3	0.725***											
	Pooled	0.716***											
BT	E1	0.212**	0.251**										
	E2	0.081	0.182*										
	E3	-0.012	-0.177*										
	Pooled	0.138	0.107										
FLBL	E1	0.730***	0.894***	0.165*									
	E2	0.703***	0.761***	0.204**									
	E3	0.699***	0.847***	-0.135									
	Pooled	0.796***	0.855***	0.093									
FLBW	E1	0.592***	0.632***	-0.213*	0.747***								
	E2	0.581***	0.517***	-0.190**	0.621***								
	E3	0.617***	0.705***	-0.464***	0.724***								
	Pooled	0.674***	0.662***	-0.369***	0.728***								
FLSL	E1	0.460***	0.759***	0.245**	0.740***	0.570***							
	E2	0.415***	0.700***	0.148*	0.616***	0.407***							
	E3	0.549***	0.816***	-0.112	0.734***	0.571***							
	Pooled	0.520***	0.786***	0.118	0.692***	0.517***							
PEDL	E1	0.154*	0.394***	0.063	0.376***	0.419***	0.654***						
	E2	0.094	0.444***	0.054	0.369***	0.224**	0.502***						
	E3	-0.012	0.373***	-0.235***	0.237***	0.202**	0.502***						
	Pooled	0.119	0.461***	-0.033	0.360***	0.269***	0.549***						
PEX	E1	-0.211**	-0.095	-0.132	-0.108	0.071	0.013	0.748***					
	E2	-0.197**	0.104	0.005	0.02	-0.037	0.034	0.756***					
	E3	-0.397***	-0.143*	-0.191**	-0.241***	-0.168*	-0.123	0.797***					
	Pooled	-0.309***	-0.06	-0.148*	-0.143*	-0.097	-0.017	0.716***					

Table 21. Cont..

	Environment	DF[1]	PLHT	BT	FLBL	FLBW	FLSL	PEDL	PEX	INFL	INFW	W5P	SPY
INFL	E1	0.719***	0.880***	0.195*	0.903***	0.726***	0.731***	0.408***	-0.083				
	E2	0.673***	0.775***	0.037	0.780***	0.636***	0.620***	0.259***	-0.098				
	E3	0.707***	0.853***	-0.195*	0.833***	0.681***	0.776***	0.262***	-0.241***				
	Pooled	0.776***	0.861***	0.014	0.864***	0.709***	0.694***	0.357***	-0.172*				
INFW	E1	0.626***	0.660***	-0.124	0.714***	0.770***	0.415***	0.138	-0.161	0.709***			
	E2	0.423***	0.514***	-0.157*	0.462***	0.450***	0.293***	0.113	-0.044	0.466***			
	E3	0.570***	0.636***	-0.425***	0.652***	0.771***	0.463***	0.05	-0.266***	0.631***			
	Pooled	0.630***	0.608***	-0.345***	0.676***	0.746***	0.408***	0.117	-0.197**	0.646***			
W5P	E1	0.547***	0.591***	-0.177*	0.644***	0.674***	0.390***	0.122	-0.161	0.594***	0.787***		
	E2	0.544***	0.553***	-0.176*	0.468***	0.513***	0.363***	0.132	-0.038	0.532***	0.580***		
	E3	0.537***	0.722***	-0.419***	0.670***	0.721***	0.559***	0.214***	-0.145*	0.667***	0.726***		
	Pooled	0.597***	0.678***	-0.344***	0.682***	0.755***	0.500***	0.245***	-0.122	0.664***	0.842***		
SPY	E1	0.419***	0.651***	0.238**	0.589***	0.382***	0.456***	0.116	-0.213*	0.533***	0.446***	0.518***	
	E2	0.414***	0.536***	0.026	0.413***	0.320***	0.405***	0.155*	-0.063	0.504***	0.369***	0.529***	
	E3	0.489***	0.637***	0.122	0.628***	0.467***	0.567***	0.141*	-0.234***	0.573***	0.368***	0.500***	
	Pooled	0.477***	0.698***	0.118	0.616***	0.455***	0.535***	0.189**	-0.197**	0.621***	0.467***	0.570***	
PY	E1	0.384***	0.651***	0.233**	0.567***	0.332***	0.435***	0.102	-0.228**	0.513***	0.419***	0.461***	0.952***
	E2	0.415***	0.578***	0.064	0.448***	0.332***	0.426***	0.215**	-0.002	0.504***	0.415***	0.514***	0.932***
	E3	0.358***	0.487***	0.160*	0.505***	0.305***	0.499***	0.133	-0.197**	0.412***	0.178*	0.387***	0.716***
	Pooled	0.450***	0.678***	0.155*	0.627***	0.409***	0.548***	0.217**	-0.191**	0.582***	0.436***	0.514***	0.899***

1=DF = Days to 50 per cent flowering, PLHT = Plant height (cm), BT = Basal tiller number, FLBL = Flag leaf blade length (mm), FLBW = Flag leaf blade width (mm), FLSL = Flag leaf sheath length (mm), PEDL = Peduncle length (mm), PEX = Panicle exertion (mm), INFL = Inflorescence length (mm), INFW = Inflorescence width (mm), W5P = Weight of five panicles (g), SPY = Single plant yield (g), PY = Grain yield per Plot (Kg ha^{-1})

2=* denotes significant at $P<0.05$, ** significant at $P<0.01$, *** highly significant at $P<0.001$

Table 22. Useful correlations (r> 0.50) between quantitative traits in foxtail millet core collection in three environments, *Rabi*/summer 2009-10 at Coimbatore (E1) and Madurai (E2) and the Rainy season 2010 in ICRISAT (E3), Patancheru, India and pooled

Pair of traits recorded meaningful correlation		E1	E2	E3	Pooled
Days to 50 per cent flowering	Plant height (cm)	0.676	0.571	0.725	0.716
	Flag leaf blade length (mm)	0.730	0.703	0.699	0.796
	Flag leaf blade width (mm)	0.592	0.581	0.617	0.674
	Flag leaf sheath length (mm)	-	-	0.549	0.520
	Inflorescence length (mm)	0.719	0.673	0.707	0.776
	Inflorescence width (mm)	0.626	-	0.570	0.63
	Weight of five panicles (g)	0.547	0.544	0.537	0.597
Plant height (cm)	Flag leaf blade length (mm)	0.894	0.761	0.847	0.855
	Flag leaf blade width (mm)	0.632	0.517	0.705	0.662
	Flag leaf sheath length (mm)	0.759	0.700	0.816	0.786
	Inflorescence length (mm)	0.880	0.775	0.853	0.861
	Inflorescence width (mm)	0.660	0.514	0.636	0.608
	Weight of five panicles (g)	0.591	0.553	0.722	0.678
	Single plant yield (g)	0.651	0.536	0.637	0.698
	Grain yield per plot (Kg ha^{-1})	0.651	0.578	-	0.678
Flag leaf blade length (mm)	Flag leaf blade width (mm)	0.747	0.621	0.724	0.728
	Flag leaf sheath length (mm)	0.740	0.616	0.734	0.692
	Inflorescence length (mm)	0.903	0.780	0.833	0.864
	Inflorescence width (mm)	0.714	-	0.652	0.676
	Weight of five panicles (g)	0.644	-	0.670	0.682
	Single plant yield (g)	0.589	-	0.628	0.616
	Grain yield per plot (Kg ha^{-1})	0.567	-	0.505	0.627
Flag leaf blade width (mm)	Flag leaf sheath length (mm)	0.570	-	0.571	0.517
	Inflorescence length (mm)	0.726	0.636	0.681	0.709
	Inflorescence width (mm)	0.770	0.450	0.771	0.746
	Weight of five panicles (g)	0.674	0.513	0.721	0.755
Flag leaf sheath length (mm)	Peduncle length (mm)	0.654	0.502	0.502	0.549
	Inflorescence length (mm)	0.731	0.620	0.776	0.694
	Weight of five panicles (g)	-	-	0.559	0.500
	Single plant yield (g)	-	-	0.567	0.535
	Grain yield per plot (Kg ha^{-1})	-	-	-	0.548
Peduncle length (mm)	Panicle exertion (mm)	0.748	0.756	0.797	0.716
Inflorescence length (mm)	Inflorescence width	0.709	-	0.631	0.646
	Weight of five panicles	0.594	0.532	0.667	0.664
	Single plant yield	0.533	0.504	0.573	0.621
	Grain yield per plot (Kg ha^{-1})	0.513	0.504	-	0.582
Inflorescence width (mm)	Weight of five panicles (g)	0.787	0.580	0.726	0.842
Weight of five panicles (g)	Single plant yield (g)	0.518	0.529	0.500	0.570
	Grain yield per plot (Kg ha^{-1})	-	0.514	-	0.514
Single plant yield (g)	Grain yield per Plot (Kg ha^{-1})	0.952	0.932	0.716	0.899

Table 23. Direct (Diagonal) and indirect effect of 12 quantitative traits on grain yield in foxtail millet core collection in three environments, *Rabi*/summer 2009-10 at Coimbatore (E1) and Madurai (E2) and the Rainy season 2010 in ICRISAT (E3), Patancheru, India and pooled

Characters	Environments	DF[1]	PLHT	BT	FLBL	FLBW	FLSL	PEDL	PEX	INFL	INFW	W5P	SPY	PY
DF	E1	-0.052	0.126	-0.008	0.038	-0.052	-0.060	0.027	0.035	-0.039	0.034	-0.040	0.384	0.393
	E2	0.004	0.046	0.003	0.004	0.012	0.001	0.002	-0.007	-0.045	0.039	-0.021	0.386	0.424
	E3	0.027	-0.165	0.000	0.201	0.001	-0.864	-0.031	1.116	-0.206	-0.168	0.135	0.329	0.375
	Pooled	-0.027	0.159	-0.005	0.085	-0.057	-0.067	0.031	0.072	-0.164	0.042	-0.068	0.438	0.439
PLHT	E1	-0.036	0.182	-0.009	0.045	-0.052	-0.087	0.066	0.013	-0.045	0.035	-0.042	0.567	0.637
	E2	0.002	0.079	0.007	0.005	0.011	0.002	0.011	0.004	-0.052	0.048	-0.022	0.503	0.598
	E3	0.021	-0.216	-0.009	0.242	0.002	-1.238	1.109	0.418	-0.242	-0.180	0.179	0.427	0.513
	Pooled	-0.020	0.216	-0.004	0.097	-0.058	-0.100	0.124	0.016	-0.186	0.044	-0.078	0.640	0.691
BT	E1	-0.012	0.045	-0.036	0.008	0.017	-0.027	0.010	0.020	-0.010	-0.007	0.012	0.206	0.226
	E2	0.000	0.015	0.036	0.001	-0.004	0.000	0.001	0.000	-0.002	-0.015	0.007	0.022	0.061
	E3	0.000	0.042	0.044	-0.039	-0.001	0.183	-0.772	0.557	0.055	0.130	-0.108	0.080	0.171
	Pooled	-0.004	0.025	-0.037	0.011	0.031	-0.017	-0.007	0.033	-0.007	-0.021	0.036	0.125	0.168
FLBL	E1	-0.039	0.160	-0.006	0.051	-0.061	-0.083	0.063	0.016	-0.047	0.038	-0.046	0.511	0.557
	E2	0.003	0.061	0.008	0.006	0.013	0.001	0.009	0.001	-0.052	0.043	-0.019	0.390	0.464
	E3	0.020	-0.191	-0.006	0.275	0.002	-1.103	0.653	0.716	-0.237	-0.185	0.168	0.425	0.537
	Pooled	-0.022	0.195	-0.004	0.107	-0.063	-0.090	0.098	0.034	-0.187	0.046	-0.077	0.570	0.607
FLBW	E1	-0.032	0.113	0.007	0.037	-0.084	-0.065	0.068	-0.011	-0.037	0.040	-0.048	0.330	0.318
	E2	0.002	0.043	-0.007	0.004	0.019	0.001	0.005	-0.002	-0.044	0.045	-0.021	0.313	0.358
	E3	0.018	-0.160	-0.022	0.204	0.002	-0.861	0.545	0.526	-0.193	-0.223	0.182	0.311	0.329
	Pooled	-0.019	0.152	0.014	0.081	-0.083	-0.068	0.079	0.022	-0.157	0.052	-0.086	0.417	0.404
FLSL	E1	-0.027	0.133	-0.008	0.036	-0.046	-0.119	0.105	-0.003	-0.036	0.021	-0.027	0.378	0.407
	E2	0.002	0.057	0.006	0.004	0.008	0.002	0.013	0.001	-0.042	0.028	-0.015	0.387	0.451
	E3	0.016	-0.186	-0.006	0.210	0.001	-1.441	1.401	0.374	-0.223	-0.131	0.143	0.388	0.546
	Pooled	-0.016	0.183	-0.005	0.081	-0.048	-0.118	0.153	0.009	-0.159	0.029	-0.058	0.515	0.566

Table 23. Cont..

Characters	Environments	DF[1]	PLHT	BT	FLBL	FLBW	FLSL	PEDL	PEX	INFL	INFW	W5P	SPY	PY
PEDL	E1	-0.008	0.071	-0.002	0.019	-0.034	-0.074	0.169	-0.114	-0.021	0.007	-0.009	0.097	0.101
	E2	0.000	0.036	0.002	0.002	0.004	0.001	0.024	0.026	-0.018	0.011	-0.005	0.143	0.226
	E3	0.000	-0.084	-0.012	0.063	0.000	-0.712	2.837	-2.011	-0.074	-0.010	0.056	0.098	0.151
	Pooled	-0.003	0.102	0.001	0.040	-0.025	-0.068	0.264	-0.169	-0.077	0.007	-0.025	0.162	0.209
PEX	E1	0.012	-0.015	0.005	-0.005	-0.006	-0.003	0.124	-0.156	0.004	-0.008	0.011	-0.182	-0.219
	E2	-0.001	0.008	0.000	0.000	-0.001	0.000	0.019	0.034	0.006	-0.004	0.002	-0.065	-0.002
	E3	-0.012	0.035	-0.010	-0.077	0.000	0.211	2.235	-2.552	0.073	0.082	-0.038	-0.163	-0.216
	Pooled	0.009	-0.015	0.005	-0.016	0.008	0.005	0.198	-0.225	0.036	-0.014	0.015	-0.188	-0.182
INFL	E1	-0.039	0.157	-0.007	0.045	-0.059	-0.082	0.067	0.012	-0.053	0.037	-0.042	0.463	0.499
	E2	0.003	0.062	0.001	0.005	0.013	0.001	0.007	-0.003	-0.066	0.043	-0.021	0.472	0.517
	E3	0.021	-0.193	-0.009	0.240	0.002	-1.185	0.779	0.688	-0.271	-0.181	0.168	0.386	0.445
	Pooled	-0.022	0.194	-0.001	0.096	-0.063	-0.090	0.098	0.039	-0.208	0.045	-0.076	0.564	0.576
INFW	E1	-0.033	0.118	0.004	0.036	-0.063	-0.047	0.023	0.024	-0.037	0.054	-0.056	0.389	0.412
	E2	0.002	0.043	-0.006	0.003	0.010	0.001	0.003	-0.002	-0.032	0.088	-0.024	0.362	0.448
	E3	0.017	-0.141	-0.021	0.184	0.002	-0.683	0.103	0.754	-0.178	-0.276	0.184	0.243	0.188
	Pooled	-0.018	0.142	0.012	0.074	-0.066	-0.052	0.030	0.046	-0.142	0.066	-0.095	0.441	0.438
W5P	E1	-0.029	0.106	0.006	0.032	-0.055	-0.044	0.020	0.024	-0.031	0.042	-0.072	0.453	0.452
	E2	0.002	0.044	-0.007	0.003	0.011	0.001	0.003	-0.001	-0.035	0.054	-0.039	0.492	0.528
	E3	0.015	-0.162	-0.020	0.194	0.002	-0.863	0.666	0.404	-0.191	-0.213	0.239	0.339	0.410
	Pooled	-0.016	0.150	0.012	0.072	-0.063	-0.061	0.057	0.030	-0.139	0.056	-0.113	0.534	0.519
SPY	E1	-0.023	0.116	-0.008	0.029	-0.031	-0.050	0.019	0.032	-0.027	0.023	-0.037	0.891	0.934
	E2	0.002	0.044	0.001	0.003	0.007	0.001	0.004	-0.002	-0.034	0.035	-0.021	0.911	0.951
	E3	0.014	-0.146	0.006	0.185	0.001	-0.886	0.443	0.659	-0.166	-0.106	0.128	0.631	0.763
	Pooled	-0.013	0.149	-0.005	0.066	-0.037	-0.065	0.046	0.046	-0.126	0.031	-0.065	0.929	0.956

1=DF = Days to 50 per cent flowering, PLHT = Plant height (cm), BT = Basal tiller number, FLBL = Flag leaf blade length (mm), FLBW = Flag leaf blade width (mm), FLSL = Flag leaf sheath length (mm), PEDL = Peduncle length (mm), PEX = Panicle exertion (mm), INFL = Inflorescence length (mm), INFW = Inflorescence width (mm), W5P = Weight of five panicles (g), SPY = Single plant yield (g), PY = Grain yield per plot (Kg ha^{-1})

Residual variance: 0.115 in E1, 0.085 in E2, 0.348 in E3 and 0.071 in pooled

Table 24. Shannon-Weaver diversity indices (H') for various quantitative traits in foxtail millet core collection in three environments, *Rabi*/summer 2009-10 at Coimbatore (E1) and Madurai (E2) and the Rainy season 2010 in ICRISAT (E3), Patancheru, India and pooled

Quantitative traits		DF[1]	PLHT	BT	FLBL	FLBW	FLSL	PEDL	PEX	INFL	INFW	W5P	SPY	PY	Mean
Environment	E1	0.57	0.61	0.59	0.57	0.62	0.61	0.61	0.60	0.57	0.61	0.55	0.59	0.59	0.59±0.006
	E2	0.55	0.59	0.58	0.59	0.61	0.60	0.64	0.63	0.61	0.57	0.55	0.55	0.56	0.57±0.008
	E3	0.53	0.58	0.55	0.58	0.62	0.60	0.62	0.60	0.59	0.56	0.59	0.59	0.59	0.58±0.007
	Pooled	0.57	0.59	0.60	0.59	0.61	0.61	0.62	0.62	0.56	0.61	0.58	0.57	0.59	0.59±0.006
	Mean	0.55±0.010	0.59 ±0.005	0.58±0.012	0.58±0.004	0.62±0.002	0.61±0.004	0.62±0.007	0.61±0.008	0.58±0.012	0.59±0.013	0.57±0.010	0.57±0.009	0.58±0.006	
Environment	Races	DF	PLHT	BT	FLBL	FLBW	FLSL	PEDL	PEX	INFL	INFW	W5P	SPY	PY	Mean
E1	*Indica*	0.50	0.60	0.61	0.56	0.59	0.60	0.61	0.62	0.56	0.59	0.58	0.60	0.61	0.59±0.009
	Maxima	0.56	0.56	0.43	0.56	0.56	0.59	0.61	0.56	0.55	0.52	0.54	0.49	0.41	0.53±0.016
	Moharia	0.35	0.51	0.55	0.48	0.53	0.57	0.55	0.54	0.47	0.46	0.37	0.50	0.50	0.49±0.019
	Mean	0.47±0.061	0.56±0.028	0.53±0.054	0.53±0.026	0.56±0.019	0.59±0.009	0.59±0.021	0.57±0.023	0.53±0.027	0.52±0.039	0.50±0.063	0.53±0.037	0.51±0.058	
E2	*Indica*	0.50	0.59	0.62	0.56	0.60	0.61	0.62	0.61	0.61	0.62	0.60	0.60	0.61	0.60±0.009
	Maxima	0.53	0.58	0.41	0.57	0.59	0.60	0.59	0.56	0.51	0.48	0.51	0.41	0.40	0.52±0.021
	Moharia	0.27	0.54	0.57	0.53	0.50	0.54	0.58	0.55	0.45	0.47	0.28	0.44	0.43	0.47±0.028
	Mean	0.44±0.084	0.57±0.014	0.53±0.064	0.55±0.014	0.56±0.032	0.58±0.021	0.59±0.013	0.57±0.020	0.52±0.048	0.53±0.050	0.46±0.095	0.48±0.058	0.48±0.065	
E3	*Indica*	0.37	0.60	0.58	0.59	0.61	0.61	0.62	0.62	0.57	0.59	0.61	0.64	0.62	0.59±0.019
	Maxima	0.61	0.57	0.29	0.57	0.57	0.52	0.59	0.51	0.55	0.46	0.56	0.58	0.55	0.53±0.023
	Moharia	0.41	0.50	0.57	0.50	0.59	0.52	0.57	0.52	0.51	0.49	0.36	0.45	0.46	0.50±0.018
	Mean	0.46±0.076	0.56±0.032	0.48±0.096	0.55±0.025	0.59±0.012	0.55±0.030	0.59±0.013	0.55±0.033	0.55±0.017	0.51±0.041	0.51±0.077	0.56±0.055	0.54±0.047	
Pooled	*Indica*	0.44	0.61	0.59	0.57	0.59	0.64	0.62	0.62	0.58	0.60	0.59	0.58	0.61	0.59±0.013
	Maxima	0.56	0.58	0.42	0.58	0.56	0.58	0.61	0.62	0.56	0.50	0.48	0.45	0.42	0.53±0.019
	Moharia	0.39	0.48	0.54	0.48	0.45	0.51	0.61	0.59	0.45	0.46	0.24	0.47	0.45	0.47±0.025
	Mean	0.46±0.048	0.55±0.037	0.51±0.051	0.55±0.031	0.53±0.042	0.58±0.039	0.612±0.003	0.61±0.009	0.53±0.040	0.52±0.041	0.44±0.103	0.50±0.041	0.49±0.060	

1=DF = Days to 50 per cent flowering, PLHT = Plant height (cm), BT = Basal tiller number, FLBL = Flag leaf blade length (mm), FLBW = Flag leaf blade width (mm), FLSL = Flag leaf sheath length (mm), PEDL = Peduncle length (mm), PEX = Panicle exertion (mm), INFL = Inflorescence length (mm), INFW = Inflorescence width (mm), W5P = weight of five panicles (g), SPY = Single plant yield (g), PY = Grain yield per plot (Kg ha^{-1})

Table 25. Phenotypic diversity index in the foxtail millet core collection in three environments, *Rabi*/summer 2009-10 at Coimbatore (E1) and Madurai (E2) and rainy season 2010 in ICRISAT, Patancheru (E3), India and pooled

	E1	E2	E3	Pooled
Mean diversity	0.255	0.255	0.250	0.253
Minimum diversity	0.006	0.006	0.001	0.003
Between	ISe 999 and ISe 869	ISe 1820 and ISe 909; ISe 1408 and ISe 985	ISe 846 and ISe 663	ISe 1820 and ISe 909
Maximum diversity	0.635	0.608	0.595	0.640
Between	ISe 1687 and ISe 1254	ISe 1687 and ISe 1254	ISe 1597 and ISe 1312	ISe1687 and ISe1254

Table 26. List of ten most diverse pair of accessions with dissimilarity value in foxtail millet core collection in three environments, *Rabi*/summer 2009-10 at Coimbatore (E1) and Madurai (E2) and rainy season 2010 in ICRISAT, Patancheru (E3), India and pooled

	E1		E2		E3		Pooled	
List of ten diverse pairs of accessions								
S.No	Between pair of accessions	Diversity values	Between pair of accessions	Diversity values	Between pair of accessions	Diversity values	Between pair of accessions	Diversity values
1	ISe1687 and ISe 1254	0.635	ISe 1687 and ISe 1254	0.608	ISe 1597 and ISe 1312	0.595	ISe 1687 and ISe 1254	0.640
2	ISe1687 and ISe 1201	0.613	ISe 1597 and ISe 1312	0.573	ISe 1687 and ISe 1254	0.575	ISe 1597 and ISe 1312	0.610
3	ISe1881 and ISe 1312	0.600	ISe 1597 and ISe 1320	0.560	ISe 1419 and ISe 1037	0.561	ISe 1687 and ISe 1201	0.584
4	ISe1685 and ISe 827	0.584	ISe 1597 and ISe 1234	0.555	ISe 1597 and ISe 1320	0.560	ISe 1881 and ISe 1312	0.580
5	ISe1789 and ISe 1687	0.564	ISe 1736 and ISe403	0.544	ISe 1687 and ISe 1312	0.548	ISe 1597 and ISe 1320	0.569
6	ISe 1687 and ISe 1312	0.561	ISe 1597 and ISe403	0.536	ISe 1312 and ISe 719	0.548	ISe 1687 and ISe 1129	0.564
7	ISe 1736 and ISe 403	0.560	ISe 1687 and ISe 1638	0.531	ISe 1419 and ISe 1320	0.545	ISe 1687 and ISe 1312	0.564
8	ISe 1687 and ISe 1335	0.559	ISe 1687 and ISe 1201	0.531	ISe 1419 and ISe 1302	0.542	ISe 1685 and ISe 827	0.560
9	ISe 1286 and ISe 1059	0.558	ISe 1687 and ISe 1209	0.530	ISe 1687 and ISe 1129	0.540	ISe 1286 and ISe 1059	0.557
10	ISe 1511 and ISe 1312	0.555	ISe 1597 and ISe 813	0.530	ISe 1419 and ISe 1312	0.537	ISe 1687 and ISe 1118	0.551

Table 27. Vector loadings and percentage of variation explained by the first three principal components (PCs) in foxtail millet core collection in three environments, *Rabi*/summer 2009-10 at Coimbatore (E1) and Madurai (E2) and rainy season 2010 in ICRISAT, Patancheru (E3), India and pooled

PCs	Eigen value	Variation explained (%)	Cumulative Value (%)	Eigenvectors												
				DF[1]	PLHT	BT	FLBL	FLBW	FLSL	PEDL	PEX	INFL	INFW	W5P	SPY	PY
		E1														
PC1	6.67	51.3	51.3	0.305	0.356	0.059	0.362	0.305	0.288	0.153	-0.042	0.352	0.307	0.287	0.273	0.262
PC2	1.98	15.3	66.6	-0.088	0.013	-0.117	0.025	0.161	0.214	0.613	0.630	0.053	-0.066	-0.098	-0.237	-0.245
PC3	1.56	12.0	78.6	-0.039	0.131	0.654	0.009	-0.324	0.217	0.177	0.048	0.023	-0.351	-0.345	0.237	0.262
		E1														
PC1	6.08	46.8	46.8	0.306	0.359	0.020	0.346	0.298	0.295	0.164	0.005	0.353	0.269	0.295	0.287	0.298
PC2	1.91	14.6	61.5	-0.182	0.131	0.182	0.068	-0.105	0.201	0.625	0.634	-0.045	-0.156	-0.172	-0.102	-0.048
PC3	1.32	10.1	71.6	0.124	0.119	0.755	0.179	-0.218	0.181	-0.159	-0.298	0.086	-0.294	-0.282	0.022	0.022
		E3														
PC1	7.06	54.3	54.3	0.300	0.356	-0.100	0.347	0.319	0.318	0.105	-0.106	0.346	0.290	0.315	0.277	0.220
PC2	2.09	16.1	70.4	-0.198	0.057	-0.418	-0.042	0.091	0.082	0.581	0.603	-0.002	0.026	0.106	-0.160	-0.165
PC3	1.65	12.7	83.1	-0.062	0.089	0.476	0.047	-0.261	0.225	0.344	0.232	0.017	-0.391	-0.177	0.322	0.424
		Pooled														
PC1	7.16	55.1	55.1	0.301	0.353	-0.008	0.348	0.310	0.301	0.144	-0.061	0.346	0.295	0.304	0.280	0.272
PC2	1.90	14.6	69.7	-0.166	0.081	-0.106	0.009	0.024	0.178	0.655	0.678	0.007	-0.111	-0.041	-0.109	-0.085
PC3	1.67	12.8	82.6	0.011	0.124	0.688	0.059	-0.330	0.201	0.093	-0.036	0.028	-0.348	-0.292	0.243	0.286

1=DF = Days to 50 per cent flowering, PLHT = Plant height (cm), BT = Basal tiller number, FLBL = Flag leaf blade length (mm), FLBW = Flag leaf blade width (mm), FLSL = Flag leaf sheath length (mm), PEDL = Peduncle length (mm), PEX = Panicle exertion (mm), INFL = Inflorescence length (mm), INFW = Inflorescence width (mm), W5P = Weight of five panicles (g), SPY = Single plant yield (g), PY = Grain yield per plot (Kg ha-1)

Table 28. Race wise vector loadings and percentage of variation explained by the first three principal components (PCs) in foxtail millet core collection evaluated at Coimbatore 2009/10 *Rabi*/summer

PCs	Eigen value	Variability (%)	Cumulative value (%)	Eigenvectors												
				DF[1]	PLHT	BT	FLBL	FLBW	FLSL	PEDL	PEX	INFL	INFW	W5P	SPY	PY
Indica																
PC1	4.51	34.7	34.7	0.357	0.346	-0.016	0.400	0.368	0.246	0.154	0.031	0.404	0.346	0.296	0.050	0.006
PC2	2.32	17.8	52.5	0.110	0.167	0.089	0.032	-0.156	-0.149	-0.442	-0.442	-0.009	0.024	0.118	0.502	0.498
PC3	1.85	14.2	66.7	-0.140	0.138	0.332	-0.017	-0.092	0.388	0.462	0.324	-0.043	-0.252	-0.151	0.375	0.381
Maxima																
PC1	8.10	62.3	62.3	0.314	0.327	0.068	0.342	0.262	0.246	-0.029	-0.166	0.313	0.325	0.308	0.335	0.324
PC2	2.23	17.2	79.4	-0.059	0.117	-0.237	0.080	0.243	0.352	0.645	0.535	0.079	-0.135	-0.049	-0.042	-0.079
PC3	1.27	9.8	89.2	0.170	0.141	0.784	-0.068	-0.333	0.198	0.173	0.061	0.158	-0.235	-0.253	0.041	0.047
Moharia																
PC1	7.55	58.1	58.1	0.303	0.351	0.061	0.337	0.318	0.268	0.237	0.040	0.349	0.317	0.281	0.264	0.256
PC2	1.67	12.9	70.9	-0.173	0.062	0.160	-0.027	-0.158	0.066	0.558	0.702	0.044	-0.077	-0.314	0.002	-0.003
PC3	1.51	11.6	82.5	0.035	-0.045	0.640	-0.065	-0.235	-0.102	-0.059	-0.199	-0.083	-0.200	-0.114	0.466	0.445

1=DF = Days to 50 per cent flowering, PLHT = Plant height (cm), BT = Basal tiller number, FLBL = Flag leaf blade length (mm), FLBW = Flag leaf blade width (mm), FLSL = Flag leaf sheath length (mm), PEDL = Peduncle length (mm), PEX = Panicle exertion (mm), INFL = Inflorescence length (mm), INFW = Inflorescence width (mm), W5P = Weight of five panicles (g), SPY = Single plant yield (g), PY = Grain yield per plot (Kg ha-1)

Table 29. Race wise vector loadings and percentage of variation explained by the first three principal components (PCs) in foxtail millet core collection evaluated at Madurai 2009/10 *Rabi*/summer

PCs	Eigen value	Variability (%)	Cumulative value (%)	Eigenvectors												
				DF[1]	PLHT	BT	FLBL	FLBW	FLSL	PEDL	PEX	INFL	INFW	W5P	SPY	PY
Indica																
PC1	4.11	31.6	31.6	0.332	0.372	-0.030	0.386	0.390	0.247	0.095	-0.022	0.422	0.218	0.294	0.194	0.174
PC2	2.02	15.5	47.2	-0.172	0.202	0.085	0.143	0.035	0.164	0.594	0.543	-0.068	0.055	-0.117	-0.335	-0.304
PC3	1.87	14.4	61.5	-0.283	0.040	-0.077	-0.232	-0.114	0.057	0.276	0.325	-0.125	-0.011	0.089	0.549	0.579
Maxima																
PC1	7.13	54.8	54.8	0.336	0.339	0.005	0.346	0.242	0.286	0.119	-0.044	0.302	0.273	0.303	0.348	0.343
PC2	2.24	17.2	72.1	-0.085	0.104	0.021	0.042	-0.011	0.309	0.622	0.601	0.094	-0.314	-0.075	-0.118	-0.098
PC3	1.36	10.4	82.5	0.119	0.113	0.811	0.024	-0.484	-0.070	-0.053	0.012	0.095	-0.104	-0.129	0.135	0.131
Moharia																
PC1	6.30	48.5	48.5	0.342	0.344	0.075	0.341	0.351	0.254	0.094	-0.035	0.364	0.318	0.331	0.184	0.261
PC2	2.13	16.4	64.9	-0.063	0.143	0.175	0.081	-0.107	0.159	0.620	0.644	-0.010	-0.080	-0.250	-0.140	0.116
PC3	1.30	10.0	74.9	-0.072	0.036	0.458	-0.024	-0.175	-0.427	-0.131	0.033	-0.083	0.011	-0.108	0.488	0.543

1=DF = Days to 50 per cent flowering, PLHT = Plant height (cm), BT = Basal tiller number, FLBL = Flag leaf blade length (mm), FLBW = Flag leaf blade width (mm), FLSL = Flag leaf sheath length (mm), PEDL = Peduncle length (mm), PEX = Panicle exertion (mm), INFL = Inflorescence length (mm), INFW = Inflorescence width (mm), W5P = Weight of five panicles (g), SPY = Single plant yield (g), PY = Grain yield per plot (Kg ha-1)

Table 30. Race wise vector loadings and percentage of variation explained by the first three principal components (PCs) in foxtail millet core collection evaluated at ICRISAT, Patancheru 2010 rainy season

PCs	Eigen Value	Variability (%)	Cumulative %	Eigenvectors												
				DF[1]	PLHT	BT	FLBL	FLBW	FLSL	PEDL	PEX	INFL	INFW	W5P	SPY	PY
Indica																
PC1	5.34	41.1	41.1	0.299	0.387	-0.198	0.324	0.375	0.269	0.090	-0.061	0.400	0.364	0.308	0.072	-0.017
PC2	2.2	17.1	58.2	-0.281	-0.024	-0.398	-0.095	0.047	0.032	0.574	0.611	-0.058	-0.008	0.128	-0.143	-0.083
PC3	1.98	15.3	73.5	-0.089	0.120	0.269	0.004	-0.063	0.277	0.246	0.105	-0.033	-0.184	0.045	0.590	0.607
Maxima																
PC1	7.37	56.7	56.7	0.337	0.325	-0.146	0.350	0.317	0.248	-0.043	-0.179	0.292	0.321	0.301	0.328	0.233
PC2	2.45	18.8	75.5	-0.166	0.201	-0.312	0.081	0.037	0.337	0.622	0.508	0.102	-0.152	0.080	-0.160	-0.058
PC3	1.99	7.7	83.2	0.013	0.240	0.570	0.166	-0.282	0.347	0.014	-0.165	0.415	-0.097	-0.142	-0.126	-0.381
Moharia																
PC1	7.86	60.4	60.5	0.255	0.338	-0.143	0.338	0.328	0.332	0.168	0.015	0.330	0.329	0.333	0.278	0.186
PC2	2.23	17.1	77.6	-0.273	0.133	-0.230	-0.080	-0.120	0.120	0.570	0.635	-0.026	0.012	-0.023	-0.076	-0.290
PC3	1.10	8.4	85.9	-0.052	0.036	0.737	0.143	-0.146	0.089	0.185	0.177	0.217	-0.253	-0.244	0.366	0.183

1=DF = Days to 50 per cent flowering, PLHT = Plant height (cm), BT = Basal tiller number, FLBL = Flag leaf blade length (mm), FLBW = Flag leaf blade width (mm), FLSL = Flag leaf sheath length (mm), PEDL = Peduncle length (mm), PEX = Panicle exertion (mm), INFL = Inflorescence length (mm), INFW = Inflorescence width (mm), W5P = Weight of five panicles (g), SPY = Single plant yield (g), PY = Grain yield per plot (Kg ha-1)

Table 31. Race wise vector loadings and percentage of variation explained by the first three principal components (PCs) in foxtail millet core collection estimated using pooled data of three environments

PCs	Eigen value	Variability (%)	Cumulative %	Eigenvectors												
				DF[1]	PLHT	BT	FLBL	FLBW	FLSL	PEDL	PEX	INFL	INFW	W5P	SPY	PY
Indica																
F1	5.06	39.0	39.0	0.337	0.368	-0.129	0.372	0.382	0.223	0.094	-0.031	0.403	0.331	0.334	0.074	0.022
F2	2.14	16.5	55.4	0.031	0.156	0.291	-0.028	-0.145	0.185	-0.126	-0.228	0.021	-0.178	-0.025	0.602	0.609
F3	2.00	15.4	70.8	-0.269	0.123	-0.087	-0.055	-0.041	0.214	0.647	0.612	-0.079	-0.079	0.078	0.139	0.154
Maxima																
F1	8.09	62.2	62.2	0.324	0.330	-0.003	0.343	0.281	0.258	0.012	-0.136	0.304	0.310	0.309	0.336	0.328
F2	2.37	18.2	80.4	-0.103	0.136	-0.246	0.061	0.135	0.343	0.638	0.557	0.080	-0.183	-0.023	-0.090	-0.066
F3	1.24	9.5	89.9	0.122	0.153	0.801	0.019	-0.341	0.151	0.130	0.083	0.202	-0.240	-0.215	0.081	0.074
MSoharia																
F1	8.01	61.6	61.6	0.302	0.341	0.010	0.330	0.332	0.309	0.162	-0.027	0.340	0.327	0.302	0.266	0.257
F2	1.92	14.7	76.4	-0.095	0.110	0.174	-0.021	-0.133	0.110	0.623	0.696	0.031	-0.036	-0.204	-0.040	-0.005
F3	1.39	10.7	87.1	0.055	-0.022	0.726	0.021	-0.182	-0.108	-0.090	-0.149	0.001	-0.211	-0.186	0.358	0.432

1=DF = Days to 50 per cent flowering, PLHT = Plant height (cm), BT = Basal tiller number, FLBL = Flag leaf blade length (mm), FLBW = Flag leaf blade width (mm), FLSL = Flag leaf sheath length (mm), PEDL = Peduncle length (mm), PEX = Panicle exertion (mm), INFL = Inflorescence length (mm), INFW = Inflorescence width (mm), W5P = Weight of five panicles (g), SPY = Single plant yield (g), PY = Grain yield per plot (Kg ha-1)

Table 32a. Performance of 15 early maturity accessions in foxtail millet core collection for various quantitative traits based on pooled BLUPs of three environments

Accession name	DF[1]	PLHT	BT	FLBL	FLBW	FLSL	PEDL	PEX	INFL	INFW	W5P	SPY	PY
ISe 1201	31.8	51	2	86.6	11.5	71.7	221.9	152.5	95.6	10.6	7.4	4.1	360
ISe 1312	34.7	46	3.5	104.8	9.5	95.5	244.8	151.6	45.9	8.5	3.2	3.3	196
ISe 1320	35.7	48.7	2.5	129.4	11.9	96.3	251.1	156.7	52.5	9.8	4.5	7	533
ISe 1234	36.2	44.5	3.6	140.9	11.4	102.3	227.1	127.1	54.4	11	5.6	6.9	443
ISe 1563	36.3	75.4	1.9	169.4	14.4	114.5	329.6	218.1	80.9	10.8	7.2	4.7	361
ISe827	36.9	57	2.7	111.2	14.6	92.6	341.4	253.4	46.3	11	5.2	4.8	386
ISe1335	37.4	41.3	2.7	114.6	11.2	88.6	254.5	168.3	41.1	8.1	12.3	4.2	283
ISe1151	37.8	62.3	2.7	143.2	15.5	106.7	233.9	134.5	78	11.3	20.9	14.2	196
ISe1258	37.8	67.6	1.5	191.9	19	113.6	308.8	198	108.4	13	17.2	6	413
ISe1286	38	55.3	4.8	115.7	11.3	88.6	286.4	198.9	50.2	10.2	5.1	3.9	288
ISe1254	38.5	56.6	1.4	95.5	12.4	81.5	286.8	208.4	42.8	10.3	3.8	3.4	283
ISe1655	38.5	97	3.3	220.6	15.2	140.5	359.8	217.7	143.3	18.4	23.5	10.5	634
ISe1181	38.7	80.1	2.5	174.3	17.8	113.2	294.2	183.6	107.8	12.3	13.8	5.6	211
ISe1161	39	67.9	3.3	154.2	13.1	132.9	275.9	216.1	51.7	11.7	4.9	4	398
ISe1638	39.4	68.9	1.4	180.1	15.4	111	324.1	216.1	96.2	13.3	5.8	7.1	359
Mean	37.1	61.3	2.7	142.2	13.6	103.3	282.7	186.7	73	11.4	9.4	6	356.3
Standard Error	0.51	3.92	0.25	10.05	0.69	4.8	11.25	9.46	8.07	0.62	1.7	0.77	31.6
Range	7.5	55.8	3.5	134	9.5	68.8	137.9	126.3	102.2	10.3	20.3	10.9	438.0
Variance	3.9	230.6	0.9	1516.4	7.1	342.3	1899.5	1342.8	975.7	5.9	43.3	8.8	14975.1
Minimum	31.8	41.3	1.4	86.6	9.5	71.7	221.9	127.1	41.1	8.1	3.2	3.3	196.0
Maximum	39.4	97.01	4.8	220.6	19	140.5	359.8	253.4	143.3	18.4	23.5	14.3	634.0
Control cultivars													
ISe 1468	58.0	104.9	3.3	291.4	19.3	124.5	322.9	201.2	135.5	21.1	40.1	27.3	1914.0
ISe 1541	76.2	116.5	3.0	354.9	22.0	130.3	199.6	68.9	198.9	35.6	55.1	38.5	2077.0
ISe 375	52.9	100.5	1.4	261.8	21.7	113.1	259.9	149.0	100.5	25.2	59.6	28.4	1926.0
ISe 376	58.1	103.2	1.2	293.9	26.3	118.5	258.6	141.7	115.4	25.1	56.7	26.9	1794.0
Mean	61.29	106.28	2.23	300.5	22.31	121.6	260.25	140.2	137.58	26.73	52.88	30.26	1927.8
Control mean + LSD	62.7	114.6	2.7	316.1	23.7	133.6	279.0	153.4	151.6	28.2	55.8	33.2	2090.6
Control mean-LSD	59.9	98.0	1.8	284.9	21.0	109.6	241.5	127.0	123.5	25.3	49.9	27.4	1765.0
Entire core collection													
Mean	53.3	96.7	3.4	253.0	18.1	133.1	301.6	171.6	139.4	16.2	24.0	18.5	1201.0
LSD	1.42	8.28	0.42	15.56	1.35	12.02	18.74	13.22	14.06	1.46	2.94	2.91	162.80
CV (%)	2.9	9.3	13.4	6.7	8.2	10.0	6.8	8.4	11.0	9.9	13.3	17.2	14.8

1=DF = Days to 50 per cent flowering, PLHT = Plant height (cm), BT = Basal tiller number, FLBL = Flag leaf blade length (mm), FLBW = Flag leaf blade width (mm), FLSL = Flag leaf sheath length (mm), PEDL = Peduncle length (mm), PEX = Panicle exertion (mm), INFL = Inflorescence length (mm), INFW = Inflorescence width (mm), W5P = Weight of five panicles (g), SPY = Single plant yield (g), PY = Grain yield per plot (Kg ha-1)

Table 32b. Performance of 15 tall plants (tallness) in foxtail millet core collection for various quantitative traits based on pooled BLUPs of three environments

Accession name	PLHT[1]	DF	BT	FLBL	FLBW	FLSL	PEDL	PEX	INFL	INFW	W5P	SPY	PY
ISe1736	121.1	69.7	3.4	280.9	21.5	165.3	337.9	175.0	192.1	19.2	41.6	27.5	1961
ISe1881	121.9	58.5	4.2	290.5	17.3	165.9	323.3	160.7	196.4	17.5	35.5	43.1	2225
ISe1687	122.1	68.3	3.3	329.4	24.7	147.8	258.9	107.4	201.4	23.1	46.4	38.0	2013
ISe1597	122.2	80.9	2.6	423.4	26.7	130.9	283.3	147.4	257.1	23.7	52.6	34.8	1870
ISe999	122.4	56.3	5.1	283.3	18.5	152.9	296.0	145.2	162.0	15.7	17.2	19.9	1496
ISe983	123.5	62.8	2.0	314.1	21.8	169.2	328.5	161.6	186.1	22.2	35.0	13.9	992
ISe1511	124.5	62.2	3.4	323.3	19.2	146.9	295.1	147.8	197.7	19.3	41.5	27.1	1762
ISe717	125.4	62.5	3.0	308.9	20.2	161.7	278.9	109.9	203.5	18.6	31.0	21.9	1668
ISe751	125.7	103.1	3.6	425.3	25.4	164.4	306.6	144.4	241.2	21.9	34.1	16.4	853
ISe1474	127.8	59.3	2.7	285.3	21.0	128.9	292.9	174.4	211.1	19.5	42.5	37.1	1980
ISe748	128.8	97.5	5.0	349.2	25.8	159.2	306.4	153.9	255.1	22.3	43.0	21.2	902
ISe1059	131.2	66.5	2.9	315.9	23.6	150.1	325.9	195.4	194.9	21.1	35.6	31.0	1889
ISe1419	131.6	90.1	2.9	359.7	21.2	138.0	256.1	120.0	231.9	25.9	39.6	7.8	560
ISe769	136.7	89.9	3.8	360.4	27.2	166.4	304.4	137.2	212.1	23.1	47.2	16.9	1208
ISe1387	140.4	79.8	4.3	400.4	26.8	173.9	340.6	169.1	221.3	23.1	28.7	9.1	596
Mean	127.0	73.8	3.5	336.7	22.7	154.8	302.3	150.0	210.9	21.1	38.1	24.4	1465.0
Standard Error	1.49	3.94	0.23	12.60	0.84	3.63	6.75	6.35	6.80	0.70	2.23	2.80	145.06
Standard Deviation	5.8	15.3	0.9	48.8	3.2	14.0	26.1	24.6	26.3	2.7	8.6	10.8	561.8
Sample Variance	33.3	233.1	0.8	2383.0	10.5	197.2	683.2	604.5	693.0	7.4	74.7	117.3	315628.7
Range	19.3	46.8	3.2	144.4	9.9	45.0	84.5	88.0	95.1	10.2	35.3	35.3	1665.0
Minimum	121.1	56.3	2.0	280.9	17.3	128.9	256.1	107.4	162.0	15.7	17.2	7.8	560.0
Maximum	140.4	103.1	5.1	425.3	27.2	173.9	340.6	195.4	257.1	25.9	52.6	43.1	2225.0
Control cultivars													
ISe 1468	104.9	58.0	3.3	291.4	19.3	124.5	322.9	201.2	135.5	21.1	40.1	27.3	1914
ISe 1541	116.5	76.2	3.0	354.9	22.0	130.3	199.6	68.9	198.9	35.6	55.1	38.5	2077
ISe 375	100.5	52.9	1.4	261.8	21.7	113.1	259.9	149.0	100.5	25.2	59.6	28.4	1926
ISe 376	103.2	58.1	1.2	293.9	26.3	118.5	258.6	141.7	115.4	25.1	56.7	26.9	1794
Mean	106.3	61.3	2.2	300.5	22.3	121.6	260.3	140.2	137.6	26.7	52.9	30.3	1927.8
Control mean + LSD	114.6	62.7	2.7	316.1	23.7	133.6	279.0	153.4	151.6	28.2	55.8	33.2	2090.6
Control mean-LSD	98.0	59.9	1.8	284.9	21.0	109.6	241.5	127.0	123.5	25.3	49.9	27.4	1765
Entire core collection													
Mean	96.7	53.3	3.4	253.0	18.1	133.1	301.6	171.6	139.4	16.2	24.0	18.5	1201.0
LSD	8.28	1.42	0.42	15.56	1.35	12.02	18.74	13.22	14.06	1.46	2.94	2.91	162.80
CV (%)	9.3	2.9	13.4	6.7	8.2	10.0	6.8	8.4	11.0	9.9	13.3	17.2	14.8

1=DF = Days to 50 per cent flowering, PLHT = Plant height (cm), BT = Basal tiller number, FLBL = Flag leaf blade length (mm), FLBW = Flag leaf blade width (mm), FLSL = Flag leaf sheath length (mm), PEDL = Peduncle length (mm), PEX = Panicle exertion (mm), INFL = Inflorescence length (mm), INFW = Inflorescence width (mm), W5P = Weight of five panicles (g), SPY = Single plant yield (g), PY = Grain yield per plot (Kg ha-1)

Table 32c. Performance of 15 maximum basal tiller number accessions in foxtail millet core collection for various quantitative traits based on pooled BLUPs of three environments

Accession name	BT[1]	DF	PLHT	FLBL	FLBW	FLSL	PEDL	PEX	INFL	INFW	W5P	SPY	PY
ISe1846	4.8	52.8	108.5	265.6	15.6	136.2	278.8	136.9	149.8	14.8	27.3	32.6	2080
ISe1286	4.8	38.0	55.3	115.7	11.3	88.6	286.4	198.9	50.2	10.2	5.1	3.9	288
ISe1299	4.9	43.2	59.7	157.3	12.2	96.6	250.8	156.6	61.2	10.6	9.5	9.0	878
ISe914	5.0	56.4	113.7	305.0	18.3	152.3	310.7	165.0	163.5	12.8	17.7	22.3	1278
ISe748	5.0	97.5	128.8	349.2	25.8	159.2	306.4	153.9	255.1	22.3	43.0	21.2	902
ISe1305	5.0	42.7	70.6	155.0	10.1	116.8	361.1	247.8	70.8	10.7	10.3	9.2	537
ISe362	5.0	57.4	106.3	299.6	18.2	156.4	306.0	151.7	164.8	13.4	18.2	24.9	1597
ISe1664	5.0	59.0	110.7	275.0	18.6	136.4	325.6	191.8	153.3	14.4	19.2	12.3	791
ISe1269	5.1	56.8	108.4	269.3	17.3	157.2	322.5	167.7	166.1	13.5	22.1	25.1	1744
ISe999	5.1	56.3	122.4	283.3	18.5	152.9	296.0	145.2	162.0	15.7	17.2	19.9	1496
ISe710	5.4	54.9	102.5	280.9	17.4	151.9	284.3	134.4	153.1	14.3	22.2	18.8	1146
ISe1009	5.5	47.0	60.5	170.4	11.5	102.4	251.7	151.6	60.0	10.6	4.1	6.8	568
ISe1408	5.9	49.9	89.1	243.6	16.1	131.7	289.7	160.3	111.6	13.8	13.6	27.1	1941
ISe1129	5.9	41.3	46.4	123.3	10.2	75.9	225.2	151.6	49.2	10.0	3.3	4.6	283
ISe1162	6.0	55.4	93.6	235.3	15.9	132.1	319.6	186.3	138.9	11.8	12.4	22.3	1566
Mean	5.2	53.9	91.8	235.2	15.8	129.8	294.3	166.7	127.3	13.3	16.4	17.3	1139.7
Standard Error	0.11	3.57	6.86	18.73	1.08	7.09	8.82	7.56	15.14	0.80	2.64	2.32	151.57
Standard Deviation	0.4	13.8	26.6	72.5	4.2	27.5	34.2	29.3	58.6	3.1	10.2	9.0	587.0
Sample Variance	0.2	191.1	706.4	5261.5	17.6	754.9	1167.0	858.1	3437.3	9.7	104.6	81.0	344599.4
Range	1.2	59.4	82.4	233.5	15.7	83.3	135.9	113.4	205.9	12.3	39.7	28.7	1797.0
Minimum	4.8	38.0	46.4	115.7	10.1	75.9	225.2	134.4	49.2	10.0	3.3	3.9	283.0
Maximum	6.0	97.5	128.8	349.2	25.8	159.2	361.1	247.8	255.1	22.3	43.0	32.6	2080.0
Control cultivars													
ISe 1468	3.3	58.0	104.9	291.4	19.3	124.5	322.9	201.2	135.5	21.1	40.1	27.3	1914.0
ISe 1541	3.0	76.2	116.5	354.9	22.0	130.3	199.6	68.9	198.9	35.6	55.1	38.5	2077.0
ISe 375	1.4	52.9	100.5	261.8	21.7	113.1	259.9	149.0	100.5	25.2	59.6	28.4	1926.0
ISe 376	1.2	58.1	103.2	293.9	26.3	118.5	258.6	141.7	115.4	25.1	56.7	26.9	1794.0
Mean	2.2	61.3	106.3	300.5	22.3	121.6	260.3	140.2	137.6	26.7	52.9	30.3	1927.8
Control mean + LSD	2.7	62.7	114.6	316.1	23.7	133.6	279.0	153.4	151.6	28.2	55.8	33.2	2090.6
Control mean-LSD	1.8	59.9	98.0	284.9	21.0	109.6	241.5	127.0	123.5	25.3	49.9	27.4	1765.0
Entire core collection													
Mean	3.4	96.7	53.3	253.0	18.1	133.1	301.6	171.6	139.4	16.2	24.0	18.5	1201.0
LSD	0.42	8.28	1.42	15.56	1.35	12.02	18.74	13.22	14.06	1.46	2.94	2.91	162.80
CV (%)	13.4	9.3	2.9	6.7	8.2	10.0	6.8	8.4	11.0	9.9	13.3	17.2	14.8

1=DF = Days to 50 per cent flowering, PLHT = Plant height (cm), BT = Basal tiller number, FLBL = Flag leaf blade length (mm), FLBW = Flag leaf blade width (mm), FLSL = Flag leaf sheath length (mm), PEDL = Peduncle length (mm), PEX = Panicle exertion (mm), INFL = Inflorescence length (mm), INFW = Inflorescence width (mm), W5P = Weight of five panicles (g), SPY = Single plant yield (g), PY = Grain yield per plot (Kg ha-1)

Table 32d. Performance of 15 maximum flag leaf blade length (mm) accessions in foxtail millet core collection for various quantitative traits based on pooled BLUPs of three environments

Accession name	FLBL[1]	DF	PLHT	BT	FLBW	FLSL	PEDL	PEX	INFL	INFW	W5P	SPY	PY
ISe717	308.9	62.5	125.4	3.0	20.2	161.7	278.9	109.9	203.5	18.6	31.0	21.9	1668
ISe1666	309.2	54.1	110.4	2.6	19.8	128.5	342.3	216.7	178.9	20.7	58.4	21.2	1429
ISe983	314.1	62.8	123.5	2.0	21.8	169.2	328.5	161.6	186.1	22.2	35.0	13.9	992
ISe1059	315.9	66.5	131.2	2.9	23.6	150.1	325.9	195.4	194.9	21.1	35.6	31.0	1889
ISe2	316.2	50.0	112.1	3.8	17.5	151.1	337.9	189.4	168.9	18.2	32.0	22.2	1416
ISe144	323.2	53.2	116.6	3.0	21.9	138.5	340.0	204.4	185.3	19.5	31.9	20.9	1330
ISe1511	323.3	62.2	124.5	3.4	19.2	146.9	295.1	147.8	197.7	19.3	41.5	27.1	1762
ISe132	325.8	51.6	116.7	3.8	19.7	152.9	348.0	197.8	189.3	18.5	39.3	16.9	933
ISe1687	329.4	68.3	122.1	3.3	24.7	147.8	258.9	107.4	201.4	23.1	46.4	38.0	2013
ISe748	349.2	97.5	128.8	5.0	25.8	159.2	306.4	153.9	255.1	22.3	43.0	21.2	902
ISe1419	359.7	90.1	131.6	2.9	21.2	138.0	256.1	120.0	231.9	25.9	39.6	7.8	560
ISe769	360.4	89.9	136.7	3.8	27.2	166.4	304.4	137.2	212.1	23.1	47.2	16.9	1208
ISe1387	400.4	79.8	140.4	4.3	26.8	173.9	340.6	169.1	221.3	23.1	28.7	9.1	596
ISe1597	423.4	80.9	122.2	2.6	26.7	130.9	283.3	147.4	257.1	23.7	52.6	34.8	1870
ISe751	425.3	103.1	125.7	3.6	25.4	164.4	306.6	144.4	241.2	21.9	34.1	16.4	853
Mean	345.6	71.5	124.5	3.3	22.8	152.0	310.2	160.2	208.3	21.4	39.7	21.3	1294.7
Standard Error	10.44	4.52	2.18	0.20	0.82	3.59	7.92	8.94	7.09	0.58	2.21	2.22	123.43
Standard Deviation	40.5	17.5	8.5	0.8	3.2	13.9	30.7	34.6	27.5	2.3	8.5	8.6	478.0
Sample Variance	1635.9	306.6	71.6	0.6	10.0	193.4	940.8	1200.2	754.0	5.1	73.0	74.2	228506.1
Range	116.4	53.1	30.0	3.0	9.7	45.4	91.9	109.3	88.2	7.7	29.8	30.2	1453.0
Minimum	308.9	50.0	110.4	2.0	17.5	128.5	256.1	107.4	168.9	18.2	28.7	7.8	560.0
Maximum	425.3	103.1	140.4	5.0	27.2	173.9	348.0	216.7	257.1	25.9	58.4	38.0	2013.0
Control cultivars													
ISe 1468	291.4	58.0	104.9	3.3	19.3	124.5	322.9	201.2	135.5	21.1	40.1	27.3	1914.0
ISe 1541	354.9	76.2	116.5	3.0	22.0	130.3	199.6	68.9	198.9	35.6	55.1	38.5	2077.0
ISe 375	261.8	52.9	100.5	1.4	21.7	113.1	259.9	149.0	100.5	25.2	59.6	28.4	1926.0
ISe 376	293.9	58.1	103.2	1.2	26.3	118.5	258.6	141.7	115.4	25.1	56.7	26.9	1794.0
Mean	300.5	61.3	106.3	2.2	22.3	121.6	260.3	140.2	137.6	26.7	52.9	30.3	1927.8
Control mean + LSD	316.1	62.7	114.6	2.7	23.7	133.6	279.0	153.4	151.6	28.2	55.8	33.2	2090.6
Control mean-LSD	284.9	59.9	98.0	1.8	21.0	109.6	241.5	127.0	123.5	25.3	49.9	27.4	1765.0
Entire core collection													
Mean	253.0	53.3	96.7	3.4	18.1	133.1	301.6	171.6	139.4	16.2	24.0	18.5	1201.0
LSD	15.56	1.42	8.28	0.42	1.35	12.02	18.74	13.22	14.06	1.46	2.94	2.91	162.80
CV (%)	6.7	2.9	9.3	13.4	8.2	10.0	6.8	8.4	11.0	9.9	13.3	17.2	14.8

1=DF = Days to 50 per cent flowering, PLHT = Plant height (cm), BT = Basal tiller number, FLBL = Flag leaf blade length (mm), FLBW = Flag leaf blade width (mm), FLSL = Flag leaf sheath length (mm), PEDL = Peduncle length (mm), PEX = Panicle exertion (mm), INFL = Inflorescence length (mm), INFW = Inflorescence width (mm), W5P = Weight of five panicles (g), SPY = Single plant yield (g), PY = Grain yield per plot (Kg ha-1)

Table 32e. Performance of15 maximum flag leaf width (mm) accessions in foxtail millet core collection for various quantitative traits based on pooled BLUPs of three environments

Accession name	FLBW[1]	DF	PLHT	BT	FLBL	FLSL	PEDL	PEX	INFL	INFW	W5P	SPY	PY
ISe144	21.9	53.2	116.6	3.0	323.2	138.5	340.0	204.4	185.3	19.5	31.9	20.9	1330
ISe375	22.3	58.0	96.0	1.7	250.2	122.1	275.7	156.8	103.9	25.4	53.7	19.9	1466
ISe1745	22.5	58.5	114.0	2.2	286.5	159.1	337.8	181.2	170.1	17.5	33.0	21.7	1602
ISe1251	22.8	49.7	107.7	1.9	266.3	158.4	329.5	173.6	160.4	20.7	51.4	28.1	1141
ISe1059	23.6	66.5	131.2	2.9	315.9	150.1	325.9	195.4	194.9	21.1	35.6	31.0	1889
ISe1575	23.8	55.9	84.8	1.3	245.6	128.5	323.1	197.3	140.1	18.6	22.3	11.0	489
ISe900	24.1	55.6	113.9	2.0	295.2	145.2	287.4	144.3	169.9	19.3	27.1	17.3	1238
ISe1685	24.3	84.0	119.1	2.6	305.7	125.1	232.9	109.7	247.6	25.9	44.5	34.4	1959
ISe1687	24.7	68.3	122.1	3.3	329.4	147.8	258.9	107.4	201.4	23.1	46.4	38.0	2013
ISe751	25.4	103.1	125.7	3.6	425.3	164.4	306.6	144.4	241.2	21.9	34.1	16.4	853
ISe748	25.8	97.5	128.8	5.0	349.2	159.2	306.4	153.9	255.1	22.3	43.0	21.2	902
ISe1597	26.7	80.9	122.2	2.6	423.4	130.9	283.3	147.4	257.1	23.7	52.6	34.8	1870
ISe1593	26.8	51.2	83.4	1.1	248.9	129.0	318.1	191.7	136.2	20.5	34.7	13.1	758
ISe1387	26.8	79.8	140.4	4.3	400.4	173.9	340.6	169.1	221.3	23.1	28.7	9.1	596
ISe769	27.2	89.9	136.7	3.8	360.4	166.4	304.4	137.2	212.1	23.1	47.2	16.9	1208
Mean	24.6	70.2	116.2	2.8	321.7	146.6	304.7	160.9	193.1	21.7	39.1	22.3	1287.6
Standard Error	0.46	4.58	4.43	0.29	15.60	4.33	8.19	7.82	12.08	0.63	2.57	2.33	130.47
Standard Deviation	1.8	17.7	17.1	1.1	60.4	16.8	31.7	30.3	46.8	2.4	10.0	9.0	505.3
Variance	3.2	314.7	293.8	1.2	3649.2	281.1	1005.1	917.0	2189.5	5.9	99.1	81.7	255337.7
Range	5.3	53.4	57.0	3.9	179.7	51.8	107.7	97.0	153.2	8.4	31.4	28.9	1524.0
Minimum	21.9	49.7	83.4	1.1	245.6	122.1	232.9	107.4	103.9	17.5	22.3	9.1	489.0
Maximum	27.2	103.1	140.4	5.0	425.3	173.9	340.6	204.4	257.1	25.9	53.7	38.0	2013.0
Control cultivars													
ISe 1468	19.3	58.0	104.9	3.3	291.4	124.5	322.9	201.2	135.5	21.1	40.1	27.3	1914
ISe 1541	22.0	76.2	116.5	3.0	354.9	130.3	199.6	68.9	198.9	35.6	55.1	38.5	2077
ISe 375	21.7	52.9	100.5	1.4	261.8	113.1	259.9	149.0	100.5	25.2	59.6	28.4	1926
ISe 376	26.3	58.1	103.2	1.2	293.9	118.5	258.6	141.7	115.4	25.1	56.7	26.9	1794
Mean	22.3	61.3	106.3	2.2	300.5	121.6	260.3	140.2	137.6	26.7	52.9	30.3	1927.8
Control mean + LSD	23.7	62.7	114.6	2.7	316.1	133.6	279.0	153.4	151.6	28.2	55.8	33.2	2090.6
Control mean-LSD	21.0	59.9	98.0	1.8	284.9	109.6	241.5	127.0	123.5	25.3	49.9	27.4	1765.0
Entire core collection													
Mean	18.1	53.3	96.7	3.4	253.0	133.1	301.6	171.6	139.4	16.2	24.0	18.5	1201.0
LSD	1.35	1.42	8.28	0.42	15.56	12.02	18.74	13.22	14.06	1.46	2.94	2.91	162.80
CV (%)	8.2	2.9	9.3	13.4	6.7	10.0	6.8	8.4	11.0	9.9	13.3	17.2	14.8

1=DF = Days to 50 per cent flowering, PLHT = Plant height (cm), BT = Basal tiller number, FLBL = Flag leaf blade length (mm), FLBW = Flag leaf blade width (mm), FLSL = Flag leaf sheath length (mm), PEDL = Peduncle length (mm), PEX = Panicle exertion (mm), INFL = Inflorescence length (mm), INFW = Inflorescence width (mm), W5P = Weight of five panicles (g), SPY = Single plant yield (g), PY = Grain yield per plot (Kg ha-1)

Table 32f. Performance of 15 maximum inflorescence length (mm) accessions in foxtail millet core collection for various quantitative traits based on pooled BLUPs of three environments

Accession Name	INFL[1]	DF	PLHT	BT	FLBL	FLBW	FLSL	PEDL	PEX	INFW	W5P	SPY	PY
ISe1059	194.9	66.5	131.2	2.9	315.9	23.6	150.1	325.9	195.4	21.1	35.6	31.0	1889
ISe1881	196.4	58.5	121.9	4.2	290.5	17.3	165.9	323.3	160.7	17.5	35.5	43.1	2225
ISe1511	197.7	62.2	124.5	3.4	323.3	19.2	146.9	295.1	147.8	19.3	41.5	27.1	1762
ISe1687	201.4	68.3	122.1	3.3	329.4	24.7	147.8	258.9	107.4	23.1	46.4	38.0	2013
ISe717	203.5	62.5	125.4	3.0	308.9	20.2	161.7	278.9	109.9	18.6	31.0	21.9	1668
ISe1725	208.4	53.2	120.9	1.7	286.1	20.0	139.4	301.6	161.2	20.1	32.6	26.3	1808
ISe1454	209.7	61.7	115.1	1.8	297.0	20.8	175.3	341.7	168.8	21.0	54.5	15.8	1100
ISe1474	211.1	59.3	127.8	2.7	285.3	21.0	128.9	292.9	174.4	19.5	42.5	37.1	1980
ISe769	212.1	89.9	136.7	3.8	360.4	27.2	166.4	304.4	137.2	23.1	47.2	16.9	1208
ISe1387	221.3	79.8	140.4	4.3	400.4	26.8	173.9	340.6	169.1	23.1	28.7	9.1	596
ISe1419	231.9	90.1	131.6	2.9	359.7	21.2	138.0	256.1	120.0	25.9	39.6	7.8	560
ISe751	241.2	103.1	125.7	3.6	425.3	25.4	164.4	306.6	144.4	21.9	34.1	16.4	853
ISe1685	247.6	84.0	119.1	2.6	305.7	24.3	125.1	232.9	109.7	25.9	44.5	34.4	1959
ISe748	255.1	97.5	128.8	5.0	349.2	25.8	159.2	306.4	153.9	22.3	43.0	21.2	902
ISe1597	257.1	80.9	122.2	2.6	423.4	26.7	130.9	283.3	147.4	23.7	52.6	34.8	1870
Mean	219.3	74.5	126.2	3.2	337.4	23.0	151.6	296.6	147.2	21.7	40.6	25.4	1492.9
Standard Error	5.62	4.08	1.73	0.23	12.34	0.81	4.27	8.00	6.78	0.64	1.99	2.82	145.26
Standard Deviation	21.8	15.8	6.7	0.9	47.8	3.2	16.5	31.0	26.3	2.5	7.7	10.9	562.6
Variance	474.3	249.2	45.1	0.8	2284.1	9.9	273.2	960.6	690.1	6.2	59.5	118.9	316525.6
Range	62.2	49.9	25.3	3.2	140.0	9.9	50.2	108.8	88.0	8.5	25.8	35.3	1665.0
Minimum	194.9	53.2	115.1	1.7	285.3	17.3	125.1	232.9	107.4	17.5	28.7	7.8	560.0
Maximum	257.1	103.1	140.4	5.0	425.3	27.2	175.3	341.7	195.4	25.9	54.5	43.1	2225.0
Control cultivars													
ISe 1468	135.5	58.0	104.9	3.3	291.4	19.3	124.5	322.9	201.2	21.1	40.1	27.3	1914
ISe 1541	198.9	76.2	116.5	3.0	354.9	22.0	130.3	199.6	68.9	35.6	55.1	38.5	2077
ISe 375	100.5	52.9	100.5	1.4	261.8	21.7	113.1	259.9	149.0	25.2	59.6	28.4	1926
ISe 376	115.4	58.1	103.2	1.2	293.9	26.3	118.5	258.6	141.7	25.1	56.7	26.9	1794
Mean	137.6	61.3	106.3	2.2	300.5	22.3	121.6	260.3	140.2	26.7	52.9	30.3	1927.8
Control mean + LSD	151.6	62.7	114.6	2.7	316.1	23.7	133.6	279.0	153.4	28.2	55.8	33.2	2090.6
Control mean-LSD	123.5	59.9	98.0	1.8	284.9	21.0	109.6	241.5	127.0	25.3	49.9	27.4	1765.0
Entire core collection													
Mean	139.4	53.3	96.7	3.4	253.0	18.1	133.1	301.6	171.6	16.2	24.0	18.5	1201.0
LSD	14.06	1.42	8.28	0.42	15.56	1.35	12.02	18.74	13.22	1.46	2.94	2.91	162.80
CV (%)	11.0	2.9	9.3	13.4	6.7	8.2	10.0	6.8	8.4	9.9	13.3	17.2	14.8

1=DF = Days to 50 per cent flowering, PLHT = Plant height (cm), BT = Basal tiller number, FLBL = Flag leaf blade length (mm), FLBW = Flag leaf blade width (mm), FLSL = Flag leaf sheath length (mm), PEDL = Peduncle length (mm), PEX = Panicle exertion (mm), INFL = Inflorescence length (mm), INFW = Inflorescence width (mm), W5P = Weight of five panicles (g), SPY = Single plant yield (g), PY = Grain yield per plot (Kg ha-1)

Table 32g. Performance of 15 maximum inflorescence width (mm) accessions in foxtail millet core collection for various quantitative traits based on pooled BLUPs of three environments

Accession Name	INFW[1]	DF	PLHT	BT	FLBL	FLBW	FLSL	PEDL	PEX	INFL	W5P	SPY	PY
ISe1251	20.7	49.7	107.7	1.9	266.3	22.8	158.4	329.5	173.6	160.4	51.4	28.1	1141
ISe1454	21.0	61.7	115.1	1.8	297.0	20.8	175.3	341.7	168.8	209.7	54.5	15.8	1100
ISe1059	21.1	66.5	131.2	2.9	315.9	23.6	150.1	325.9	195.4	194.9	35.6	31.0	1889
ISe1610	21.7	58.0	102.7	2.5	270.6	19.9	130.0	321.3	194.0	130.6	28.3	18.3	1190
ISe751	21.9	103.1	125.7	3.6	425.3	25.4	164.4	306.6	144.4	241.2	34.1	16.4	853
ISe983	22.2	62.8	123.5	2.0	314.1	21.8	169.2	328.5	161.6	186.1	35.0	13.9	992
ISe748	22.3	97.5	128.8	5.0	349.2	25.8	159.2	306.4	153.9	255.1	43.0	21.2	902
ISe18	22.6	48.3	108.5	3.6	282.7	17.6	121.0	331.3	213.3	137.0	35.9	20.0	1308
ISe769	23.1	89.9	136.7	3.8	360.4	27.2	166.4	304.4	137.2	212.1	47.2	16.9	1208
ISe1387	23.1	79.8	140.4	4.3	400.4	26.8	173.9	340.6	169.1	221.3	28.7	9.1	596
ISe1687	23.1	68.3	122.1	3.3	329.4	24.7	147.8	258.9	107.4	201.4	46.4	38.0	2013
ISe1597	23.7	80.9	122.2	2.6	423.4	26.7	130.9	283.3	147.4	257.1	52.6	34.8	1870
ISe375	25.4	58.0	96.0	1.7	250.2	22.3	122.1	275.7	156.8	103.9	53.7	19.9	1466
ISe1419	25.9	90.1	131.6	2.9	359.7	21.2	138.0	256.1	120.0	231.9	39.6	7.8	560
ISe1685	25.9	84.0	119.1	2.6	305.7	24.3	125.1	232.9	109.7	247.6	44.5	34.4	1959
Mean	22.9	73.2	120.8	3.0	330.0	23.4	148.8	302.9	156.8	199.4	42.0	21.7	1269.8
Standard Error	0.44	4.48	3.28	0.25	14.35	0.72	5.04	8.77	7.96	12.30	2.30	2.43	123.65
Standard Deviation	1.7	17.4	12.7	1.0	55.6	2.8	19.5	34.0	30.8	47.6	8.9	9.4	478.9
Variance	2.9	301.2	161.5	0.9	3090.0	7.8	381.6	1153.0	951.0	2269.7	79.1	88.8	229324.9
Range	5.3	54.8	44.4	3.3	175.1	9.6	54.3	108.8	105.9	153.2	26.2	30.2	1453.0
Minimum	20.7	48.3	96.0	1.7	250.2	17.6	121.0	232.9	107.4	103.9	28.3	7.8	560.0
Maximum	25.9	103.1	140.4	5.0	425.3	27.2	175.3	341.7	213.3	257.1	54.5	38.0	2013.0
Control cultivars													
ISe 1468	21.1	58.0	104.9	3.3	291.4	19.3	124.5	322.9	201.2	135.5	40.1	27.3	1914
ISe 1541	35.6	76.2	116.5	3.0	354.9	22.0	130.3	199.6	68.9	198.9	55.1	38.5	2077
ISe 375	25.2	52.9	100.5	1.4	261.8	21.7	113.1	259.9	149.0	100.5	59.6	28.4	1926
ISe 376	25.1	58.1	103.2	1.2	293.9	26.3	118.5	258.6	141.7	115.4	56.7	26.9	1794
Mean	26.7	61.3	106.3	2.2	300.5	22.3	121.6	260.3	140.2	137.6	52.9	30.3	1927.8
Control mean + LSD	28.2	62.7	114.6	2.7	316.1	23.7	133.6	279.0	153.4	151.6	55.8	33.2	2090.6
Control mean-LSD	25.3	59.9	98.0	1.8	284.9	21.0	109.6	241.5	127.0	123.5	49.9	27.4	1765.0
Entire core collection													
Mean	16.2	53.3	96.7	3.4	253.0	18.1	133.1	301.6	171.6	139.4	24.0	18.5	1201.0
LSD	1.46	1.42	8.28	0.42	15.56	1.35	12.02	18.74	13.22	14.06	2.94	2.91	162.80
CV (%)	9.9	2.9	9.3	13.4	6.7	8.2	10.0	6.8	8.4	11.0	13.3	17.2	14.8

1=DF = Days to 50 per cent flowering, PLHT = Plant height (cm), BT = Basal tiller number, FLBL = Flag leaf blade length (mm), FLBW = Flag leaf blade width (mm), FLSL = Flag leaf sheath length (mm), PEDL = Peduncle length (mm), PEX = Panicle exertion (mm), INFL = Inflorescence length (mm), INFW = Inflorescence width (mm), W5P = Weight of five panicles (g), SPY = Single plant yield (g), PY = Grain yield per plot (Kg ha-1)

Table 32h. Performance of 15 maximum weight of five panicles (g) accessions in foxtail millet core collection for various quantitative traits based on pooled BLUPs of three environments

Accession Name.	W5P[1]	DF	PLHT	BT	FLBL	FLBW	FLSL	PEDL	PEX	INFL	INFW	SPY	PY
ISe302	38.0	51.2	105.5	3.6	286.6	19.2	128.8	305.0	178.5	143.8	19.7	24.2	1643
ISe132	39.3	51.6	116.7	3.8	325.8	19.7	152.9	348.0	197.8	189.3	18.5	16.9	933
ISe1419	39.6	90.1	131.6	2.9	359.7	21.2	138.0	256.1	120.0	231.9	25.9	7.8	560
ISe1511	41.5	62.2	124.5	3.4	323.3	19.2	146.9	295.1	147.8	197.7	19.3	27.1	1762
ISe1736	41.6	69.7	121.1	3.4	280.9	21.5	165.3	337.9	175.0	192.1	19.2	27.5	1961
ISe1474	42.5	59.3	127.8	2.7	285.3	21.0	128.9	292.9	174.4	211.1	19.5	37.1	1980
ISe748	43.0	97.5	128.8	5.0	349.2	25.8	159.2	306.4	153.9	255.1	22.3	21.2	902
ISe1685	44.5	84.0	119.1	2.6	305.7	24.3	125.1	232.9	109.7	247.6	25.9	34.4	1959
ISe1687	46.4	68.3	122.1	3.3	329.4	24.7	147.8	258.9	107.4	201.4	23.1	38.0	2013
ISe769	47.2	89.9	136.7	3.8	360.4	27.2	166.4	304.4	137.2	212.1	23.1	16.9	1208
ISe1251	51.4	49.7	107.7	1.9	266.3	22.8	158.4	329.5	173.6	160.4	20.7	28.1	1141
ISe1597	52.6	80.9	122.2	2.6	423.4	26.7	130.9	283.3	147.4	257.1	23.7	34.8	1870
ISe375	53.7	58.0	96.0	1.7	250.2	22.3	122.1	275.7	156.8	103.9	25.4	19.9	1466
ISe1454	54.5	61.7	115.1	1.8	297.0	20.8	175.3	341.7	168.8	209.7	21.0	15.8	1100
ISe1666	58.4	54.1	110.4	2.6	309.2	19.8	128.5	342.3	216.7	178.9	20.7	21.2	1429
Mean	46.3	68.6	119.0	3.0	316.8	22.4	145.0	300.7	157.7	199.5	21.9	24.7	1461.8
Standard Error	1.65	4.14	2.79	0.23	11.38	0.70	4.47	9.07	7.98	10.81	0.66	2.28	120.79
Standard Deviation	6.4	16.0	10.8	0.9	44.1	2.7	17.3	35.1	30.9	41.9	2.5	8.8	467.8
Variance	40.8	256.6	116.6	0.8	1942.0	7.3	300.4	1234.3	955.1	1752.2	6.5	77.6	218850.7
Range	20.5	47.8	40.7	3.3	173.2	8.0	53.2	115.1	109.3	153.2	7.5	30.2	1453.0
Minimum	38.0	49.7	96.0	1.7	250.2	19.2	122.1	232.9	107.4	103.9	18.5	7.8	560.0
Maximum	58.4	97.5	136.7	5.0	423.4	27.2	175.3	348.0	216.7	257.1	25.9	38.0	2013.0
Control cultivars													
ISe 1468	40.1	58.0	104.9	3.3	291.4	19.3	124.5	322.9	201.2	135.5	21.1	27.3	1914
ISe 1541	55.1	76.2	116.5	3.0	354.9	22.0	130.3	199.6	68.9	198.9	35.6	38.5	2077
ISe 375	59.6	52.9	100.5	1.4	261.8	21.7	113.1	259.9	149.0	100.5	25.2	28.4	1926
ISe 376	56.7	58.1	103.2	1.2	293.9	26.3	118.5	258.6	141.7	115.4	25.1	26.9	1794
Mean	52.9	61.3	106.3	2.2	300.5	22.3	121.6	260.3	140.2	137.6	26.7	30.3	1927.8
Control mean + LSD	55.8	62.7	114.6	2.7	316.1	23.7	133.6	279.0	153.4	151.6	28.2	33.2	2090.6
Control mean-LSD	49.9	59.9	98.0	1.8	284.9	21.0	109.6	241.5	127.0	123.5	25.3	27.4	1765.0
Entire core collection													
Mean	24.0	53.3	96.7	3.4	253.0	18.1	133.1	301.6	171.6	139.4	16.2	18.5	1201.0
LSD	2.94	1.42	8.28	0.42	15.56	1.35	12.02	18.74	13.22	14.06	1.46	2.91	162.80
CV (%)	13.3	2.9	9.3	13.4	6.7	8.2	10.0	6.8	8.4	11.0	9.9	17.2	14.8

1=DF = Days to 50 per cent flowering, PLHT = Plant height (cm), BT = Basal tiller number, FLBL = Flag leaf blade length (mm), FLBW = Flag leaf blade width (mm), FLSL = Flag leaf sheath length (mm), PEDL = Peduncle length (mm), PEX = Panicle exertion (mm), INFL = Inflorescence length (mm), INFW = Inflorescence width (mm), W5P = Weight of five panicles (g), SPY = Single plant yield (g), PY = Grain yield per plot (Kg ha-1)

Table 32i. Performance of 15 maximum single plant yield (g) accessions in foxtail millet core collection for various quantitative traits based on pooled BLUPs of three environments

Accession Name	SPY[1]	DF	PLHT	BT	FLBL	FLBW	FLSL	PEDL	PEX	INFL	INFW	W5P	PY
ISe1767	28.8	52.1	110.7	4.1	304.6	17.8	137.3	344.8	210.4	169.3	15.0	27.3	1974
ISe1000	29.2	60.2	110.6	4.7	283.9	17.1	150.6	301.7	140.8	140.1	13.1	23.5	1946
ISe388	30.8	58.9	109.7	4.4	265.6	18.5	156.4	327.9	174.0	155.0	14.9	29.1	1971
ISe1059	31.0	66.5	131.2	2.9	315.9	23.6	150.1	325.9	195.4	194.9	21.1	35.6	1889
ISe238	31.4	60.1	114.0	3.6	273.2	19.1	165.2	335.7	174.5	153.5	16.0	22.5	1629
ISe1846	32.6	52.8	108.5	4.8	265.6	15.6	136.2	278.8	136.9	149.8	14.8	27.3	2080
ISe1685	34.4	84.0	119.1	2.6	305.7	24.3	125.1	232.9	109.7	247.6	25.9	44.5	1959
ISe1597	34.8	80.9	122.2	2.6	423.4	26.7	130.9	283.3	147.4	257.1	23.7	52.6	1870
ISe1406	35.1	45.0	119.4	3.4	240.4	16.8	158.3	272.3	195.5	112.8	17.3	36.6	1917
ISe1888	35.4	50.7	98.3	3.8	261.3	18.6	154.0	280.4	128.4	158.0	16.8	21.7	2240
ISe364	37.0	61.9	105.4	4.1	249.7	18.2	128.2	325.9	201.5	142.5	14.2	32.8	2084
ISe1474	37.1	59.3	127.8	2.7	285.3	21.0	128.9	292.9	174.4	211.1	19.5	42.5	1980
ISe956	37.4	56.8	117.6	3.4	278.8	17.5	145.7	339.2	196.3	152.7	13.8	31.0	2081
ISe1687	38.0	68.3	122.1	3.3	329.4	24.7	147.8	258.9	107.4	201.4	23.1	46.4	2013
ISe1881	43.1	58.5	121.9	4.2	290.5	17.3	165.9	323.3	160.7	196.4	17.5	35.5	2225
Mean	34.4	61.1	115.9	3.6	291.6	19.8	145.4	301.6	163.6	176.2	17.8	33.9	1990.5
Standard Error	1.00	2.72	2.28	0.19	11.34	0.88	3.50	8.61	8.69	10.53	1.03	2.40	38.26
Standard Deviation	3.9	10.5	8.8	0.7	43.9	3.4	13.6	33.4	33.7	40.8	4.0	9.3	148.2
Variance	14.9	111.0	77.7	0.6	1929.2	11.6	183.5	1112.0	1133.9	1664.6	16.0	86.3	21952.3
Range	14.3	39.0	32.9	2.2	183.0	11.0	40.8	111.9	103.0	144.3	12.9	30.8	611.0
Minimum	28.8	45.0	98.3	2.6	240.4	15.6	125.1	232.9	107.4	112.8	13.1	21.7	1629.0
Maximum	43.1	84.0	131.2	4.8	423.4	26.7	165.9	344.8	210.4	257.1	25.9	52.6	2240.0
Control cultivars													
ISe 1468	27.3	58.0	104.9	3.3	291.4	19.3	124.5	322.9	201.2	135.5	21.1	40.1	1914
ISe 1541	38.5	76.2	116.5	3.0	354.9	22.0	130.3	199.6	68.9	198.9	35.6	55.1	2077
ISe 375	28.4	52.9	100.5	1.4	261.8	21.7	113.1	259.9	149.0	100.5	25.2	59.6	1926
ISe 376	26.9	58.1	103.2	1.2	293.9	26.3	118.5	258.6	141.7	115.4	25.1	56.7	1794
Mean	30.3	61.3	106.3	2.2	300.5	22.3	121.6	260.3	140.2	137.6	26.7	52.9	1927.8
Control mean + LSD	33.2	62.7	114.6	2.7	316.1	23.7	133.6	279.0	153.4	151.6	28.2	55.8	2090.6
Control mean-LSD	27.4	59.9	98.0	1.8	284.9	21.0	109.6	241.5	127.0	123.5	25.3	49.9	1765.0
Entire core collection													
Mean	18.5	53.3	96.7	3.4	253.0	18.1	133.1	301.6	171.6	139.4	16.2	24.0	1201.0
LSD	2.91	1.42	8.28	0.42	15.56	1.35	12.02	18.74	13.22	14.06	1.46	2.94	162.80
CV (%)	17.2	2.9	9.3	13.4	6.7	8.2	10.0	6.8	8.4	11.0	9.9	13.3	14.8

1=DF = Days to 50 per cent flowering, PLHT = Plant height (cm), BT = Basal tiller number, FLBL = Flag leaf blade length (mm), FLBW = Flag leaf blade width (mm), FLSL = Flag leaf sheath length (mm), PEDL = Peduncle length (mm), PEX = Panicle exertion (mm), INFL = Inflorescence length (mm), INFW = Inflorescence width (mm), W5P = Weight of five panicles (g), SPY = Single plant yield (g), PY = Grain yield per plot (Kg ha-1)

Table 32j. Performance of 15 maximum grain yield per plot (Kg ha^{-1}) accessions in foxtail millet core collection for various quantitative traits based on pooled BLUPs of three environments

Accession Name	PY[1]	DF	PLHT	BT	FLBL	FLBW	FLSL	PEDL	PEX	INFL	INFW	W5P	SPY
ISe1805	1928	53.2	104.8	3.9	273.0	18.2	149.8	300.1	152.5	151.1	17.4	28.6	27.9
ISe1780	1931	53.6	114.2	2.9	278.6	20.3	143.8	334.9	193.9	179.5	20.3	23.0	26.7
ISe1408	1941	49.9	89.1	5.9	243.6	16.1	131.7	289.7	160.3	111.6	13.8	13.6	27.1
ISe1000	1946	60.2	110.6	4.7	283.9	17.1	150.6	301.7	140.8	140.1	13.1	23.5	29.2
ISe1685	1959	84.0	119.1	2.6	305.7	24.3	125.1	232.9	109.7	247.6	25.9	44.5	34.4
ISe1736	1961	69.7	121.1	3.4	280.9	21.5	165.3	337.9	175.0	192.1	19.2	41.6	27.5
ISe388	1971	58.9	109.7	4.4	265.6	18.5	156.4	327.9	174.0	155.0	14.9	29.1	30.8
ISe1767	1974	52.1	110.7	4.1	304.6	17.8	137.3	344.8	210.4	169.3	15.0	27.3	28.8
ISe1474	1980	59.3	127.8	2.7	285.3	21.0	128.9	292.9	174.4	211.1	19.5	42.5	37.1
ISe1687	2013	68.3	122.1	3.3	329.4	24.7	147.8	258.9	107.4	201.4	23.1	46.4	38.0
ISe1846	2080	52.8	108.5	4.8	265.6	15.6	136.2	278.8	136.9	149.8	14.8	27.3	32.6
ISe956	2081	56.8	117.6	3.4	278.8	17.5	145.7	339.2	196.3	152.7	13.8	31.0	37.4
ISe364	2084	61.9	105.4	4.1	249.7	18.2	128.2	325.9	201.5	142.5	14.2	32.8	37.0
ISe1881	2225	58.5	121.9	4.2	290.5	17.3	165.9	323.3	160.7	196.4	17.5	35.5	43.1
ISe1888	2240	50.7	98.3	3.8	261.3	18.6	154.0	280.4	128.4	158.0	16.8	21.7	35.4
Mean	2020.9	59.3	112.1	3.9	279.8	19.1	144.5	304.6	161.5	170.6	17.3	31.2	32.9
Standard Error	26.12	2.33	2.62	0.23	5.74	0.70	3.36	8.47	8.33	8.85	0.96	2.42	1.30
Standard Deviation	101.2	9.0	10.2	0.9	22.2	2.7	13.0	32.8	32.3	34.3	3.7	9.4	5.0
Variance	10235.6	81.7	103.3	0.8	494.2	7.4	169.3	1075.3	1041.4	1175.9	14.0	87.9	25.3
Range	312.0	34.1	38.6	3.3	85.8	9.0	40.8	111.9	103.0	136.0	12.9	32.8	16.4
Minimum	1928.0	49.9	89.1	2.6	243.6	15.6	125.1	232.9	107.4	111.6	13.1	13.6	26.7
Maximum	2240.0	84.0	127.8	5.9	329.4	24.7	165.9	344.8	210.4	247.6	25.9	46.4	43.1
Control cultivars													
ISe 1468	1914	58.0	104.9	3.3	291.4	19.3	124.5	322.9	201.2	135.5	21.1	40.1	27.3
ISe 1541	2077	76.2	116.5	3.0	354.9	22.0	130.3	199.6	68.9	198.9	35.6	55.1	38.5
ISe 375	1926	52.9	100.5	1.4	261.8	21.7	113.1	259.9	149.0	100.5	25.2	59.6	28.4
ISe 376	1794	58.1	103.2	1.2	293.9	26.3	118.5	258.6	141.7	115.4	25.1	56.7	26.9
Mean	1927.8	61.3	106.3	2.2	300.5	22.3	121.6	260.3	140.2	137.6	26.7	52.9	30.3
Control mean + LSD	2090.6	62.7	114.6	2.7	316.1	23.7	133.6	279.0	153.4	151.6	28.2	55.8	33.2
Control mean-LSD	1765.0	59.9	98.0	1.8	284.9	21.0	109.6	241.5	127.0	123.5	25.3	49.9	27.4
Entire core collection													
Mean	1201.0	53.3	96.7	3.4	253.0	18.1	133.1	301.6	171.6	139.4	16.2	24.0	18.5
LSD	162.80	1.42	8.28	0.42	15.56	1.35	12.02	18.74	13.22	14.06	1.46	2.94	2.91
CV (%)	14.8	2.9	9.3	13.4	6.7	8.2	10.0	6.8	8.4	11.0	9.9	13.3	17.2

1=DF = Days to 50 per cent flowering, PLHT = Plant height (cm), BT = Basal tiller number, FLBL = Flag leaf blade length (mm), FLBW = Flag leaf blade width (mm), FLSL = Flag leaf sheath length (mm), PEDL = Peduncle length (mm), PEX = Panicle exertion (mm), INFL = Inflorescence length (mm), INFW = Inflorescence width (mm), W5P = Weight of five panicles (g), SPY = Single plant yield (g), PY = Grain yield per plot (Kg ha^{-1})

Table 33. Summary statistics of 84 SSR markers diversity in entire core collection, among three different races and among clusters based on unweighted neighbor joining clusters in foxtail millet core collection

Statistics	Overall	Classification based on race			Cluster based on Unweighted Neighbor-Joining tree			
		Indica	Maxima	Moharia	Cluster 1	Cluster 2	Cluster 3	Cluster 4
Sample size	155	102	24	29	87	37	19	14
Total number of alleles	1356	997	784	844	845	853	633	521
Number of alleles per locus	16.14 (4-35)[1]	11.87 (2-25)	9.33 (2-19)	10.05 (2-21)	10.06 (1-24)	10.15 (1-21)	7.54 (2-16)	6.2 (1-13)
Gene Diversity	0.72 (0.06-0.95)	0.65 (0.02-0.93)	0.74 (0.08-0.92)	0.74 (0.13-0.94)	0.62 (0-0.92)	0.71 (0-0.94)	0.70 (0.10-0.93)	0.69 (0.13-0.92)
Heterozygosity	0.06 (0-0.56)	0.06 (0-0.56)	0.08 (0-0.39)	0.06 (0-0.73)	0.07 (0-0.51)	0.05 (0-0.56)	0.05 (0-75)	0.05 (0-64.29)
PIC	0.70 (0.06-0.95)	0.63 (0.02-0.93)	0.72 (0.08-0.91)	0.72 (0.12-0.94)	0.60 (0-0.92)	0.69 (0-0.92)	0.68 (0.09-0.92)	0.66 (0.12-0.91)
Rare allele	368	100	0	0	62	0	0	0
Common allele	906	803	688	760	688	757	531	390
Most frequent allele	82	94	96	84	95	96	102	131
Unique allele	61	44	77	47	62	53	31	33
No. of monomorphic SSR loci	-	-	-	-	3	1	-	2

1= Values in parentheses represent the range

Table 34. Allelic richness, gene diversity, heterozygosity (%), polymorphic information content (PIC), allele range, rare allele, common allele and most frequent alleles of the 84 SSR markers in foxtail millet core collection (155 accessions)

S. No	Marker	Allele	Gene diversity	Hetero-zygosity	PIC	Range	Rare alleles	Common alleles	Most frequent alleles
1	p38	8	0.75	0.05	0.71	170-192	2	4	2
2	p58	10	0.41	0.03	0.40	168-222	5	4	1
3	p61	13	0.84	0.05	0.82	218-244	1	10	2
4	b123	12	0.60	0.03	0.58	123-157	2	9	1
5	p33	8	0.24	0.00	0.23	177-215	3	4	1
6	b202	8	0.68	0.03	0.65	197-243	1	6	1
7	b111	16	0.85	0.04	0.83	186-220	5	10	1
8	b223	19	0.90	0.07	0.89	136-174	3	16	0
9	p10	16	0.79	0.05	0.76	198-256	6	8	2
10	b234	18	0.90	0.06	0.89	289-341	3	15	0
11	p3	26	0.92	0.08	0.91	186-270	7	19	0
12	b196	4	0.06	0.00	0.06	177-187	1	2	1
13	b110	7	0.55	0.01	0.46	253-287	2	3	2
14	p87	17	0.80	0.02	0.78	205-249	5	10	2
15	p42	9	0.75	0.03	0.71	187-205	2	6	1
16	b226	5	0.49	0.04	0.42	273-283	1	2	2
17	p92	5	0.32	0.00	0.30	174-186	0	4	1
18	b151	6	0.28	0.00	0.27	133-179	2	3	1
19	b227	21	0.88	0.07	0.88	150-204	7	13	1
20	p91	6	0.11	0.01	0.11	188-206	4	1	1
21	p2	13	0.86	0.22	0.85	147-211	2	10	1
22	b109	30	0.94	0.05	0.94	139-283	6	24	0
23	b159	14	0.74	0.02	0.72	184-216	5	8	1
24	p17x	7	0.54	0.01	0.50	228-278	2	3	2
25	b225	19	0.83	0.03	0.81	122-166	5	13	1
26	b242	27	0.94	0.08	0.94	145-205	8	19	0
27	b142	20	0.75	0.07	0.74	195-255	5	14	1
28	p41	23	0.93	0.03	0.93	201-255	3	20	0
29	p16	9	0.55	0.16	0.53	213-233	2	6	1
30	p34	9	0.76	0.01	0.72	153-177	1	6	2
31	b269	14	0.82	0.03	0.81	148-198	1	12	1
32	b185	24	0.92	0.07	0.91	133-199	6	18	0
33	b200	21	0.76	0.03	0.75	352-406	6	14	1
34	p75	21	0.91	0.07	0.90	208-265	2	18	1
35	b186	22	0.84	0.05	0.83	159-221	8	13	1
36	p4	31	0.92	0.07	0.91	180-280	8	22	1
37	b190	16	0.82	0.05	0.80	285-319	5	9	2
38	p9	25	0.85	0.04	0.84	186-266	7	17	1
39	p56	4	0.18	0.00	0.17	194-220	1	2	1
40	b217	23	0.91	0.07	0.90	288-346	6	17	0
41	b255	17	0.81	0.04	0.79	121-165	4	12	1
42	p20	16	0.88	0.04	0.87	203-239	1	14	1
43	p100	13	0.64	0.03	0.61	247-315	5	7	1
44	b129	14	0.60	0.06	0.58	128-168	6	7	1

Table 34. Cont..

S. No	Marker	Allele	Gene diversity	Hetero-zygosity	PIC	Range	Rare alleles	Common alleles	Most frequent alleles
45	b188	17	0.85	0.03	0.83	192-260	4	11	2
46	b105	26	0.93	0.06	0.93	174-244	3	23	0
47	p21	5	0.58	0.00	0.51	220-276	1	2	2
48	b187	27	0.94	0.04	0.93	188-244	5	22	0
49	b258	11	0.39	0.00	0.38	205-275	5	5	1
50	b251	17	0.89	0.08	0.88	269-311	4	13	0
51	p50	27	0.93	0.02	0.92	197-255	8	19	0
52	b107	22	0.91	0.08	0.90	246-296	7	15	0
53	b153	18	0.81	0.05	0.79	169-237	6	10	2
54	b163	14	0.73	0.01	0.71	183-225	4	9	1
55	b260	29	0.95	0.05	0.95	151-221	5	24	0
56	b166	19	0.92	0.07	0.91	195-247	5	14	0
57	b165	26	0.94	0.05	0.93	252-314	6	20	0
58	b125	19	0.83	0.03	0.81	341-383	6	11	2
59	p59	18	0.85	0.03	0.83	176-210	4	13	1
60	p88	15	0.89	0.03	0.87	190-246	4	11	0
61	b171	35	0.94	0.03	0.94	177-276	11	24	0
62	b236	28	0.94	0.02	0.93	109-183	5	23	0
63	p85	11	0.74	0.01	0.70	179-227	4	5	2
64	p8	17	0.68	0.00	0.65	180-230	8	8	1
65	b126	14	0.82	0.05	0.80	186-226	3	9	2
66	b246	27	0.93	0.05	0.92	131-194	8	19	0
67	b174	28	0.93	0.09	0.93	165-225	8	20	0
68	b115	10	0.66	0.03	0.63	187-223	1	8	1
69	m2	5	0.31	0.00	0.29	165-175	1	3	1
70	b247	27	0.82	0.09	0.81	99-187	11	15	1
71	p98	8	0.51	0.00	0.49	161-178	2	5	1
72	p44	16	0.87	0.07	0.85	158-228	6	9	1
73	ICMM02C05	5	0.11	0.01	0.11	100-202	1	3	1
74	ICMM02C24	21	0.73	0.24	0.69	306-376	12	7	2
75	ICMM02D07	11	0.81	0.56	0.78	226-256	2	8	1
76	ICMM02D15B	11	0.22	0.14	0.21	132-166	7	3	1
77	P13	13	0.83	0.11	0.81	104-174	3	8	2
78	P2	8	0.64	0.26	0.60	110-124	1	5	2
79	P5	10	0.59	0.10	0.57	202-310	0	9	1
80	UGEP102	7	0.65	0.10	0.62	176-204	1	5	1
81	UGEP3	20	0.78	0.28	0.77	100-206	5	14	1
82	UGEP56	20	0.63	0.31	0.61	124-174	9	10	1
83	UGEP8	8	0.22	0.01	0.22	202-302	3	4	1
84	UGEP81	20	0.69	0.05	0.66	102-236	12	6	2

Table 35. List 61 unique alleles in foxtail millet core collection along with SSR markers and accessions

S. No	Accession Name	Race	Sub race	Origin	SSR marker	Unique alleles	Genotype (alleles)
1	ISe31	Indica	Nana	India	p44	158	158/210
2	ISe156	Indica	Nana	India	b129	152	144/152
3	ISe289	Indica	Profusa	India	p38	178	178/190
4	ISe289	Indica	Profusa	India	b187	242	222/242
5	ISe289	Indica	Profusa	India	b166	207	207/229
6	ISe525	Indica	Nana	USA	b171	191	191/199
7	ISe748	Indica	Glabra	India	b126	226	194/226
8	ISe795	Indica	Erecta	India	p100	277	263/277
9	ISe827	Maxima	Compacta	China	b109	201	181/201
10	ISe827	Maxima	Compacta	China	ICMM02C24	360	338/360
11	ISe828	Maxima	Compacta	China	b111	188	188/208
12	ISe828	Maxima	Compacta	China	p4	256	246/256
13	ISe828	Maxima	Compacta	China	b125	357	347/357
14	ISe828	Maxima	Compacta	China	b247	135	99/135
15	ISe846	Indica	Nana	India	p10	206	200/206
16	ISe907	Indica	Nana	India	UGEP56	146	142/146
17	ISe963	Indica	Nana	India	b125	341	341/347
18	ISe969	Indica	Nana	India	ICMM02C24	344	338/344
19	ISe985	Indica	Nana	India	b217	324	294/324
20	ISe995	Indica	Nana	India	UGEP81	134	118/134
21	Ise 1009	Moharia	Aristata	Lebanon	ICMM02C24	354	354/376
22	ISe1037	Moharia	Aristata	Lebanon	p100	269	263/269
23	ISe1037	Moharia	Aristata	Lebanon	b247	185	185/187
24	ISe1037	Moharia	Aristata	Lebanon	b247	187	185/187
25	ISe1037	Moharia	Aristata	Lebanon	ICMM02C24	306	306/308
26	ISe1037	Moharia	Aristata	Lebanon	ICMM02C24	308	306/308
27	ISe1059	Maxima	Spongiosa	India	UGEP81	174	174/178
28	ISe1067	Maxima	Compacta	Syria	b227	204	176/204
29	ISe1067	Maxima	Compacta	Syria	b200	406	360/406
30	ISe1136	Indica	Nana	Syria	b242	197	165/197
31	ISe1181	Maxima	Compacta	China	p2	171	163/171
32	ISe1181	Maxima	Compacta	China	UGEP3	108	108/206
33	ISe1201	Maxima	Compacta	China	p2	211	207/211

Table 35. Cont..

S. No	Accession Name	Race	Sub race	Origin	SSR marker	Unique alleles	Genotype (alleles)
34	ISe1204	Maxima	Compacta	Russia and CISs	b185	195	133/195
35	ISe1209	Moharia	Fusiformis	Russia and CISs	ICMM02C24	320	320/340
36	ISe1227	Moharia	Glabra	Russia and CISs	UGEP56	164	136/164
37	ISe1251	Maxima	Compacta	Russia and CISs	b109	283	165/283
38	ISe1251	Maxima	Compacta	Russia and CISs	b200	356	356/360
39	ISe1286	Moharia	Glabra	Turkey	b247	165	165/167
40	ISe1299	Moharia	Glabra	Iran	b247	169	167/169
41	ISe1299	Moharia	Glabra	Iran	UGEP56	144	144/154
42	ISe1387	Indica	Glabra	Sri Lanka	ICMM02D15B	166	138/166
43	ISe1474	Indica	Glabra	United Kingdom	b227	196	194/196
44	ISe1575	Maxima	Compacta	Korea,	ICMM02D15B	164	154/164
45	ISe1605	Indica	Nana	India	UGEP3	174	174/184
46	ISe1610	Indica	Glabra	Malawi	ICMM02D15B	132	132/142
47	ISe1610	Indica	Glabra	Malawi	ICMM02D15B	142	132/142
48	ISe1610	Indica	Glabra	Malawi	UGEP81	200	178/200
49	ISe1638	Moharia	Glabra	Taiwan	b107	288	268/288
50	ISe1638	Moharia	Glabra	Taiwan	ICMM02D15B	136	136/146
51	ISe1655	Indica	Glabra	Taiwan	UGEP3	176	176/180
52	ISe1666	Maxima	Spongiosa	India	UGEP102	204	184/204
53	ISe1685	Indica	Profusa	India	ICMM02C24	364	340/364
54	ISe1687	Maxima	Spongiosa	India	ICMM02C24	362	348/362
55	ISe1704	Indica	Nana	India	UGEP8	214	214/216
56	ISe1704	Indica	Nana	India	UGEP8	216	214/216
57	ISe1725	Maxima	Compacta	Nepal	p42	197	189/197
58	ISe1725	Maxima	Compacta	Nepal	p91	192	192/202
59	ISe1773	Indica	Nana	India	p44	228	210/228
60	ISe1851	Indica	Nana	India	b165	302	290/302
61	ISe1892	Indica	Nana	USA	ICMM02D07	252	246/252

Table 36. Allelic richness, major allele frequency, gene diversity, heterozygosity (%), polymorphic information content (PIC) of the 84 SSR loci in biological races of foxtail millet core collection

S. No	Marker	Indica				Maxima				Moharia			
		Allele No	Gene Diversity	Hetero zygosity	PIC	Allele No	Gene Diversity	Hetero zygosity	PIC	Allele No	Gene Diversity	Hetero zygosity	PIC
1	p38	8.00	0.75	0.03	0.71	5.00	0.68	0.09	0.62	6.00	0.69	0.07	0.64
2	p58	5.00	0.35	0.03	0.33	7.00	0.68	0.09	0.63	5.00	0.27	0.00	0.26
3	p61	12.00	0.76	0.07	0.73	10.00	0.86	0.00	0.84	11.00	0.88	0.00	0.87
4	b123	6.00	0.42	0.02	0.39	9.00	0.81	0.04	0.79	9.00	0.80	0.07	0.78
5	p33	2.00	0.02	0.00	0.02	6.00	0.65	0.00	0.62	5.00	0.44	0.00	0.42
6	b202	5.00	0.52	0.02	0.49	6.00	0.77	0.04	0.74	6.00	0.63	0.04	0.59
7	b111	10.00	0.81	0.04	0.79	10.00	0.87	0.04	0.85	10.00	0.87	0.04	0.85
8	b223	18.00	0.88	0.05	0.87	12.00	0.89	0.08	0.88	13.00	0.89	0.14	0.88
9	p10	12.00	0.68	0.06	0.65	9.00	0.78	0.00	0.75	8.00	0.75	0.03	0.73
10	b234	14.00	0.89	0.05	0.88	12.00	0.84	0.08	0.82	11.00	0.87	0.07	0.86
11	p3	16.00	0.90	0.09	0.89	15.00	0.90	0.13	0.90	16.00	0.89	0.03	0.88
12	b196	2.00	0.02	0.00	0.02	2.00	0.08	0.00	0.08	3.00	0.19	0.00	0.18
13	b110	6.00	0.47	0.01	0.41	4.00	0.52	0.00	0.45	2.00	0.31	0.03	0.26
14	p87	8.00	0.73	0.02	0.69	8.00	0.81	0.04	0.79	15.00	0.88	0.00	0.87
15	p42	7.00	0.63	0.03	0.59	8.00	0.78	0.08	0.75	5.00	0.76	0.00	0.72
16	b226	5.00	0.43	0.05	0.36	4.00	0.57	0.00	0.48	4.00	0.55	0.04	0.48
17	p92	4.00	0.32	0.00	0.29	4.00	0.23	0.00	0.22	4.00	0.35	0.00	0.33
18	b151	4.00	0.24	0.00	0.23	3.00	0.39	0.00	0.34	4.00	0.28	0.00	0.27
19	b227	17.00	0.86	0.08	0.85	12.00	0.87	0.13	0.86	11.00	0.84	0.00	0.83
20	p91	2.00	0.02	0.00	0.02	5.00	0.23	0.08	0.22	2.00	0.29	0.00	0.24
21	p2	9.00	0.84	0.20	0.82	10.00	0.81	0.38	0.79	9.00	0.79	0.14	0.77
22	b109	24.00	0.91	0.02	0.91	19.00	0.92	0.17	0.92	18.00	0.92	0.04	0.92
23	b159	9.00	0.65	0.02	0.62	9.00	0.81	0.00	0.79	8.00	0.85	0.04	0.83
24	p17x	5.00	0.29	0.01	0.27	5.00	0.73	0.05	0.68	6.00	0.72	0.00	0.68
25	b225	13.00	0.74	0.03	0.72	12.00	0.84	0.00	0.83	13.00	0.87	0.07	0.86
26	b242	21.00	0.92	0.10	0.92	13.00	0.90	0.13	0.89	15.00	0.91	0.00	0.90
27	b142	17.00	0.61	0.03	0.60	10.00	0.80	0.13	0.78	11.00	0.88	0.14	0.87
28	b41	20.00	0.92	0.03	0.91	12.00	0.84	0.10	0.83	12.00	0.89	0.00	0.88
29	p16	6.00	0.38	0.11	0.36	5.00	0.64	0.33	0.60	9.00	0.81	0.21	0.79
30	p34	7.00	0.73	0.02	0.68	5.00	0.52	0.00	0.50	6.00	0.77	0.00	0.74
31	p269	10.00	0.73	0.04	0.70	9.00	0.82	0.00	0.79	12.00	0.89	0.04	0.88
32	b185	17.00	0.88	0.08	0.87	16.00	0.91	0.13	0.91	14.00	0.90	0.00	0.89
33	b200	11.00	0.61	0.02	0.58	12.00	0.87	0.10	0.86	15.00	0.91	0.00	0.91
34	p75	18.00	0.90	0.07	0.89	12.00	0.89	0.08	0.88	7.00	0.79	0.04	0.76
35	b186	8.00	0.75	0.05	0.72	12.00	0.85	0.09	0.83	15.00	0.92	0.00	0.92
36	p4	23.00	0.87	0.07	0.87	15.00	0.91	0.04	0.90	18.00	0.93	0.07	0.92
37	b190	10.00	0.77	0.06	0.73	10.00	0.84	0.05	0.82	10.00	0.86	0.00	0.84
38	p9	16.00	0.82	0.05	0.80	14.00	0.87	0.04	0.86	13.00	0.87	0.00	0.86
39	p56	2.00	0.06	0.00	0.06	4.00	0.57	0.00	0.50	2.00	0.13	0.00	0.12
40	b217	18.00	0.88	0.05	0.87	13.00	0.89	0.14	0.88	17.00	0.93	0.07	0.92
41	b255	12.00	0.71	0.04	0.68	11.00	0.84	0.04	0.82	12.00	0.87	0.04	0.86
42	p20	13.00	0.85	0.05	0.83	9.00	0.85	0.00	0.83	10.00	0.88	0.04	0.87

Table 36. Cont..

S. No	Marker	Indica				Maxima				Moharia			
		Allele No	Gene Diversity	Hetero zygosity	PIC	Allele No	Gene Diversity	Hetero zygosity	PIC	Allele No	Gene Diversity	Hetero zygosity	PIC
43	p100	11.00	0.62	0.01	0.58	5.00	0.63	0.00	0.59	8.00	0.68	0.11	0.64
44	b129	8.00	0.35	0.04	0.34	9.00	0.81	0.17	0.79	8.00	0.80	0.03	0.78
45	b188	12.00	0.82	0.01	0.80	9.00	0.82	0.09	0.80	11.00	0.87	0.04	0.86
46	b105	24.00	0.91	0.07	0.91	13.00	0.91	0.05	0.90	17.00	0.91	0.03	0.91
47	p21	5.00	0.40	0.00	0.36	3.00	0.64	0.00	0.57	4.00	0.40	0.00	0.36
48	b187	25.00	0.93	0.04	0.93	15.00	0.91	0.08	0.90	12.00	0.89	0.00	0.88
49	b258	6.00	0.19	0.00	0.18	6.00	0.63	0.00	0.59	7.00	0.67	0.00	0.63
50	b251	16.00	0.88	0.08	0.87	9.00	0.80	0.04	0.78	11.00	0.86	0.11	0.84
51	p50	23.00	0.89	0.03	0.88	13.00	0.89	0.00	0.88	10.00	0.86	0.00	0.85
52	b107	17.00	0.89	0.07	0.88	14.00	0.89	0.14	0.88	13.00	0.90	0.07	0.89
53	b153	14.00	0.75	0.05	0.72	10.00	0.82	0.13	0.80	10.00	0.79	0.00	0.76
54	b163	8.00	0.54	0.00	0.51	9.00	0.84	0.09	0.83	12.00	0.88	0.00	0.86
55	b260	24.00	0.93	0.07	0.93	12.00	0.90	0.04	0.89	19.00	0.93	0.00	0.93
56	b166	15.00	0.90	0.07	0.89	13.00	0.90	0.09	0.89	16.00	0.89	0.03	0.88
57	b165	24.00	0.92	0.04	0.92	16.00	0.92	0.13	0.91	15.00	0.90	0.00	0.90
58	b125	14.00	0.74	0.03	0.70	13.00	0.88	0.05	0.87	12.00	0.87	0.00	0.86
59	p59	13.00	0.76	0.01	0.73	11.00	0.86	0.09	0.85	13.00	0.90	0.03	0.89
60	p88	11.00	0.86	0.02	0.84	11.00	0.88	0.00	0.86	11.00	0.88	0.08	0.87
61	b171	24.00	0.90	0.03	0.90	15.00	0.91	0.05	0.91	19.00	0.94	0.00	0.93
62	p236	23.00	0.91	0.02	0.91	15.00	0.91	0.04	0.91	14.00	0.91	0.00	0.90
63	p85	4.00	0.67	0.00	0.61	8.00	0.82	0.08	0.80	8.00	0.75	0.00	0.72
64	p8	6.00	0.51	0.00	0.48	9.00	0.77	0.00	0.74	13.00	0.83	0.00	0.82
65	b126	12.00	0.77	0.06	0.74	10.00	0.87	0.00	0.86	7.00	0.77	0.04	0.73
66	b246	20.00	0.90	0.04	0.89	12.00	0.91	0.00	0.90	18.00	0.93	0.10	0.92
67	b174	20.00	0.92	0.09	0.92	14.00	0.89	0.13	0.88	21.00	0.94	0.07	0.94
68	b115	9.00	0.59	0.04	0.56	7.00	0.74	0.04	0.71	7.00	0.72	0.00	0.68
69	m2	4.00	0.26	0.00	0.23	3.00	0.23	0.00	0.21	2.00	0.44	0.00	0.34
70	b247	12.00	0.70	0.07	0.68	13.00	0.89	0.14	0.89	21.00	0.93	0.10	0.92
71	p98	2.00	0.21	0.00	0.19	6.00	0.63	0.00	0.57	7.00	0.72	0.00	0.69
72	p44	13.00	0.83	0.07	0.81	10.00	0.88	0.04	0.87	9.00	0.82	0.07	0.79
73	ICMM02C05	2.00	0.02	0.00	0.02	3.00	0.18	0.00	0.17	4.00	0.31	0.04	0.29
74	ICMM02C24	15.00	0.71	0.24	0.67	9.00	0.69	0.17	0.64	11.00	0.74	0.31	0.71
75	ICMM02D07	11.00	0.81	0.56	0.79	7.00	0.70	0.38	0.67	8.00	0.82	0.73	0.80
76	ICMM02D15B	7.00	0.21	0.16	0.20	4.00	0.20	0.17	0.19	6.00	0.26	0.04	0.25
77	P13	11.00	0.82	0.13	0.80	8.00	0.80	0.05	0.77	10.00	0.83	0.07	0.81
78	P2	7.00	0.64	0.22	0.59	4.00	0.59	0.29	0.51	6.00	0.64	0.34	0.60
79	P5	10.00	0.59	0.09	0.56	9.00	0.63	0.09	0.60	5.00	0.51	0.15	0.47
80	UGEP102	6.00	0.65	0.08	0.62	6.00	0.73	0.25	0.69	5.00	0.47	0.04	0.45
81	UGEP3	16.00	0.75	0.26	0.74	13.00	0.86	0.39	0.85	9.00	0.75	0.26	0.73
82	UGEP56	18.00	0.67	0.33	0.65	11.00	0.46	0.27	0.45	11.00	0.62	0.25	0.59
83	UGEP8	8.00	0.26	0.01	0.25	3.00	0.16	0.00	0.16	3.00	0.14	0.00	0.14
84	UGEP81	15.00	0.61	0.03	0.58	6.00	0.71	0.05	0.66	9.00	0.76	0.11	0.73

Table 37. List 44 unique alleles present in the race *indica* in foxtail millet core collection along with SSR markers and accessions

S. No	Accession name	Race	Sub race	Origin	Marker	Allele	Genotype (alleles)
1	ISe31	Indica	Nana	India	p44	158	158/210
2	ISe31	Indica	Nana	India	b247	137	99/137
3	ISe132	Indica	Nana	India	b129	152	152/152
4	ISe237	Indica	Nana	India	b105	232	220/232
5	ISe238	Indica	Nana	India	b185	161	161/175
6	ISe289	Indica	Profusa	India	b166	207	207/229
7	ISe289	Indica	Profusa	India	p38	178	178/190
8	ISe289	Indica	Profusa	India	b187	242	222/242
9	ISe525	Indica	Nana	USA	b171	191	191/199
10	ISe748	Indica	Glabra	India	b126	226	194/226
11	ISe758	Indica	Glabra	India	b247	111	99/111
12	ISe758	Indica	Glabra	India	b107	296	276/296
13	ISe785	Indica	Nana	India	P5	304	304/307
14	ISe795	Indica	Erecta	India	p100	277	263/277
15	ISe795	Indica	Erecta	India	UGEP56	174	166/174
16	ISe846	Indica	Nana	India	p10	206	200/206
17	ISe907	Indica	Nana	India	b242	159	159/187
18	ISe907	Indica	Nana	India	UGEP56	142	142/146
19	ISe907	Indica	Nana	India	UGEP56	146	142/146
20	ISe914	Indica	Nana	India	ICMM02C24	348	340/348
21	ISe963	Indica	Nana	India	b125	341	341/347
22	ISe969	Indica	Nana	India	ICMM02C24	344	338/344
23	ISe985	Indica	Nana	India	b217	324	294/324
24	ISe995	Indica	Nana	India	UGEP81	134	118/134
25	ISe1136	Indica	Nana	Syria	b242	197	165/197
26	ISe1387	Indica	Glabra	Sri Lanka	ICMM02D15B	166	138/166
27	ISe1474	Indica	Glabra	United Kingdom	b227	194	194/196
28	ISe1474	Indica	Glabra	United Kingdom	b227	196	194/196
29	ISe1597	Indica	Glabra	India	ICMM02D07	226	226/238
30	ISe1605	Indica	Nana	India	UGEP3	174	174/184
31	ISe1610	Indica	Glabra	Malawi	ICMM02D15B	132	132/142
32	ISe1610	Indica	Glabra	Malawi	ICMM02D15B	142	132/142
33	ISe1610	Indica	Glabra	Malawi	UGEP81	200	178/200
34	ISe1655	Indica	Glabra	Taiwan	p16	225	215/225
35	ISe1655	Indica	Glabra	Taiwan	b129	136	136/144
36	ISe1655	Indica	Glabra	Taiwan	UGEP3	176	176/180
37	ISe1685	Indica	Profusa	India	ICMM02C24	364	340/364

Table 37. Cont..

S. No	Accession name	Race	Sub race	Origin	Marker	Allele	Genotype (alleles)
38	ISe1685	Indica	Profusa	India	b185	189	133/189
39	ISe1704	Indica	Nana	India	UGEP8	214	214/216
40	ISe1704	Indica	Nana	India	UGEP8	216	214/216
41	ISe1773	Indica	Nana	India	p44	228	210/228
42	ISe1851	Indica	Nana	India	b165	302	290/302
43	ISe1881	Indica	Nana	India	p20	221	215/221
44	ISe1892	Indica	Nana	USA	ICMM02D07	252	246/252

Table 38. List 77 unique alleles present in the race *maxima* in foxtail millet core collection along with SSR markers and accessions

S. No	Accession name	Race	Sub race	Origin	Marker	Allele	Genotype (alleles)
1	ISe746	Maxima	Compacta	India	b142	231	221/231
2	ISe746	Maxima	Compacta	India	UGEP56	154	154/160
3	ISe746	Maxima	Compacta	India	UGEP56	160	154/160
4	ISe792	Maxima	Compacta	India	ICMM02D07	240	234/240
5	ISe792	Maxima	Compacta	India	UGEP56	124	124/130
6	ISe792	Maxima	Compacta	India	UGEP56	130	124/130
7	ISe827	Maxima	Compacta	China	b109	181	181/201
8	ISe827	Maxima	Compacta	China	b109	201	181/201
9	ISe827	Maxima	Compacta	China	b187	194	194/204
10	ISe827	Maxima	Compacta	China	b251	281	281/293
11	ISe827	Maxima	Compacta	China	ICMM02C24	338	338/360
12	ISe827	Maxima	Compacta	China	ICMM02C24	360	338/360
13	ISe827	Maxima	Compacta	China	P5	202	202/307
14	ISe827	Maxima	Compacta	China	UGEP56	152	152/158
15	ISe827	Maxima	Compacta	China	UGEP56	158	152/158
16	ISe827	Maxima	Compacta	China	p2	153	153/159
17	ISe827	Maxima	Compacta	China	b105	212	226/212
18	ISe827	Maxima	Compacta	China	b105	226	226/212
19	ISe828	Maxima	Compacta	China	b223	142	142/150
20	ISe828	Maxima	Compacta	China	p42	193	193/199
21	ISe828	Maxima	Compacta	China	b109	173	173/187
22	ISe828	Maxima	Compacta	China	b109	187	173/187

Table 38. Cont..

S. No	Accession name	Race	Sub race	Origin	Marker	Allele	Genotype (alleles)
23	ISe828	Maxima	Compacta	China	b242	159	159/171
24	ISe828	Maxima	Compacta	China	p4	256	246/256
25	ISe828	Maxima	Compacta	China	p9	230	230/244
26	ISe828	Maxima	Compacta	China	b165	282	268/282
27	ISe828	Maxima	Compacta	China	b174	211	197/211
28	ISe828	Maxima	Compacta	China	p58	168	168/170
29	ISe828	Maxima	Compacta	China	b111	188	188/208
30	ISe828	Maxima	Compacta	China	b186	217	169/217
31	ISe828	Maxima	Compacta	China	b163	217	207/217
32	ISe828	Maxima	Compacta	China	b217	304	304/310
33	ISe828	Maxima	Compacta	China	b166	229	223/229
34	ISe828	Maxima	Compacta	China	b125	357	347/357
35	ISe828	Maxima	Compacta	China	b171	230	230/244
36	ISe828	Maxima	Compacta	China	b247	135	99/135
37	ISe828	Maxima	Compacta	China	b41	251	235/251
38	ISe1059	Maxima	Spongiosa	India	UGEP56	138	136/138
39	ISe1059	Maxima	Spongiosa	India	UGEP81	174	174/178
40	ISe1067	Maxima	Compacta	Syria	b227	176	176/204
41	ISe1067	Maxima	Compacta	Syria	b227	204	176/204
42	ISe1067	Maxima	Compacta	Syria	p91	198	198/202
43	ISe1067	Maxima	Compacta	Syria	b185	149	149/183
44	ISe1067	Maxima	Compacta	Syria	b165	292	264/292
45	ISe1067	Maxima	Compacta	Syria	b200	406	360/406
46	ISe1181	Maxima	Compacta	China	UGEP3	108	108/206
47	ISe1181	Maxima	Compacta	China	p2	171	163/171
48	ISe1187	Maxima	Compacta	China	UGEP56	166	166/174
49	ISe1187	Maxima	Compacta	China	UGEP56	174	166/174
50	ISe1201	Maxima	Compacta	China	p2	211	207/211
51	ISe1201	Maxima	Compacta	China	b107	286	286/290
52	ISe1201	Maxima	Compacta	China	b107	290	286/290
53	ISe1204	Maxima	Compacta	Russia and CISs	b185	195	133/195
54	ISe1251	Maxima	Compacta	Russia and CISs	b123	151	147/151
55	ISe1251	Maxima	Compacta	Russia and CISs	b109	165	165/283

Table 38. Cont..

S. No	Accession name	Race	Sub race	Origin	Marker	Allele	Genotype (alleles)
56	ISe1251	Maxima	Compacta	Russia and CISs	b109	283	165/283
57	ISe1251	Maxima	Compacta	Russia and CISs	b174	205	201/205
58	ISe1251	Maxima	Compacta	Russia and CISs	b202	241	225/241
59	ISe1251	Maxima	Compacta	Russia and CISs	b200	356	356/360
60	ISe1251	Maxima	Compacta	Russia and CISs	b41	215	215/233
61	ISe1258	Maxima	Compacta	Russia and CISs	ICMM02D07	232	232/246
62	ISe1338	Maxima	Compacta	Turkey	p3	244	189/244
63	ISe1338	Maxima	Compacta	Turkey	P5	301	301/310
64	ISe1563	Maxima	Compacta	Korea	UGEP3	188	182/188
65	ISe1575	Maxima	Compacta	Korea	ICMM02D15B	154	154/164
66	ISe1575	Maxima	Compacta	Korea	ICMM02D15B	164	154/164
67	ISe1593	Maxima	Compacta	Korea	b217	318	318/328
68	ISe1666	Maxima	Spongiosa	India	b142	253	221/253
69	ISe1666	Maxima	Spongiosa	India	UGEP102	204	184/204
70	ISe1687	Maxima	Spongiosa	India	ICMM02C24	348	348/362
71	ISe1687	Maxima	Spongiosa	India	ICMM02C24	362	348/362
72	ISe1725	Maxima	Compacta	Nepal	p42	197	189/197
73	ISe1725	Maxima	Compacta	Nepal	p91	192	192/202
74	ISe1725	Maxima	Compacta	Nepal	UGEP3	204	184/204
75	ISe1725	Maxima	Compacta	Nepal	p17x	253	230/253
76	ISe1725	Maxima	Compacta	Nepal	b247	115	115/129
77	ISe1736	Maxima	Compacta	Nepal	b234	291	291/305

Table 39. List of 47 unique alleles present in the race *moharia* in foxtail millet core collection along with SSR markers and accessions

S. No	Accession name	Race	Sub race	Origin	Marker	Unique allele	Genotype (alleles)
1	ISe364	Moharia	Aristata	India	b174	205	199/205
2	ISe364	Moharia	Aristata	India	b109	183	183/189
3	ISe364	Moharia	Aristata	India	b109	189	183/189
4	ISe403	Moharia	Aristata	India	b234	317	317/323
5	ISe403	Moharia	Aristata	India	b234	323	317/323
6	ISe458	Moharia	Aristata	USA	UGEP56	138	138/142
7	ISe458	Moharia	Aristata	USA	UGEP56	142	138/142
8	ISe719	Moharia	Aristata	Pakistan	p16	213	213/227
9	ISe719	Moharia	Aristata	Pakistan	b217	312	306/312
10	ISe719	Moharia	Aristata	Pakistan	b251	301	287/301
11	ISe719	Moharia	Aristata	Pakistan	p38	192	188/192
12	ISe719	Moharia	Aristata	Pakistan	p88	218	214/218
13	ISe1009	Moharia	Aristata	Lebanon	ICMM02C24	354	354/376
14	ISe1026	Moharia	Aristata	Lebanon	p44	220	172/220
15	ISe1037	Moharia	Aristata	Lebanon	b217	304	304/316
16	ISe1037	Moharia	Aristata	Lebanon	b217	316	304/316
17	ISe1037	Moharia	Aristata	Lebanon	b246	162	146/162
18	ISe1037	Moharia	Aristata	Lebanon	b247	185	185/187
19	ISe1037	Moharia	Aristata	Lebanon	b247	187	185/187
20	ISe1037	Moharia	Aristata	Lebanon	p100	269	263/269
21	ISe1037	Moharia	Aristata	Lebanon	ICMM02C24	306	306/308
22	ISe1037	Moharia	Aristata	Lebanon	ICMM02C24	308	306/308
23	ISe1118	Moharia	Glabra	Syria	ICMM02D07	240	240/246
24	ISe1151	Moharia	Glabra	Syria	UGEP56	152	152/162
25	ISe1161	Moharia	Glabra	Syria	p100	247	247/265
26	ISe1177	Moharia	Aristata	Syria	P2	122	122/124
27	ISe1177	Moharia	Aristata	Syria	p100	303	263/303
28	ISe1209	Moharia	Fusiformis	Russia and CISs	ICMM02C24	320	320/340
29	ISe1209	Moharia	Fusiformis	Russia and CISs	ICMM02C24	340	320/340
30	ISe1227	Moharia	Glabra	Russia and CISs	UGEP56	164	136/164
31	ISe1286	Moharia	Glabra	Turkey	b105	218	210/218
32	ISe1286	Moharia	Glabra	Turkey	b247	165	165/167
33	ISe1299	Moharia	Glabra	Iran	b247	169	167/169
34	ISe1299	Moharia	Glabra	Iran	UGEP56	144	144/154
35	ISe1299	Moharia	Glabra	Iran	UGEP56	154	144/154
36	ISe1299	Moharia	Glabra	Iran	UGEP81	182	182/184

Table 39. Cont..

S. No	Accession name	Race	Sub race	Origin	Marker	Unique allele	Genotype (alleles)
37	ISe1312	Moharia	Glabra	Unknown	ICMM02C24	328	328/332
38	ISe1335	Moharia	Glabra	Hungary	b225	162	134/162
39	ISe1638	Moharia	Glabra	Taiwan	b107	288	268/288
40	ISe1638	Moharia	Glabra	Taiwan	p59	188	188/196
41	ISe1638	Moharia	Glabra	Taiwan	b246	174	146/174
42	ISe1638	Moharia	Glabra	Taiwan	b174	187	187/201
43	ISe1638	Moharia	Glabra	Taiwan	b142	201	201/219
44	ISe1638	Moharia	Glabra	Taiwan	b126	190	190/206
45	ISe1638	Moharia	Glabra	Taiwan	b126	206	190/206
46	ISe1638	Moharia	Glabra	Taiwan	ICMM02D15B	136	136/146
47	ISe1638	Moharia	Glabra	Taiwan	ICMM02D15B	146	136/146

Table 42. Allelic richness, gene diversity, heterozygosity and polymorphic information content (PIC) of four cluster identified by Unweighted neighbor-joining tree based on the simple matching dissimilarity matrix of 84 SSR markers infoxtail millet core collection

S. No	Marker	Cluster I				Cluster II				Cluster III				Cluster IV			
		Allele No	Gene Diversity	Hetero zygosity	PIC	Allele No	Gene Diversity	Hetero zygosity	PIC	Allele No	Gene Diversity	Hetero zygosity	PIC	Allele No	Gene Diversity	Hetero zygosity	PIC
1	p38	7	0.73	0.06	0.69	7	0.78	0.06	0.75	4	0.65	0.00	0.59	3	0.56	0.00	0.47
2	p58	3	0.32	0.05	0.29	5	0.48	0.03	0.45	2	0.11	0.00	0.10	6	0.73	0.00	0.69
3	p61	6	0.74	0.08	0.69	12	0.85	0.00	0.83	9	0.84	0.00	0.82	6	0.73	0.00	0.70
4	b123	4	0.37	0.03	0.33	7	0.64	0.06	0.60	8	0.83	0.00	0.81	6	0.80	0.00	0.77
5	p33	1	0.00	0.00	0.00	4	0.16	0.00	0.16	3	0.41	0.00	0.37	6	0.79	0.00	0.75
6	b202	4	0.37	0.01	0.34	6	0.76	0.10	0.72	3	0.36	0.00	0.33	4	0.68	0.00	0.63
7	b111	9	0.79	0.07	0.77	10	0.85	0.00	0.84	8	0.84	0.00	0.83	8	0.85	0.00	0.83
8	b223	14	0.86	0.08	0.84	14	0.91	0.03	0.90	11	0.89	0.11	0.88	8	0.85	0.07	0.83
9	p10	8	0.58	0.08	0.53	12	0.84	0.00	0.83	6	0.72	0.00	0.68	6	0.63	0.00	0.60
10	b234	14	0.88	0.10	0.87	14	0.87	0.03	0.86	9	0.84	0.00	0.82	6	0.78	0.00	0.75
11	p3	14	0.88	0.10	0.87	13	0.87	0.09	0.86	11	0.85	0.05	0.84	8	0.84	0.00	0.82
12	b196	1	0.00	0.00	0.00	2	0.06	0.00	0.05	2	0.19	0.00	0.17	3	0.26	0.00	0.24
13	b110	5	0.33	0.02	0.31	3	0.49	0.00	0.41	2	0.10	0.00	0.09	4	0.37	0.00	0.35
14	p87	5	0.70	0.04	0.65	11	0.82	0.00	0.80	12	0.90	0.00	0.89	4	0.70	0.00	0.65
15	p42	8	0.63	0.06	0.59	6	0.77	0.00	0.73	4	0.63	0.00	0.57	6	0.79	0.00	0.76
16	b226	4	0.45	0.07	0.37	4	0.34	0.00	0.32	4	0.51	0.00	0.47	3	0.26	0.00	0.24
17	p92	3	0.30	0.00	0.27	4	0.38	0.00	0.35	4	0.43	0.00	0.39	1	0.00	0.00	0.00
18	b151	3	0.15	0.00	0.15	4	0.43	0.00	0.40	3	0.34	0.00	0.31	3	0.44	0.00	0.39
19	b227	14	0.84	0.08	0.82	15	0.88	0.09	0.87	9	0.84	0.05	0.83	6	0.73	0.00	0.70
20	p91	3	0.03	0.01	0.03	1	0.00	0.00	0.00	2	0.36	0.05	0.30	4	0.37	0.00	0.35
21	p2	8	0.82	0.28	0.80	9	0.84	0.15	0.82	7	0.72	0.05	0.70	8	0.81	0.25	0.79
22	b109	21	0.90	0.06	0.89	21	0.94	0.06	0.94	12	0.89	0.00	0.88	8	0.84	0.00	0.82
23	b159	8	0.57	0.01	0.54	7	0.80	0.03	0.78	7	0.81	0.00	0.79	6	0.78	0.08	0.74
24	p17x	4	0.09	0.02	0.09	5	0.64	0.00	0.58	5	0.64	0.00	0.59	4	0.73	0.00	0.68

Table 42. Cont..

S. No	Marker	Cluster I				Cluster II				Cluster III				Cluster IV			
		Allele No	Gene Diversity	Hetero zygosity	PIC	Allele No	Gene Diversity	Hetero zygosity	PIC	Allele No	Gene Diversity	Hetero zygosity	PIC	Allele No	Gene Diversity	Hetero zygosity	PIC
25	b225	12	0.64	0.05	0.61	11	0.86	0.00	0.85	11	0.88	0.05	0.87	8	0.81	0.00	0.79
26	b242	19	0.92	0.11	0.92	17	0.91	0.06	0.90	10	0.82	0.05	0.80	9	0.85	0.00	0.83
27	b142	15	0.58	0.06	0.57	10	0.69	0.09	0.67	7	0.83	0.00	0.81	8	0.83	0.14	0.81
28	b41	18	0.91	0.05	0.91	16	0.91	0.03	0.91	8	0.84	0.00	0.82	7	0.83	0.00	0.81
29	p16	4	0.36	0.13	0.34	7	0.37	0.11	0.36	7	0.76	0.11	0.72	4	0.73	0.57	0.68
30	p34	5	0.67	0.02	0.63	7	0.79	0.00	0.76	6	0.75	0.00	0.72	2	0.26	0.00	0.23
31	b269	8	0.67	0.05	0.63	9	0.85	0.00	0.83	9	0.85	0.00	0.83	8	0.80	0.07	0.78
32	b185	14	0.87	0.09	0.86	16	0.90	0.03	0.89	8	0.84	0.05	0.82	9	0.84	0.07	0.83
33	b200	6	0.48	0.02	0.45	13	0.84	0.03	0.83	12	0.88	0.05	0.87	7	0.82	0.00	0.80
34	p75	16	0.87	0.09	0.86	16	0.90	0.03	0.90	5	0.78	0.00	0.75	8	0.82	0.07	0.80
35	b186	6	0.71	0.07	0.67	9	0.82	0.03	0.79	10	0.87	0.00	0.86	9	0.85	0.00	0.83
36	p4	19	0.85	0.08	0.84	18	0.92	0.06	0.91	10	0.88	0.05	0.87	9	0.85	0.00	0.83
37	b190	9	0.75	0.07	0.72	9	0.80	0.03	0.77	8	0.80	0.00	0.78	6	0.76	0.00	0.72
38	p9	15	0.83	0.05	0.81	10	0.60	0.06	0.58	10	0.86	0.00	0.84	12	0.92	0.00	0.91
39	p56	1	0.00	0.00	0.00	3	0.21	0.00	0.19	2	0.19	0.00	0.17	3	0.59	0.00	0.52
40	b217	14	0.85	0.08	0.84	17	0.93	0.06	0.92	12	0.90	0.00	0.89	12	0.91	0.08	0.90
41	b255	11	0.59	0.07	0.56	10	0.86	0.00	0.84	11	0.88	0.00	0.86	8	0.79	0.00	0.77
42	p20	11	0.80	0.05	0.78	11	0.85	0.03	0.83	9	0.85	0.06	0.83	7	0.82	0.00	0.79
43	p100	8	0.56	0.02	0.52	9	0.74	0.03	0.71	5	0.60	0.05	0.56	4	0.61	0.00	0.54
44	b129	7	0.25	0.01	0.24	6	0.64	0.11	0.59	6	0.73	0.05	0.69	9	0.86	0.21	0.85
45	b188	11	0.80	0.04	0.77	10	0.84	0.00	0.82	8	0.84	0.06	0.82	7	0.84	0.00	0.82
46	b105	21	0.90	0.06	0.89	20	0.93	0.09	0.93	14	0.91	0.05	0.91	9	0.88	0.00	0.86
47	p21	5	0.27	0.00	0.26	3	0.51	0.00	0.41	2	0.20	0.00	0.18	2	0.46	0.00	0.35
48	b187	24	0.92	0.06	0.92	17	0.92	0.03	0.92	11	0.89	0.00	0.88	7	0.84	0.00	0.82
49	b258	4	0.09	0.00	0.09	7	0.40	0.00	0.39	6	0.75	0.00	0.71	5	0.73	0.00	0.69
50	b251	12	0.87	0.11	0.85	12	0.87	0.06	0.85	8	0.86	0.00	0.84	5	0.72	0.00	0.69
51	p50	17	0.86	0.04	0.85	20	0.93	0.00	0.93	5	0.74	0.00	0.70	5	0.74	0.00	0.69
52	b107	13	0.88	0.09	0.87	15	0.90	0.06	0.89	9	0.82	0.00	0.80	10	0.86	0.18	0.85
53	b153	9	0.68	0.07	0.62	13	0.86	0.06	0.84	7	0.73	0.00	0.70	8	0.77	0.00	0.74
54	b163	8	0.52	0.01	0.48	7	0.71	0.00	0.68	10	0.84	0.05	0.82	5	0.71	0.00	0.67
55	b260	19	0.92	0.08	0.92	20	0.93	0.03	0.92	13	0.90	0.00	0.89	8	0.83	0.00	0.81
56	b166	14	0.89	0.10	0.88	13	0.90	0.03	0.89	13	0.91	0.00	0.90	9	0.88	0.00	0.86
57	b165	23	0.92	0.06	0.91	17	0.92	0.03	0.92	12	0.88	0.06	0.87	9	0.85	0.00	0.83

Table 42. Cont..

S. No	Marker	Cluster I				Cluster II				Cluster III				Cluster IV			
		Allele No	Gene Diversity	Hetero zygosity	PIC	Allele No	Gene Diversity	Hetero zygosity	PIC	Allele No	Gene Diversity	Hetero zygosity	PIC	Allele No	Gene Diversity	Hetero zygosity	PIC
58	b125	8	0.67	0.05	0.62	13	0.86	0.00	0.85	10	0.88	0.00	0.86	4	0.69	0.00	0.64
59	p59	10	0.69	0.01	0.65	13	0.87	0.03	0.85	11	0.88	0.05	0.86	8	0.77	0.08	0.75
60	p88	10	0.85	0.03	0.84	9	0.81	0.03	0.78	8	0.85	0.00	0.83	7	0.82	0.00	0.79
61	b171	21	0.90	0.05	0.89	20	0.94	0.00	0.93	13	0.90	0.00	0.90	6	0.79	0.00	0.76
62	p236	16	0.89	0.03	0.88	19	0.94	0.00	0.93	10	0.88	0.00	0.86	9	0.87	0.00	0.85
63	p85	5	0.68	0.01	0.62	5	0.65	0.03	0.58	7	0.68	0.00	0.66	7	0.76	0.00	0.73
64	p8	4	0.45	0.00	0.41	10	0.76	0.00	0.73	8	0.79	0.00	0.76	7	0.74	0.00	0.72
65	b126	8	0.70	0.06	0.65	12	0.87	0.03	0.86	5	0.67	0.00	0.62	7	0.82	0.07	0.80
66	b246	19	0.89	0.06	0.88	17	0.93	0.00	0.92	11	0.87	0.05	0.86	9	0.86	0.09	0.85
67	b174	18	0.92	0.14	0.91	16	0.90	0.03	0.89	15	0.93	0.00	0.92	9	0.81	0.07	0.80
68	b115	6	0.45	0.06	0.42	9	0.78	0.00	0.75	6	0.74	0.00	0.70	5	0.65	0.00	0.60
69	m2	4	0.23	0.00	0.21	3	0.25	0.00	0.23	2	0.49	0.00	0.37	2	0.13	0.00	0.12
70	b247	14	0.66	0.12	0.63	10	0.85	0.00	0.83	16	0.93	0.11	0.92	6	0.80	0.08	0.76
71	p98	3	0.25	0.00	0.22	4	0.34	0.00	0.32	4	0.55	0.00	0.50	6	0.68	0.00	0.65
72	p44	11	0.80	0.07	0.78	10	0.86	0.09	0.85	7	0.76	0.00	0.72	9	0.83	0.07	0.81
73	ICMM02C05	3	0.07	0.01	0.07	2	0.06	0.00	0.06	4	0.31	0.00	0.30	2	0.15	0.00	0.14
74	ICMM02C24	15	0.73	0.26	0.70	12	0.69	0.20	0.64	7	0.75	0.38	0.72	4	0.56	0.08	0.47
75	ICMM02D07	11	0.81	0.51	0.79	7	0.76	0.57	0.73	8	0.77	0.75	0.74	5	0.67	0.64	0.62
76	ICMM02D15B	4	0.15	0.11	0.14	6	0.32	0.24	0.30	3	0.20	0.00	0.19	6	0.37	0.29	0.36
77	P13	11	0.82	0.12	0.79	7	0.74	0.06	0.70	8	0.78	0.11	0.75	6	0.81	0.10	0.78
78	P2	7	0.68	0.18	0.63	7	0.61	0.43	0.57	4	0.47	0.42	0.44	2	0.50	0.07	0.37
79	P5	10	0.63	0.08	0.60	8	0.53	0.09	0.51	6	0.59	0.26	0.54	3	0.27	0.00	0.26
80	UGEP102	7	0.64	0.09	0.61	5	0.69	0.09	0.65	4	0.31	0.12	0.29	4	0.73	0.14	0.69
81	UGEP3	15	0.75	0.26	0.74	13	0.75	0.38	0.73	7	0.67	0.20	0.64	13	0.89	0.29	0.88
82	UGEP56	18	0.68	0.36	0.67	10	0.54	0.24	0.53	7	0.66	0.33	0.60	5	0.37	0.14	0.35
83	UGEP8	8	0.34	0.01	0.33	2	0.07	0.00	0.06	2	0.10	0.00	0.09	1	0.00	0.00	0.00
84	UGEP81	10	0.52	0.03	0.49	10	0.75	0.06	0.72	9	0.79	0.16	0.76	4	0.63	0.00	0.56

Table 43. List of ten pairs of most diverse accessions in foxtail millet core collection based of 84 SSR markers

S. No	Most diverse pairs		Dissimilarity value
1	ISe 1320 and ISe 1162	(*moharia and moharia*)	0.956
2	ISe 338 and ISe 1320	(*indica and moharia*)	0.944
3	ISe 1773 and ISe 1320	(*indica and moharia*)	0.943
4	ISe 179 and ISe 1320	(*indica and moharia*)	0.938
5	ISe 907 and ISe 1320	(*indica and moharia*)	0.937
6	ISe 1808 and ISe 1320	(*indica and moharia*)	0.934
7	ISe 1808 and ISe 1547	(*indica and moharia*)	0.932
8	ISe 195 and ISe 1320	(*indica and moharia*)	0.931
9	ISe 946 and ISe 1547	(*indica and moharia*)	0.931
10	ISe 1320 and ISe 1137	(*moharia and indica*)	0.925

Table 41. Details of the accessions present in four clusters identified by unweighted neighbor joining tree based on 84 SSR markers

Cluster I : Total 87 accessions + 2 control		
80 accessions in *indica* + 1 control	4 accessions in *maxima* + 1 control	3 accessions in *moharia*
	ISe 1541 (Control)	ISe 1013
	ISe 1666	ISe 364
	ISe 1725	ISe 403
	ISe 792	
	ISe 828	
Cluster II: Total 35 accessions + 2 control		
22 accessions in indica	7 accessions in *maxima* + 2 controls	6 accessions in *moharia*
22 accessions	ISe1059	ISe1026
	ISe1251	ISe1674
	ISe1687	ISe458
	ISe1736	ISe719
	ISe827	ISe735
	ISe375	ISe 1177
	ISe 746	
	ISe375 (Control)	
	ISe376 (Control)	
Cluster III: Total 19 accessions		
Moharia	2 accessions *maxima*	
17	ISe1067	
	ISe1338	
Cluster IV: Total 14 accessions		
11 accessions in *maxima*	3 accessions in *moharia*	
	ISe1151	
	ISe1209	
	ISe1638	

Table 44. Principal Coordinates Analysis (PCoA) of foxtail millet core collection accessions using 84 SSR markers based on estimates of Nei (1973) distance

Axis	PC 1	PC2	PC3
% Variation	34.7	16.6	14.9
Cumulative %	34.7	51.3	66.2
Eigen Value	89.7	42.9	38.4
ISe1305	1.456	-0.205	0.285
ISe1254	1.386	-0.361	0.353
ISe1575	1.331	0.936	0.594
ISe1312	1.311	0.171	0.362
ISe1227	1.306	-0.250	0.137
ISe1161	1.301	-0.118	0.201
ISe1234	1.279	-0.114	0.246
ISe1335	1.256	0.056	0.324
ISe1119	1.212	-0.438	0.230
ISe1163	1.209	-0.201	0.353
ISe1320	1.209	0.315	0.586
ISe1209	1.179	0.445	0.415
ISe1547	1.178	0.814	0.350
ISe1338	1.170	-0.550	0.195
ISe1187	1.161	-0.102	0.399
ISe1299	1.143	-0.644	0.308
ISe1593	1.139	0.882	0.399
ISe1563	1.121	0.161	0.245
ISe1009	1.116	-0.169	0.294
ISe1181	1.114	0.211	0.340
ISe1581	1.107	0.700	0.283
ISe1118	1.105	-0.434	0.029
ISe1638	1.103	0.070	0.510
ISe1204	1.098	0.124	0.285
ISe1129	1.096	-0.183	0.047
ISe1067	1.074	-0.012	0.537
ISe1647	1.062	0.274	0.293
ISe1286	1.047	-0.081	0.097
ISe1302	0.988	-0.153	0.167
ISe1201	0.972	0.042	0.473
ISe1458	0.935	0.136	-0.197
ISe1655	0.915	-0.030	-0.033
ISe1687	0.877	-0.020	-0.355
ISe1258	0.875	-0.080	0.431

Axis	PC 1	PC2	PC3
ISe1474	0.867	0.511	0.335
ISe1332	0.852	-0.438	0.257
ISe375_C	0.840	0.429	-2.798
ISe813	0.818	0.261	-2.635
ISe375	0.792	0.431	-2.811
ISe1736	0.773	-0.019	-0.219
ISe376_C	0.729	0.378	-2.699
ISe1454	0.719	-0.261	-0.139
ISe1151	0.695	-0.269	0.318
ISe1685	0.686	-0.094	-0.200
ISe1059	0.642	-0.067	-0.297
ISe1026	0.637	0.094	-0.054
ISe1745	0.621	0.144	-0.160
ISe735	0.576	-0.072	-0.190
ISe1460	0.466	-0.116	-0.031
ISe1136	0.452	-0.378	-0.028
ISe1674	0.388	-0.235	0.061
ISe1597	0.353	0.337	-0.053
ISe746	0.346	-0.187	-0.467
ISe1177	0.342	-0.081	-0.202
ISe1137	0.299	-0.243	-0.049
ISe1387	0.291	-0.083	0.064
ISe1251	0.281	0.251	0.271
ISe1134	0.239	-0.083	-0.064
ISe751	0.158	-0.187	-0.174
ISe769	0.083	-0.407	-0.163
ISe1610	0.078	0.012	0.053
ISe458	0.076	-0.277	-0.433
ISe144	0.075	0.470	0.137
ISe1789	-0.024	0.312	0.288
ISe1419	-0.041	-0.115	0.217
ISe745	-0.048	0.100	-0.034
ISe195	-0.058	-0.450	-0.061
ISe1037	-0.061	0.014	0.167
ISe1806	-0.065	0.059	-0.152
ISe719	-0.076	-0.555	-0.030
ISe758	-0.083	0.415	-0.101

Table 44. Cont..

Axis	PC 1	PC2	PC3
ISe828	-0.092	-0.230	0.205
ISe1629	-0.114	-0.516	-0.068
ISe900	-0.142	-0.816	0.146
ISe179	-0.146	-0.471	-0.057
ISe200	-0.207	0.448	0.112
ISe1773	-0.220	0.608	-0.268
ISe90	-0.221	-0.479	-0.187
ISe1162	-0.246	-0.812	-0.048
ISe838	-0.263	-0.725	0.219
ISe914	-0.288	-0.920	0.236
ISe1406	-0.322	0.010	0.258
ISe1846	-0.322	-0.106	-0.073
ISe946	-0.322	-0.870	-0.054
ISe827	-0.346	-0.399	0.031
ISe364	-0.362	0.665	-0.264
ISe1762	-0.363	0.327	0.300
ISe983	-0.363	-0.965	-0.185
ISe748	-0.366	0.071	-0.047
ISe963	-0.380	-0.787	0.118
ISe1808	-0.391	-0.329	-0.073
ISe717	-0.400	-0.485	-0.317
ISe132	-0.410	0.354	0.294
ISe1511	-0.410	0.765	0.005
ISe1725	-0.431	0.778	0.238
ISe1900	-0.453	-0.078	-0.028
ISe156	-0.479	0.545	0.187
ISe525	-0.480	0.292	0.208
ISe160	-0.507	0.174	-0.160
ISe846	-0.517	-0.293	0.159
ISe663	-0.531	-1.068	-0.191
ISe869	-0.532	-0.842	0.097
ISe907	-0.533	-0.467	0.032
ISe792	-0.534	0.019	-0.076
ISe289	-0.544	0.355	-0.287
ISe985	-0.547	-0.620	-0.008
ISe254	-0.575	0.719	0.114
ISe710	-0.577	-0.264	-0.117
ISe796	-0.587	0.022	0.113
ISe1851	-0.600	0.257	0.040
ISe1805	-0.604	0.373	0.169
ISe1269	-0.610	-0.534	0.238
ISe49	-0.611	0.253	0.268
ISe1704	-0.618	-0.025	-0.036
ISe795	-0.620	-0.173	-0.064
ISe1402	-0.626	0.428	0.193
ISe785	-0.626	0.237	-0.262
ISe999	-0.633	-1.053	0.248
ISe1664	-0.647	0.286	0.021
ISe842	-0.656	-0.398	0.264
ISe1666	-0.665	0.646	0.048
ISe995	-0.672	-0.825	-0.375
ISe1780	-0.677	0.561	0.192
ISe771	-0.687	-0.256	-0.033
ISe2	-0.691	0.760	0.281
ISe237	-0.710	0.216	0.303
ISe398	-0.710	1.075	-0.091
ISe1605	-0.713	0.271	-0.298
ISe238	-0.714	0.302	0.120
ISe1541_C	-0.721	0.541	-0.112
ISe267	-0.725	0.985	0.117
ISe1400	-0.732	0.017	0.068
ISe1858	-0.739	0.370	0.385
ISe1408	-0.745	1.288	0.342
ISe507	-0.745	0.047	-0.345
ISe31	-0.753	0.820	-0.047
ISe1892	-0.758	0.226	-0.053
ISe1354	-0.764	-0.065	0.366
ISe1859	-0.781	0.080	0.168
ISe388	-0.781	-0.557	-0.140
ISe1000	-0.802	-1.199	-0.067
ISe1468_C	-0.810	1.342	0.156
ISe480	-0.814	-0.153	-0.254
ISe403	-0.821	0.061	0.002
ISe302	-0.822	1.353	0.203
ISe18	-0.824	0.633	0.038
ISe909	-0.829	0.001	-0.374
ISe936	-0.830	-0.072	0.179
ISe969	-0.844	-1.438	-0.064
ISe1881	-0.860	0.364	0.186
ISe840	-0.862	-1.458	-0.085
ISe1820	-0.883	0.175	0.048
ISe1888	-0.884	0.362	0.368
ISe362	-0.892	0.711	-0.112
ISe96	-0.898	-0.089	0.194
ISe783	-0.947	-0.063	-0.038
ISe1767	-0.977	0.387	0.237
ISe956	-1.036	0.030	-0.144
ISe931	-1.053	-1.499	-0.119

Table 48. Details of the accessions present in each subpopulation detected by STRUCTURE analysis

Sub Population I : Total 59 accessions				Total
	Moharia (27)[1]	Maxima (18)	Indica (14)	59
Afghanistan	2	-	-	2
China	-	5	-	5
Hungary	1	-	-	1
India	1	3	7	10
Iran	1	-	-	1
Korea,	-	4	-	4
Lebanon	3	-	-	3
Malawi	-	-	1	1
Nepal	-	1	-	1
Pakistan	2	-	-	2
Russia and CIS	4	2	-	6
Spain	1	-	-	1
Sri Lanka	-	-	1	1
Syria	7	1	3	11
Taiwan	1	1	1	3
Turkey	1	1	-	2
United Kingdom	-	-	1	1
USA	2	-	-	2
Unknown	1	-	-	1
Sub Population II : Total 4 accessions + 2 Controls				
	Maxima (3+ two controls)	Indica (1)	Moharia (0)	4 + 2 Controls
India	1 + (2 Controls)	1	-	-
Korea	1	-	-	-
Russia and CIS	1	-	-	-
Sub Population III: Total 7 Genotypes				
	Indica (7)	Maxima	Moharia	7
India	7	-	-	-
Sub Population IV: Total 85 accessions + 2 Controls				
	Indica (81)	Moharia (2)	Maxima (2+2 Control)	85 + 2 Controls
China	1	-	-	1
Ethiopia	1	-	-	1
India	71	2	1+ (2 Controls)	74 + (2 Controls)
Kenya	1	-	-	1
Malwi	1	-	-	1
Nepal	0	-	1	1
Pakistan	1	-	-	1
South Africa	1	-	-	1
Syria	1	-	-	1
USA	3	-	-	3

1=Numbers in parenthesis indicate number of accessions in each group

Table 49. Summary statistics of foxtail millet core collection accessions based subpopulations detected by STRUCTURE analysis using 84 SSR markers

Statistics	Overall	Subpopulation detected by STRUCTURE software			
		SP1	SP2	SP3	SP4
Sample size	155	59	4	7	85
Total number of alleles	1356	1150	213	226	840
Number of alleles per locus	16.14	13.69	2.54	2.69	10
	(4-35)[1]	(3-30)	(1-4)	(1-8)	(1-23)
Gene Diversity	0.72	0.76	0.5	0.42	0.63
	(0.06-0.95)	(0.11-0.96)	(0-075)	(0-0.84)	(0-0.93)
Heterozygosity	0.06	0.06	0.03	0.06	0.06
	(0-0.56)	(0-0.64)	(0-0.50)	(0-0.86)	(0-0.51)
PIC	0.70	0.75	0.43	0.37	0.60
	(0.06-0.95)	(0.10-0.95)	(0-0.70)	(0-0.82)	(0-0.93)
No of SSR loci monomorphic to particular group	-	-	8	13	2

1=Numbers in parenthesis indicate range

Table 52. Details of marker trait association (MTAs) detected for different agronomic traits in foxtail millet core collection in three environments, Coimbatore (E1), Madurai (E2) during Rabi/summer 2009/10 and ICRISAT (E3), Patancheru during rainy season 2010 and pooled

Traits	LOCUS	E1	E2	E3	Total	POOLED
Days to 50% flowering	b200	*[1]		**	2	*
	p100			**	1	
	b115			**	1	*
	b202	*	*	**	3	**
	b258		*		1	*
	b225	*	*		2	*
	b251		*		1	*
	P13			**	1	
	p17x	*	*	*	3	**
	m2			*	1	
	p34	**	**	**	3	**
	TOTAL	5	6	8		8
Plant height (cm)	b111	*	*	*	3	**
	b123	*	**		2	*
	B153			*	1	
	b186			*	1	
	b200			**	1	
	b202		**		1	*
	B225			*	1	
	b234	**	*		2	**
	b251	*		*	2	**
	b258	*		**	2	
	ICMMO2CO5	**	*	**	3	**
	ICMM02D15B	*			1	*
	ICMM02C24			**	1	*
	m2	*	**	**	3	**
	p2	**			1	
	p16		*		1	
	p17x	*	*		2	
	p33		**		1	
	p8		*	**	2	*
	p98	**	**	**	3	**
	TOTAL	11	11	12		11
Basal tiller number	b111	**	*		2	
	b123		*		1	
	b151			*	1	
	b200	*	**		2	*
	b202	*			1	
	b41		**		1	
	p17x		*		1	
	P2	*			1	*
	p34	**			1	*
	p56			*	1	*
	p8	**	**	*	3	**

Table 52. Cont..

Traits	LOCUS	E1	E2	E3	Total	POOLED
	p87	*			1	*
	P98	**			1	*
	UGEP81	**		**	2	*
	TOTAL	9	6	4		8
Flag leaf blade length (mm)	b111	*			1	*
	b123	**			1	
	b163	*			1	
	b153			*	1	
	b186	**			1	*
	b200	*		*	2	*
	b202	**	**	*	3	**
	b234	**			1	*
	ICMMO2C05	**	**	*	3	**
	ICMM02D15B	**	*		2	*
	m2	*		**	2	**
	p2	*			1	
	p17x	**	**		2	**
	b258	**			1	
	p34		**		1	*
	p61			**	1	
	p8			**	1	*
	p98	**		**	2	**
	TOTAL	14	5	8		12
Flag leaf blade width (mm)	b111	*			1	
	b126	*			1	*
	b153	*			1	
	b186	**			1	
	b200	**			1	
	b202		*		1	
	ICMM02C05	**	**		2	**
	m2			*	1	
	P13		*		1	
	P2				0	*
	p34		**	*	2	*
	p56			*	1	
	p61			**	1	
	p8	**		**	2	**
	p98	**	*	**	3	**
	TOTAL	8	5	6		6
Flag leaf sheath length (mm)	b123	**	**	*	3	**
	B111			*	1	
	b125	*			1	
	b129	**			1	
	b142			*	1	
	b151	*		**	2	*
	b153			**	1	
	b163	*			1	
	b186	**		**	2	**
	b188	*		**	2	**
	b200			**	1	
	b226			**	1	

Table 52. Cont..

Traits	LOCUS	E1	E2	E3	Total	POOLED
	b234		*		1	*
	b258			**	1	
	ICMM02C05			*	1	
	ICMM02C24			*	1	
	ICMMO2D15B		*		1	
	m2			**	1	*
	P13	*			1	
	p17x	**			1	**
	p58	*	*		2	*
	p8	*		**	2	*
	p85		*		1	
	p98	**	**	**	3	**
	TOTAL	12	6	15		10
Peduncle length (mm)	b115	*			1	
	b123	*		*	2	*
	b129	**			1	
	b142			*	1	
	b151	*		*	2	
	b166				0	*
	b186	**		**	2	**
	b188	*			1	
	b196	*		**	2	**
	b200	*		*	2	*
	b202		*		1	*
	b234				0	*
	b258			*	1	
	ICMM02C05		*		1	*
	p16	**		*	2	
	p17x	*			1	
	p33	*			1	
	p59	**			1	*
	p8	**			1	*
	p85	*			1	
	p87			**	1	*
	p91	**			1	*
	p98	*		*	2	**
	UGEP81			**	1	
	TOTAL	16	2	11		13
Panicle exertion (mm)	b115	*			1	
	b123	**		*	2	*
	b125	*			1	
	b142	*		*	2	*
	b159	*			1	
	b166	**			1	**
	b186	**			1	*
	b196	*		**	2	**
	b200	**		*	2	
	b202	**		**	2	**
	b226		*	*	2	*
	b234	*		**	2	**

Table 52. Cont..

Traits	LOCUS	E1	E2	E3	Total	POOLED
	b251	*			1	
	p16	**			1	
	p56	*			1	
	p59	*			1	
	p61	*			1	
	p75			**	1	
	p88	**			1	
	p91	*			1	*
	TOTAL	18	1	8		9
Inflorescence length (mm)	b111	**			1	
	b123	*			1	*
	b153	*		**	2	*
	b200	*		*	2	*
	b202			**	1	
	b225			**	1	*
	b234	*			1	
	b251	*	*		2	
	b258			**	1	
	ICMM02C05			*	1	
	ICMM02C24			*	1	
	ICMM02D15B	**	*		2	*
	m2	*		**	2	*
	P13			*	1	
	p17x	**			1	
	p20	*			1	
	p33		**		1	
	p34		*	*	2	*
	p8			*	1	
	p92	*			1	
	p98			**	1	**
	TOTAL	10	4	12		8
Inflorescence width (mm)	b111	*			1	
	b196			**	1	
	ICMM02C24	*			1	
	p16		*		1	
	P2	*			1	
	p56			*	1	
	p61			**	1	
	p98	*	*		2	*
	TOTAL	4	2	3		1
Weight of five panicle (g)	b123	**	**		2	**
	b153	**			1	**
	b202	*			1	
	b225			*	1	
	b234		*		1	
	b258	*			1	
	ICMM02C05		*	*	2	*
	ICMM02C24			*	1	
	p56			**	1	

Table 52. Cont..

Traits	LOCUS	E1	E2	E3	Total	POOLED
	p58	*	*		2	*
	p8			**	1	
	p98	**	**	**	3	**
	UGEP102		**		1	
	TOTAL	6	6	6		5
Single plant yield (g)	b123			**	1	*
	b142	*	*		2	*
	b153	*			1	
	b159		*	**	2	*
	b190	*	*		2	*
	b200	*		*	2	*
	b225			*	1	
	b234	**			1	*
	b41	*			1	*
	ICMM02C05			*	1	
	m2			*	1	
	p16			**	1	
	p2	*			1	*
	P5	*			1	*
	p56	*	*		2	**
	p61	*	**		2	*
	p8		*		1	
	p98		*	**	2	*
	TOTAL	10	7	8		12
Plot yield (Kg ha^{-1})	b115	*			1	
	b123			*	1	
	b142	*			1	*
	b159		*		1	
	b190		*		1	
	b200		*		1	*
	b234	*	*	*	3	*
	b251			*	1	
	b41	*			1	
	ICMM02C05			*	1	
	P5	*	*		2	*
	p61		*		1	*
	p98	*	*		2	*
	p17x		*		1	
	m2			*	1	
	TOTAL	6	8	5		6

** and ** represents the presence of marker trait association (MTA) at P≤0.05 and 0.01, respectively*

Table 53. Association of SSR markers (*P*≤5) with quantitative traits along with chromosome location, F markers, P markers and R^2 values from POOLED BLUPs of three environments

Trait	Locus	Chromosome located	F_Marker	p_Marker	R2 (%)
Days to 50 % flowering	b115	2	2.07	0.0263	9.71
	b225	3	1.76	0.0294	13.73
	p34	4	3.43	4.75E-04	14
	p17x	5	2.84	0.01	8.09
	b200	7	1.74	0.0327	14.88
	b202	7	2.68	0.0049	12.58
	b258	8	2.04	0.0332	6.03
	b251	9	1.62	0.0487	9.27
Plant height (cm)	p8	1	2.04	0.0169	10.16
	p98	3	4.71	8.73E-05	1.56
	b234	6	2.39	0.0011	10.6
	b123	7	2.04	0.0188	8.94
	b202	7	2.14	0.0253	8.11
	b251	9	2.07	0.0056	7.2
	m2	9	3.55	0.0085	5.82
	ICMM02C05	-	4.26	0.0013	2.95
	ICMM02C24	-	1.71	0.0337	9.22
	ICMM02D15B	-	1.98	0.0346	5.45
	b111	5	2.72	6.10E-04	9.89
Basal tiller Number	p8	1	3.34	8.72E-05	12.89
	p87	1	1.82	0.0292	8.69
	p56	2	3.08	0.0294	1.95
	p98	3	2.7	0.0115	4.8
	p34	4	1.96	0.0415	3.88
	b200	7	1.96	0.0122	9.13
	P2	-	1.99	0.0299	5.46
	UGEP81	-	1.84	0.0223	5.12
Flag leaf blade Length (mm)	p8	1	1.83	0.0367	10.58
	b186	3	1.69	0.032	16.79
	p98	3	3.11	0.0044	12.52
	p34	4	1.94	0.0446	9.16
	b111	5	1.92	0.0199	9.23
	p17x	5	2.89	0.0052	8.54
	b234	6	1.87	0.0152	10.75
	b200	7	1.69	0.04	13.64
	b202	7	2.96	0.0021	11.87
	m2	9	3.4	0.0108	6.29
	ICMM02C05	-	4.13	0.0016	2.43
	ICMM02D15B	-	2.23	0.0163	5.65

Table 53. Cont..

Trait	Locus	Chromosome located	F_Marker	p_Marker	R2 (%)
Flag leaf blade Width (mm)	b126	1	1.86	0.0241	3.33
	p8	1	2.74	0.001	6.22
	p98	3	3.76	8.95E-04	3.87
	p34	4	2.18	0.0219	2.68
	ICMM02C05	-	3.29	0.0079	1.02
	P2	-	1.91	0.0382	1.54
Flag leaf sheath Length (mm)	p58	1	2.21	0.0141	1.55
	p8	1	1.84	0.0353	2.19
	b151	2	2.83	0.018	0.72
	b186	3	2.09	0.0044	7.38
	p98	3	4.7	8.93E-05	5.34
	b188	5	2.15	0.0082	2.83
	p17x	5	2.76	0.0073	1.84
	b234	6	1.88	0.0144	2.18
	b123	7	2.56	0.0026	1.94
	m2	9	2.74	0.0308	0.78
Peduncle length (mm)	p8	1	1.96	0.0223	8.05
	p87	1	1.9	0.0211	16.31
	b186	3	2.8	9.74E-05	30.27
	p98	3	3.62	0.0013	11.01
	b196	5	5.62	0.0011	3.25
	b234	6	1.74	0.0283	3.05
	b123	7	2.13	0.0135	5.44
	b200	7	1.84	0.0215	16.74
	b202	7	2.4	0.0117	5.96
	p59	7	1.92	0.0175	12.85
	b166	9	1.67	0.0349	7.19
	p91	9	2.48	0.0256	4.23
	ICMM02C05	-	2.51	0.0331	1.27
Panicle exertion (mm)	b186	3	1.8	0.0194	19.52
	b226	3	3.08	0.0112	9.02
	b234	6	2.03	0.007	9.99
	b123	7	2.04	0.0188	9.88
	b142	7	1.78	0.0251	25.3
	b202	7	2.97	0.002	10.12
	b166	9	1.93	0.0097	14.13
	p91	9	2.43	0.0289	5.79
	b196	5	4.83	0.003	4.29
Inflorescence length (mm)	b153	1	1.75	0.0355	1.06
	b225	3	1.94	0.0135	2.03
	p98	3	2.9	0.0072	1.75
	p34	4	1.93	0.0457	0.85

Table 53. Cont..

Trait	Locus	Chromosome located	F_Marker	p_Marker	R2 (%)
	b123	7	1.9	0.0315	1.13
	b200	7	1.65	0.0475	1.07
	m2	9	3.23	0.0142	0.66
	ICMM02D15B	-	2.05	0.0286	0.89
Inflorescence width (mm)	p98	3	2.46	0.0205	4.37
Weight of five panicles (g)	b153	1	2.09	0.0082	6.45
	p58	1	1.97	0.0311	4.86
	p98	3	4.66	9.80E-05	8.04
	b123	7	2.54	0.0029	7.45
	ICMM02C05	-	2.79	0.0199	2.35
Single plant yield (g)	p56	2	3.99	0.0091	1.52
	p61	3	2.09	0.0157	5.5
	p98	3	2.36	0.0258	3.28
	p2	4	1.68	0.0424	3.29
	b159	6	1.94	0.0276	3.05
	b190	6	2.01	0.0136	4.65
	b234	6	1.89	0.0135	3.69
	b142	7	1.95	0.0114	4.55
	b200	7	1.72	0.0355	7.31
	b41	9	1.68	0.034	5.53
	P5	-	1.92	0.0331	3.91
Plot yield Kg ha^{-1}	p61	3	2.16	0.0123	4.63
	p98	3	2.14	0.0428	2
	b234	6	2.06	0.0061	3.16
	b142	7	1.84	0.0189	3.35
	b200	7	1.8	0.0251	5.8
	P5	-	2.41	0.0059	3.14

Table 54a. List of 49 highly significant (*P*≤0.01) marker trait associations detected in Coimbatore (E1), Rabi/summer 2009/10.

Trait	Locus	Chromosome located	p_Marker	R2 (%)
Days to 50% flowering	p34	4	0.004	1.98
Plant height (cm)	p98	3	0.001	24.36
	b234	6	0.001	23.08
	p2	4	0.003	24.15
	ICMM02C05	-	0.008	5.48
Basal tiller number	p8	1	0.00002	14.23
	p34	4	0.003	7.43
	UGEP81	-	0.003	8.09
	p98	3	0.007	6.45
	b111	5	0.008	13.14
Flag leaf blade length (mm)	p17x	5	0.001	19.18
	ICMM02C05	-	0.003	7.25
	b258	8	0.004	15.78
	ICMM02D15B	-	0.004	13.81
	b123	7	0.005	23.34
	b186	3	0.006	36.25
	p98	3	0.008	25.75
	b202	7	0.008	21.81
Flag leaf blade width (mm)	p8	1	0.0003	7.82
	p98	3	0.001	5.05
	b186	3	0.004	10.54
	ICMM02C05	-	0.006	1.54
	b200	7	0.008	10.59
Flag leaf sheath length (mm)	p98	3	0.00002	14.62
	p17x	5	0.0001	6.66
	b186	3	0.001	16.53
	b123	7	0.002	5.09
	b129	5	0.003	6.66

Table 54a. Cont..

Trait	Locus	Chromosome located	p_Marker	R2 (%)
Peduncle length (mm)	b186	3	0.0002	14.25
	p59	7	0.003	8.9
	p16	1	0.004	6.84
	p98	3	0.006	8.01
	p8	1	0.006	6.49
	b129	5	0.010	6.56
Panicle exertion (mm)	b166	9	0.001	14.32
	b202	7	0.002	6.63
	b123	7	0.004	9.24
	b186	3	0.005	18.77
	p16	1	0.006	10.72
	p91	9	0.006	6.5
	b200	7	0.010	23.68
Inflorescence width (mm)	p17x	5	0.003	19.87
	ICMM02D15B	-	0.005	13.68
	b111	5	0.006	21.83
Weight of five panicles (g)	p98	3	0.0002	9.63
	b123	7	0.0003	12.61
	b153	1	0.006	10.02
Single plant yield (g)	b234	6	0.010	5.43
Plot yield (Kg ha^{-1})	P5	-	0.004	6.32

Table 54b. List of 23 highly significant (*P*≤0.01) marker trait associations detected in Madurai (E2), Rabi/Summer 2009/10

Trait	Locus	Chromosome located	p_Marker	R2 (%)
Days to 50% flowering	p34	4	0.007	24.9
Plant height (cm)	p98	3	0.001	4.07
	b202	7	0.002	4.18
	b123	7	0.003	3.29
	p33	1	0.009	2
	m2	9	0.009	1.79
Basal tiller number	p8	1	0.002	16.69
	b200	7	0.009	15.92
	b41	9	0.010	24.13
Flag leaf blade length (mm)	ICMM02C05	-	0.001	0.85
	p17x	5	0.004	2.31
	p34	4	0.008	2.29
	b202	7	0.010	2.17
Flag leaf blade width	p34	4	0.0004	9.54
	ICMM02C05	-	0.008	2.81
Flag lead sheath length	p98	3	0.008	4.6
	b123	7	0.01	1.33
Inflorescence length	p34	4	0.003	1.72
Weight of five panicles	b123	7	0.0002	12.68
	p98	3	0.0003	9.86
	UGEP102	-	0.010	4.15
Single plant yield (g)	p61	3	0.002	8.15
Plot yield (Kg ha-1	p61	3	0.0002	9.07

Table 54c. List of 61 highly significant ($P \leq 0.01$) marker trait associations detected in ICRISAT, Patancheru (E3), rainy season 2010

Trait	Locus	Chromosome located	p_Marker	R2 (%)
Days to 50% flowering	p34	4	3E-06	31.43
	b115	2	0.0002	22.85
	b202	7	0.0004	27.89
	P13	-	0.0004	32.26
	b200	7	0.005	29.05
	p100	4	0.009	14.54
Plant height (cm)	p98	3	0.00001	28.29
	p8	1	0.00004	25.66
	b111	5	0.001	18.91
	b200	7	0.002	27.29
	ICMM02C05	-	0.003	5.99
	ICMM02C24	-	0.006	22.18
	b258	8	0.009	14.31
	m2	9	0.01	11.15
Basal tiller number	UGEP81	-	0.006	8.05
Flag leaf blade length (mm)	p98	3	0.00001	3.25
	m2	9	0.001	1.09
	p8	1	0.003	1.92
	b200	7	0.005	3.32
	b202	7	0.006	1.5
	b153	1	0.006	1.13
	p61	3	0.008	0.84
Flag leaf blade width (mm)	p8	1	0.001	5.63
	p98	3	0.001	4.36
	p61	3	0.010	3.44
Flag leaf sheath length (mm)	p98	3	0.00001	8.36
	b200	7	0.001	11.13
	m2	9	0.001	3.31
	b188	5	0.002	10.42
	p8	1	0.005	5.71
	b153	1	0.005	7
	b186	3	0.006	9.76
	b151	2	0.007	2.47
	b258	8	0.008	2.66
	b226	3	0.009	1.63
Peduncle length (mm)	b196	5	0.0001	5.06
	p87	1	0.0004	18.89
	b186	3	0.001	25.34

Table 54c. Cont..

Trait	Locus	Chromosome located	p_Marker	R2 (%)
	UGEP81	-	0.009	15.57
Panicle exertion (mm)	b196	5	0.001	4.13
	b202	7	0.005	8.39
	b234	6	0.007	5.83
	p75	5	0.008	26.01
Inflorescence length (mm)	p98	3	0.0001	5.49
	b153	1	0.001	5.44
	b225	3	0.002	6.56
	m2	9	0.002	2.71
	b258	8	0.002	1.33
	b202	7	0.006	4.11
Inflorescence width (mm)	b196	5	0.001	1.72
	p61	3	0.002	4.35
Weight of five panicles (g)	p8	1	0.001	6.13
	p56	2	0.001	1.6
	p98	3	0.001	4.06
Single plant yield (g)	b123	7	3E-06	17.5
	p98	3	0.001	8.93
	p16	1	0.003	10.29
	b159	6	0.01	7.05
Plot yield (Kg ha^{-1})	b123	7	0.002	10.24
	b234	6	0.004	14.17
	b251	9	0.007	13.8

Table 54d. List of 37 highly significant marker trait associations at *P*≤0.01 identified in pooled BLUPs of three environments

Trait	Locus	Chromosome located	p_Marker	R2 (%)
Days to 50% flowering	b202*[1]	7	0.0049	12.57
	p34*	4	4.75E-04	14
	p17x*	5	0.01	8.09
Plant height (cm)	b234	6	0.0011	10.59
	b251	9	0.0056	7.2
	ICMM02C05*	-	0.0013	2.95
	m2*	9	0.0085	5.8
	p98*	3	8.73E-05	1.5
	b111*	5	6.10E-04	9.88
Basal tiller number	p8*	1	8.72E-05	11.87
Flag leaf blade length (mm)	b202*	7	0.0021	11.86
	ICMM02C05*	-	0.0016	2.43
	m2	9	0.0108	6.3
	p17x	5	0.0052	8.54
	p98	3	0.0044	12.5
Flag leaf blade width (mm)	ICMM02C05	-	0.0079	1.02
	p8	1	0.001	6.22
	p98*	3	8.95E-04	3.87
Flag leaf sheath length (mm)	b123*	7	0.0026	1.94
	b186	3	0.0044	7.38
	b188	5	0.0082	2.83
	p17x	5	0.0073	1.84
	p98*	3	8.93E-05	5.34
Peduncle length (mm)	b186	3	9.74E-05	30.27
	b196	5	0.0011	3.25
	p98	3	0.0013	11.01
Panicle exertion (mm)	b166	9	0.0097	14.13
	b196	5	0.003	4.29
	b202	7	0.002	10.12
	b234	6	0.007	9.99
Inflorescence length (mm)	p98	3	0.0072	1.75
Weight of five panicles (g)	b123	7	0.0029	7.45
	b153	1	0.0082	6.45
	p98*	3	9.80E-05	8.04
Single plant yield (g)	p56	2	0.0091	1.52
Plot yield (Kg ha^{-1})	P5	-	0.0059	3.14
	b234*	6	0.0061	3.16

1=marker followed by * denotes the stable marker trait association (MTA) across the environments and pooled

CHAPTER V

DISCUSSION

Foxtail millet (*Setaria italica* (L.) Beauv.) is one of the oldest cereal crops contributed to human civilization not only in the past, but also still used as a staple food in China and India (Wang *et al.,* 2009a). Its importance has continually decreased in the last 80 years (Austin, 2006) mainly because of poor seedling establishment, need for hand weeding and lack of breeding effort for improved yield (Ahanchede *et al.,* 2004) beside lack of proper utilization of existing genetic resources.

In general, foxtail millet is valued as a crop of short growth duration, which is fairly resistant to insect pests and diseases (Upadhyaya *et al.,* 2008a), adaptable to varied soil and environmental conditions due to its high photosynthesis and water use efficiency. It has high nutritional and medicinal value and also it has low glycemic index (GI) which makes it as an ideal food for people suffering from diabetes (Anju and Sarita, 2010; Thathola *et al.,* 2010). Foxtail millet grains contain vitamins B1, B2, B6, C and E (Coulibaly and Chen, 2011). It may be cooked and eaten like rice, either as whole grain or broken; flour used for making porridge and puddings. Foxtail millet is also used as bird feed for feeding cage birds and the by-product of the foxtail millet is used as animal feed extensively in China (En *et al.,* 2008). At present, foxtail millet is regaining its value and emerging as important crop after realizing the nutritional and health benefits of foxtail millet and adaptability to changing climate.

In view of the several merits of this crop and very limited research undergone, Upadhyaya *et al.* (2008a) developed a core collection (155 accessions) in foxtail millet. Further, there is a need for the study of phenotypic and genetic diversity for its effective utilization in development of improved cultivars. Therefore, the present investigation was formulated to study the phenotypic and genetic diversity in foxtail millet core collection, to study the population structure and to identify SSR markers associated with quantitative traits using association mapping. The results obtained on phenotypic and genetic (molecular) diversity aspects are discussed as below briefly.

5.1. QUALITATIVE TRAITS

5.1.1. Frequency distribution

The frequency distributions of different phenotypic classes of the 12 qualitative traits revealed a large variation for each trait. In the entire foxtail millet core collection, green plant pigmentation (81.3%), green leaf colour (84.5%), erect growth habit (95.5%), high culm branching (41.9%), long bristle length (40.0%), dense panicle lobing (53.6%), compact inflorescence (76.8%), compact lobe (91.0%), yellow grain colour (91.6%), non lodging (49.7%), leaves almost green at maturity (47.1%) senescence score and good overall plant aspect score (43.2%) were the most predominant classes of the 12 qualitative traits.

Green plant pigmentation, green leaf colour, erect growth habit, compact inflorescence, compact lobe, yellow grain colour and non lodging plants were the most prevalent classes across three races, whereas the traits like culm branching, bristle length, panicle lobing, leaf senescence and overall plant aspects differed with races. Medium (44.1%) culm branching was the most prevalent class found among the accessions present in the race *indica* whereas, low culm branching in *maxima* (75.0%) and high culm branching in *moharia* (72.4%) were the most prevalent classes. Intermediate culm branching in the race *indica*, low culm branching in *maxima* and high culm branching in *moharia* were the characteristics of three races (Prasada Rao *et al.,* 1986). Most of the accessions present in the race *indica* had long bristle length (50.0%), whereas 79.2 per cent of the accessions in *maxima* and 51.7 per cent of the accessions in *moharia* had short bristle and medium bristle length, respectively.

The race *indica* (58.8%) and *maxima* (83.3%) were predominated with dense lobed accessions and *moharia* predominated with non lobed (69%) accessions. The race *maxima* is characterized by spikelets closely arranged on elongated lateral branches, giving the inflorescence a lobed appearance. Dense lobed, large inflorescences are the characteristics of the race *maxima* (Prasada Rao *et al.,* 1986). Leaves almost green at maturity class was the most prevalent among the accessions present in *indica* (57.8%) whereas 41.7 per cent of the accessions in *maxima* and 34.5 per cent of the accessions in *moharia* had leaves completely and moderately green at maturity, respectively. Overall plant aspect was classified into very good, good, average, poor and very poor. Good plant score was found to be the most common in the race *indica* (53.9%) and *maxima* (41.7%) whereas 51.7 per cent of the accessions showed poor plant aspect in the race *moharia*.

The early flowering, short plant stature, more tillers with numerous side branches, short inflorescence length and low yield were the main reason for poor plant aspect of the race *moharia*. Cultivars of race *moharia* often resemble members of wild ssp. *viridis* in phenotype. Short plant type (25-100cm), with 5-52 (average 8.6) tillers per plants, tillers usually branched to produce a well developed terminal inflorescence and several, smaller lateral inflorescences are the characteristics of the race *moharia* as described by Prasada Rao *et al.* (1986). The results of this study support the earlier report of Upadhyaya *et al.* (2008a) in foxtail millet core collection and entire germplasm collection conserved at ICRISAT.

5.1.2 Shannon Weaver Diversity Indices

The Shannon-Weaver diversity indices (H′) were estimated for 12 qualitative traits in the core collection and for each race to compare H′ values in foxtail millet core collection. Leaf senescence (0.46), bristle length (0.45) and culm branching (0.45) in *indica*, over all plant aspects (0.59) and leaf senescence (0.58) in *maxima,* and leaf senescence (0.60) and plant lodging (0.52) in *moharia* had the highest H′ value. The accessions of *moharia* had slightly higher pooled H′ value (0.32±0.048) across the traits followed by *indica* (0.30±0.041) and *maxima* (0.30±0.049). Among the qualitative traits studied, leaf senescence (0.55) and over all plant aspects (0.55) had the highest H′ followed by culm branching (0.47), bristle length (0.47) and plant lodging (0.44) in the entire core collection. Growth habit (0.09) and grain colour (0.15) had the lower H′ index in the entire core collection.

5.2 QUANTITATIVE CHARACTERS

The data on 13 quantitative traits of individual environment and pooled data were analyzed for the entire core collection and each race separately to estimate variance components due to genotype (σ^2_g) and genotype × environments (σ^2_{ge}), to compare mean and variance, to estimate phenotypic diversity, Shannon-Weaver diversity index (H') and principle component analysis (PCA). The results of various analyses are discussed below.

5.2.1 Variance components

The REML analysis indicated that the σ^2_g was significant for all the traits in all three environments and pooled data in the foxtail millet core collection indicating the presence of high level of variability for all the traits. In pooled analysis, σ^2_{ge} interaction was significant for all the

traits indicating the differential response of genotypes to different environments and the core collection interacting with environment. Wald's statistics was significant for all the traits except flag leaf sheath length indicating that the three environments were adequate to differentiate the core collection accessions.

5.2.2 Variability Studies

Progress in any crop improvement program depends mainly on the variability existing in the metric traits of the base population. Genetic variability studies provide basic information regarding the genetic properties of the population based on which breeding methods are formulated for further improvement of the crop. These studies are also helpful to know about the nature and extent of variability that can be attributed to different causes, sensitive nature of the crop to environmental influences, heritability of the characters and genetic advance that can be realized in practical breeding. Hence, to have a comprehensive idea, it is necessary to have an analytical assessment of yield components.

5.2.1.1 Phenotypic and genotypic coefficient of variation (PCV and GCV)

In the present study, the traits such as days to 50 per cent flowering, plant height, basal tiller number, flag leaf blade length, inflorescence length, inflorescence width, weight of five panicles, single plant yield and grain yield per plot (Kg ha^{-1}) showed high estimates of PCV and GCV, and narrow difference between them in all three environments and for pooled data indicated the low effects of environments and greater role of genetic factors on the expression of these traits. Similar findings have been reported in foxtail millet for days to 50 per cent flowering and plant height (Cill and Randhawa, 1975), basal tiller number (Nirmalakumari and Vetriventhan, 2010; Nirmalakumari *et al.,* 2008; Reddy and Jhansilakshmi, 1991a; Cill and Randhawa, 1975) and grain yield (Nirmalakumari and Vetriventhan, 2010; Basheeruddin and Sahib, 2004; Selvarani and Gomathinayagam, 2000b; Rathod, 1995; Cill and Randhawa, 1975).

5.2.1.2 Heritability and genetic gain

Heritability is a quantitative measure which provides information about the correspondence between genotypic variance and phenotypic variance, *i.e.,* the ratio of variance due to heritable differences (σ^2g) to the total phenotypic variance (σ^2p) and expressed as per cent. In the present study, all the traits namely days to 50 per cent flowering, plant height, basal

tiller number, flag leaf blade length, flag leaf blade width, flag leaf sheath length, panicle exertion, peduncle length, inflorescence length, inflorescent width, weight of five panicles, single plant yield and grain yield per plot (Kg ha^{-1}) showed the high estimates of broad sense heritability (h^2_b) indicating the reliability of the estimates for variation between entries and effectiveness of selection in this material for these traits. Populations which are genetically more uniform are expected to show lower heritability than the genetically variable population. Also, more variable environmental condition reduces the magnitude of heritability and more uniform environmental condition increases it (Dabholkar, 1999). Hence, high heritability of these traits in this study may be due to highly variable and genetically diverse accessions present in the core collection and probably due to uniform conditions within environments.

Since heritability is also influenced by environment, the information on heritability alone may not help in pin pointing characters enforcing selection. Nevertheless, the heritability estimates in conjunction with the predicted genetic gain will be more reliable (Johnson *et al.,* 1955). Heritability gives the information on the magnitude of inheritance of quantitative traits, while genetic advance will be helpful in formulating suitable selection procedures.

The grain yield and its components like days to 50 per cent flowering, plant height, basal tiller number, flag leaf blade length, flag leaf blade width, flag leaf sheath length, panicle exertion, peduncle length, inflorescence length, inflorescent width, weight of five panicles and single plant yield showed high genetic advance as per cent of mean coupled with high estimates of h^2_b indicated that, the variation are attributable to high level of heritable variation and selection would be effective for improvement of this traits. The high estimates of heritability coupled with high genetic advance as per cent of mean reported by the earlier studies in foxtail millet for days to 50 per cent flowering (Nirmalakumari *et al.,* 2008), plant height (Nirmalakumari and Vetriventhan, 2010; Basheeruddin and Sahib, 2004; Selvarani and Gomathinayagam, 2000b), basal tillers number (Nirmalakumari and Vetriventhan, 2010; Nirmalakumari *et al.,* 2008, Reddy and Jhansilakshmi, 1991a; Cill and Randhawa, 1975), flag leaf blade length, flag leaf blade width, peduncle length and panicle exertion (Nirmalakumari *et al.,* 2008), inflorescence length (Nirmalakumari and Vetriventhan, 2010; Nirmalakumari *et al.,* 2008; Lakshmanan and Guggari, 2001), weight of five panicles (Reddy and Jhansilakshmi, 1991a) and grain yield (Nirmalakumari and Vetriventhan, 2010; Nirmalakumari *et al.,* 2008; Lakshmanan and Guggari, 2001; Selvarani and Gomathinayagam, 2000b).

5.2.2 Range

In the foxtail millet core collection, a wide range of variation was observed for all the traits of three different races and three environments as well in overall pooled data. This indicated the differential response of the genotypes to different environments and wide range of diversity in the core collection.

5.2.3 Mean performance of foxtail millet core collection

5.2.3.1 Mean performance within and between three environments

The mean of each environment was computed for all 13 quantitative traits and compared with other environments using the Newman-Keuls procedure. The three environments and pooled data did not differ significantly for overall mean of core collection for days to 50 per cent flowering, plant height, flag leaf sheath length, peduncle length and weight of five panicles indicating less influence of the environment on the expression of these traits, whereas the remaining eight traits (basal tillers number, flag leaf blade length, flag leaf blade width, panicle exertion, inflorescence length, inflorescence width, single plant yield and grain yield per plot (Kg ha^{-1}) were significantly different between environments indicating the greater influence of the environments on the expression of these traits.

Mean days to 50 per cent flowering (53.7±0.76), plant height (100.3±4.45), basal tillers number (4.2±0.29), flag leaf blade width (19.0±0.91), inflorescence length (149.5±8.61), inflorescence width (16.9±0.65), weight of five panicles (25.6±1.74), single plant yield (23.9±2.18) and grain yield per plot (Kg ha^{-1}) (1612.4±121.1) were maximum in E1 as compared to E2 and E3. Peduncle length (309.4±9.024) and panicle exertion (182.3±6.90) in E2, and flag leaf blade length (275.8±14.13) and flag leaf sheath length (135.0±6.39) in E3 were showed the maximum mean performance. This differential response was due to the different evaluation conditions in all three environments. In E1 and E2, foxtail millet was evaluated under irrigated during Rabi/summer 2009/10 and in E3 under as rainfed during rainy season 2010. And also, there was heavy rain in E3 at initial establishment stage was the main reason for the reduced yield and other traits in E3. Therefore, maximum yield can be achieved by growing it in well managed condition with adequate irrigation.

5.2.3.2 Mean performance of three biological races within and between environments

Mean of different traits were calculated for each of the three races in each environment separately and pooled data were tested using the Newman-Keuls procedure. The means of three races differed significantly in each of the three environments or two out of three environments for the traits like days to 50 per cent flowering, plant height, basal tillers number, flag leaf blade length, flag leaf sheath length, inflorescence length, single plant yield and grain yield per plot (Kg ha^{-1}).

The traits like flag leaf blade width, peduncle length, inflorescence width and weigh of five panicles did not show significant differences between *indica* and *maxima* however both these races differed significantly from *moharia* in all three environments and overall in pooled data. Basal tiller number was lowest in *maxima* and different significantly from *indica* and *moharia* in all three environments and pooled. This followed the properties of three races, intermediate basal tillers number in *indica*, maximum tillers in *moharia* and few unbranched tillers in *maxima* are the characteristics of the races (Prasada Rao *et al.,* 1986).

The tall and late flowering accessions were from race *indica*. That were characterized with greater flag leaf blade length, flag leaf sheath length, peduncle length, inflorescence length, single plant yield and grain yield per plot (Kg ha^{-1}) in all three environments and pooled.

The accessions of *moharia* were earliest in flowering, have short height, maximum basal tiller and lowest flag leaf blade length, flag leaf blade width, flag leaf sheath length, peduncle length, inflorescence length inflorescence width, weight of five panicles, single plant yield and grain yield per plot (Kg ha^{-1}). Prasada Rao *et al.* (1986) reported that high number of basal tillers (5-52, average 8.6) is characteristic feature of race *moharia*.

The accessions of *maxima* were intermediate in days to 50 per cent flowering, plant height, flag leaf blade length, flag leaf sheath length, peduncle length, inflorescence length, inflorescence width, single plant yield and grain yield per plot (Kg ha^{-1}) and the maximum flag leaf blade width, panicle exertion, weight of five panicles with less number of basal tillers. Prasada Rao *et al.* (1986) described that plants with 45-100cm tall and low (1-8 with an average of 1.6) unbranched tillers as characteristic feature of the race *maxima.*

Mean of the race *indica* significantly differ in each environment for all the traits except days to 50 per cent flowering and flag leaf sheath length. In case of the race *maxima*, basal tillers number, flag leaf blade length, single plant yield and grain yield per plot (Kg ha^{-1}) show

significant difference between environments, however *moharia* show significant difference only for the trait single plant yield and grain yield per plot (Kg ha^{-1}).

5.2.4 Variance

Variances of 13 quantitative traits were calculated for individual environment separately and for pooled data of entire core collection and for three races separately. The homogeneity of variances of three was tested using Levene's test. Variances were homogenous between environments for only four quantitative traits *viz.*, days to 50 per cent flowering, flag leaf blade length, flag leaf sheath length and panicle exertion out of 13 quantitative traits studied. Variances were homogenous between three different races for only two trait (days to 50% flowering and single plant yield) in E1, nine traits in E2 (days to 50% flowering, basal tiller number, flag leaf blade length, flag leaf blade width, peduncle length, panicle exertion, inflorescence length, inflorescence width and single plant yield) and six traits in E3 (days to 50% flowering, flag leaf blade width, flag leaf sheath length, inflorescence width, single plant yield and grain yield per plot (Kg ha^{-1}). This explains the diversity of the races present in the core collection. For days to 50 per cent flowering and single plant yield variances were homogenous between races in all three environments, and pooled data.

Homogeneity of variance was also tested race-wise between environments. The quantitative traits like days to 50 per cent flowering, flag leaf blade length, flag leaf blade width and inflorescence length of race *indica* and for days to 50 per cent flowering, plant height, flag leaf blade length, flag leaf sheath length, peduncle length and panicle exertion for race *maxima* were homogenous between environments. For all the quantitative traits except basal tillers number, flag leaf blade length and flag leaf blade width variance of the race *moharia* between environments were homogenous.

5.2.5. Correlations

Understanding of the interaction of the traits among themselves and with the environment is of great use in plant breeding. Correlation studies provide information on the nature and extent of association between any two quantitative traits and it would be possible to genetic enhancement of a trait through selection of a correlated trait (associated response). Grain yield is a complex character and jointly determined by a number of related traits. An insight into the association between grain yield and other correlated traits helps to improve the efficiency of

selection. In general, the correlation between yield and other characters as well as among the component characters will vary with the material handled by the breeder.

In the present investigation, the phenotypic correlations were estimated among 12 quantitative traits that are closely related to grain yield using BLUPs in foxtail millet core collection in each environment separately and overall three environments.

Out of 78 correlations for the particular environment, a total of 64 correlations were significant in E1, 60 in E2, 70 in E3 and 65 in pooled at $P \leq 0.05$ which indicated the importance of the traits investigated in this study. The grain yield per plot (Kg ha^{-1}) was significantly and positively correlated with days to 50 per cent flowering, plant height, flag leaf blade length, flag leaf blade width, flag leaf sheath length, inflorescence length, inflorescence width, weight of five panicles, single plant yield in all three environments and in pooled analysis. Basal tillers number in E1, E3 and pooled had significant positive correlation with grain yield per plot (Kg ha^{-1}). Peduncle length had significant positive correlation in E2 and pooled. It would be inferred that, selection for high yield would be effective through selection for these traits. Besides these traits showed high heritability coupled with high genetic advance as per cent mean, hence selection is desirable. Positive correlation of days to 50 per cent flowering (Nirmalakumari and Vetriventhan, 2010), plant height (Nirmalakumari and Vetriventhan, 2010; Channappagoudar *et al.,* 2008; Murugan and Nirmalakumari, 2006; Santhakumar, 1999), basal tiller number (Nirmalakumari and Vetriventhan, 2010; Islam *et al.,* 1990; Navale and Harinarayana, 1987; Cill and Randhawa, 1975), inflorescence length (Nirmalakumari and Vetriventhan, 2010; Murugan and Nirmalakumari, 2006, Santhakumar, 1999), inflorescence width (Cill and Randhawa, 1975), weight of main ear (Murugan and Nirmalakumari, 2006) with grain yield were reported in foxtail millet. Panicle exertion is the only character which showed significant negative correlation with grain yield per plot (Kg ha^{-1}) in E1 (-0.228), E3 (-0.197) and pooled (-0.191).

Days to 50 per cent flowering was significant positively correlated with plant height, flag leaf blade length, flag leaf blade width, flag leaf sheath length, inflorescence length, inflorescence width, weight of five panicles, single plant yield and grain yield per plot (Kg ha^{-1}) indicated the simultaneous enhancement of these traits through the selection in positive direction for days to 50 per cent flowering. Upadhyaya *et al.* (2008) reported the positive correlation of days to 50 per cent flowering with flag leaf blade length, flag leaf blade width, flag leaf sheath length, inflorescence length, inflorescence width and weight of five panicles. Therefore, it can be

inferred that selection should be in positive side for days to 50 per cent flowering, plant height, flag leaf blade length, flag leaf blade width, flag leaf sheath length, inflorescence length, inflorescence width, weight of five panicles, single plant yield along with low panicle exertion which will in turn automatically increase the grain yield in foxtail millet.

In the present study, a total 35 useful (r>0.500 or <-0.500) correlations were observed in E1, 29 in E2, 36 in E3 and 40 in pooled. grain yield per plot (Kg ha^{-1}) had useful positive correlation with plant height in E1 (0.651), E2 (0.578) and pooled (0.678), flag leaf blade length in E1 (0.567), E3 (0.505) and pooled (0.627), flag leaf sheath length in pooled (0.548), inflorescence length in E1 (0.513), E2 (0.504) and pooled (0.582) and weight of five panicles in E2 (0.514) and pooled (0.514). Single plant yield had useful positive correlation in all three environments and pooled with grain yield per plot (Kg ha^{-1}) (0.952 in E1, 0.932 in E2, 0.716 in E3 and 0.899 in pooled). This indicated the strong association of plant height, flag leaf blade length, flag leaf sheath length, inflorescence length, weight of five panicles, single plant yield with grain yield per plot (Kg ha^{-1})

The useful correlation of (1) days to 50 per cent flowering with plant height, flag leaf blade length, flag leaf blade width, flag leaf sheath length, inflorescence length, inflorescence width and weight of five panicles, (2) plant height with flag leaf blade length, flag leaf blade width, flag leaf sheath length, inflorescence length, inflorescence width, weight of five panicles, single plant yield and grain yield per plot (Kg ha^{-1}), (3) flag leaf blade length with flag leaf blade width, flag leaf sheath length, inflorescence length, inflorescence width, weight of five panicles, single plant yield and grain yield per plot (Kg ha^{-1}), (4) flag leaf blade width with flag leaf sheath length, inflorescence length, inflorescence width and weight of five panicles, (5) flag leaf sheath length with peduncle length, inflorescence length, weight of five panicles, single plant yield and grain yield per plot (Kg ha^{-1}), (6) peduncle length with panicle exertion, (7) inflorescence length with inflorescence width, weight of five panicle, single plant yield and grain yield per plot (Kg ha^{-1}), (8) inflorescence width with weight of five panicles, single plant yield and grain yield per plot (Kg ha^{-1}), (9) weight of five panicles with single plant yield and grain yield per plot (Kg ha^{-1}) and (10) single plant yield with grain yield per plot (Kg ha^{-1}) in pooled data. Out of 40 useful correlations present in pooled, 26 were present in all three environments. Upadhyaya *et al.* (2008) reported the useful correlation between plant height *vs* inflorescence length, flag leaf

blade length *vs* inflorescence length, peduncle length *vs* panicle exertion in foxtail millet entire and core collection.

5.2.6 Path coefficient analysis

The correlation measured the relationship existing between pairs of traits. But dependent traits are an interaction product of many mutually associated components. The path analysis takes into account the cause and effect relationship between the variables by partitioning the association into direct and indirect effects through other independent variables.

In this study, the direct effect of single plant yield on grain yield per plot (Kg ha^{-1}) was positive and high in all the environments separately and in pooled analysis (0.891 in E1, 0.911 in E2, 0.61 in E3 and 0.929 in pooled) which indicated the true relationship of this trait and a direct selection through this trait will be effective. The indirect effect of days to 50 per cent flowering, plant height, flag leaf blade length, flag leaf blade width, flag leaf sheath length, inflorescence length, inflorescence width and weight of five panicles through single plant yield was positive and high. It can be inferred that, the direct selection of single plant yield in foxtail millet lead to simultaneous indirect selection of days to flowering, plant height, flag leaf blade length, flag leaf blade width, flag leaf sheath length, inflorescence length, inflorescence width and weight of five panicles for increased grain yield.

The residual effect determines how best the causal factors account for the variability of the dependent factors, yield in this case. Its estimate being 0.115 in E1, 0.085 in E2 and 0.348 in E3 and 0.071 pooled, explained about 88.5 per cent of variability in the yield in E1, 91.5 per cent in E2, 65.2 per cent in E3 and overall 93 per cent in pooled data. This indicated that, the maximum proportion of the variability was captured in foxtail millet core collection. The residual variance was low in all the three environments as well in pooled data which indicated that, importance of the characters taken in this study and accounted more variation for grain yield in foxtail millet core collection.

5.3 DIVERSITY ANALYSIS

5.3.1 Shannon Weaver Diversity Indices

The Shannon-Weaver diversity indices (H′) were calculated to compare diversity index among 13 quantitative traits and three races of foxtail millet core collection. Out of 13 quantitative traits, flag leaf blade width, flag leaf sheath length, peduncle length in all three

environments and pooled along with plant height, inflorescence width in E1, panicle exertion and inflorescence length in E2, panicle exertion and weight of five panicle in E3, and panicle exertion and inflorescence width in pooled had the maximum H′ value. This shows that, the importance of these characters in contributing to divergence. Upadhyaya *et al.* (2008a) also reported the highest H' for plant height, flag leaf blade width, flag leaf sheath length, peduncle length and panicle exertion in the entire collection of foxtail millet germplasm conserved at ICRISAT and in core collection, which indicated the diversity of core collection represents the entire collection. Among the races, *indica* showed the highest pooled H′ values across the traits indicating the relatively higher diversity of this race in core collection. The race *maxima* and *moharia* showed the low pooled H′ across the traits in all three environments as well as pooled data, was probably due the less sample size represented by these two races in the core collection (*maxima*;15.5% and *moharia* ;18.7%).

5.3.2 Phenotypic diversity matrix

Phenotypic diversity matrix (Gower, 1985) was created by calculating differences between each pair of accessions for each of the 12 qualitative and 13 quantitative traits by averaging all the differences in the phenotypic values for each trait divided by their respective range. In the entire foxtail millet core collection evaluated at three different environments showed similar mean diversity, ranging from 0.250 in E3 to 0.255 in E1 which indicated the consistency of diversity between environments. Based on the diversity index, ten most diverse pairs of accessions were identified in each environment separately and overall pooled data of three environments. Most of diverse pairs of accessions in pooled data were also found in individual environment which indicated the stability of the genotypes across the environments. Hence, ISe 1687-ISe 1254, ISe 1597-ISe 1312, ISe 1687-ISe 1201, ISe 1881-ISe 1312, ISe 1597 -ISe 1320, ISe 1687-ISe 1129, ISe 1687-ISe 1312, ISe 1685-ISe 827, ISe 1286-ISe 1059, and ISe 1687-ISe 1118 were the ten most diverse pairs of accessions identified in pooled data of three environments. It would be interesting to involve these pairs of diverse accessions in development of mapping population to identify QTL and in hybridization program to study the segregating generation and selection of superior lines.

5.3.3 Principal component analysis

The PCA on the mean values of the entire core collection and races was performed which provided a reduced dimension model that could indicate measured differences among the accessions and races.

5.3.3. 1. PCA based on environments

The results revealed the importance of the first three PCs in discriminating the foxtail millet core collection in individual environment and pooled. The percentage of total variance explained by the first three PC was 70 per cent in all the environments as well as in pooled data. Days to 50 per cent flowering, plant height, flag leaf blade length, flag leaf blade width, flag leaf sheath length, inflorescence length, weight of five panicles were most important traits that made contribution in explaining variation in the first three PCs. It indicated the importance of these traits for their contribution towards divergence in foxtail millet core collection.

5.3.3.2 PCA based on races

The results of principal component analysis based on races revealed the importance of first three PCs which explained more than 60 per cent in discriminating the three races in all three environments and pooled. The percentage of total variation explained by the first three PCs in race *indica* was 66.7, 61.6, 73.5 and 70.8 per cent in E1, E2, E3, and pooled, respectively, which was less as compared to variation explained in *maxima* and *moharia* (89.2 in E1, 74.9 in E2, 86.0 in E3 and 83.2% in pooled for *maxima* and 82.5 in E1, 82.5 in E2, 83.2 in E3 and 87.1% in pooled for *moharia*) which shows the first three PCs of *maxima* and *moharia* explained more variation than *indica*.

Days to 50 per cent flowering, flag leaf blade length, flag leaf blade width, inflorescence length, inflorescence width and plant height were the most important traits explaining more variation in the first three PCs of *indica*, whereas days to 50 per cent flowering, plant height, flag leaf blade length, inflorescence length, inflorescence width, weight of five panicles, single plant yield and grain yield per plot (Kg ha^{-1}) in *maxima* and days to 50 per cent flowering, plant height, flag leaf blade length, flag leaf blade width, flag leaf sheath length, inflorescence length, inflorescence width, weight of five panicles and single plant yield in *moharia* were more important in contribution in explaining variation in first three PCs. All together, basal tillers, peduncle length and panicle exertion were made no contribution in explaining the variation in the

first three PCs in all three races across environments indicating the low importance of this traits in of foxtail millet.

5.3.4. Clustering

The hierarchical cluster analysis (Ward, 1963) was performed for individual environment and pooled based on scores of first three PCs accounting 78.6, 71.6, 83.1 and 82.5 per cent of total variance in E1, E2, E3 and pooled data, respectively. The clustering pattern in all the three environments and pooled were based on the three races. In general, accessions of *indica* were grouped into two sub-clusters *BI* and *BII*, under cluster *B*. Most of the accessions from *moharia* grouped together in cluster *A*. Accessions from *maxima* mixed with *moharia* in cluster *A* and *indica* in sub-cluster *BI*. The reason for this clustering may be that the race *indica* was probably derived from a combination of *moharia* cultivars from southwestern Asia and *maxima* cultivars from China (Prasada Rao *et al.,* 1986).

5.4. IDENTIFICATION OF TRAIT SPECIFIC SOURCES

In any crop, improvement of yield and other traits like quality, biotic and abiotic stresses can be achieved by identifying gene/trait specific sources. The use of genetic resources in the breeding programs have been mainly as sources of resistance to pests and diseases (Knauft and Gorbet, 1989), or as sources of male sterility, short stature or any such character with simple inheritance. Well known examples are semi-dwarf rice and wheat genotypes which contributed much to the success of green revolution. There have been fewer efforts for identifying germplasm lines for increasing yield potential than for pest resistance and nutritional quality (Halward and Wynne, 1991), because such traits are highly environment interactive and require multi-environment testing to accurately characterize them (Upadhyaya *et al.,* 2010a). Thus identification of promising resources for the environment sensitive quantitative characters is a difficult task. However, with the use of core and mini core collections of chickpea (Upadhyaya and Ortiz, 2001), sources for high grain yield (Upadhyaya *et al.*, 2007a), tolerance to drought (Kashiwagi *et al.,* 2005) and disease (Pande *et al*., 2006) have been identified. Evaluation of mini core led to the identification of 39 chickpea accessions for a combination of agronomic traits such as early maturity, seed size and grain yield (Upadhyaya *et al.,* 2007a). Similarly, new sources for tolerance to drought (Upadhyaya, 2005) and low temperature at germination (Upadhyaya *et al* 2009a), and for early-maturity (Upadhyaya *et al.,* 2006a), were identified in the

groundnut core and mini core collections. Upadhyaya *et al*. (2005) identified 15 fastigiata, 20 vulgaris, and 25 hypogaea type groundnut accessions for pod yield and its components upon multi-location evaluation of groundnut core collection for Asia region. Foxtail millet core collection was evaluated and neck blast resistant foxtail millet accessions were identified (ICRISAT Archival Report 2009). Upadhyaya *et al.* (2011a) evaluated finger millet core collection for grain nutrients and identified accessions rich in Fe, Zn, Ca and protein.

Hence, multi-environmental evaluation/characterization of foxtail millet core collection and identification of trait specific sources for different yield contributing traits will provides new sources for future breeding program in foxtail millet. The accessions from the reserve collection (remaining part of the entire collection) can also be examined selectively for additional sources of useful traits from the same cluster from which the accessions in the core collection have been identified (Upadhyaya *et al.,* 2008a).

In the present study, foxtail millet core collection evaluated in three different environments shows a wide range of variability for yield and its component traits within and between environments could be utilized for identification of new trait specific sources. Fifteen accessions were identified for each traits namely early, tall plants, and maximum values of basal tiller number, flag leaf blade length, flag leaf blade width, inflorescence length, inflorescence width, weight of five panicles, single plant yield and grain yield based on pooled BLUP of three environments and compared with mean of four control cultivars ± LSD. Most of the accessions selected as trait specific sources appeared in top 15 ranks in all the three environments or atleast in two out of three environments indicated the stability of the genotype in different environments.

Out of 155 accessions of the foxtail millet core collection, a total of 68 accessions (39 accessions in *indica*, 15 in *maxima* and 14 in *moharia*) were identified as trait specific for ten important yield contributing traits (Table 55). Multi-trait specific accessions were identified, which were found to be sources for more than one trait. Twelve accessions were identified as sources for two traits each, seven accessions were sources for three traits each, two accessions were sources for four traits each, four accessions were sources for five traits each, three accessions were sources for six traits each, two accessions were sources for seven traits each, two accessions were sources for eight traits each and ISe 1687 (*maxima*) was source for eight

traits including grain yield per plot (Kg ha^{-1}). These accessions could be utilized for simultaneous transfer of multiple traits/gene in crop improvement program.

5.5. MOLECULAR DIVERSITY

Understanding the distribution of genetic diversity among individuals, populations and gene pools is crucial for the efficient management of germplasm collections and breeding programs. Diversity analysis is routinely carried out using sequencing of selected gene(s) or by molecular markers. An extensive characterization of plant genetic resources provides an opportunity for structural dissection to mine the allelic variation, and identify diverse accessions for crop improvement (Upadhyaya *et al.,* 2010a). The DNA-based markers are promising and effective tools for measuring genetic diversity in plants germplasm and elucidating their evolutionary relationships (Pervaiz *et al.,* 2009).

Germplasm characterization based on molecular markers has gained importance due to the speed and quality of data generated. It would also provide information on the population structure, allelic richness, and diversity parameters to help breeders use genetic resources for cultivar development more effectively. Molecular characterization of the core collection would help in revealing the population structure and in assessing the genetic diversity at DNA level with reduced resources (Upadhyaya *et al.,* 2008a). The core germplasm accessions were characterized using DNA markers such as random amplified fragment DNA (RAPD) and isoenzyme in red clover (*Trifolium pretense*) (Dias *et al.,* 2008), common bean (*Phaseolus vulgaris L.*) (Skroch *et al.,* 1998) and potato (*Solanum tuberosum* L.) (Ghislain *et al.,* 1999). The AFLP markers have been used for studying the variation in core subsets of oats (Fu *et al.,* 2005).

Amongst the DNA markers, the microsatellites [also known as single sequence repeats (SSRs)] markers are now the markers of choice in most areas of molecular genetics as they are highly polymorphic even between closely related lines, require low amount of DNA, can be easily automated for high throughput screening, can be exchanged between laboratories and are highly transferable between populations. The SSR markers were co-dominant markers and good for studies of population genetics and mapping. Microsatellite (SSR) markers were utilized to reveal genetic diversity in apple *(Malus* spp.) (Hokanson *et al.,* 1998), common beans (*Phaseolus vulgaris* L.) (Blair *et al.,* 2009) core collections, US peanut mini core collection

(Kottapalli *et al.,* 2007), USDA rice minicore subset (Agrama *et al.,* 2009) and chickpea compost collection (Upadhyaya *et al.*, 2008b).

5.5.1. Molecular diversity of foxtail millet core collection

Out of 99 SSR markers in this study, 84 markers (72 foxtail millet SSRs, 3 foxtail millet EST-SSRs, 5 finger millet SSRs and 4 pearl millet SSRs) produced clear, scorable and polymorphic marker profile and were used for the further analysis.

5.5.1.1. Allelic richness

A set of 84 highly informative SSR markers detected a total of 1,356 alleles in 155 accessions of foxtail millet core collection. Of the 1,356 alleles, 368 were rare (27.14%), 906 common (66.81%) and 82 most frequent alleles (6.05%). The P5 and p92 had no rare alleles, whereas all other markers showed rare alleles which ranged from 1 (p61, b202, b196, b226, p34, p269, p56, p20, p21, b115, m2, ICMM02C05, P2 and UGEP102) to 12 (ICMM02C24 and UGEP81). In general, markers detecting a greater number of alleles per locus detected more rare alleles. The presence of many rare alleles could be due to the higher rate of mutation at SSR loci (Henderson and Peters, 1992) and highly diverse nature of the accessions present in the core collection. Rare alleles from cultivated and wild accessions could be used to select specific accessions for allele mining (Upadhyaya *et al.,* 2010a). A total of 61 unique alleles were detected in core collection, which were present only in one accession and absent in other accessions. Unique alleles are important because they may be diagnostic of particular type of genotype (Senior *et al.*, 1998). The occurrence of the highest number of rare and unique alleles in the foxtail millet core collection is an indication of the greater diversity present in this core collection and its potential as a reservoir of novel alleles for crop improvement.

The number of alleles per locus ranged from 4 (b196 and p56) to 35 (b171) which was higher than reported in barley (4-32 alleles, Matus and Hayes, 2002) and rice (3 to 32 alleles, Borbra *et al.,* 2010), and lesser than reported in chickpea (14-67 alleles, Upadhyaya et al., 2008b) and maize (2-38 alleles, Wang et al., 2008). The average of 16.14 alleles per locus was detected in foxtail millet core collection which was more than the previous studies in foxtail millet (6.16, Jia *et al.,* 2009; 14.04, Liu et al., 2011) and other crops, *e.g.,* 7.6 (Wang *et al.,* 2009b) and 4.79 (Shehzad *et al.,* 2009) in sorghum, 8.23 in maize (Yang *et al.,* 2010b) and 8.2 (Agrama et al., 2007), 15.8 (Agrama and Eizenga, 2008) and 12.4 (Borba et al*.,* 2010) in rice. Jia

et al. (2009) used only 40 accessions of foxtail millet from limited geographical origins (most from China) might be the reason for less number of alleles per locus in their study. Higher number of alleles per locus than detected in this study was reported in barley (16.3 alleles per locus, Matus and Hayes, 2002; 16.7 alleles per locus, Malyshera-Otta et al*,* 2006) and chickpea (35 alleles per locus, Upadhyaya *et al.,* 2008b).

The difference in SSR allelic richness can be explained by several factors like diversity range of the germplasm, number of accessions used, number of SSR loci and SSR repeat type (Yang et al., 2010b). A larger number of SSR loci and the use of dinucleotide repeat SSRs rather than tri- or higher may lead to a higher number of alleles and higher genetic diversity (Yang *et al.,* 2010b). The SSR markers used in this study are di-nucleotides that might be one of the reasons for higher allelic diversity. Moreover, the higher number of alleles may also be attributed to the material used in this study; core collection represents the diversity of the entire collection of foxtail millet conserved at ICRISAT, Patancheru, India.

5.5.1.2 Polymorphic information content (PIC).

The PIC value is a reflection of allele diversity and the informativeness of each marker. The PIC values ranged from 0.06 (b196) to 0.95 (b260) with an average of 0.70. This was higher than that reported in sweet sorghum (0.54, Wang *et al.,* 2009b) and rice (0.603, Pervaiz *et al.,* 2009; 0.42, Jin *et al.,* 2010), but lower than that reported in chickpea (0.854, Upadhyaya *et al.,* 2008b). SSR markers used in this study were highly informative and polymorphic. Out of 84 markers, 69 markers were highly polymorphic with PIC values more than 0.50.

5.5.1.3 Gene diversity

Gene diversity is defined as the probability that two randomly chosen alleles from the population are different. It varied from 0.06 (b196) to 0.95 (b260), with an average of 0.72. Seventy one out of 84 SSRs showed high gene diversity (>0.50) and only 13 SSR markers scored gene diversity ≤0.50. High level of polymorphism, more number of alleles and high gene diversity observed in this study indicated a wide diversity among accessions present in the foxtail millet core collection.

5.5.1.4. Heterozygosity

Eventhough, the DNA was extracted from a single plant per accessions and crop is highly self-pollinated, a varying range of heterozygosity (0 to 0.56) was detected in the investigated materials. Of 72 SSR markers which were specific to foxtail millet, only 2 SSRs [p16 (0.16) and p2 (0.22)] showed heterozygosity of >0.10. Out of 84 SSRs used, 10 SSR markers detected no heterozygosity and 11 SSR markers showed more than 0.10. Of these 11 SSR markers, three each for foxtail millet EST-SSRs (P5 and P13 and P2), finger millet SSRs (UGEP102, UGEP3 and UGEP56) and pearl millet SSRs (ICMMO2D15B, ICMMO2C24 and ICMM02D07) showed heterozygosity >0.10. The SSR markers from other crop/related species (pearl millet and finger millet) showed more heterozygosity as compared to SSRs generated from foxtail millet which were specific to foxtail millet genome. This may be due to partial homology of the genome between species. Besides out-crossing averaging about 4% (Li *et al.,* 1935) in foxtail millet or heterozygous individuals or by residual heterozygosity in germplasm (Blair *et al.,* 2009) for particular SSR loci may also be the reason for heterozygosity detected in this study.

5.5.1.5 Diverse accessions

The SSR-derived data were subjected to calculate the genetic dissimilarity. This dissimilarity matrix was used to determine the level of relatedness among the accessions present in the core collection. Pair-wise estimates of dissimilarity values ranged from 0.098 to 0.956. The minimum dissimilarity was observed between ISe 813 and ISe 375 (0.098), and the maximum dissimilarity was observed between ISe 1320 and ISe 1162 (0.956).

Based on the dissimilarity values ten pairs of most dissimilar accessions (ISe 1320-ISe 1162, ISe 338-ISe 1320, ISe 1773-ISe 1320, ISe 179-ISe 1320, ISe 907-ISe 1320, ISe 1808-ISe 1320, ISe 1808-ISe 1547, ISe 195-ISe 1320, ISe 946-ISe 1547 and ISe 1320-ISe 1137) were identified in foxtail millet core collection. Further, the pair-wise estimates of dissimilarity value was >0.500 except 123 pair of accessions out of 11,935 pairwise estimates. This indicated the highest diversity of the foxtail millet core collection. These diverse pair of accessions could be utilized in hybridization to study the segregating population and to develop mapping population for identification of QTL based on linkage mapping.

5.5.2 Molecular diversity among races within foxtail millet core collection

Biologically, the accessions of foxtail millet core collection belonged to three races namely *indica* (102 accessions), *maxima* (24 accessions) and *moharia* (29 accessions). Of 1,356 alleles detected in entire core collection, 997 (73.5%) alleles were detected in the race *indica*, 784 (57.8%) in *maxima* and 844 (62.2%) in *moharia.* Eventhough, number of accessions in the race *maxima* and *moharia* was less than the race *indica*; these two races had more than 55.0% alleles of the entire core collection. Accessions of race *moharia* often resemble members of wild ssp. *viridis* in phenotype, except that they have lost the ability of natural seed dispersal (Prasada Rao *et al.,* 1986) hence, it might have harbored more diversity than *indica* and *maxima*. The higher number of alleles in the race *indica*, may be due to the more number of accessions represented in core collection (65.8%) compared to the race *maxima* (15.5%) and *moharia* (18.7%).

Of the 997 alleles present in accessions from *indica*, 100 (10.1%) were rare, 803 (80.5%) common and 94 (9.4%) were the most frequent alleles. Out of 784 alleles in *maxima*, 688 (87.8%) were common and 96 (12.2%) most frequent alleles. In case of *moharia*, 760 (90.1%) common and 84 (9.9%) most frequent alleles were detected out of 844 alleles. Rare alleles were not detected in accessions in the race *maxima* and *moharia* and found only in the race *indica.* This can be due to the less sample size of *maxima* and *moharia* as compared to the race *indica.* A total of 44 unique alleles in indica, 77 unique alleles in maxima and 47 alleles in moharia were detected. Here, the molecular based biological (races) diversity differed with respect to allelic richness, frequency of rare allele, common allele and most frequent alleles which can be explained by difference in sample size included in each races and genetic diversity harbored in it.

The similar range of PIC values was found in all the three races, which ranged from 0.02 to 0.93 in *indica*, 0.08 to 0.91 in *maxima* and 0.12 to 0.94 with an average of 0.63 in *indica*, 0.72 in *maxima* and *moharia*. For the race *indica*, gene diversity averaged 0.65, ranging from 0.02 to 0.93 whereas the accessions from the race *maxima* varied from 0.08 to 0.92 with an average of 0.74. In the race *moharia*, the gene diversity ranged from 0.13 to 0.94 with an average 0.74. The race *maxima* and *moharia* had the maximum mean gene diversity and PIC than *indica*. The average PIC values, gene diversity in races showed the highest range which indicated the diversity of the three biological races present in the core collection and highly informative SSR markers used.

Pairwise comparison on the basis of the values of F_{st} could be interpreted as standardized population distance between two populations, *i.e.,* the proportion of the total genetic diversity that separate the population. F_{st} is typically greater than or equal to zero. If all the subpopulations are in Hardy-Weinberg equilibrium with the same allele frequency, then F_{st} =0. The overall pairwise F_{st} in this study among the three races were 0.045. The race *maxima* showed the smallest F_{st} with *moharia* (0.032), whereas *indica* showed the maximum F_{st} with *maxima* (0.053) and *moharia* (0.050). The genetic distance data were in agreement with the F_{st} estimates. The race *indica* showed the highest genetic distance with *maxima* (0.273) and *moharia* (0.254) whereas the genetic distance between *maxima* and *moharia* was the smallest (0.201).

5.5.3 Cluster analysis

Unweighted neighbor-joining tree based on simple matching dissimilarity matrix between 155 accessions of the foxtail millet core collection along with four checks highlighted broadly four clusters namely CI to CIV, respectively. The CI and CII represented by accessions from *indica*, CIII and CIV predominated with accessions from *moharia* and *maxima*, respectively. The results from the neighbor-joining phylogenetic tree corresponded well with the classification based on three biological races of foxtail millet.

5.5.4 Correlations

The correlations coefficients among number of repeat unit, number of alleles per locus, gene diversity, heterozygosity and PIC for 84 SSR markers were estimated. Number of repeat unit was highly significant and positively correlated with number of alleles per locus (0.54), gene diversity (0.51) and PIC (0.53), whereas non significant negatively correlated with heterozygosity (-0.23). Number of alleles per locus was highly significant and positively correlated with gene diversity (0.77) and PIC (0.79), and gene diversity was highly significant and positively correlated with PIC (0.99). Significant positive correlation between allele per locus and gene diversity was reported in chickpea (Upadhyaya *et al.,* 2008b) and positive correlation between PIC and number of allele, PIC and repeat unit, number of alleles per locus and repeat unit has been reported in earlier studies of foxtail millet (Jia *et al.* 2009). Pervaiz *et al.* (2009) reported the significant positive correlation with number of alleles in Asian rice.

5.5.5 Analysis of molecular marker diversity (AMOVA)

The AMOVAs were conducted to determine the variation explained within and between the races and clusters identified by neighbor joining tree. It revealed that, 7 per cent of the total genetic variance was explained by among the races while 93 per cent was among the individuals within the races. The same trend was observed when the AMOVA estimated based on four clusters identified by neighbor joining method (10 among the clusters and 90% within the clusters) which shows the consistency of the neighbor joining clusters with the racial classification.

5.6 RELATIONSHIP BETWEEN PHENOTYPIC AND GENETIC DIVERSITY

Clustering on the basis of phenotypic and molecular diversity corresponded well with each other. All the accessions from the race *indica* grouped together into two clusters and accessions from the race *maxima* and *moharia* not separated clearly in both phenotypic and molecular based cluster analysis. The correlation coefficient between the phenotypic and SSR dissimilarity matrix (Mantel test) was performed which was significant (r=0.329), indicating the significant relationship between the phenotypic and molecular diversity.

5.7 POPULATION STRUCTURE AND ASSOCIATION MAPPING

Foxtail millet is one of the most ancient domesticated crops. It is becoming a model system for studying biofuel crops and comparative genomics among the grasses (Wang *et al.,* 2010). It is more tractable experimental model because of its small diploid genome (1C=490Mb) and inbreeding nature as compared to large genomes of the outbreeding species like pearl millet (diploid, IC=2,352Mb), napiergrass (tetraploid, IC=2,254Mb) and switchgrass (tetraploid, 1C=1,372-1,666Mb, octaploid IC=2,352-3,136Mb) (Doust *et al.,* 2009). However, knowledge on the level of genetic diversity and linkage disequilibrium (LD) is very limited in this crop and its wild ancestor, green foxtail. Such information would help us to understand the domestication process of cultivated species and will allow further research in these species, including association mapping and identification of agriculturally significantly genes involved in domestication (Wang *et al.,* 2010).

The phenotypic variation of many complex traits of agriculturally or evolutionary importance is influenced by multiple quantitative trait loci (QTL), their interaction, the environment and the interaction between QTL and environment. Linkage analysis and association mapping are the two most commonly used tools for dissecting complex traits (Zhu *et*

al., 2008). Linkage analysis in plants typically localizes QTL in 10 to 20 cM intervals because of the limited number of recombination events that occur during the construction of mapping populations and evaluating a large number of lines (Doerge, 2002; Holland, 2007). Alternatively, association mapping has emerged as a tool to resolve complex trait variation down to the sequence level by exploiting historical and evolutionary recombination events at the population level (Nordborg and Tavare, 2002; Risch and Merikangas, 1996).

Presence of population structure within an association mapping population can be an obstacle to the application of association mapping as it often generates spurious genotype-phenotype associations (Yu and Buckler, 2006; Zhu *et al.,* 2008). Different methods and software tools have been developed to correct the results for population structure usually by dividing the germplasm collections into subgroups or adjusting the probability of the null hypothesis (Rafalski, 2010). To account for population structure in association analysis, two major statistical methods, genome control (Devlin and Roeder, 1999; Zheng *et al.,* 2005) and structure association (SA) (Pritchard *et al.,* 2000) were applied in early studies, both of which used random markers spaced throughout the genome, but incorporated them into statistical analysis in different approaches (Yang *et al.,* 2010b). Yu *et al.* (2006) developed a mixed linear model (MLM) approach to perform association analysis. The MLM approach, accounting for both population structure (Q) and relative kinship (K), which can be performed with the TASSEL software package (Bradbury *et al.* 2007). It is the most common method of association analysis in plants and has been successfully applied in crops like rice (Agrama *et al.,* 2007; Wen *et al.,* 2009; Borba *et al.,* 2010), wheat (Breseghello and Sorrells, 2006; Neumann *et al.,* 2011), sorghum (Murrary *et al.,* 2009), *Arabidopsis* (Zhao *et al.,* 2007) and potato (Malosetti *et al.,* 2007).

However, until now, the reports of QTL for foxtail millet are limited except the QTL reported by Doust *et al.* (2004, 2005), and Doust and Kellogg (2006). Association mapping using the existing natural variation present in the germplasm for the detection of markers associated with phenotypic variation has not been reported in foxtail millet because of limited number of SSRs markers reported in this crop. Hence, there is a need for the identification and development of more SSR markers and mapping for various agronomical traits including yield and yield components in foxtail millet.

5.7.1 Population structure in foxtail millet core collection

Analysis of population structure using 72 SSR markers located on nine linkage groups provided the evidence for the presence of significant population structure in the foxtail millet core collection and identified four subpopulations denoted as SP1 to SP4, respectively. The subpopulation SP1 represents mixed subpopulation dominated with *moharia* followed by *maxima* and *indica*. The SP2 represented by five accessions present *maxima* out of six present in this subpopulation, and the remaining accessions preset in *maxima* were distributed in SP1. The SP3 and SP4 are represented by the race *indica*.

The pairwise comparison on the basis of the values of F_{st} could be interpreted as standardized population distance between two populations. The race *maxima* showed the smallest F_{st} with *moharia* which could be the reason for mixed subpopulation of *maxima* and *moharia* in SP1, whereas *indica* showed greatest F_{st} with *maxima* and *moharia*.

The pairwise F_{st} was estimated among the subpopulations identified by STRUCTURE, the highest F_{st} between SP2 (*maxima*) and SP3 (*indica*) followed by between SP2 (*maxima*) and SP4 (*indica*) with an average of 0.143. The genetic distance data agreed with the F_{st} estimates with the mean genetic distance 0.532. Therefore, pairwise estimates of *Fst* and genetic distance based on population structure corresponded well with pairwise estimates of *Fst* and genetic distance based on races. Hence, the subpopulations identified by STRUCTURE analysis fairly corresponded well with three biological races.

5.7.1.1 Allelic richness and genetic diversity of subpopulations

The 84 SSR markers were genotyped across the 155 accessions of foxtail millet core collection detected a total of 1,150 alleles in SP1, 213 in SP2, 226 in SP3 and 840 in SP4. Maximum mean PIC value was detected in SP1 and SP4 when compared to SP2 and SP3. A total of eight SSR loci in SP2, 13 in SP3 and two in SP4 were monomorphic to the respective subpopulation. The average number of alleles per locus, gene diversity and PIC were higher in SP1 and SP4 compared to SP2 and SP3 which may be due to the difference in the sample size and diversity within the subpopulation. The maximum gene diversity, allelic richness, PIC in SP1 and SP4 can be explained by the large number of the individuals present in these subpopulation compared to SP2 and SP3.

5.7.1.2. Analysis of molecular genetic variance

The distribution of molecular genetic variation among and within the four subpopulations was estimated by AMOVA. The AMOVA revealed that 9 per cent of the total variance was among the subpopulations, while 91 per cent was among individuals within the subpopulations. The same trend was observed when the AMOVA estimated based on three basic races of foxtail millet (7% among populations and 93% within population) and unweighted neighbor joining phylogenetic tree (10% variation among population and 90% within population) which indicated the consistency of subpopulation identified by STRUCTURE with the racial classification and unweighted neighbor joining tree.

5.7.1.2. Assessment of population structure

In this study, principal coordinate analysis and neighbor-joining phylogenetic analysis was conducted to further assess the population subdivisions identified using STRUCTURE.

Plotting the first two PCs and colour coding genotypes according to three biological races shows clear separation of the race *indica*, most of which are present in SP4. The race *maxima* and *moharia* were not clearly separated as in SP1 which was identified by STRUCTURE analysis. This indicated the less genetic distance between *maxima* and *moharia* as inferred by pairwise estimates of F_{st} and genetic distance based on population structure.

Neighbor-joining tree was constructed based on the simple matching dissimilarity matrix of 84 SSR markers assayed. Color coding was given for genotypes based on subpopulations identified by STRUCTURE. SP1 (Red) and SP2 (Yellow) are the major subpopulations along with two small subpopulations named as SP2 (green) and SP3 (blue), which clearly differentiated subpopulations.

Therefore, the results of PCoA and neighbor-joining revealed genetic relationship fairly consistent with the STRUCTURE based membership assignment for most of the accessions. Also, all the three above approach (PCoA, neighbor joining tree and STRUCTURE) were fairly consistent with the racial classification of foxtail millet (Prasada Rao *et al.,* 1986). PCoA has been used to analyse population structure in barley (Malyshera-Otta *et al.,* 2006; Cockaram *et al.,* 2008) and soft winter wheat (Reif *et al.,* 2011), rice (Jin *et al.,* 2010) and PCoA along with neighbor joining tree in wild diploid alfalfa to further asses the population subdivision identified by STRUCTURE analysis. Results similar to ours have been reported by Jin *et al*. (2010) in rice and Şakiroğlu *et al.* (2010) in wild diploid alfalfa (*Medicago sative* L.).

5.7.2 Association analysis

Replication of individual accessions within a site is usually needed to increase precision in phenotypic measurement, by eliminating environmentally induce noise and measured errors. Data on replicates of each accession can then be combined to produce an estimate of the 'mean' phenotype of the accessions which is less influenced by environment or measurement errors. Additional benefit of replication can be achieved if the entire association mapping collection is replicated across multiple environments (Hall *et al.,* 2010).

In the present study, the experiment was conducted in the alpha-design with three replications in three environments. The Residual Maximum Likelihood (REML) analysis of individual environment indicated that, both σ^2_g and σ^2_{ge} interaction were significant for all the traits indicating the differential response of genotypes to different environments. Wald's statistics was significant for all the traits except flag leaf sheath length indicating that the three environments were adequate to differentiate the core collection genotypes. Further, the measure of heritability was higher for all the quantitative traits in all three environments and pooled. Altogether, this phenotypic study can provide important information on the robustness of positive association across environments and on the importance of genotype by environment interactions in shaping allelic contributions to the trait of interest (Lynch and Walsh, 1998).

The association analysis was carried out using the BLUP of individual environments separately and pooled of three environments. Marker trait associations (MTAs) detected using pooled data were considered as final MTAs detected in this study, since the pooled data represent the adjusted mean (BLUPs) of three environments for each traits under study. Association analysis identified marker trait association at $P \leq 0.05$ for all the traits evaluated in pooled data. A total of 39 SSR markers produced 108 marker trait associations ($P \leq 0.05$) of which 26 markers found to be associated with more than one trait in pooled mean over the environments (Table 56). Of the 108 significant marker trait associations, a total of 18 SSR markers showed 37 highly significant MTAs at $P \leq 0.01$ for all the traits except inflorescence width (Table 57).

In the present study, of the 18 SSR markers that showed 36 highly significant MTAs at $P \leq 0.01$, six markers are associated with two traits each. The marker b196 located on chromosome 5 associated the peduncle length and panicle exertion, b186 located on chromosome 3 associated with peduncle length and flag leaf sheath length, p8 located on

chromosome 1 associated with basal tillers number and flag leaf blade width, b123 on chromosome 7 associated with flag leaf sheath length and weight of five panicles and m2 located on chromosome 9 associated with plant height and flag leaf blade length. Four SSR markers (p17x, ICMM02C05, b202 and b234) found to be associated with three traits each. The marker p17x located on chromosome 5 associated with days to 50 per cent flowering flag leaf blade length and flag leaf sheath length, The marker ICMM02C05 associated with plant height, flag leaf blade length and flag leaf blade width, b202 located on chromosome 7 associated with panicle exertion, flag leaf blade length and days to 50 per cent flowering and b234 located on chromosome 6 associated plant height, grain yield per plot and panicle exertion. The SSR markers p98 located on chromosome 3 associated with seven traits namely plant height, flag leaf blade length, flag leaf blade width, flag leaf sheath length, peduncle length, inflorescence length and weight of five panicle.

Majority of the markers were found to be associated with more than one trait, such an association may arise due to pleiotropic effect of the linked QTL on different traits (Miller and Rawlings 1967; Culp *et al*. 1979). Closely linked QTLs affecting different traits may also lead to a single marker showing association with multiple traits which would be reflected in correlations between such traits (Rakshit *et al.,* 2010). In this study, the grain yield per plot was found to be significant and positively correlated with days to 50 per cent flowering, plant height, flag leaf blade length, flag leaf blade width, flag leaf sheath length, inflorescence length, inflorescence width, weight of five panicles, single plant yield in all three environments and pooled. The quantitative traits included in this study were also showed highly significant correlation with each other. This correlation was also evident in shared associated markers for these traits. The multiple traits associated with single marker were reported in cotton (Rakshit *et al.,* 2010) and wheat (Liu *et al.,* 2010). Agrama *et al.* (2007) reported the four SSR markers associated with two traits each.

Sixty five out of 108 MTAs at $P \leq 0.05$ found in pooled data also detected in atleast two out of three environments (50 MATs) or in all three environments (15 MTAs). The MTAs detected in all three environments as well as pooled named as stable MTAs, all these MTAs were highly significant at $P \leq 0.01$ across environments (Table 58). Our results indicate that association mapping can be successfully applied in this core collection. This may help to better understand the architecture of these traits and for discovering novel trait-related genes in further breeding

improved cultivars in foxtail millet leads to the most effective utilization of ex situ conserved genetic resources.

FUTURE LINE OF WORK

Based on results obtained in the present study and information available, the following future line of work can be proposed.

1. The foxtail millet core collection found to be diverse both phenotypic and genetic level and possesses potential variation for economic traits. Hence, it can be used effectively for the development of genetically diverse and improved cultivars.
2. The superior most diverse trait specific accessions identified could be utilized in breeding programs to improve and to widen the genetic base of foxtail millet cultivars. Multi-trait specific accessions could be utilized for simultaneous transfer of multiple traits/genes in crop improvement.
3. Most diverse pair of accessions identified based on phenotypic traits and molecular markers could be utilized for the development of mapping population and for the selection of superior lines in segregating generation.
4. MTAs identified in this study using SSR markers is the first effort in this crop and will provide information to the foxtail millet research community for further MTAs studies, identification and validation of QTL for its use in crop improvement.

Table 59. Details of the trait specific accessions identified based on pooled BLUPs

S. No	Accession name	Race	No. of traits	List of traits[1]	
1	ISe1269	*indica*	1	BT[2]	
2	ISe1406	*indica*	1	SPY	
3	ISe1610	*indica*	1	INFW	
4	ISe1655	*indica*	1	Early flowering	
5	ISe1664	*indica*	1	BT	
6	ISe1745	*indica*	1	FLBW	
7	ISe1780	*indica*	1	PY	
8	ISe18	*indica*	1	INFW	
9	ISe1805	*indica*	1	PY	
10	ISe2	*indica*	1	FLBL	
11	ISe238	*indica*	1	SPY	
12	ISe302	*indica*	1	W5P	
13	ISe362	*indica*	1	BT	
14	ISe710	*indica*	1	BT	
15	ISe900	*indica*	1	FLBW	
16	ISe914	*indica*	1	BT	
17	ISe1129	*maxima*	1	BT	
18	ISe1181	*maxima*	1	Early flowering	
19	ISe1201	*maxima*	1	Early flowering	
20	ISe1258	*maxima*	1	Early flowering	
21	ISe1563	*maxima*	1	Early flowering	
22	ISe1575	*maxima*	1	FLBW	
23	ISe1593	*maxima*	1	FLBW	
24	ISe1725	*maxima*	1	INFL	
25	ISe827	*maxima*	1	Early flowering	
26	ISe1234	*moharia*	1	Early flowering	
27	ISe1254	*moharia*	1	Early flowering	
28	ISe1305	*moharia*	1	BT	
29	ISe1312	*moharia*	1	Early flowering	
30	ISe1320	*moharia*	1	Early flowering	
31	ISe1009	*moharia*	1	BT	
32	ISe1151	*moharia*	1	Early flowering	
33	ISe1161	*moharia*	1	Early flowering	
34	ISe1162	*moharia*	1	BT	
35	ISe1299	*moharia*	1	BT	
36	ISe1335	*moharia*	1	Early flowering	
37	ISe1638	*moharia*	1	Early flowering	
38	ISe1000	*indica*	2	SPY	PY
39	ISe132	*indica*	2	FLBL	W5P

S. No	Accession name	Race	No. of traits	List of traits[1]						
40	ISe1408	*indica*	2	BT	PY					
41	ISe144	*indica*	2	FLBL	FLBW					
42	ISe1767	*indica*	2	SPY	PY					
43	ISe1888	*indica*	2	SPY	PY					
44	ISe364	*indica*	2	SPY	PY					
45	ISe388	*indica*	2	SPY	PY					
46	ISe956	*indica*	2	SPY	PY					
47	ISe999	*indica*	2	BT	Tall plants					
48	ISe1666	*maxima*	2	FLBL	W5P					
49	ISe1286	*moharia*	2	Early flowering	BT					
50	ISe1454	*indica*	3	INFL	INFW	W5P				
51	ISe1846	*indica*	3	BT	SPY	PY				
52	ISe1251	*maxima*	3	FLBW	INFW	W5P				
53	ISe375	*maxima*	3	FLBW	INFW	W5P				
54	ISe717	*indica*	3	Tall plants	FLBL	INFL				
55	ISe983	*indica*	3	Tall plants	FLBL	INFW				
56	ISe1736	*maxima*	3	Tall plants	W5P	PY				
57	ISe1881	*indica*	4	INFL	Tall plants	SPY	PY			
58	ISe1511	*indica*	4	Tall plants	FLBL	INFL	W5P			
59	ISe1474	*indica*	5	INFL	Tall plants	SPY	W5P	PY		
60	ISe1387	*indica*	5	Tall plants	FLBL	FLBW	INFL	INFW		
61	ISe1419	*indica*	5	Tall plants	FLBL	INFL	INFW	W5P		
62	ISe751	*indica*	5	Tall plants	FLBL	FLBW	INFL	INFW		
63	ISe1685	*indica*	6	FLBW	INFL	INFW	W5P	SPY	PY	
64	ISe1059	*maxima*	6	Tall plants	FLBL	FLBW	INFL	INFW	SPY	
65	ISe769	*moharia*	6	Tall plants	FLBL	FLBW	INFL	INFW	W5P	
66	ISe1597	*indica*	7	Tall plants	FLBL	FLBW	INFL	INFW	W5P	SPY
67	ISe748	*indica*	7	Tall plants	BT	FLBL	FLBW	INFL	INFW	W5P
68	ISe1687	*maxima*	8	Tall plants	FLBL	FLBW	INFL	INFW	W5P	SPY	PY

1= Higher values were considered as desirable except early flowering

2= DF = Days to 50 per cent flowering, BT = Basal tiller number, FLBL = Flag leaf blade length (mm), FLBW = Flag leaf blade width (mm), FLSL = Flag leaf sheath length (mm), PEDL = Peduncle length (mm), PEX = Panicle exertion (mm), INFL = Inflorescence length (mm), INFW = Inflorescence width (mm), W5P = Weight of five panicles (g), SPY = Single plant yield (g), PY = Grain yield per plot (Kg ha^{-1})

Table 60. Details of the SSR markers associated with traits in pooled of three environments for each traits

S.No	SSR markers	Chromosome location	No. of traits	Associated with									
1	b115	2	1	DF[1]									
2	b126	1	1	FLBW									
3	b151	2	1	FLSL									
4	b159	6	1	SPY									
5	b188	5	1	FLSL									
6	b190	6	1	SPY									
7	b226	3	1	PEX									
8	b258	8	1	DF									
9	b41	9	1	SPY									
10	ICMM02C24	-	1	PLHT									
11	p2	4	1	SPY									
12	p59	7	1	PEDL									
13	UGEP81	-	1	BT									
14	b111	5	2	FLBL	PLHT								
15	b153	2	2	INFL	W5P								
16	b166	9	2	PEDL	PEX								
17	b196	5	2	PEDL	PEX								
18	b225	3	2	DF	INFL								
19	b251	9	2	DF	PLHT								
20	P2	-	2	BT	FLBW								
21	P5	-	2	SPY	YKGPH								
22	p56	2	2	BT	SPY								
23	p58	1	2	FLSL	W5P								
24	p61	3	2	SPY	YKGPH								
25	p87	1	2	BT	PEDL								
26	p91	9	2	PEDL	PEX								
27	b142	3	3	PEX	SPY	YKGPH							
28	ICMM02D15B	-	3	FLBL	INFL	PLHT							
29	p17x	5	3	DF	FLBL	FLSL							
30	b186	3	4	FLBL	FLSL	PEDL	PEX						
31	m2	9	4	FLBL	FLSL	INFL	PLHT						
32	b202	7	5	DF	FLBL	PEDL	PEX	PLHT					
33	ICMM02C05	-	5	FLBL	FLBW	PEDL	PLHT	W5P					
34	p34	4	5	BT	DF	FLBL	FLBW	INFL					
35	b123	7	6	FLSL	INFL	PEDL	PEX	PLHT	W5P				
36	p8	1	6	BT	FLBL	FLBW	FLSL	PEDL	PLHT				
37	b200	7	7	BT	DF	FLBL	INFL	PEDL	SPY	YKGPH			
38	b234	6	7	FLBL	FLSL	PEDL	PEX	PLHT	SPY	YKGPH			
39	p98	3	11	BT	PLHT	FLBL	FLBW	FLSL	INFL	INFW	PEDL	SPY	W5P	YKGPH
		Total	108										

1= DF = Days to 50 per cent flowering, PLHT = Plant height (cm), BT = Basal tiller number, FLBL = Flag leaf blade length (mm), FLBW = Flag leaf blade width (mm), FLSL = Flag leaf sheath length (mm), PEDL = Peduncle length (mm), PEX = Panicle exertion (mm), INFL = Inflorescence length (mm), INFW = Inflorescence width (mm), W5P = weight of five panicles (g), SPY = Single plant yield (g), PY = Grain yield per plot (Kg ha^{-1})

Table 61. Details of 18 SSR markers showing 37 highly significant marker trait association (MTAs) (P<0.01)

S.No	Markers	Chromosome located	No. of Traits	Associated with						
1	b111	5	1	PLHT [1]						
2	b153	1	1	W5P						
3	b166	9	1	PEX						
4	b188	5	1	FLSL						
5	b251	9	1	PLHT						
6	p34	4	1	DF						
7	P5	-	1	YKGPH						
8	p56	2	1	SPY						
9	b196	5	2	PEDL	PEX					
10	b186	3	2	PEDL	FLSL					
11	p8	1	2	BT	FLBW					
12	b123	7	2	FLSL	W5P					
13	m2	9	2	PLHT	FLBL					
14	p17x	5	3	FLBL	FLSL	DF				
15	ICMM02C05	-	3	PLHT	FLBL	FLBW				
16	b202	7	3	DF	FLBL	PEX				
17	b234	6	3	PLHT	PEX	YKGPH				
18	p98	3	7	PLHT	FLBL	FLBW	FLSL	PEDL	INFL	W5P
		Total	37							

1= DF = Days to 50 per cent flowering, PLHT = Plant height (cm), BT = Basal tiller number, FLBL = Flag leaf blade length (mm), FLBW = Flag leaf blade width (mm), FLSL = Flag leaf sheath length (mm), PEDL = Peduncle length (mm), PEX = Panicle exertion (mm), INFL = Inflorescence length (mm), INFW = Inflorescence width (mm), W5P = weight of five panicles (g), SPY = Single plant yield (g), PY = Grain yield per plot (Kg ha^{-1})

Table 62. List of stable MTAs identified in foxtail millet core collection evaluated across three environments

Trait	Marker	Chromosome location	Based on Pooled BLUPs	
			p_Marker	R2 (%)
Days to 50 % flowering	b202	7	0.0049	12.57
Days to 50 % flowering	p17x	5	0.01	8.09
Days to 50 % flowering	p34	4	4.75E-04	14
Plant height (cm)	b111	5	6.10E-04	9.88
Plant height (cm)	ICMMO2CO5	-	0.0013	2.95
Plant height (cm)	m2	9	0.0085	5.8
Plant height (cm)	p98	3	8.73E-05	1.5
Basal tillers	p8	1	8.72E-05	11.87
Flag leaf Blade length (mm)	b202	7	0.0021	11.86
Flag leaf Blade length (mm)	ICMMO2C05	-	0.0016	2.43
Flag leaf Blade Width (mm)	p98	3	8.95E-04	3.87
Flag leaf sheath length (mm)	b123	7	0.0026	1.94
Flag leaf sheath length (mm)	p98	3	8.93E-05	5.34
Weight of five panicle (g)	p98	3	9.80E-05	8.04
Plot grain yield (Kg ha^{-1})	b234	6	0.0061	3.16

CHAPTER VI

SUMMARY

Phenotypic and molecular characterization and identification of genetically diverse trait specific sources are important for enhanced utilization of foxtail millet genetic resources in breeding improved cultivars. Hence, the current study was undertaken to understand the phenotypic and genetic diversity in foxtail millet core collection, to identify trait specific germplasm and the SSR markers associated with phenotypic variation. The genetic materials used in this study were 155 accessions of foxtail millet core collection and four controls (ISe 375, ISe 376, ISe 1468 and ISe 1541) that were evaluated at three environments [Coimbatore (E1), Madurai (E2) and ICRISAT, Patancheru (E3)]. In all the three environments, the experiment was conducted in alpha design with three replications. The data on 12 qualitative and 13 quantitative traits were recorded. For the molecular characterization of foxtail millet core collection, a total of 99 SSR markers were used. The results are summarized below.

6.1. PHENOTYPIC DIVERSITY

6.1.1. Qualitative traits

- In the entire foxtail millet core collection, green plant pigmentation, green leaf colour, erect growth habit, high culm branching, long bristle length, dense panicle lobing, compact inflorescence, compact lobe, yellow grain color, non lodging, leaves almost green at maturity (senescence score) and good overall plant aspect score were the most predominant classes in various qualitative traits.
- The proportion of green plant pigmentation, green leaf colour, erect growth habit, compact inflorescence, compact lobe, yellow grain colour and non lodging plants were the most prevalent classes across three races. However, the traits like culm branching, bristle length, panicle lobing, leaf senescence and overall plant aspects were different in the three races, *indica*, *maxima* and *moharia*.
- Medium culm branching, long bristles, dense lobed inflorescence, leaves almost green at maturity and good plant aspect score were the most prevalent classes found in accessions of race *indica* whereas, low culm branching, short bristles, dense lobed inflorescence, leaves completely green at maturity (senescence score) and good plant aspect score were the most common classes of observed in race *maxima.* In case of the race *moharia*, high

culm branching, short bristles, non lobed inflorescence, leaves moderately green at maturity (senescence score) and poor plant aspects were the most prevalent classes.

- The Shannon-Weaver diversity indices (H′) estimates were computed for 12 qualitative traits. Culm branching, bristle length, plant lodging, senescence and overall plant aspects showed the maximum H′ values in all three races and in the entire core collection indicating the importance of these qualitative traits in contributing towards diversity in core collection and in the races.

6.1.2. Quantitative traits

- REML analysis of data indicated that variance components due to genotype (σ^2_g) and genotype × environment (σ^2_{ge}) interaction were significant for all quantitative traits. This indicated sufficient variability for all the traits in core collection and the core collection accessions interacted with environment.
- The wider range of various traits was observed in different environment and for different races of the foxtail millet core collection
- High genetic advance as per cent of mean coupled with high estimates of broad sense heritability (h^2_b) (>60%) were observed in all three environments separately and pooled data indicating that, the variation for most traits were heritable variation and selection would be effective for improvement of these traits.
- Mean days to 50 per cent flowering, plant height, flag leaf sheath length, peduncle length and weight of five panicles of three environments did not differ significantly indicating less influence of the environment on the expression of these traits, whereas the remaining eight traits (basal tillers number, flag leaf blade length, flag leaf blade width, panicle exertion, inflorescence length, inflorescence width, single plant yield and grain yield per plot (Kg ha^{-1}) were significantly differed with environments indicating the greater influence of the environments on the expression of these traits.
- Among the race, the mean days to 50 per cent flowering, plant height, basal tillers number, flag leaf blade length, flag leaf sheath length, inflorescence length, single plant yield and grain yield per plot (Kg ha^{-1}) differ significantly in each races in all three environments or two out of three environments indicated the importance of these traits in differentiating the three races.

- Flag leaf blade width, peduncle length, inflorescence width and weight of five panicles did not differ significantly between *indica* and *maxima* and both of these two races differed significantly from *moharia* in all three environments and overall pooled data. Basal tiller number was the lowest in *maxima* and significantly differed from *indica* and *moharia* in all three environments and in pooled data.
- Variances were homogenous between environments for four quantitative traits, days to 50 per cent flowering, flag leaf blade length, flag leaf sheath length and panicle exertion.
- Variances were homogenous between three races for two trait (days to 50% flowering and single plant yield) in E1, nine traits in E2 (days to 50% flowering, basal tiller number, flag leaf blade length, flag leaf blade width, peduncle length, panicle exertion, inflorescence length, inflorescence width and single plant yield) and six traits in E3 (days to 50% flowering, flag leaf blade width, flag leaf sheath length, inflorescence width, single plant yield and grain yield per plot (Kg ha^{-1})).
- Grain yield per plot (Kg ha^{-1}) was highly significant and positively correlated with all the traits except panicle exertion. It could be inferred that, the selection in positive direction for all the traits (plant height, flag leaf blade length, flag leaf sheath length, inflorescence length, weight of five panicles, single plant yield with grain yield per plot (Kg ha^{-1})) except panicle exertion for genetic enhancement of grain yield.
- Flag leaf blade width, flag leaf sheath length, peduncle length in all three environments and pooled along with plant height and inflorescence width in E1, panicle exertion and inflorescence length in E2, panicle exertion and weight of five panicle in E3, and panicle exertion and inflorescence width in pooled had the maximum H'. This indicated the importance of these characters in contributing toward divergence.
- The races *indica* had the highest pooled H' across the quantitative traits in all three environments and pooled indicated the relatively higher diversity of this race in core collection compared to the *maxima* and *moharia*.
- Days to 50 per cent flowering, plant height, basal tiller number, flag leaf blade length, flag leaf blade width, peduncle length, panicle exertion and inflorescence length occurred in the first three PCs of all three environments separately, indicated their importance for characterization in foxtail millet germplasm accessions.

- Ten pairs of most diverse accessions were identified based on phenotypic distance (Gower, 1985) for each environment separately and for pooled data of three environments. These diverse accessions could be utilized in development of mapping population and in hybridization program to generate the segregating population for the selection of superior lines.
- The clustering of core collection accessions using scores of first three principal components (PCs) corresponded well with foxtail millet racial classification.
- The trait-specific sources for ten economically important yield traits (15 accessions for each trait) namely early flowering, tall plants, and maximum basal tiller number, flag leaf blade length, flag leaf blade width, inflorescence length, inflorescence width, weight of five panicles and single plant yield and grain yield per plot (Kg ha^{-1}) have been identified. Multi-trait specific accessions were identified, which were sources for more than one trait. Finally, out of 155 core accessions, a total of 68 accessions were identified as sources for ten important yield contributing traits.

6.2. MOLECULAR DIVERSITY

A total of 99 SSR markers were used initially to genotype the foxtail millet core collection. Of these, 84 SSR markers produced clear, scorable and polymorphic marker profiles and were used for further analysis.

6.2.1. Allelic richness and genetic diversity

- The SSR markers used in this study were highly polymorphic and informative, and detected a total of 1,356 alleles with an average of 16.14 alleles per locus. Of these, 368 were rare alleles (27.14%); 906 common alleles (66.81%); and 82 the most frequent alleles (6.05%). Total of 61 unique alleles were detected in core collection, which were specific to a particular accession. The 84 SSR markers detected a total of 997 (73.53%) alleles in *indica*, 784 (57.82%) in *maxima* and 844 (62.24%) in *moharia*.
- The unweighted neighbor-joining tree based on simple matching dissimilarity matrix of 155 accessions of the foxtail millet core collection highlighted broadly four clusters which corresponded well with the classification based on three biological races of foxtail millet.

- The genetic relationship among races was studied based on F_{st} and genetic distance. The race *maxima* had the smallest F_{st} and genetic distance with *moharia*, whereas *indica* had the maximum F_{st} and genetic distance with *maxima* and *moharia*.
- The correlation coefficient between the phenotypic and SSR dissimilarity matrix (Mantel test) was performed which was significant (r=0.329), indicating the significant relationship between the phenotypic and molecular diversity.
- Finally, ten pairs of most diverse accessions were identified based on dissimilarity matrix using molecular data. The pair-wise estimates of dissimilarity value was >0.50 except in 123 pairs out of 11,935 pairwise estimates. This indicated the presence of greater genetic diversity in foxtail millet core collection.

6.2.2. Population structure and association mapping

- The STRUCTURE analysis provided evidence for the presence of population structure and identified four subpopulations (SPI to SPIV). Further, consistency of this population structure was assessed by principal coordinate and un-weighted neighbor joining phylogenetic analysis, which showed consistent relationship with population structure identified by STRUCTURE analysis and racial classification.
- The mixed linear model (MLM) (Q+K model) as implemented in TASSEL v2.1 was used to find marker traits associations (MTAs). The number of significant MTAs was 130 in E1, 69 in E2 and 106 in E3 at $P \leq 0.05$ whereas 49 MTAs in E1, 23 MTAs in E2 and 61 MTAs in E3 were found to be highly significant at $P \leq 0.01$.
- The MTAs detected using pooled BLUPs of three environments was considered as final MTAs, since it represents the average performance of the accessions over the three environments. In pooled BLUPs of three environments, a total of 39 SSR markers showed 108 MTAs ($P \leq 0.05$) of which 26 markers found to be associated with more than one trait.
- However, out of 108 significant MTAs detected in pooled, only 18 SSR markers showed 37 highly significant MTAs at $P \leq 0.01$ for all the traits except inflorescence width.
- Of these 37 MTAs in pooled data, 15 were identified as stable and highly significant MTAs across the environments.

Figure 2. Geographical distribution of 155 foxtail millet core collection accessions

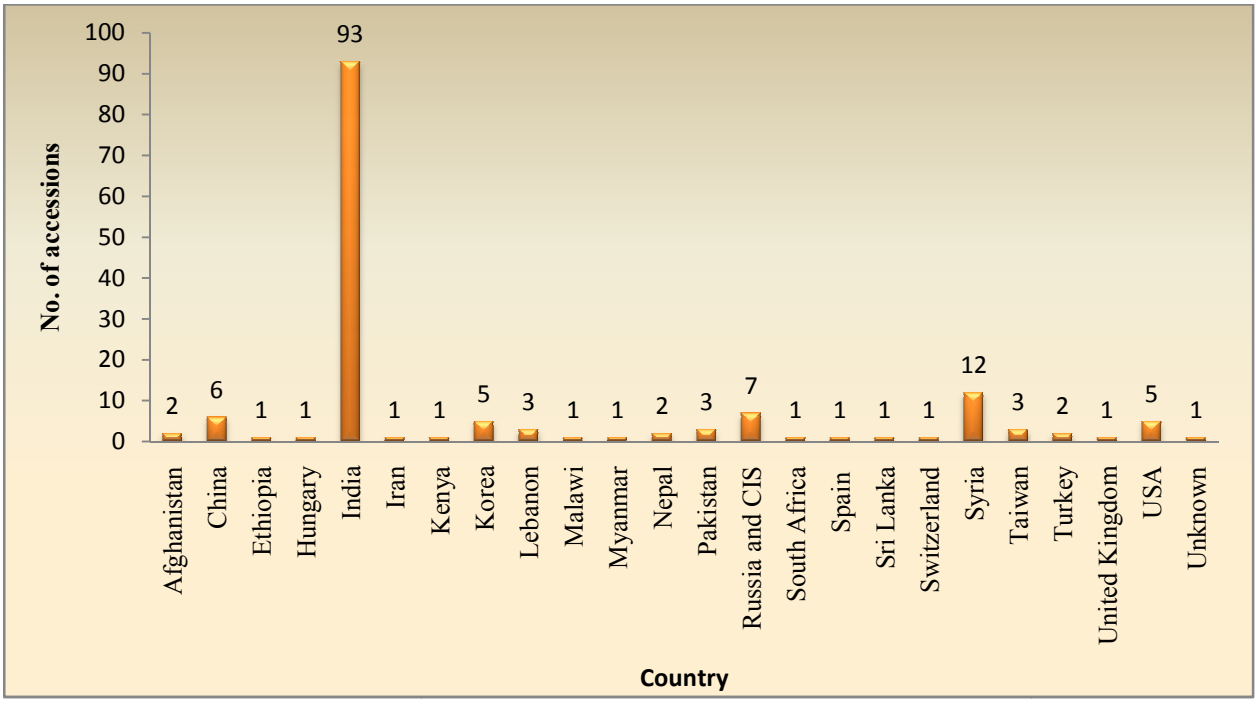


Figure 3. Number of accessions in each race and subraces in foxtail millet core collection

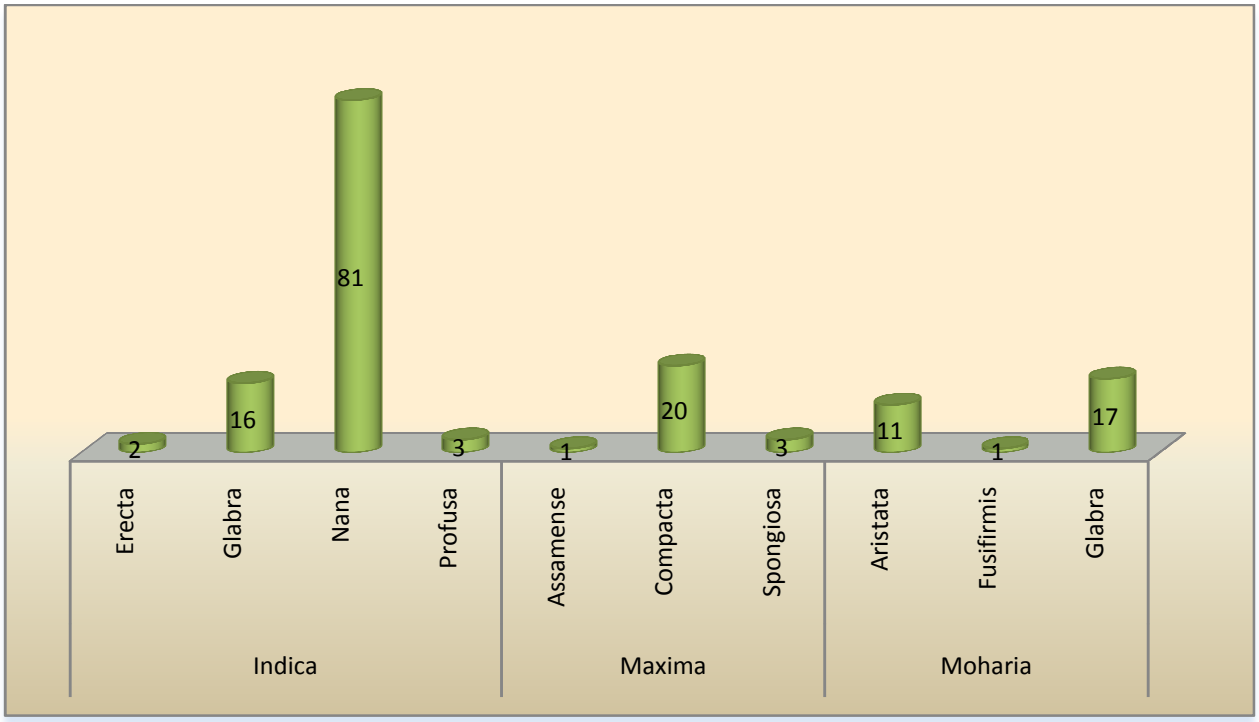


Figure 4. Phenotypic, genotypic coefficient of variation and heritability (%) for grain yield and yield contributing traits in foxtail millet core collection based on pooled BLUPs of three environments

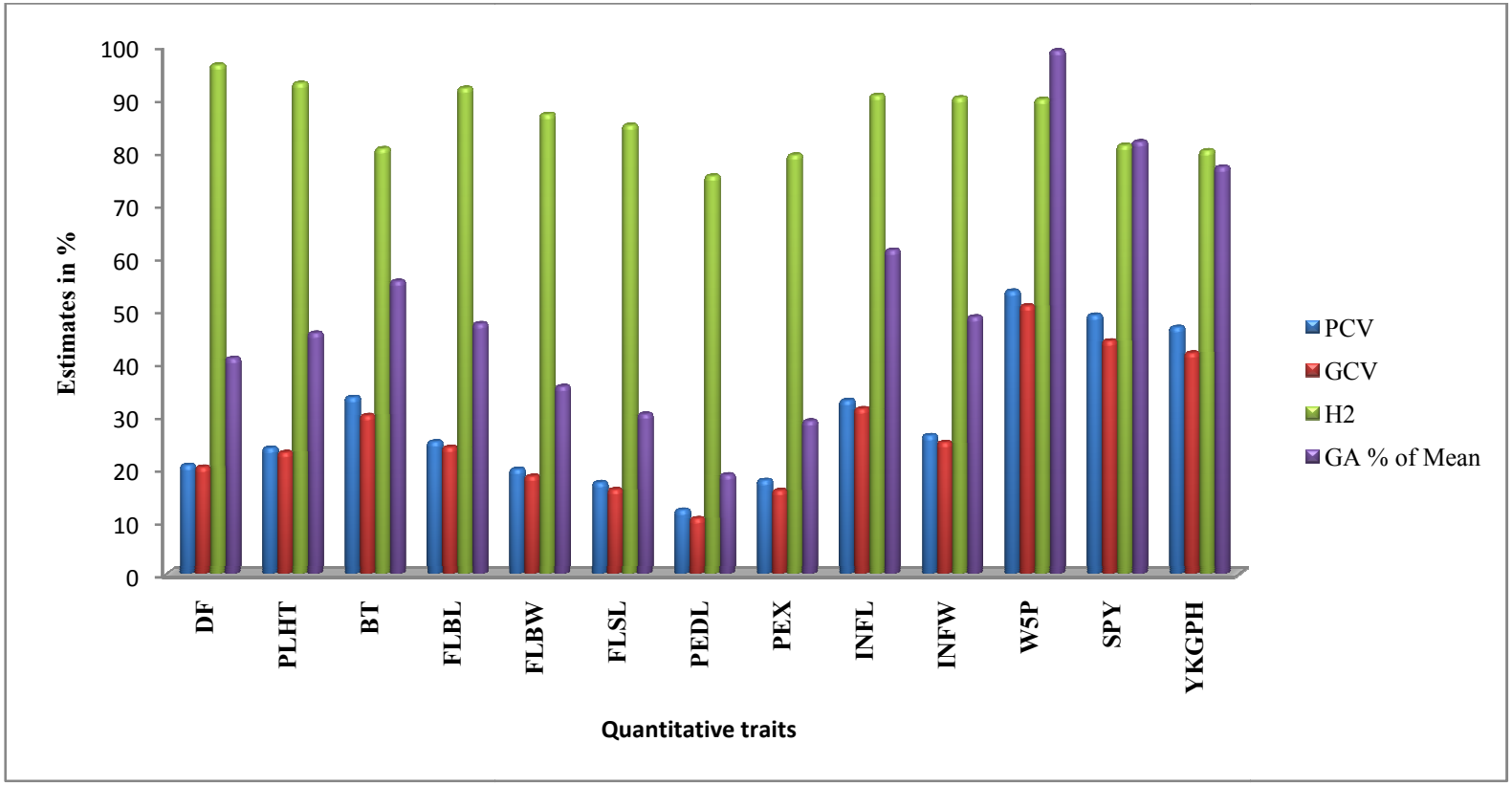
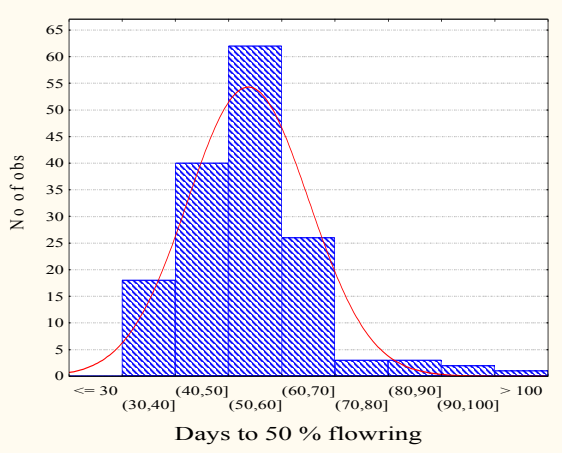
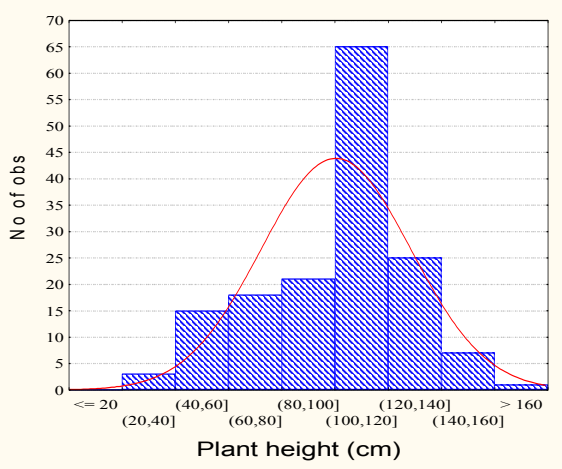


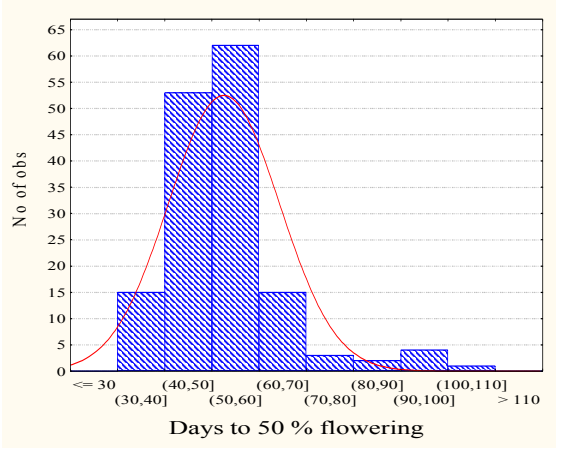
Figure 5. Frequency distribution of quantitative traits evaluated at Coimbatore (E1), Madurai (E2) during Rabi/summer 2009/10 and ICRISAT, Patancheru (E3) during rainy season 2010

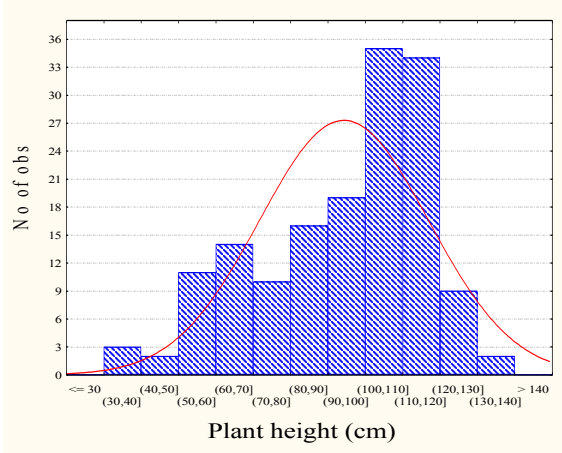
E1_Coimbatore



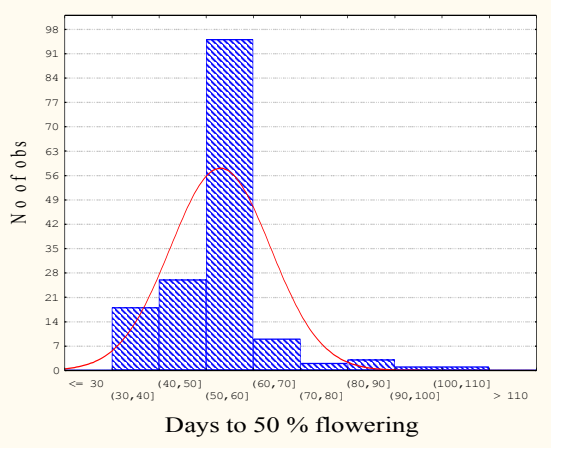


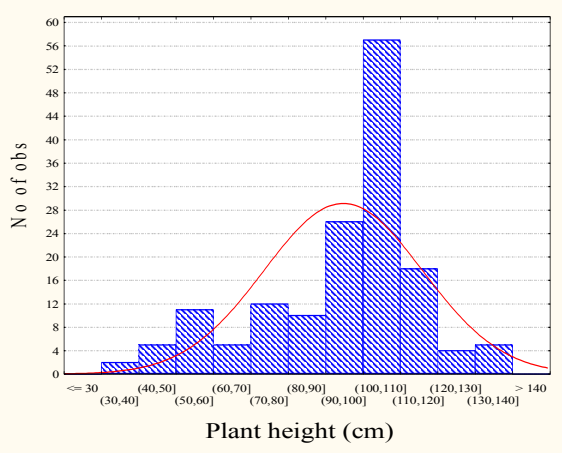
E2_Madurai



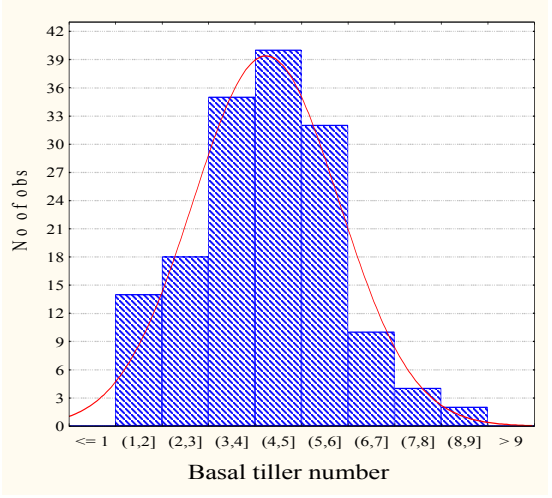


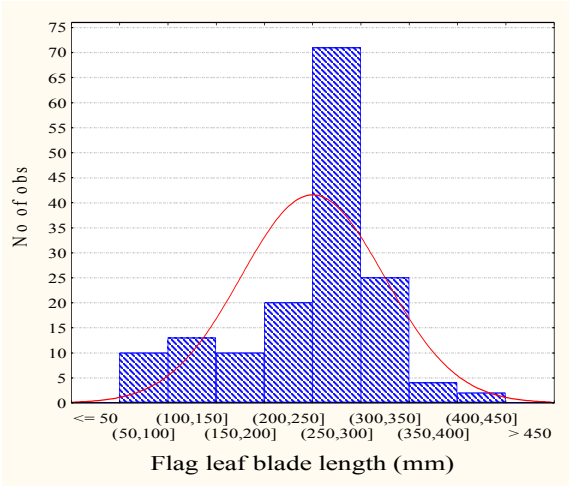
E3_ICRISAR, Patancheru



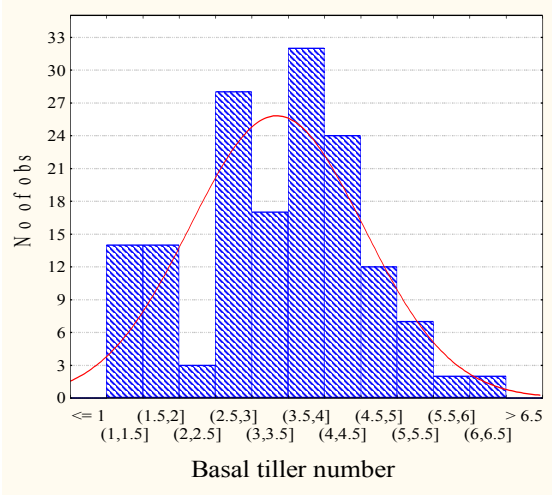


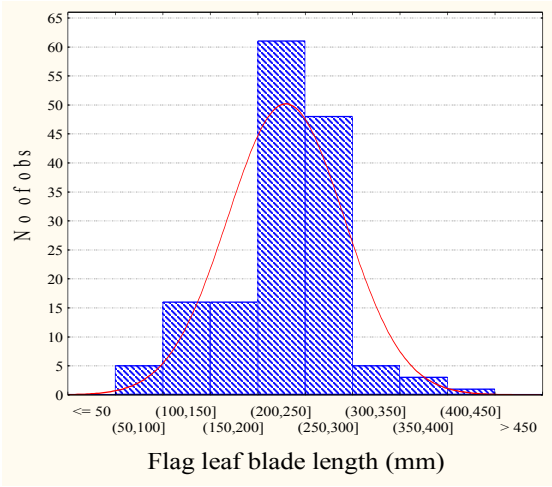
E1_Coimbatore



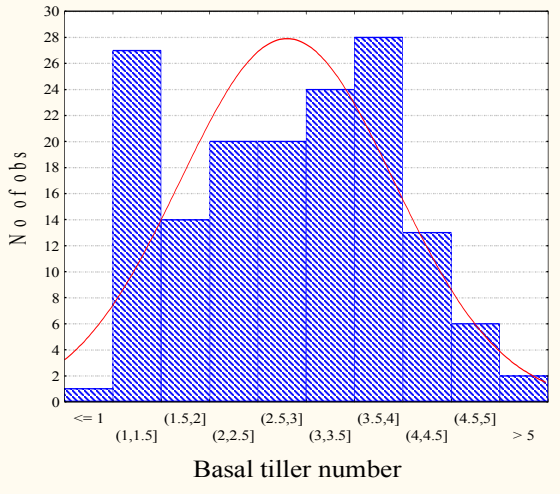


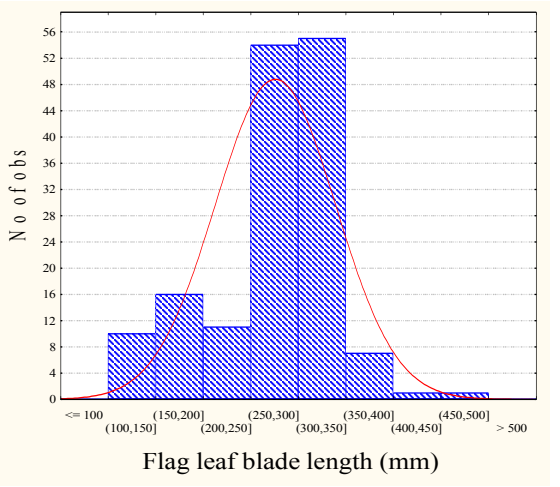
E2_Madurai



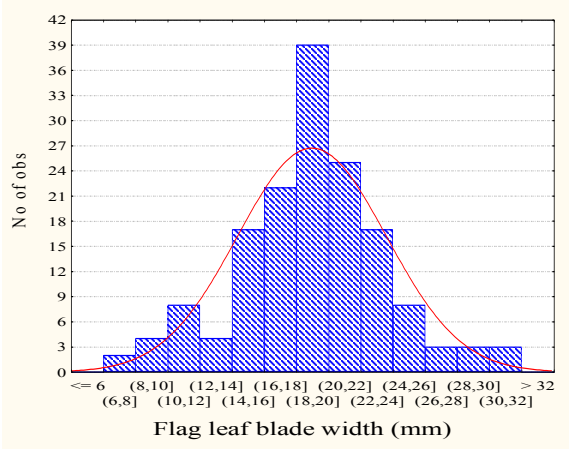


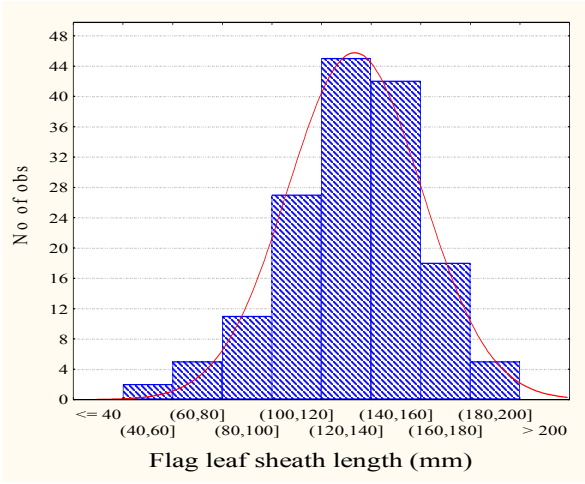
E3_ICRISAR, Patancheru





E1_Coimbatore





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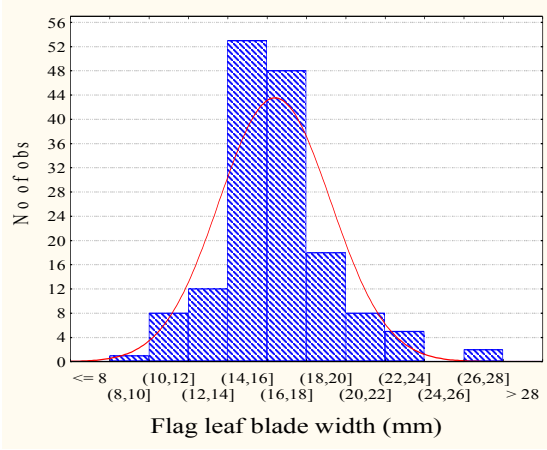
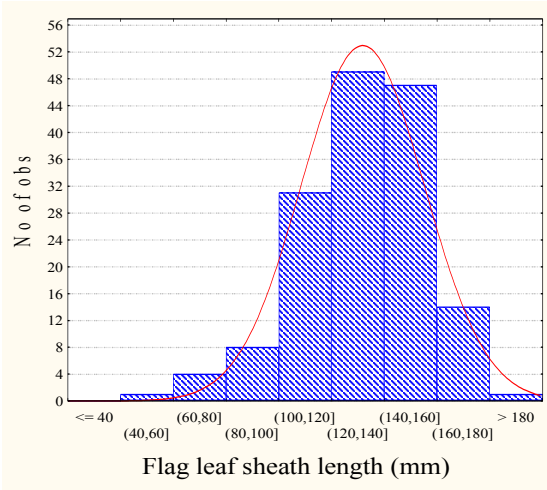
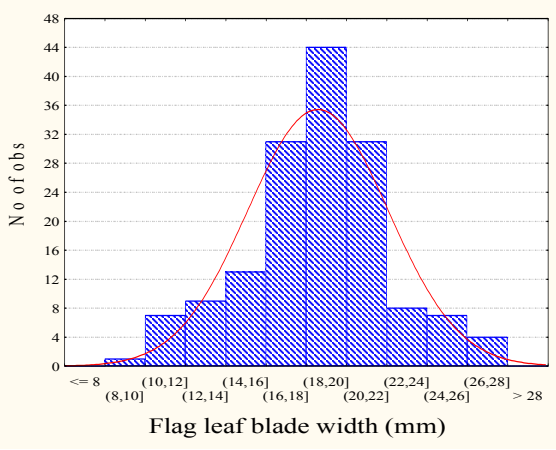
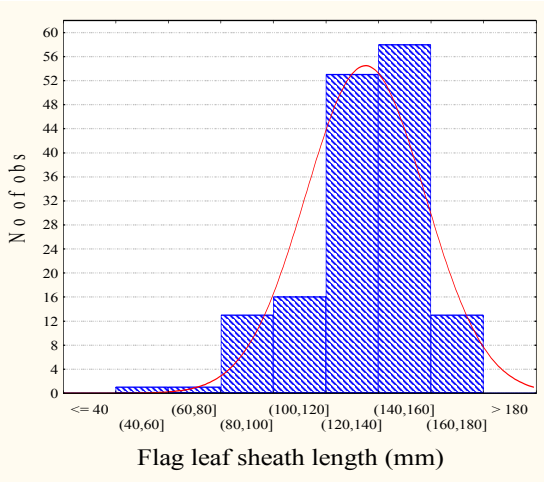


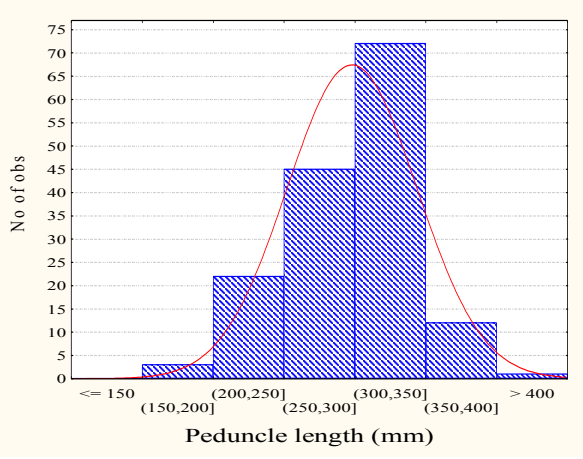


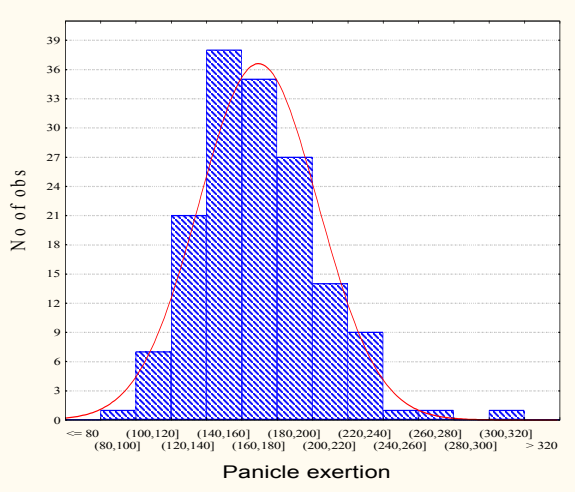
E3_ICRISAR, Patancheru





E1_Coimbatore





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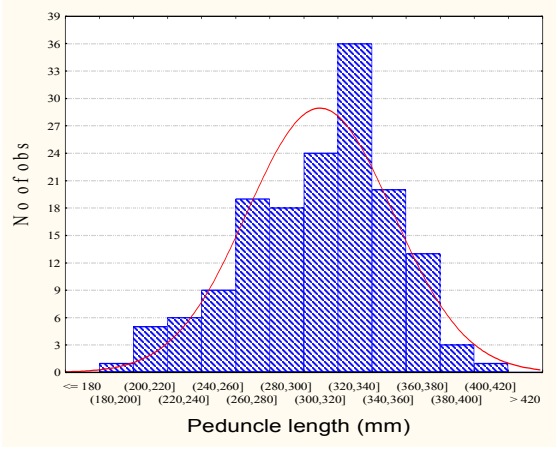
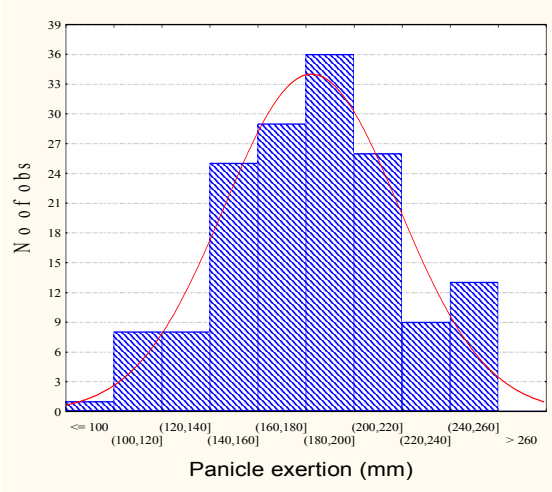
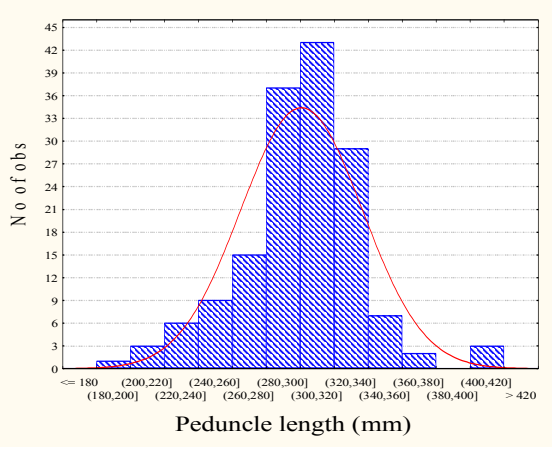
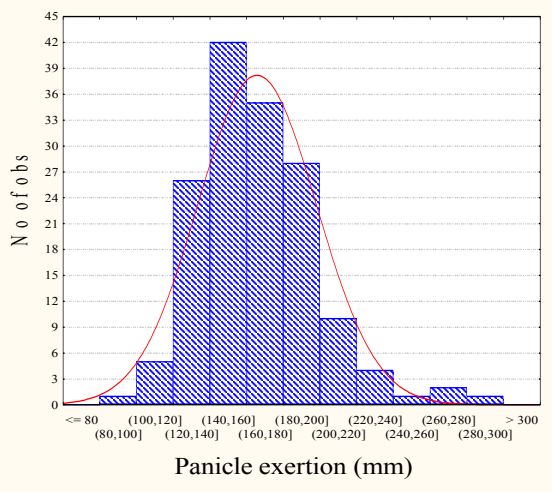


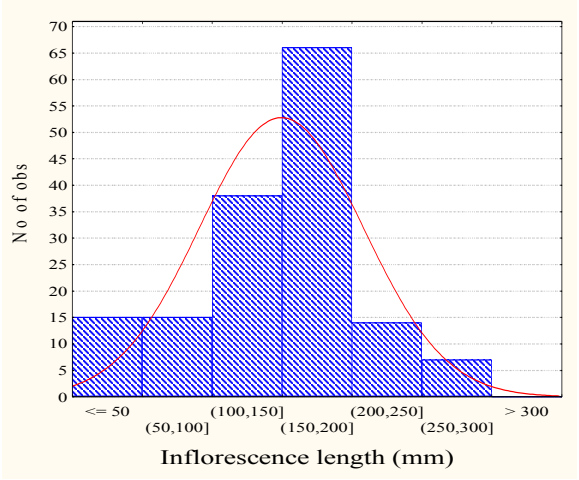


E3_ICRISAR, Patancheru

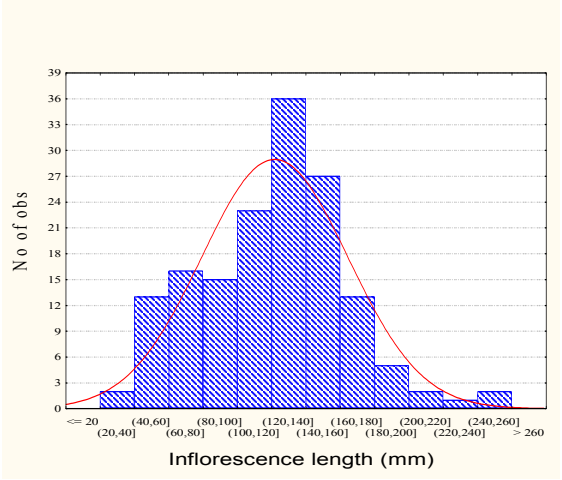




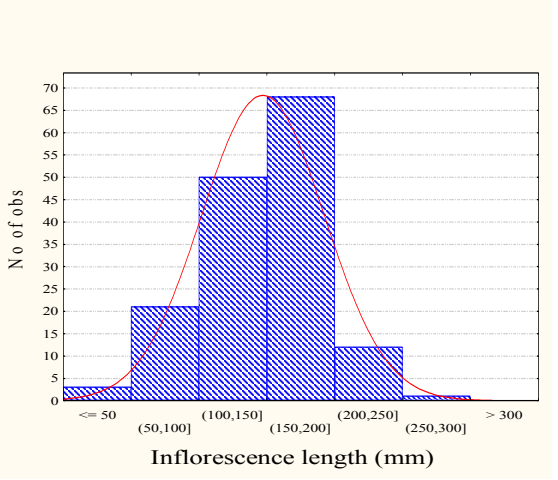
E1_Coimbatore

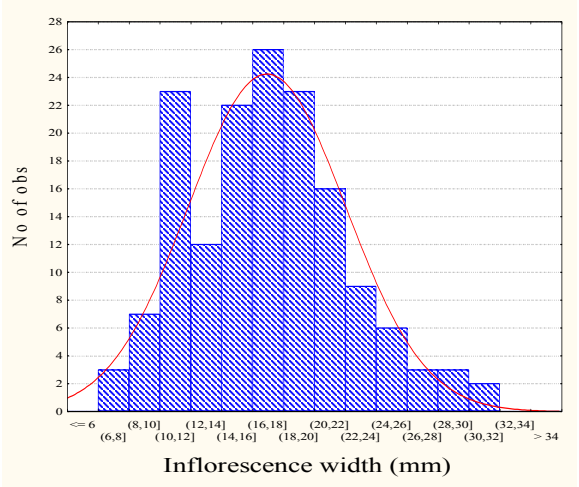


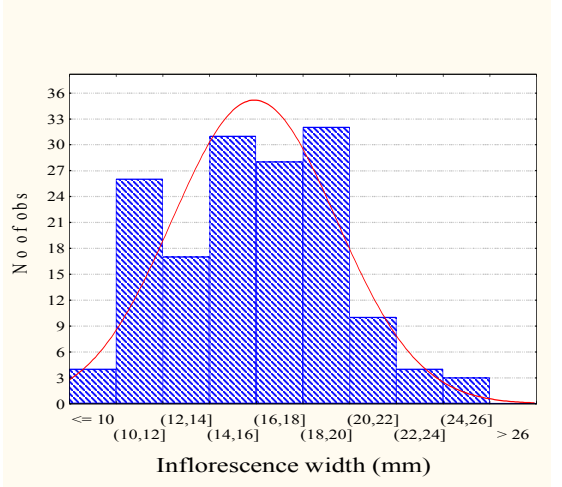
E2_Madurai

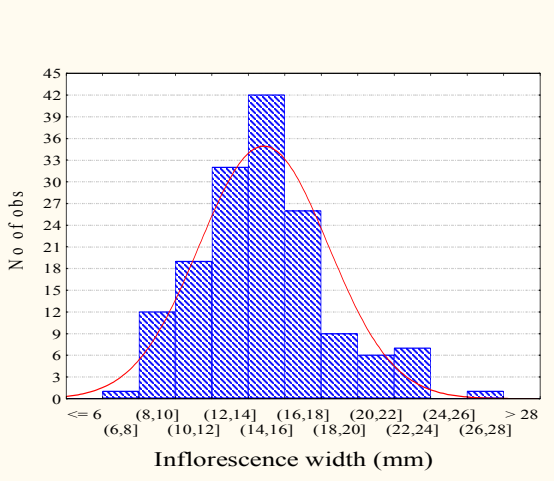


E3_ICRISAR, Patancheru

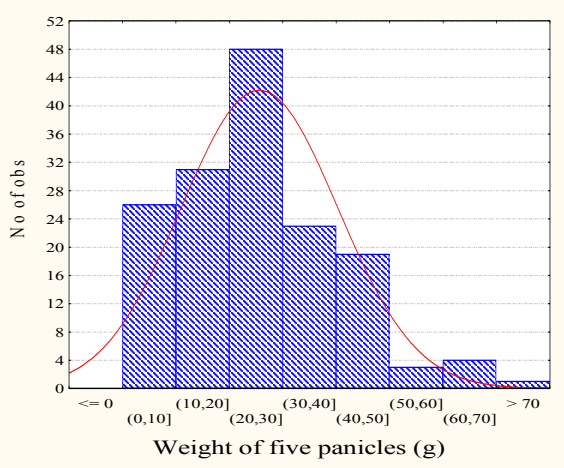


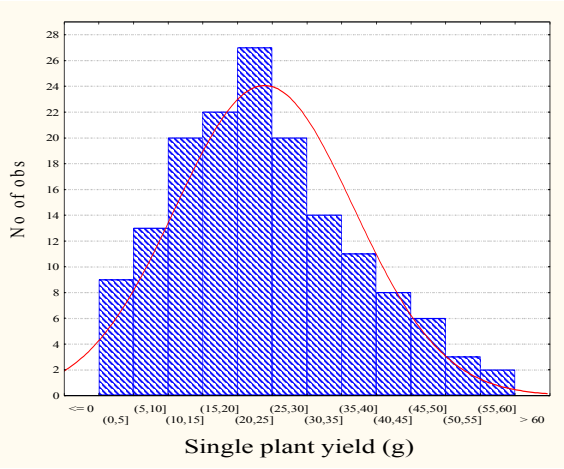




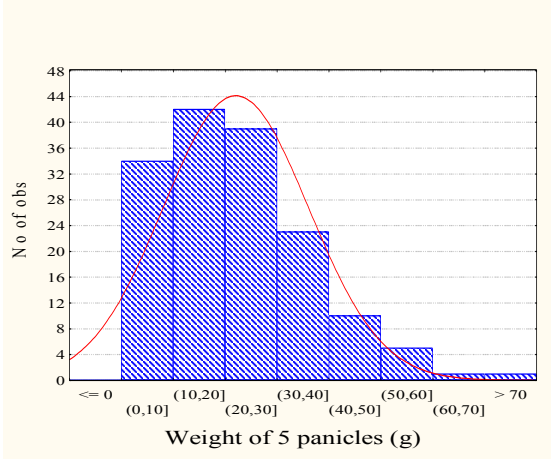


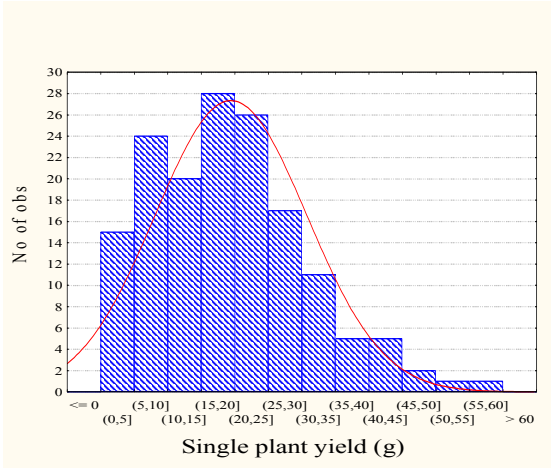
E1_Coimbatore



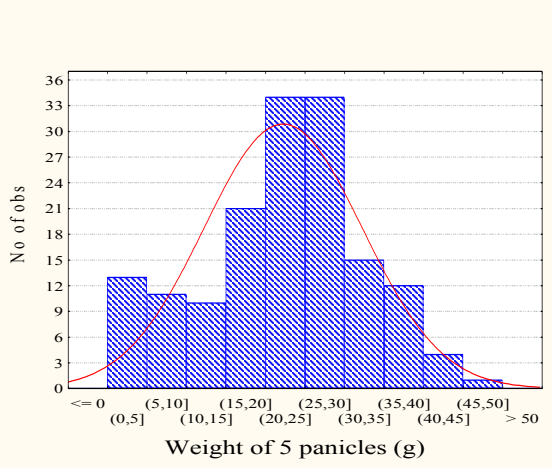


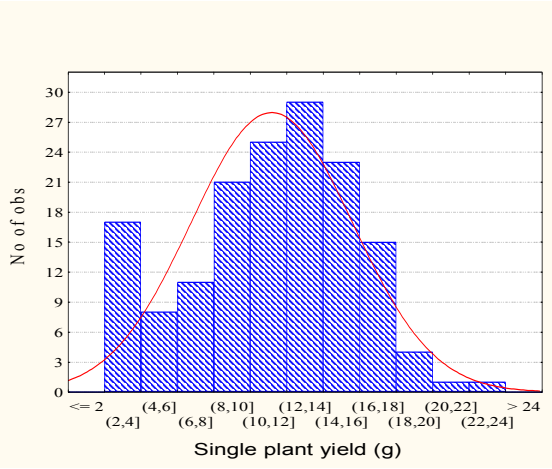
E2_Madurai



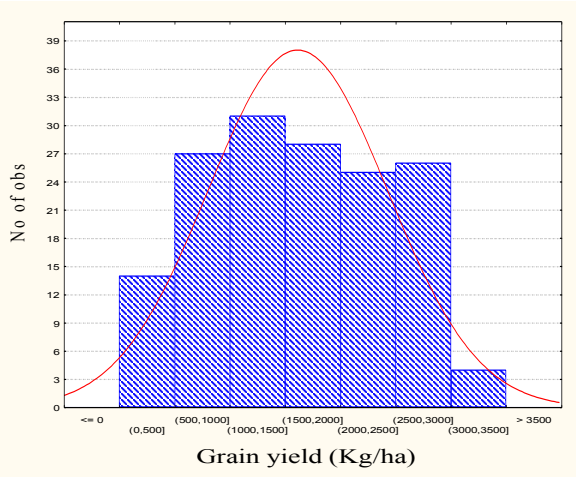


E3_ICRISAR, Patancheru

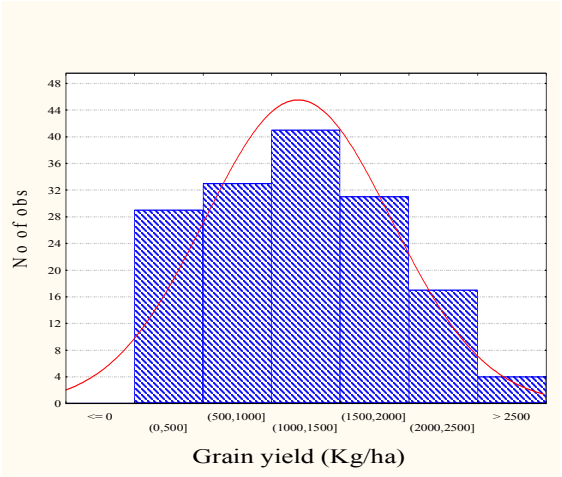




E1_Coimbatore



E2_Madurai



E3_ICRISAR, Patancheru

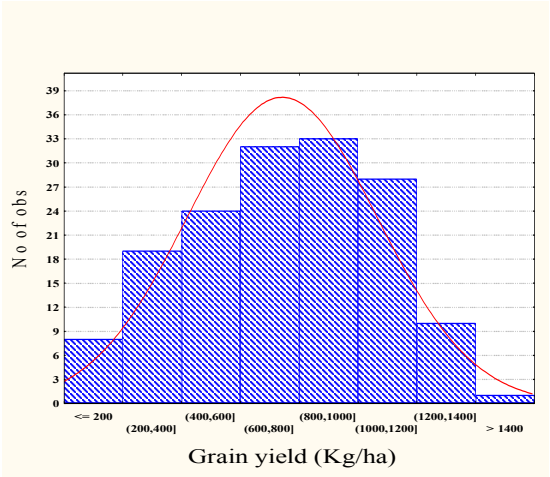


Figure 6. Frequency distribution of phenotypic dissimilarity values between pairs accessions present in foxtail millet core collection

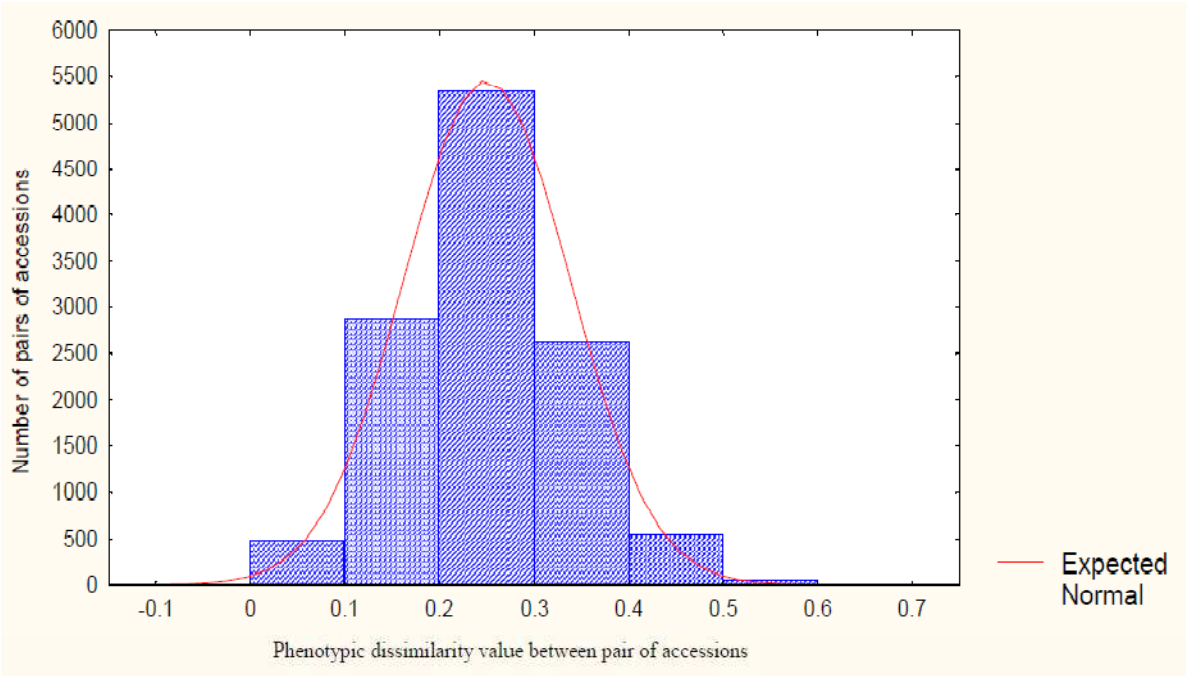
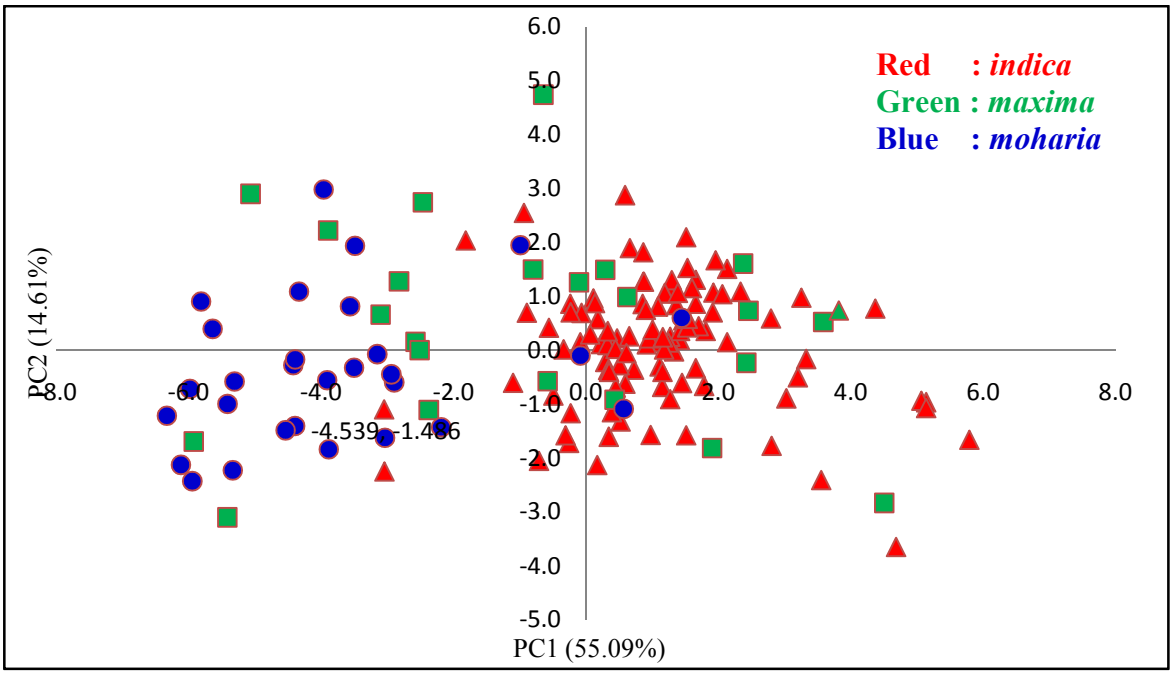


Figure 7. Scatter plot of first two principal components (PCs) of foxtail millet core collection accessions based on three races using pooled BLUPs of three environments



Note: PC1 and PC2 are the first and the second principal components, respectively. Numbers in parentheses refers to the proportion of variance explained by the principal coordinate

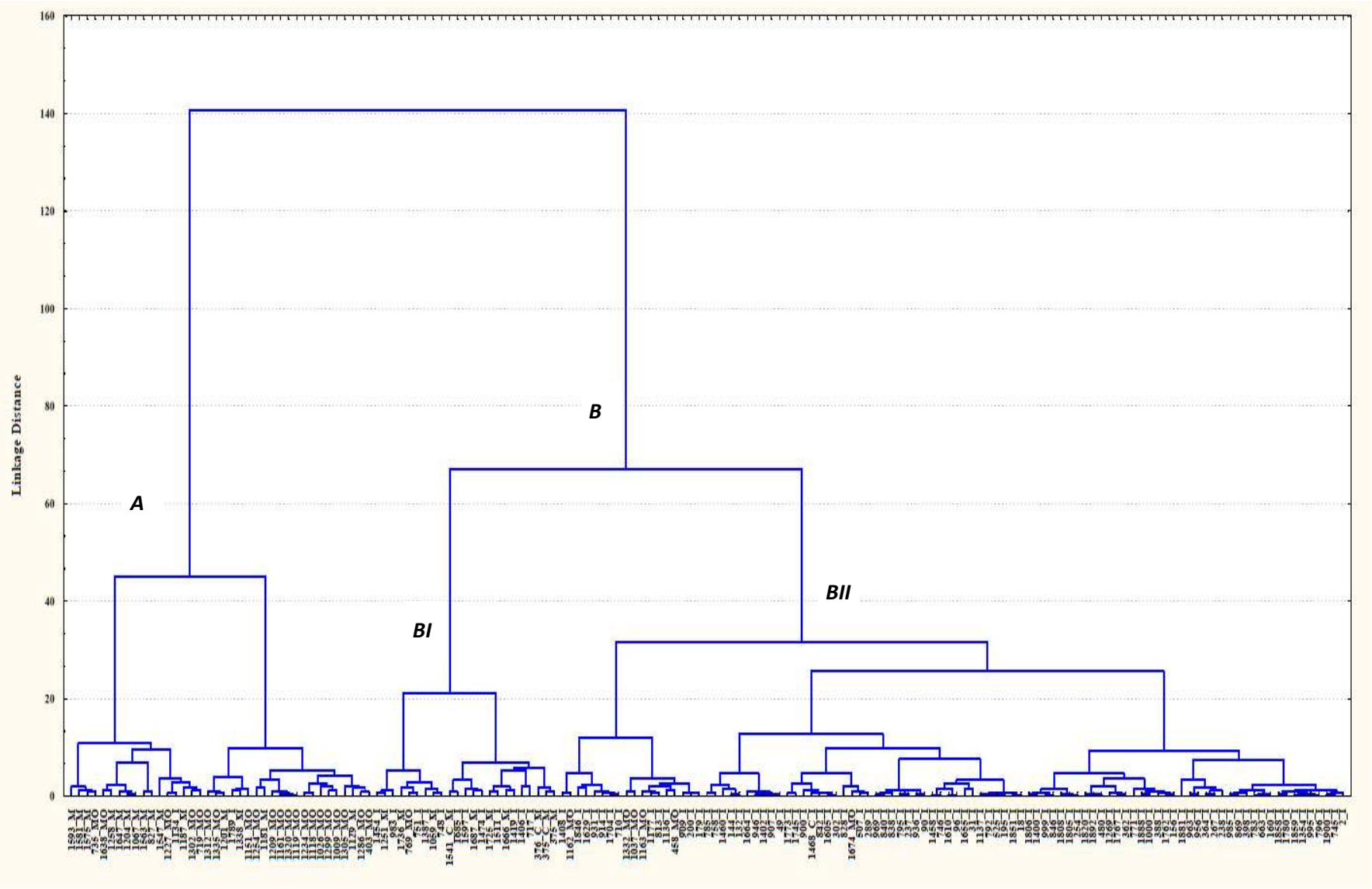


Figure 8. The hierarchical cluster (Ward, 1963) of E1 (Coimbatore) using the scores of first three PCs.

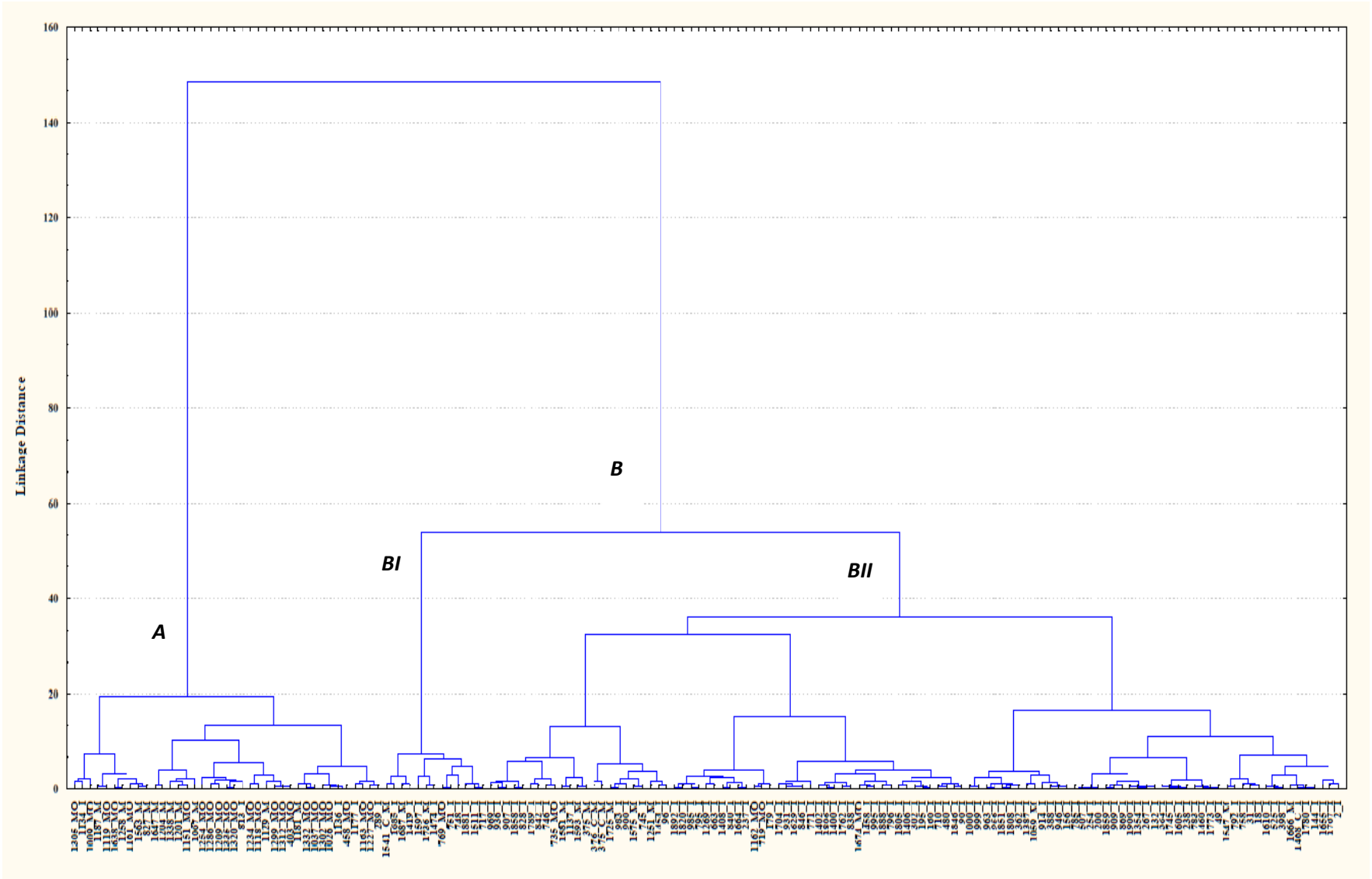


Figure 9. The hierarchical cluster (Ward, 1963) of E2 (Madurai) using the scores of first three PCs.

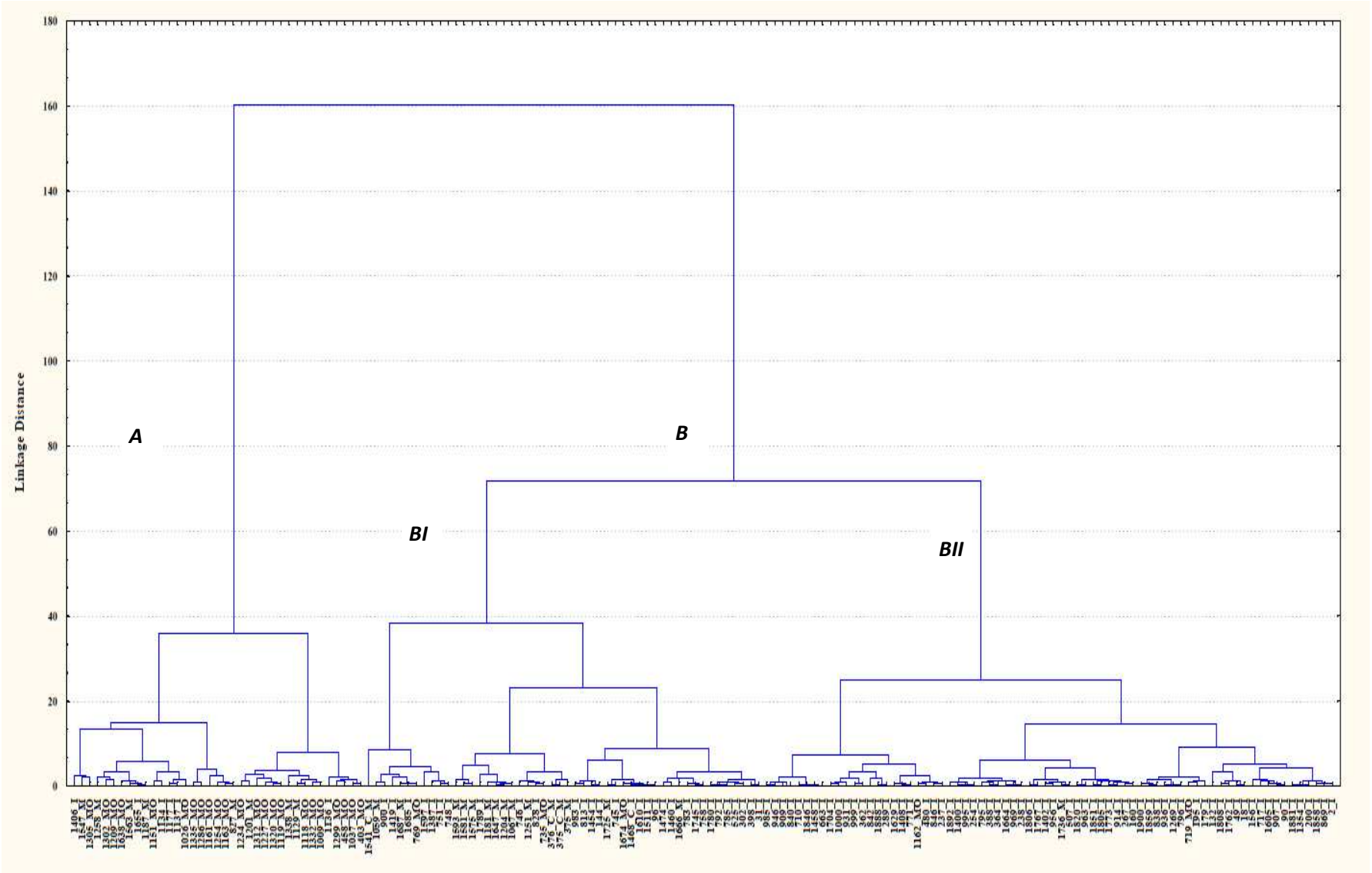


Figure 10. The hierarchical cluster (Ward, 1963) of E3 (ICRISAT, Patancheru) using the scores of first three PCs.

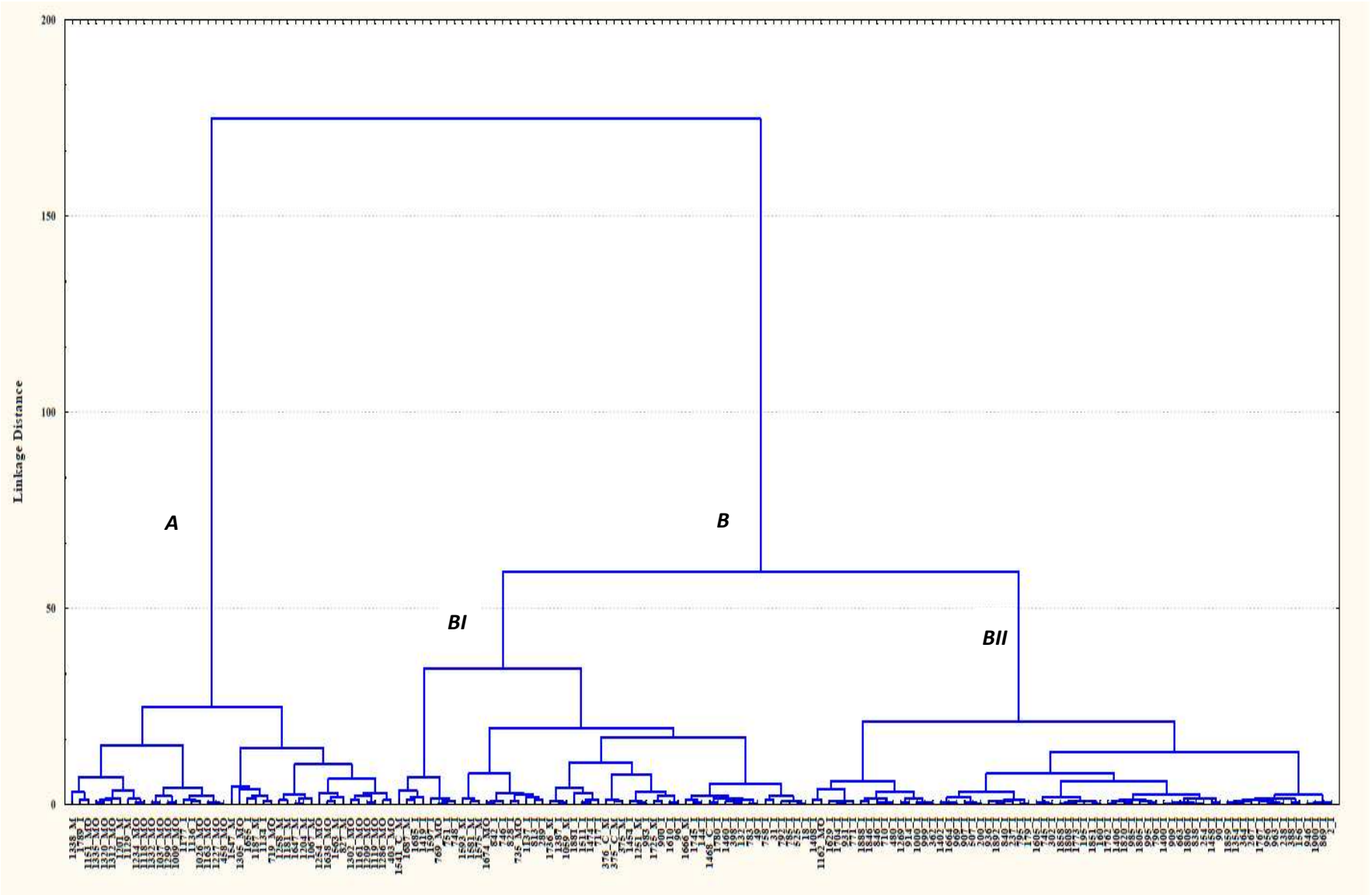


Figure 11. The hierarchical cluster (Ward, 1963) of Pooled data of three environments using first three PCs

Figure 12. Distribution of number of alleles per locus among 84 SSR markers along with linkage group used for genotyping foxtail millet core collection

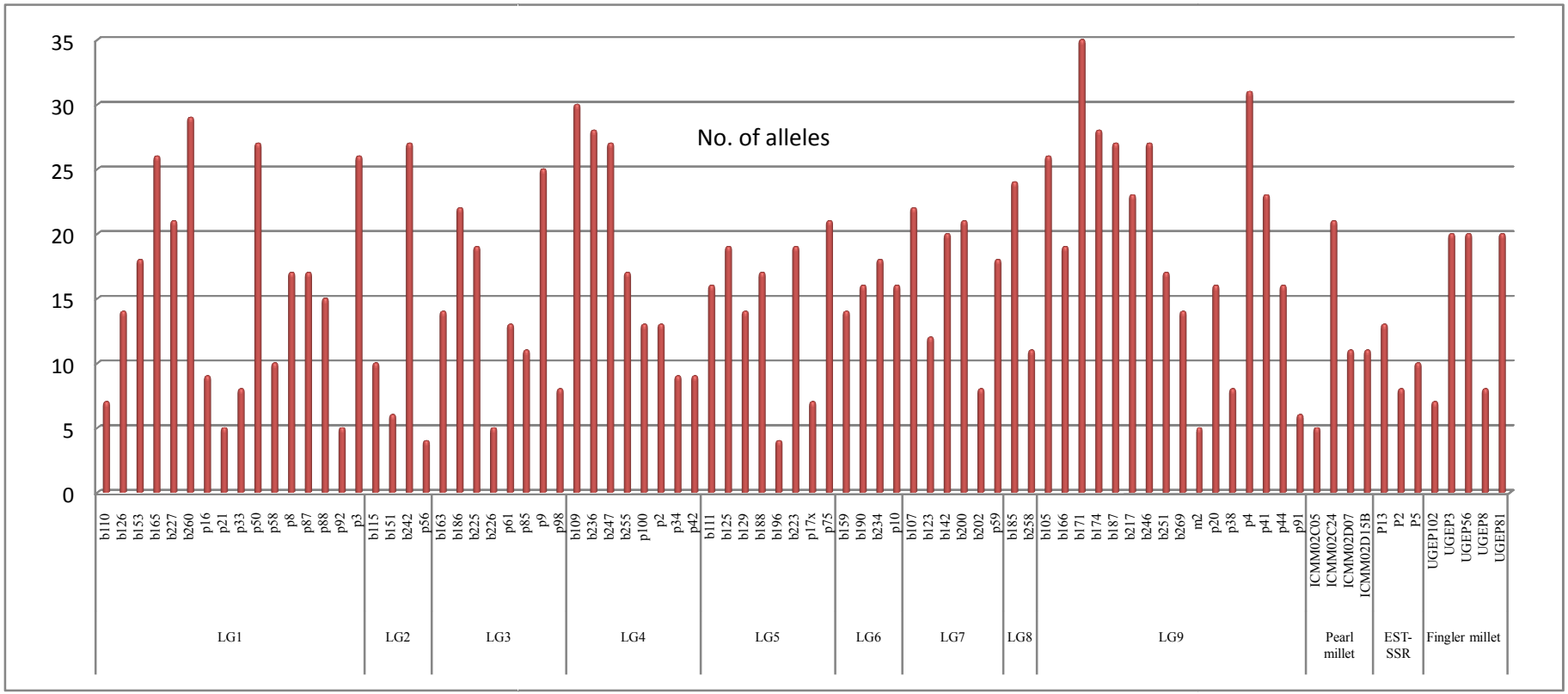


Figure 13. Distribution of rare, common and most frequent alleles in entire core collection and three races in foxtail millet core collection using 84 SSR markers

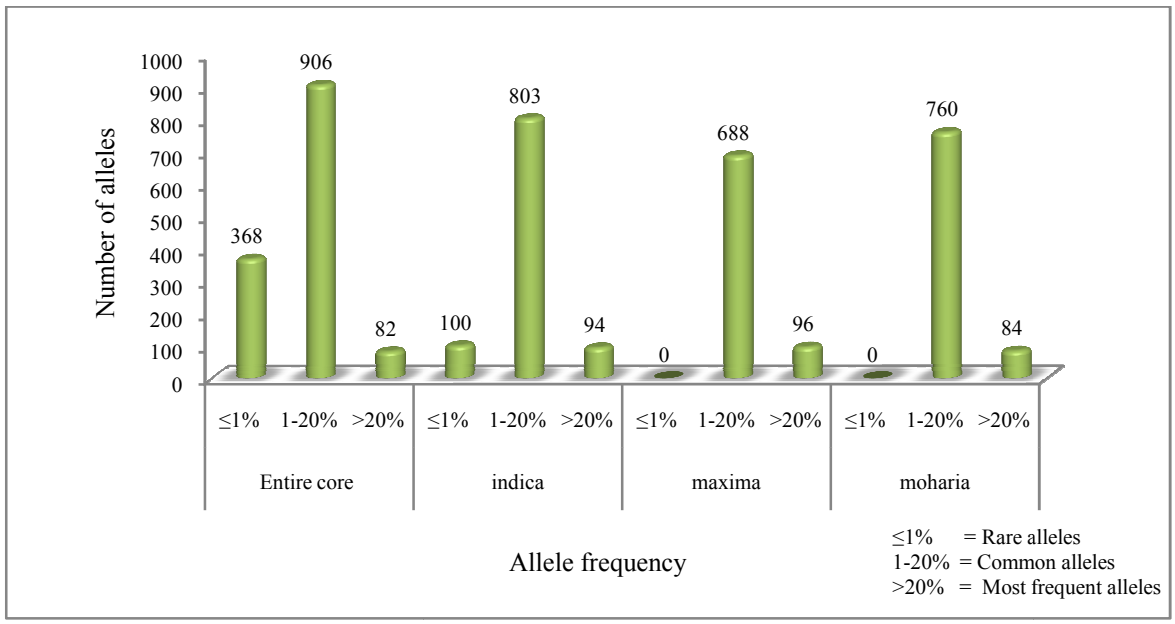
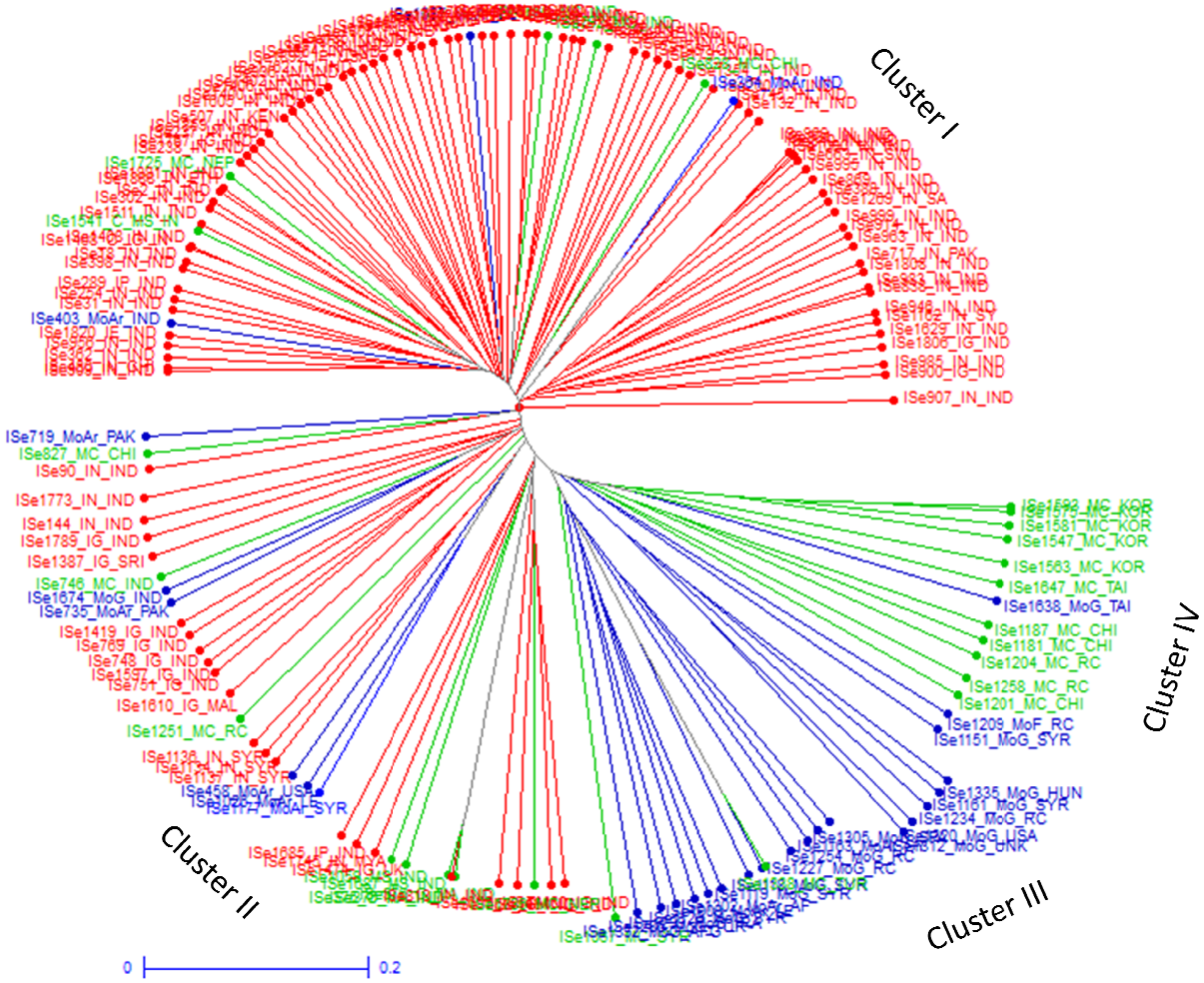


Figure 14. Unweighted neighbor-joining tree based on the simple matching dissimilarity matrix of 84 SSR markers genotyped across the foxtail millet core collection



Red: Indica **Green: Maxima** **Blue: Moharia**

Figure 15. Frequency distribution of dissimilarity index based on 84 SSR markers between pair of accessions

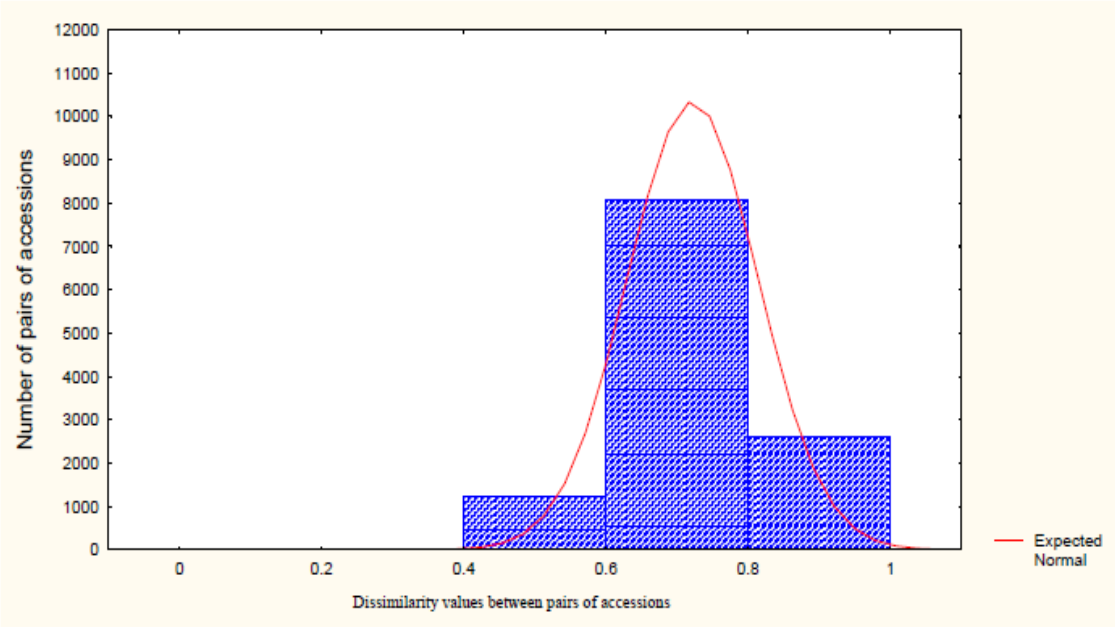


Figure 16. Principal coordinates analysis (PCoA) of foxtail millet core collection (colour coding based on three races) accessions using 84 SSR markers based on Nei (1973) distance estimates.

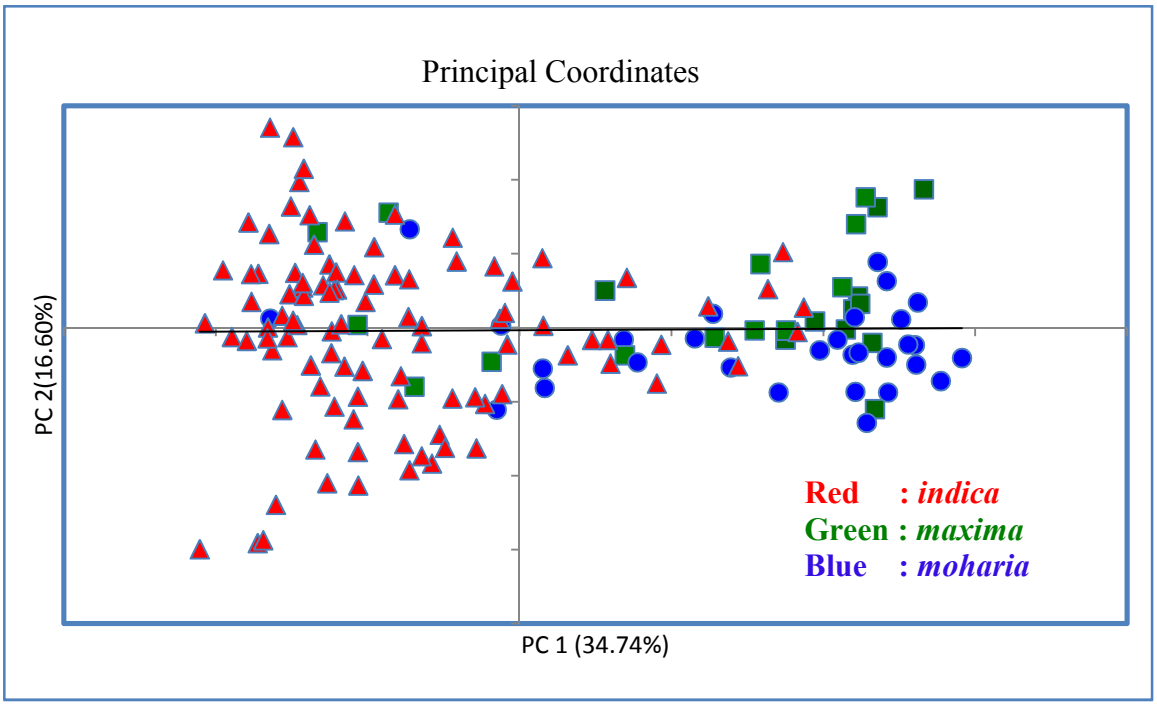


Figure 17. Scatter plot based on phenotypic and molecular marker dissimilarity between pair of accessions

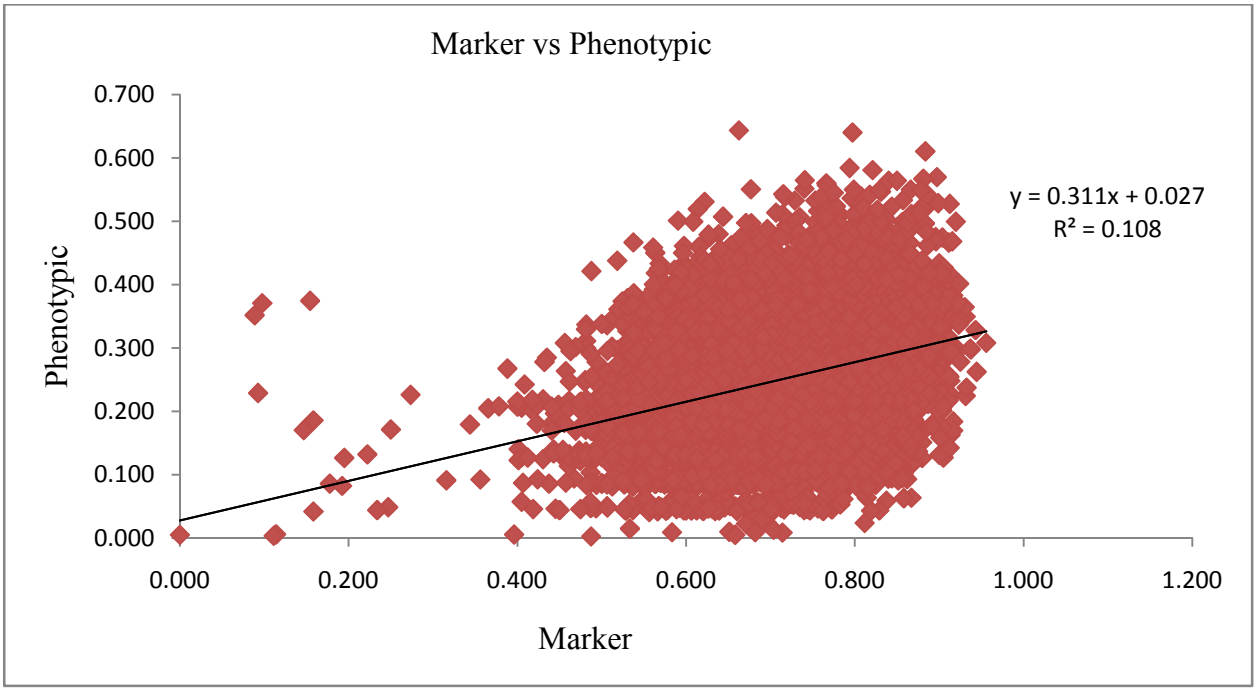


Figure 18. Rate of change in *LnP(D)* between successive *K* (*K* averaged over the five run)

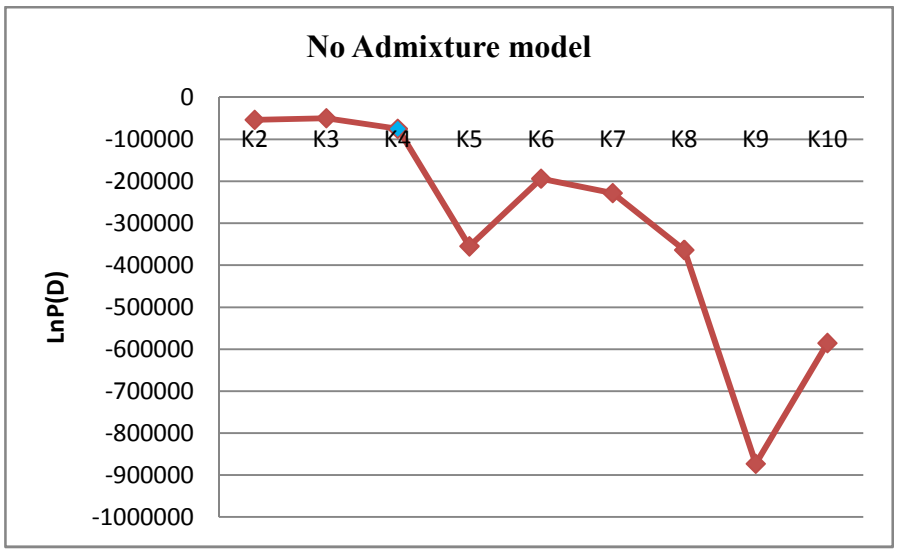
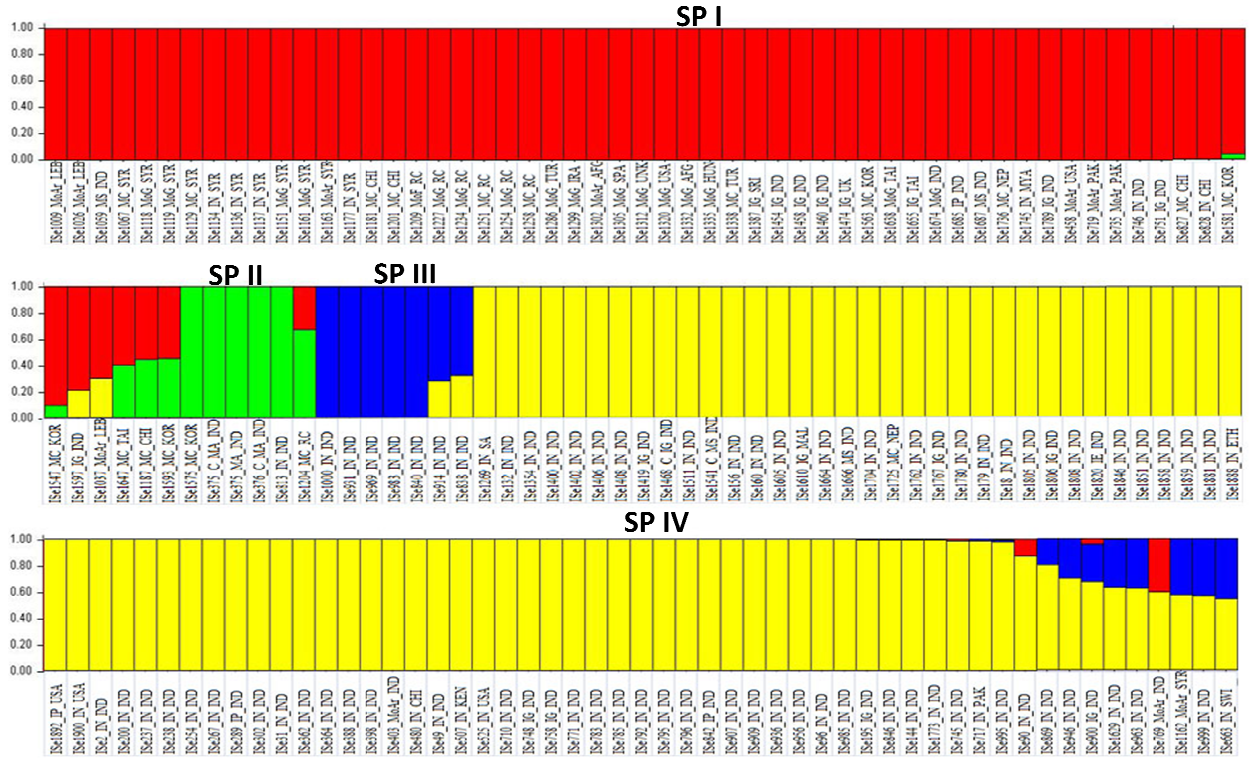
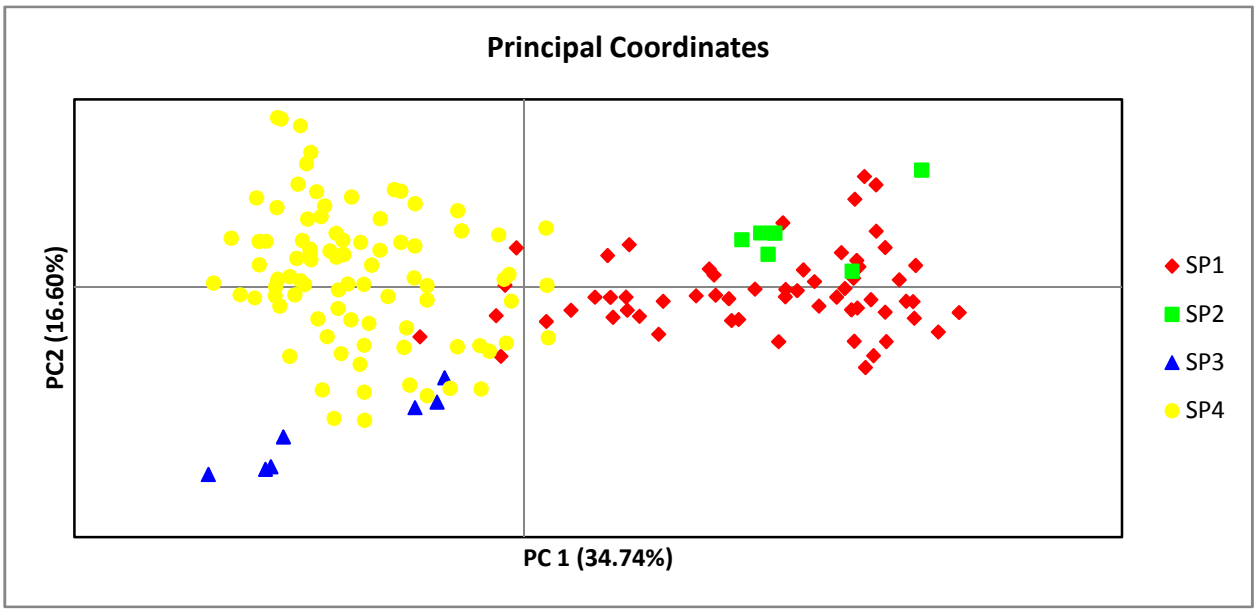


Figure 19. Population structure of foxtail millet core collection based on 84 SSR markers (k=4) revealed by STRUCTURE analysis



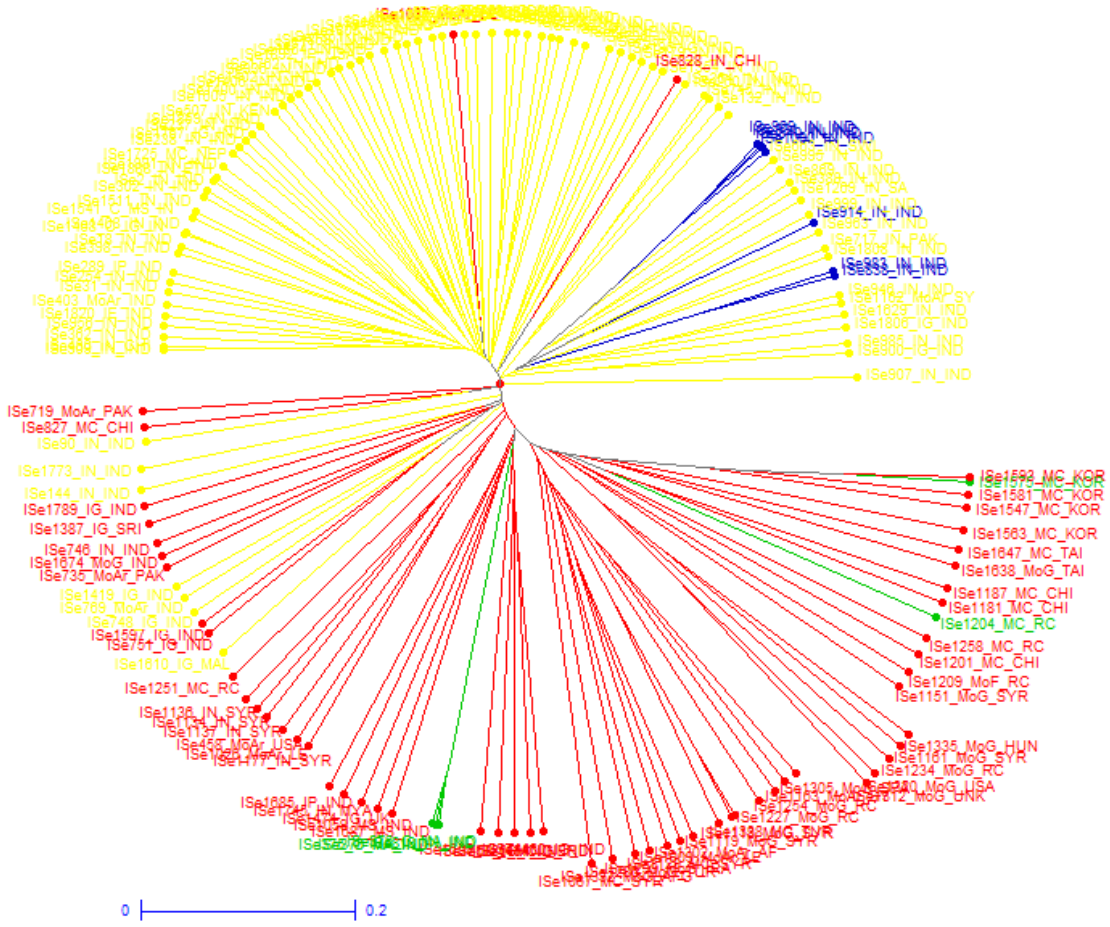
Note: Number on the y axis show the subgroup membership and the number on the x axis show the accession number

Figure 20. Principal coordinates analysis (PCoA) of foxtail millet core collection accessions using 84 SSR markers based on Nei (1973) distance estimates and colour coding based on subpopulation identified by STRUCTURE analysis



[Note: PC1 and PC2 are the first and the second principal coordinates, respectively. Numbers in parentheses refers to the proportion of variance explained by the principal coordinate]

Figure 21. Unweighted neighbor-joining tree based on the simple matching dissimilarity matrix of 84 SSR markers genotyped across the foxtail millet core collection



Red: SP1 **Green: SP2** **Blue: SP3** **Yellow: SP4**

Figure 22. The pattern of LD for 72 SSR loci indicating correlations of allele frequency (r^2) value against genetic distance (cM) between all loci pairs

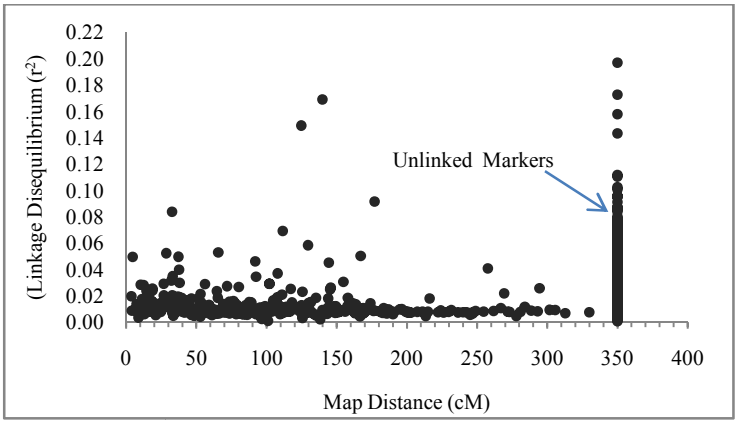
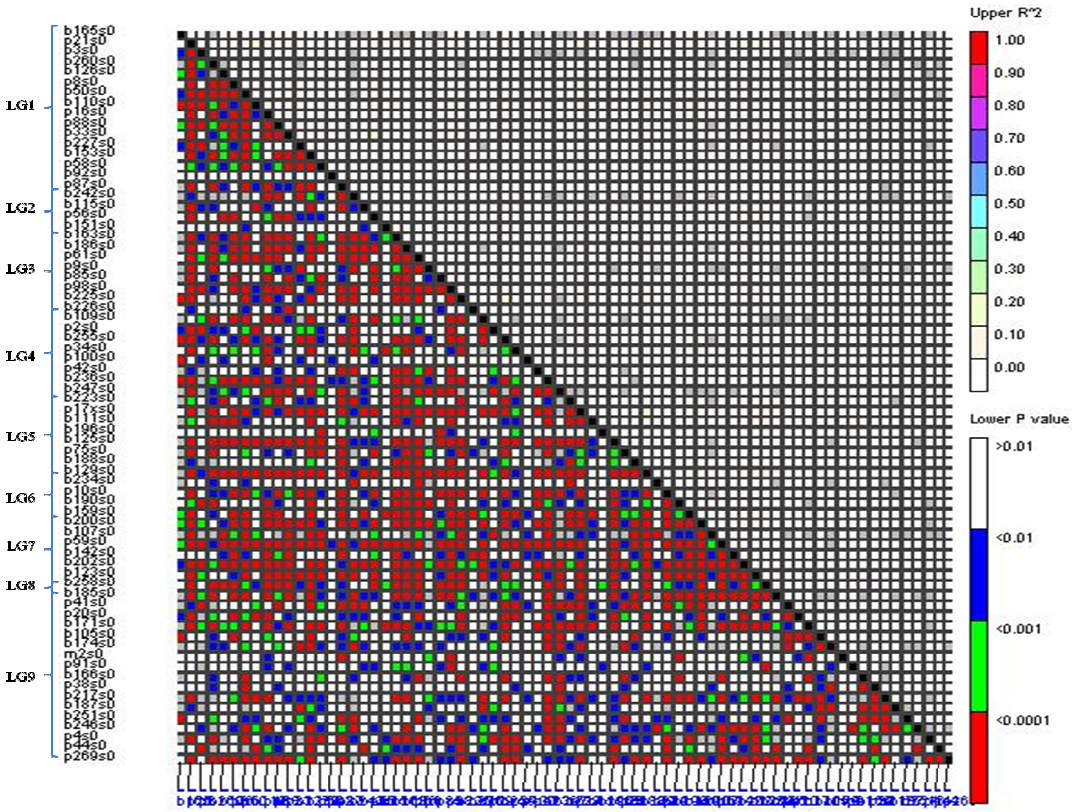
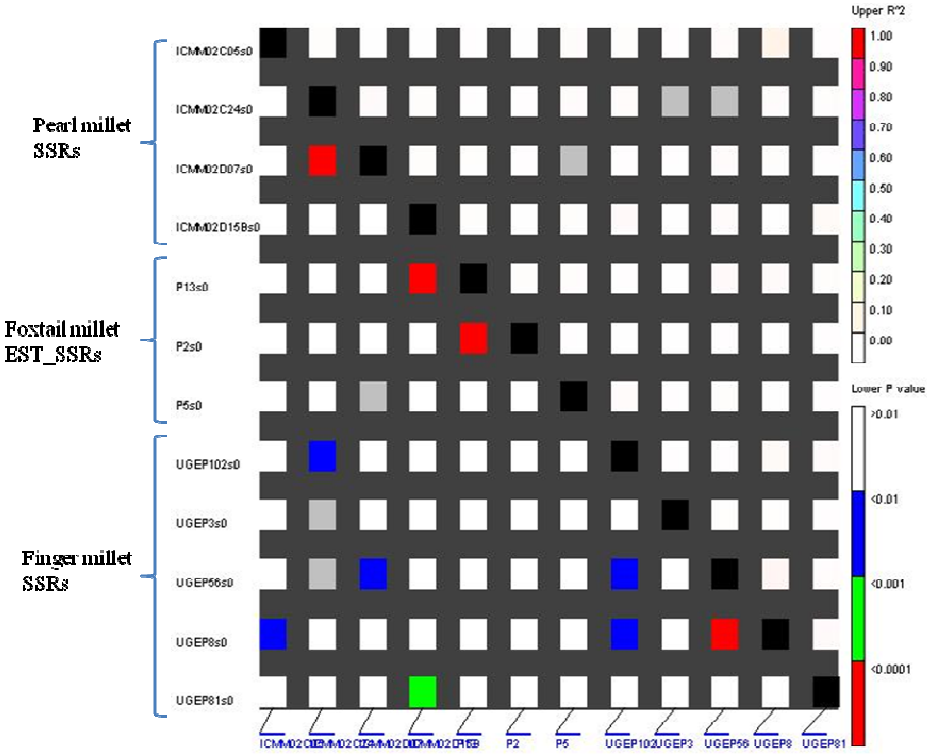


Figure 23. Linkage disequilibrium (LD) plot generated based 155 accessions of foxtail millet and 72 mapped SSR markers



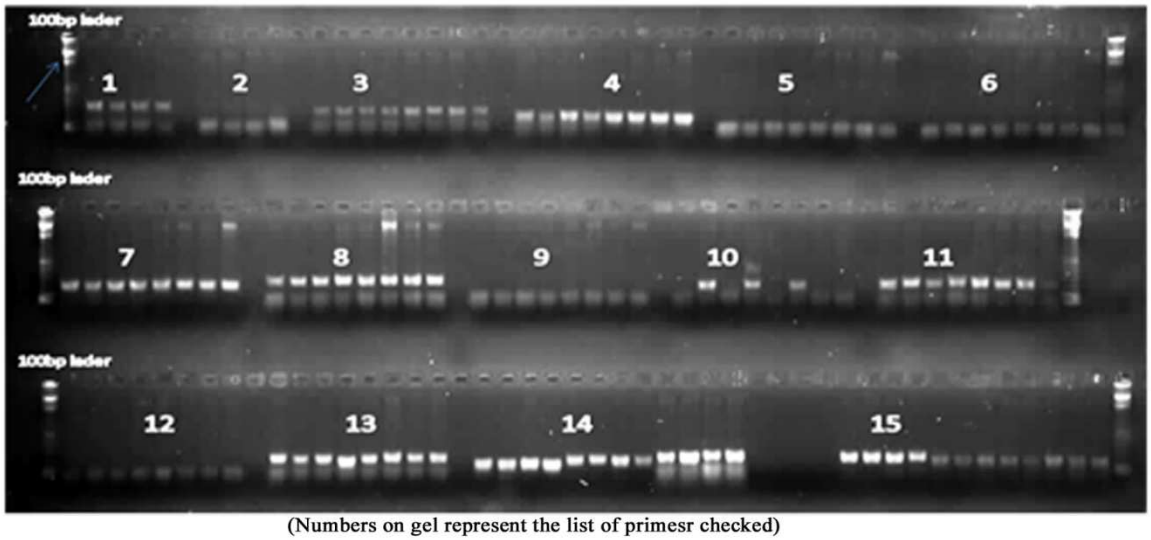
Note: Each cell represents the relationship between two markers with the colour codes for the presence of significant LD. Colored bar code for the significant threshold levels, LG: Linkage group

Figure 24. Linkage disequilibrium (LD) plot generated based 155 accessions of foxtail millet and 12 SSRs which are unmapped on foxtail millet genome



Note: Each cell represents the relationship between two markers with the colour codes for the presence of significant LD. Colored bar code for the significant threshold levels

Plate 5A. PCR products tested for amplification on 1.2 per cent agarose



(Numbers on gel represent the list of primesr checked)

Plate 5B. Allele sizing of the data obtained from ABI 3730xl Genetic Analyser using Genemapper® software version 4.0 (Applied Biosystems, USA)

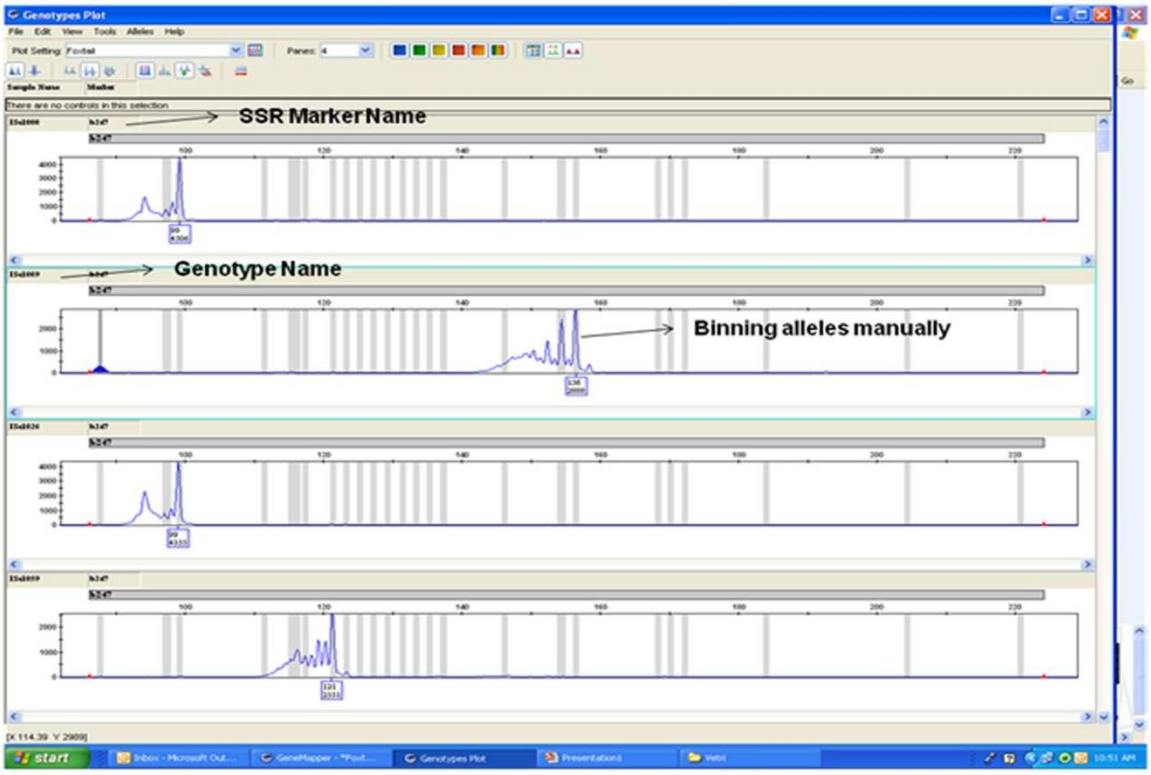


Plate 4. Grain colour (Yellow, Black, Black and White and Red)

a. Yellow (ISe 717)

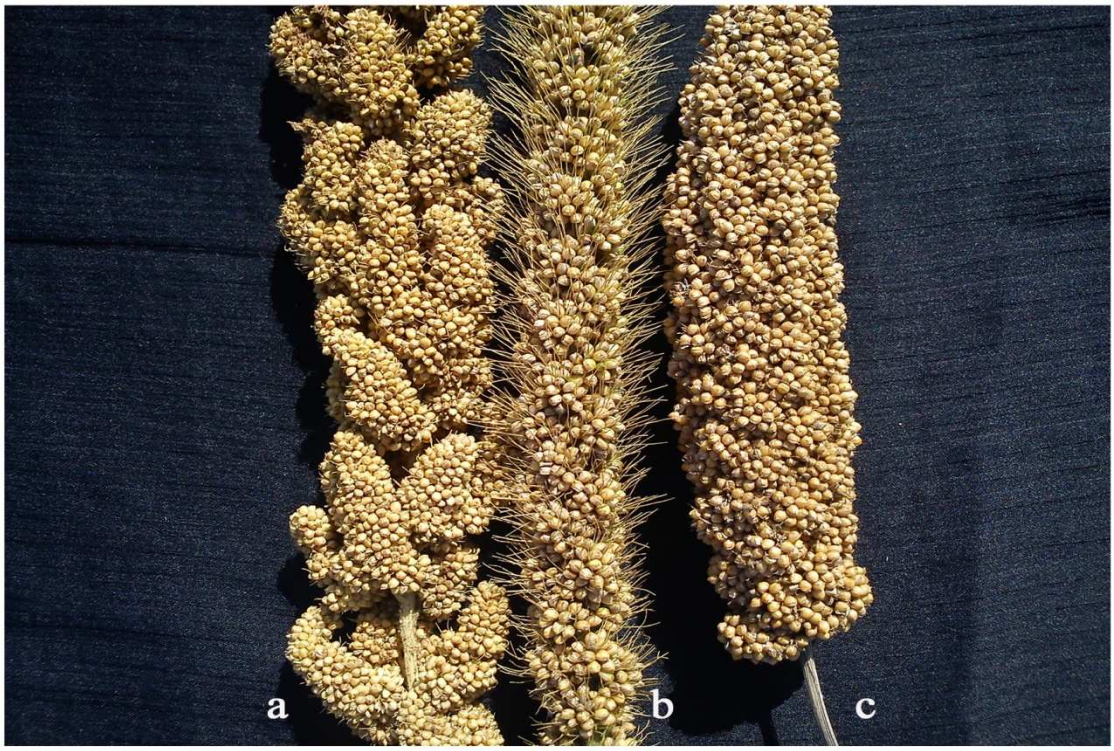
b. Black (ISe 31)

c. Black and white (ISe 1419)

d. Red (ISe 160)

Plate 3. Inflorescence and lobe compactness

A. Inforescence compactness (a. Loose, b. Medium and c. Compact)



B. Lobe Compactness (a. Loose, b. Medium and c. Compact

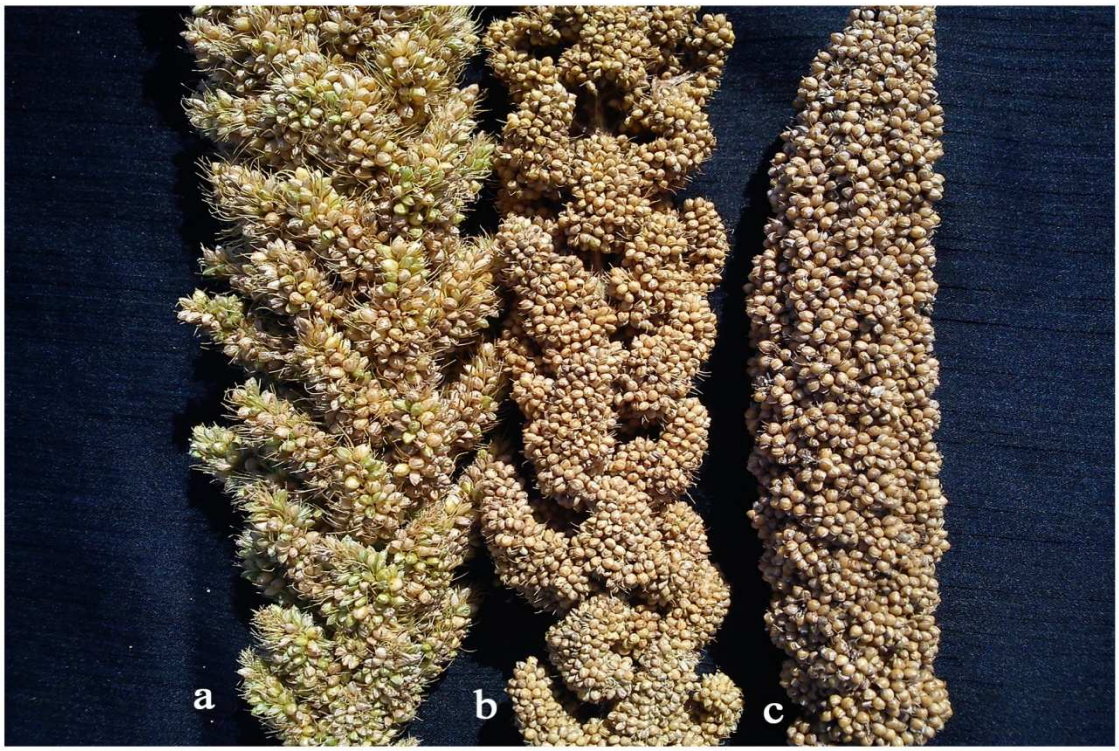
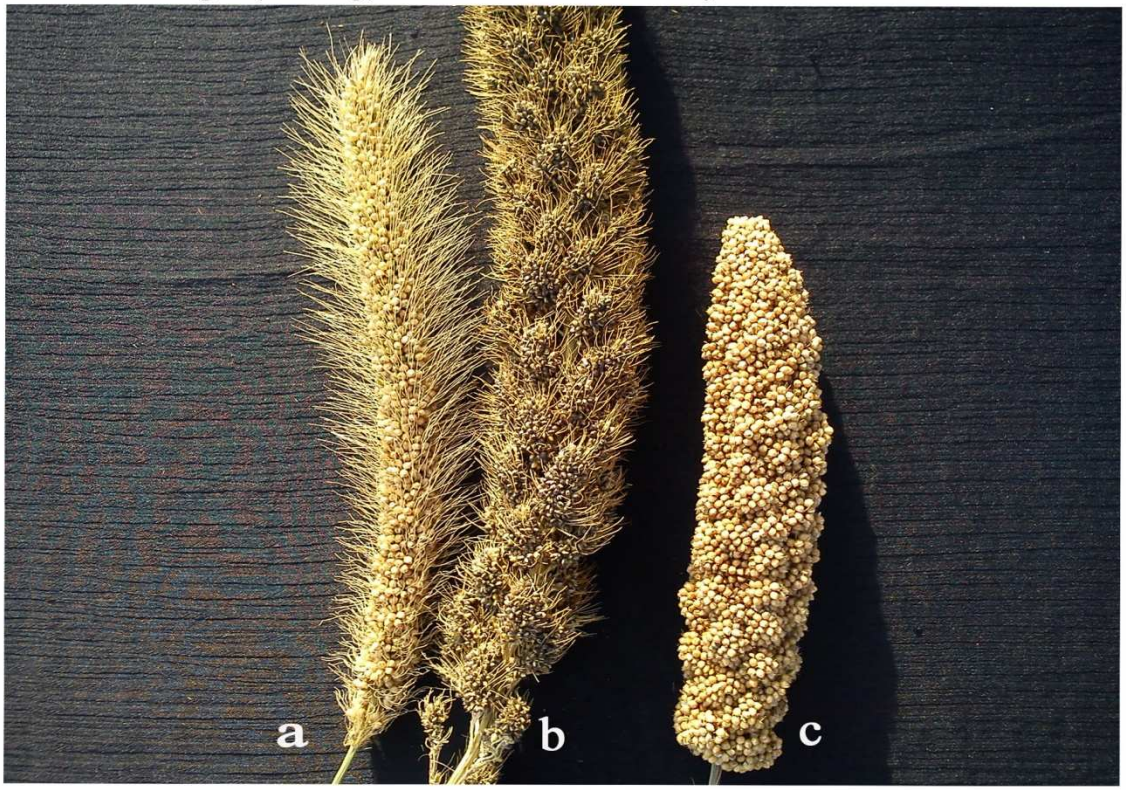


Plate 2. Bristle length and panicle lobing

A. Bristle length (a. Long, b. Medium and c. Short)



B. Panicle lobing (a. Non lobed, b. Medium lobed and c. Dense lobed)

A. Pigmentation

a. Green

b. Pigmented

c. Deep purple

B. Culm branching

a. Low

b. Medium

c. High

Plate 6. Diversity in plant height and inflorescence length

A. Plant height

B. Inflorescence length

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Appendix 1. Scores of 12 qualitative traits for 155 accessions in foxtail millet core collection

ISe	PP[1]	LFCL	GH	CB	BL	PL	INFC	LC	GRC	LO	SENE	PAS
2	1	1	1	2	1	3	3	3	1	1	2	2
18	1	3	1	2	2	3	2	2	1	1	2	2
31	1	1	1	2	2	3	2	3	5	2	1	2
49	1	3	1	2	1	3	2	3	1	1	3	2
90	1	3	1	2	1	3	3	3	1	2	3	3
96	1	1	1	2	2	3	3	3	1	2	2	2
132	1	1	1	2	2	2	3	3	1	3	3	2
144	1	1	1	2	3	3	3	3	1	2	2	2
156	1	1	1	2	1	2	3	3	1	1	2	2
160	2	1	1	2	1	2	3	3	2	1	2	3
179	1	1	1	1	1	2	3	3	1	3	3	2
195	1	1	1	2	1	2	3	3	1	2	3	3
200	1	3	1	1	1	2	3	3	1	2	4	3
237	2	1	1	1	1	2	3	3	1	2	2	2
238	1	1	1	1	1	3	3	3	1	2	2	3
254	1	1	1	2	2	3	2	3	1	2	2	2
267	1	3	1	2	2	3	3	3	1	2	3	2
289	1	1	1	1	2	3	2	3	1	2	2	2
302	1	3	1	3	2	3	2	3	1	1	1	2
362	1	1	1	1	1	2	2	3	1	2	2	3
364	1	1	1	1	3	3	3	3	1	2	1	3
375	2	1	1	3	3	3	3	3	1	1	2	1
388	1	1	1	1	2	3	3	3	1	1	3	2
398	1	1	1	2	1	3	3	3	1	1	3	2
403	2	1	1	1	2	1	2	2	1	1	4	4
458	1	3	1	1	1	1	3	3	1	2	2	3
480	1	1	1	1	1	3	3	3	1	1	2	3
507	1	3	1	2	1	3	2	3	1	1	2	2
525	1	3	1	2	2	3	3	3	1	1	2	2
663	1	1	1	1	1	2	3	3	1	1	2	2
710	1	1	1	1	1	2	3	3	1	2	2	3
717	1	1	1	2	1	3	3	3	1	3	3	2
719	1	1	2	1	1	2	1	2	1	3	3	3
735	1	1	1	3	3	3	3	3	1	1	1	1
745	1	1	1	1	2	3	2	3	1	2	4	3
746	1	1	1	3	3	3	3	3	5	2	2	2
748	1	1	1	3	3	3	3	3	2	1	3	1
751	1	1	1	1	2	3	3	3	1	2	2	2
758	1	1	1	3	3	3	3	3	1	1	1	3
769	1	1	1	3	3	3	3	3	1	2	2	3
771	2	1	1	1	1	3	2	3	1	2	2	3
783	3	2	1	3	2	3	3	3	1	1	2	1
785	2	1	1	3	1	3	3	3	2	1	2	2
792	1	1	1	3	3	3	3	3	1	1	2	4
795	1	1	1	1	3	2	3	3	1	1	3	3
796	1	1	1	2	3	3	3	3	1	3	2	2
813	3	2	1	2	2	1	3	3	1	2	4	3
827	2	1	1	3	3	1	3	3	2	2	1	4
828	1	1	1	3	3	3	3	3	1	1	1	2
838	1	1	1	2	2	3	3	3	1	1	2	3
840	1	1	1	1	1	2	3	3	1	1	2	2
842	2	1	1	2	3	3	2	3	1	2	2	2
846	1	1	1	1	1	2	3	3	1	1	2	2
869	1	1	1	2	1	3	3	3	1	2	2	2
900	1	1	1	3	3	3	3	3	1	1	2	2
907	1	1	1	2	2	2	3	3	1	2	3	3

Appendix 1. Cont..

ISe	PP[1]	LFCL	GH	CB	BL	PL	INFC	LC	GRC	LO	SENE	PAS
909	1	1	1	1	1	2	3	3	1	1	2	3
914	1	1	1	2	1	2	3	3	1	1	1	2
931	1	1	1	1	2	3	3	3	1	1	2	2
936	2	1	1	1	2	3	3	3	1	1	2	2
946	1	3	1	2	2	3	3	3	1	2	2	2
956	2	1	1	2	2	2	3	3	1	1	2	2
963	1	1	1	1	1	2	3	3	1	1	1	2
969	1	1	1	1	1	2	3	3	1	2	3	2
983	1	1	1	3	1	3	2	3	1	2	2	2
985	1	1	1	1	1	2	3	3	1	1	3	2
995	1	1	1	2	1	2	3	3	1	2	3	2
999	1	1	1	2	1	3	3	3	1	2	2	2
1000	1	1	1	2	1	2	3	3	1	1	2	2
1009	1	1	1	1	2	1	3	3	1	4	5	3
1026	1	1	1	1	1	2	3	3	1	3	3	2
1037	2	1	2	1	1	1	3	3	1	3	4	4
1059	3	2	1	2	3	3	3	3	1	1	3	1
1067	1	1	1	3	1	3	3	3	1	1	1	2
1118	1	1	1	1	2	1	3	3	1	3	3	4
1119	1	1	1	1	2	1	3	3	1	3	4	5
1129	1	1	1	1	2	1	3	3	1	1	4	4
1134	1	1	1	1	1	1	3	3	1	3	1	3
1136	1	1	1	1	1	1	3	3	1	3	3	3
1137	1	1	1	2	3	3	3	3	1	1	3	3
1151	2	1	1	1	3	2	3	3	1	2	3	4
1161	1	1	1	1	2	1	3	2	1	2	3	4
1162	1	1	1	1	1	1	3	3	1	2	2	3
1163	1	1	1	2	1	1	3	3	1	2	2	3
1177	1	1	1	1	1	1	3	3	1	3	4	3
1181	1	1	1	3	3	1	3	3	1	1	3	4
1187	1	1	1	1	2	1	3	3	1	1	1	4
1201	1	1	1	1	3	2	3	3	1	1	3	4
1204	2	1	1	2	3	3	3	3	1	2	1	3
1209	1	1	1	2	1	1	3	3	1	1	3	3
1227	1	1	1	2	2	2	2	3	1	2	1	3
1234	2	1	1	1	2	1	3	3	1	1	3	4
1251	2	1	1	2	3	3	3	3	1	2	1	2
1254	1	1	1	2	3	1	3	3	2	1	3	4
1258	1	1	1	3	3	3	3	3	1	1	3	3
1269	1	1	1	1	1	2	2	3	1	2	3	3
1286	1	1	1	1	2	2	2	2	1	2	2	4
1299	1	1	1	1	1	1	3	3	1	3	4	4
1302	2	2	1	1	2	1	3	3	1	3	4	3
1305	1	1	1	1	2	2	3	3	1	2	3	4
1312	2	1	1	2	2	1	3	3	2	1	4	4
1320	2	2	1	1	2	1	3	3	1	1	3	4
1332	1	3	1	1	2	1	3	3	1	2	4	3
1335	2	1	1	1	1	1	3	3	1	1	4	4
1338	1	1	1	3	2	3	3	3	1	2	4	4
1354	1	1	1	3	1	2	2	3	1	1	2	2
1387	1	1	1	2	2	3	3	3	1	1	1	1
1400	1	1	1	3	3	3	3	3	1	3	2	3
1402	1	1	1	1	2	3	2	3	1	1	3	3
1406	1	1	1	2	3	3	3	3	1	1	3	3
1408	1	1	1	1	1	2	3	3	1	1	3	2
1419	1	1	1	3	3	3	1	2	7	1	2	1
1454	1	1	1	3	3	3	3	3	1	2	3	1
1458	1	1	1	2	1	2	3	3	1	1	2	3

Appendix 1. Cont..

ISe	PP[1]	LFCL	GH	CB	BL	PL	INFC	LC	GRC	LO	SENE	PAS
1460	1	1	1	3	2	3	1	2	2	2	1	2
1474	1	1	1	2	3	3	3	3	1	1	1	2
1511	1	1	1	3	1	3	2	2	1	2	3	1
1547	1	1	1	3	3	3	3	3	1	3	2	3
1563	1	1	1	1	3	3	3	3	1	1	4	4
1575	2	2	1	3	3	3	3	3	1	1	1	2
1581	2	1	1	3	3	3	3	3	1	1	2	2
1593	1	2	1	3	3	3	3	3	1	1	1	2
1597	1	1	1	3	3	3	2	3	1	3	2	1
1605	1	1	1	2	2	3	2	3	1	1	2	2
1610	1	1	1	2	2	2	2	2	1	1	2	3
1629	1	1	1	1	1	2	3	3	1	2	3	3
1638	1	1	1	2	3	1	3	3	1	1	2	4
1647	1	1	1	3	3	3	3	3	1	3	4	3
1655	1	1	2	2	2	2	3	3	1	3	2	3
1664	1	1	1	1	1	2	2	3	1	1	2	2
1666	1	1	1	3	3	3	3	3	1	1	2	2
1674	1	1	1	3	2	3	3	3	1	1	2	2
1685	1	1	2	1	2	3	2	3	7	1	1	1
1687	2	1	2	3	2	3	1	2	1	2	1	1
1704	1	1	1	1	1	2	2	3	1	1	2	3
1725	1	1	4	3	1	3	3	3	1	1	2	2
1736	1	1	2	3	3	3	3	3	1	2	1	2
1745	1	1	1	3	3	3	3	3	1	1	1	2
1762	1	3	1	2	2	3	3	3	1	3	2	3
1767	1	1	1	1	1	3	3	3	1	1	2	3
1773	1	1	1	2	2	3	3	3	1	1	2	3
1780	1	3	1	2	2	3	2	3	1	1	2	2
1789	1	1	1	2	3	3	3	3	2	1	3	3
1805	2	2	1	1	1	3	3	3	1	2	3	2
1806	1	3	1	1	1	2	3	3	1	2	3	3
1808	1	1	1	2	1	3	2	3	1	1	2	2
1820	1	1	1	1	1	2	3	3	1	1	2	3
1846	1	1	1	1	2	2	3	3	1	2	2	3
1851	2	2	1	2	2	2	3	3	1	2	3	3
1858	1	1	1	1	2	3	1	1	2	3	3	2
1859	2	1	1	1	1	2	2	3	1	2	2	2
1881	1	1	1	1	1	3	1	2	1	2	2	2
1888	1	1	1	2	3	3	2	2	1	1	2	2
1892	2	2	1	1	1	2	3	3	1	2	2	2
1900	1	1	1	2	1	2	2	2	1	2	2	3
Control cultivars												
1468_C	1	1	1	1	3	3	2	2	1	1	3	1
1541_C	1	1	1	2	2	3	1	1	1	3	4	1
375_C	2	1	1	3	3	3	3	3	1	1	2	1
376_C	2	1	1	3	3	3	3	3	1	1	2	1

P1= P: Plant pigmentation, LECL: Leaf colour, GH: Growth habits, BL: Bristle length, PL: Panicle lobing, INFC: Inflorescence compactness, LC: Lobe compactness, GRC: Grain color, LO: Plant lodging, SENE: Leaf senescence, PAS: Overall plant aspects

Appendix 2. Mean performance 155 accessions in foxtail millet core collection for 13 quantitative traits at Coimbatore (E1) during 2009/10 *Rabi*/*Summer*

ISe	DF[1]	PLHT	BT	FLBL	FLBW	FLSL	PEDL	PEX	INFL	INFW	W5P	SPY	PY
2	50.0	109.6	5.2	299.6	17.2	145.8	301.7	159.0	181.3	19.9	34.6	28.0	1728.0
18	50.0	115.9	5.0	257.4	17.7	118.2	309.0	196.2	146.7	22.6	35.7	23.3	1598.0
31	60.3	100.5	3.1	292.1	23.2	137.5	347.5	214.5	137.3	18.3	42.3	12.2	857.0
49	51.3	107.7	5.0	274.6	22.4	147.3	334.8	191.1	179.7	19.8	13.5	19.6	1201.0
90	52.3	90.1	5.2	260.2	20.4	128.6	301.1	175.7	160.8	16.7	14.6	20.0	1427.0
96	59.0	104.2	1.8	276.3	21.5	140.7	314.0	177.0	164.0	14.9	36.4	28.0	1031.0
132	51.3	116.9	4.8	290.1	21.9	154.1	347.2	196.2	188.2	21.1	40.5	19.6	1050.0
144	50.0	118.0	4.2	316.0	21.6	128.3	345.9	222.9	189.5	19.6	32.1	24.7	1513.0
156	58.3	127.5	6.3	249.7	22.4	166.8	298.9	133.4	199.9	12.8	27.8	31.6	2047.0
160	49.4	111.5	5.0	268.4	19.5	140.7	319.4	182.5	152.9	18.7	35.1	27.8	1934.0
179	48.0	112.0	4.5	255.9	16.3	124.7	266.1	145.6	149.7	12.1	11.7	21.3	1261.0
195	54.0	113.9	3.4	249.0	19.0	150.8	317.4	168.6	149.0	15.4	19.8	24.9	1481.0
200	47.0	100.4	4.7	237.2	17.3	125.0	273.9	153.3	147.4	17.5	21.9	21.5	1294.0
237	54.7	113.5	5.4	281.9	16.6	132.1	302.3	174.4	159.8	12.7	17.6	27.8	1816.0
238	63.0	124.9	4.9	300.3	22.2	191.2	354.1	168.0	190.8	18.5	25.8	43.7	2014.0
254	52.0	112.6	3.5	280.6	19.7	125.9	285.3	163.8	160.8	15.1	32.6	44.6	2422.0
267	63.0	109.6	6.1	288.4	19.4	149.9	334.8	188.2	159.8	20.9	36.7	49.0	2347.0
289	56.3	99.2	4.8	288.4	19.3	114.6	270.2	160.6	140.5	22.3	28.8	15.1	1178.0
302	50.0	111.7	3.6	301.2	20.4	129.4	292.2	167.1	159.1	21.3	44.1	31.1	1996.0
362	59.3	111.3	6.7	294.7	19.3	163.6	318.4	156.8	174.5	14.0	20.4	31.0	1621.0
364	65.0	111.7	5.3	264.1	19.8	135.7	339.6	208.4	162.7	15.4	42.5	48.0	2623.0
375	60.3	101.0	2.4	271.4	22.3	130.9	230.4	105.1	121.3	28.7	64.7	26.8	2168.0
388	62.0	108.4	4.8	300.7	19.4	155.0	308.7	156.1	179.5	15.8	33.6	40.8	2712.0
398	59.3	107.4	3.7	274.6	19.5	127.7	334.7	212.1	164.0	20.0	29.0	36.8	2599.0
403	40.4	49.8	3.3	115.7	10.2	103.9	258.2	160.0	60.6	6.6	2.6	4.8	265.0
458	43.1	94.7	3.0	258.6	16.6	137.5	298.6	168.3	140.5	14.1	8.7	12.0	1010.0
480	58.0	105.0	5.5	270.4	20.2	139.2	299.8	164.2	148.7	16.3	22.4	29.8	2096.0
507	56.7	120.2	5.0	278.3	20.2	119.4	272.7	158.1	164.7	20.4	26.2	16.8	1531.0
525	45.0	113.2	3.0	271.4	17.0	125.6	311.3	190.6	185.2	18.7	24.4	24.2	1896.0
663	55.3	114.8	4.1	300.9	19.7	168.0	311.2	144.6	192.4	16.4	30.3	18.5	1134.0
710	53.7	101.2	7.2	279.9	18.7	151.7	262.6	112.8	164.9	14.6	24.0	24.0	1388.0
717	64.3	131.2	3.2	303.9	19.7	130.8	227.4	99.7	238.7	22.0	32.8	29.8	2404.0
719	42.1	86.8	4.2	195.8	15.3	117.3	347.8	236.7	121.9	18.1	8.9	15.9	1234.0
735	53.7	94.0	1.2	285.5	23.2	134.2	304.6	174.4	144.8	17.1	30.6	11.0	817.0
745	49.4	104.4	3.9	280.9	24.6	164.8	314.0	151.0	154.6	16.7	22.1	32.1	2517.0
746	52.7	101.5	2.1	300.9	22.2	153.5	294.8	137.2	158.5	15.9	20.6	16.5	1092.0
748	95.5	132.8	6.5	361.3	31.5	160.6	329.4	184.4	265.5	28.6	45.6	20.8	659.0
751	102.8	127.8	4.6	425.0	26.2	178.7	316.9	138.8	256.7	24.1	37.7	20.9	1231.0
758	50.4	102.2	4.1	297.0	24.1	144.9	378.4	237.9	192.4	17.8	25.8	14.4	1039.0
769	91.5	153.2	5.3	386.1	29.7	181.4	325.9	136.6	242.8	27.5	47.1	23.7	1680.0
771	60.6	106.7	5.6	288.8	17.3	140.7	268.6	145.2	149.3	19.5	19.4	40.9	2770.0
783	47.4	107.0	3.7	267.4	16.1	157.0	328.2	173.8	157.2	20.0	38.4	29.0	2031.0
785	49.0	108.7	5.4	283.2	21.6	154.1	381.9	231.5	209.0	17.9	31.0	12.3	826.0
792	49.7	93.8	3.4	277.9	21.6	124.4	314.7	195.3	191.0	16.7	17.9	24.9	1791.0
795	64.3	104.0	5.4	239.2	16.8	142.5	300.1	161.0	126.8	14.2	16.8	22.3	1675.0
796	60.6	98.1	6.1	302.9	19.4	165.6	311.8	167.1	180.3	22.2	31.0	22.2	1884.0
813	45.0	86.6	3.9	230.0	16.4	128.6	273.9	149.4	135.6	14.1	10.7	14.3	1068.0
827	37.4	60.6	3.9	89.2	15.2	95.6	358.2	270.7	31.5	9.6	2.6	3.0	259.0
828	47.0	77.4	3.2	232.6	23.7	110.6	240.6	135.0	149.0	22.1	23.2	19.6	1006.0
838	56.0	104.8	4.4	283.2	19.1	136.9	306.8	173.8	154.6	18.3	12.7	21.1	2011.0
840	63.3	110.4	4.6	289.1	16.0	148.7	323.5	178.0	144.8	10.9	20.9	21.7	1732.0
842	64.6	115.6	5.0	257.9	20.2	135.1	301.1	146.2	174.8	21.5	41.2	10.9	756.0
846	54.3	119.0	4.8	245.4	18.8	158.1	292.4	134.7	164.7	15.6	26.0	32.2	2413.0

Appendix 2. Cont..

ISe	DF[1]	PLHT	BT	FLBL	FLBW	FLSL	PEDL	PEX	INFL	INFW	W5P	SPY	PY
869	60.6	130.0	5.6	301.6	19.3	157.0	316.2	161.6	211.0	16.7	29.8	14.8	1067.0
900	54.3	110.4	2.3	298.9	24.5	133.6	287.1	157.3	185.5	20.7	30.0	21.6	1582.0
907	54.3	125.4	4.8	255.6	19.3	155.9	333.3	180.2	159.4	18.1	22.4	16.6	1295.0
909	49.7	108.6	5.2	243.8	15.7	132.7	270.8	141.7	139.2	17.1	26.3	23.7	1610.0
914	58.0	116.5	7.0	289.8	17.8	134.2	257.9	139.8	172.5	11.3	19.9	29.9	1887.0
931	61.3	110.8	5.5	237.9	14.4	119.1	255.6	141.1	151.3	14.3	19.4	28.2	2108.0
936	50.4	98.7	3.9	216.2	19.0	136.0	303.0	167.7	130.1	13.6	22.7	28.6	2323.0
946	50.0	119.5	4.5	308.8	19.6	139.5	326.8	201.4	160.1	18.4	19.6	25.4	1941.0
956	59.3	128.3	4.2	277.3	19.7	150.9	369.6	222.5	166.3	15.0	30.1	52.7	2898.0
963	63.6	122.6	5.0	281.2	20.7	158.8	369.6	213.9	164.3	16.2	25.7	35.7	2683.0
969	58.0	109.3	3.9	264.1	17.0	150.2	326.3	179.2	142.2	11.8	26.8	25.7	2078.0
983	64.6	144.0	3.0	333.8	25.2	185.5	342.4	157.4	220.4	25.9	34.2	18.8	1267.0
985	59.0	124.0	4.0	277.9	17.3	160.9	333.9	175.4	182.6	16.9	21.6	29.4	2041.0
995	50.7	108.1	3.7	300.6	20.5	164.8	318.4	155.5	186.8	17.6	18.3	34.4	2444.0
999	58.0	132.4	5.3	261.5	19.2	162.4	284.7	123.8	184.2	16.8	17.4	21.9	1616.0
1000	61.6	116.6	4.7	282.2	18.0	159.1	320.3	126.6	141.8	13.5	23.7	44.7	3056.0
1009	47.7	61.7	6.3	152.2	9.2	101.0	219.7	124.1	64.9	10.7	6.2	10.9	865.0
1026	47.4	62.6	3.3	235.9	14.4	92.4	227.6	141.4	88.0	10.9	9.4	17.7	1379.0
1037	41.7	80.4	5.7	171.5	11.7	112.5	321.5	159.9	118.2	12.9	7.1	21.1	1680.0
1059	67.9	142.5	3.5	326.5	27.9	145.2	329.7	207.3	246.7	26.0	44.3	39.5	2451.0
1067	48.7	48.5	3.2	128.2	20.8	126.5	325.1	125.7	107.9	16.4	23.7	4.8	371.0
1118	49.0	46.7	5.4	106.5	10.1	84.5	217.7	139.8	47.4	9.0	5.9	7.2	383.0
1119	41.7	43.3	3.8	82.9	14.7	97.7	248.1	156.5	54.7	11.0	3.3	14.1	710.0
1129	42.1	44.2	7.2	93.4	8.7	76.0	227.6	159.0	37.4	9.0	3.4	6.8	586.0
1134	52.7	83.8	5.7	259.2	15.9	132.1	356.3	229.3	211.0	10.2	19.4	11.5	754.0
1136	44.4	82.2	5.8	236.2	16.6	116.7	299.5	188.2	125.5	11.9	12.3	17.1	1228.0
1137	59.6	90.6	4.3	196.2	22.0	109.9	299.3	222.6	147.4	18.5	24.9	25.5	1842.0
1151	39.1	43.5	3.4	64.4	15.6	64.8	160.3	122.5	32.1	9.5	21.6	3.4	287.0
1161	39.4	60.5	3.5	107.3	12.1	172.4	188.3	143.3	34.0	10.6	3.0	4.2	304.0
1162	54.3	102.4	8.8	257.9	16.1	138.9	315.9	169.7	120.8	11.7	15.3	33.7	2325.0
1163	55.0	69.9	6.6	259.5	17.3	112.2	252.2	148.1	105.0	10.2	15.6	14.0	927.0
1177	51.3	84.7	4.7	269.4	17.8	114.6	256.3	146.5	116.7	10.7	11.2	16.1	1250.0
1181	38.4	64.5	2.3	140.7	17.9	105.4	285.3	186.0	72.0	10.5	9.4	5.7	335.0
1187	46.7	78.0	2.7	194.9	18.9	148.4	378.4	234.1	102.4	12.1	9.4	6.6	460.0
1201	31.1	28.1	2.7	66.1	7.8	55.0	206.7	155.5	47.2	9.1	7.7	5.5	475.0
1204	39.7	65.3	1.2	166.9	18.4	119.4	297.6	183.4	67.1	16.4	30.3	16.7	996.0
1209	46.7	48.6	2.6	105.4	14.7	92.5	242.9	157.8	35.7	12.0	9.2	12.8	832.0
1227	51.7	86.8	4.8	270.4	18.2	158.2	344.3	192.1	156.2	11.2	16.3	12.6	736.0
1234	38.7	40.5	4.0	133.4	10.7	99.5	210.5	116.4	44.3	10.3	7.3	10.4	765.0
1251	47.7	105.5	2.5	298.9	28.2	163.9	351.9	190.5	192.7	24.0	67.2	41.5	1262.0
1254	39.7	56.1	1.2	79.9	12.1	79.9	249.0	202.3	28.0	10.2	2.3	4.3	541.0
1258	37.4	69.9	1.3	187.3	23.0	108.7	311.2	208.8	133.0	13.3	21.8	8.3	586.0
1269	58.3	116.6	5.1	285.2	19.2	158.8	323.2	166.7	175.4	13.1	25.0	42.9	2897.0
1286	39.1	47.5	6.8	83.5	11.9	73.9	250.2	184.4	46.9	10.6	8.2	6.2	517.0
1299	46.0	70.8	5.7	145.3	10.3	99.0	251.9	159.0	69.0	11.0	9.9	13.9	953.0
1302	47.7	71.2	5.4	197.5	15.9	103.6	329.5	232.8	85.1	10.3	11.2	9.6	478.0
1305	44.7	55.0	7.7	70.1	6.8	87.3	291.3	212.3	31.3	9.3	10.7	11.8	884.0
1312	36.1	43.2	3.0	98.4	8.4	81.5	221.7	147.2	36.1	8.0	3.1	3.7	172.0
1320	35.8	49.3	2.7	140.3	12.3	105.4	251.4	149.9	59.0	10.4	6.7	12.0	901.0
1332	48.4	58.0	4.7	114.7	13.0	127.7	295.1	171.9	78.2	9.1	5.4	21.0	1672.0
1335	38.7	33.8	2.7	79.3	8.2	69.3	200.5	138.8	26.0	7.7	17.8	5.5	502.0
1338	43.4	39.2	1.5	114.4	18.9	52.0	178.6	142.7	57.3	19.2	4.9	7.0	362.0
1354	56.7	121.8	5.0	277.3	20.2	141.6	320.6	182.8	178.7	18.6	24.9	36.2	2647.0
1387	80.9	162.0	5.3	440.1	30.9	176.9	360.7	185.3	262.9	27.6	28.0	11.2	830.0
1400	57.0	128.2	5.0	276.0	18.8	142.8	280.6	140.8	163.0	15.1	25.4	21.8	1525.0
1402	47.0	113.6	5.1	263.5	19.8	151.1	339.9	192.1	168.6	19.9	23.5	22.9	1402.0
1406	46.0	138.4	3.7	276.0	15.5	125.6	204.2	122.8	44.6	17.8	47.8	56.8	2867.0

Appendix 2. Cont..

ISe	DF[1]	PLHT	BT	FLBL	FLBW	FLSL	PEDL	PEX	INFL	INFW	W5P	SPY	PY
1408	48.0	90.1	8.3	259.2	16.1	138.3	297.3	162.6	132.4	13.3	15.0	37.7	2942.0
1419	86.9	138.4	4.3	390.6	19.4	132.4	245.6	116.4	261.5	30.5	48.4	5.7	580.0
1454	64.0	118.4	2.1	300.3	23.1	179.6	374.6	196.6	245.6	21.4	70.6	17.7	1320.0
1458	53.0	105.6	3.2	232.0	19.7	133.3	292.9	168.3	156.5	14.9	43.5	20.1	1341.0
1460	53.3	109.1	4.0	303.5	22.4	180.5	393.5	208.8	198.9	18.0	43.8	19.0	1501.0
1474	63.6	149.5	4.5	320.6	21.3	121.1	225.7	135.3	264.3	21.9	55.2	48.9	2823.0
1511	64.0	147.7	3.7	335.4	19.7	150.2	296.0	140.8	217.8	23.3	52.0	37.4	2541.0
1547	48.0	91.7	1.4	219.5	23.0	129.4	423.2	300.2	100.1	15.1	22.9	23.7	1689.0
1563	36.1	65.0	1.4	109.5	11.0	99.8	341.5	249.2	52.9	10.7	4.1	6.4	530.0
1575	60.6	77.4	1.1	247.7	29.1	108.7	314.0	211.6	134.5	21.5	21.9	16.9	566.0
1581	44.0	74.9	1.7	218.5	22.1	129.7	328.9	203.9	84.6	16.9	37.4	17.8	1271.0
1593	52.7	76.1	1.2	258.9	30.6	130.9	336.9	210.8	137.7	21.7	49.9	18.9	1276.0
1597	79.9	119.2	3.9	393.2	24.4	112.2	247.1	139.8	240.7	23.6	66.4	47.3	2723.0
1605	54.3	118.7	3.8	266.8	20.9	130.5	284.2	157.8	187.5	19.8	41.3	26.4	2137.0
1610	60.6	105.0	2.7	261.5	21.7	127.7	317.8	195.0	142.3	20.4	27.0	23.0	1376.0
1629	49.0	87.0	5.9	263.8	15.9	108.8	222.0	118.0	139.9	14.4	11.2	31.9	2180.0
1638	38.7	70.2	1.2	180.2	15.3	112.2	325.7	219.7	89.0	13.8	8.2	5.2	439.0
1647	39.7	68.8	1.1	186.6	15.9	119.1	295.7	181.8	87.7	15.4	28.6	4.6	392.0
1655	36.4	95.6	4.3	236.6	18.7	151.7	335.8	187.3	152.3	25.0	17.9	13.8	808.0
1664	58.3	129.1	5.9	287.1	21.3	148.7	343.4	198.2	175.8	17.3	18.8	18.7	1108.0
1666	54.7	116.1	3.0	334.4	22.5	122.3	297.9	180.5	197.9	25.9	65.9	29.9	2436.0
1674	48.7	93.3	2.8	285.8	24.8	110.8	258.2	153.3	131.1	17.8	32.6	34.1	2574.0
1685	88.9	120.0	2.6	303.5	27.2	115.2	212.1	101.0	281.8	31.5	49.4	46.3	2820.0
1687	72.9	128.9	5.4	342.6	25.3	159.7	262.0	101.9	239.0	28.1	49.1	51.5	2786.0
1704	50.0	98.9	4.7	237.9	15.7	143.4	280.6	140.1	174.5	16.5	9.9	35.0	2493.0
1725	53.3	143.1	2.7	323.2	23.8	119.1	285.6	161.6	258.3	24.1	38.2	37.6	2837.0
1736	76.9	143.0	5.4	308.8	23.6	181.1	334.5	154.2	230.9	22.9	52.4	37.0	2827.0
1745	60.3	119.2	2.4	281.2	25.6	167.1	328.9	163.5	192.1	20.5	39.5	29.7	2416.0
1762	56.0	118.6	3.9	283.5	20.5	149.6	307.1	161.0	156.8	14.6	17.8	45.6	3013.0
1767	50.7	114.3	5.0	319.3	16.1	135.1	324.6	193.8	184.9	15.8	31.3	39.0	2625.0
1773	55.0	106.1	3.1	311.1	20.4	143.4	327.8	188.2	189.8	22.1	46.4	34.2	2366.0
1780	54.0	132.1	4.5	253.6	21.6	129.6	313.6	188.5	203.8	23.9	24.4	35.0	2749.0
1789	39.7	51.9	1.4	134.0	11.9	86.3	213.0	131.6	43.3	10.6	23.4	4.9	516.0
1805	53.7	107.8	3.5	236.7	19.0	141.9	298.6	160.0	154.6	18.5	28.8	38.8	2821.0
1806	53.7	102.7	5.1	274.6	18.2	132.1	289.4	161.3	151.0	18.9	21.2	31.1	2534.0
1808	53.3	111.0	3.9	263.5	18.8	150.8	283.1	131.4	155.5	16.8	29.0	29.4	2175.0
1820	56.3	109.8	4.8	243.5	18.6	144.3	318.1	177.3	146.1	17.5	19.8	35.1	2663.0
1846	52.0	122.1	6.7	258.2	14.8	117.9	238.3	124.7	145.7	15.6	29.1	43.3	2815.0
1851	49.7	114.1	3.9	290.4	21.1	135.7	302.7	170.9	177.1	17.9	20.1	19.2	1516.0
1858	49.0	126.7	5.7	270.4	20.0	176.0	332.2	157.3	189.1	20.4	41.5	22.6	1812.0
1859	50.4	128.2	4.9	295.0	22.2	142.5	310.2	171.2	184.2	16.9	23.5	30.8	2562.0
1881	60.0	137.6	7.9	305.2	19.8	165.9	339.0	178.0	223.7	21.8	40.5	59.0	3068.0
1888	48.4	103.9	4.6	279.9	19.8	175.4	312.8	138.2	185.5	19.2	21.2	50.8	3290.0
1892	67.6	127.8	4.9	288.1	17.1	137.8	303.6	167.4	160.1	15.7	19.1	20.0	1693.0
1900	60.3	125.7	4.4	293.7	20.4	149.3	317.8	171.5	169.9	19.0	23.0	27.5	2009.0
Control cultivars													
1468	63.6	103.1	4.3	281.5	21.2	121.7	313.0	196.5	131.7	22.9	45.1	34.3	2596.0
1541	77.6	125.1	3.9	350.8	21.3	121.4	207.7	96.2	221.8	33.4	63.4	48.8	2768.0
375	53.0	108.1	1.9	293.7	24.3	116.8	247.9	135.6	113.8	30.7	78.4	38.3	2826.0
376	62.6	111.1	1.6	311.1	30.2	123.2	226.6	107.1	131.4	30.2	77.2	38.1	2703.0

1= DF = Days to 50 per cent flowering, PLHT = Plant height (cm), BT = Basal tiller number, FLBL = Flag leaf blade length (mm), FLBW = Flag leaf blade width (mm), FLSL = Flag leaf sheath length (mm), PEDL = Peduncle length (mm), PEX = Panicle exertion (mm), INFL = Inflorescence length (mm), INFW = Inflorescence width (mm), W5P = Weight of five panicles (g), SPY = Single plant yield (g), PY = Grain yield per plot (Kg ha-1)

Appendix 3. Mean performance 155 accessions in foxtail millet core collection for 13 quantitative traits at Madurai (E2) during 2009/10 *Rabi*/*Summer*

ISe	DF[1]	PLHT	BT	FLBL	FLBW	FLSL	PEDL	PEX	INFL	INFW	W5P	SPY	PY
2	45.0	114.2	2.9	296.3	16.2	152.4	384.7	236.4	141.5	18.3	31.6	21.7	1418.0
18	44.4	102.7	3.3	252.8	15.4	116.1	371.3	259.0	104.5	24.8	36.2	19.0	1219.0
31	59.3	111.5	2.5	246.5	18.2	127.8	339.0	238.0	107.8	16.4	33.6	13.5	842.0
49	49.0	123.8	3.3	268.9	18.8	140.1	326.2	189.7	147.5	22.8	22.0	13.3	829.0
90	51.0	101.3	4.0	289.4	20.3	152.0	279.0	130.1	159.4	16.6	9.6	11.1	678.0
96	58.3	110.8	1.9	276.2	20.4	150.4	336.5	189.7	174.6	17.5	32.1	24.2	1578.0
132	50.0	114.6	4.8	282.4	15.7	125.5	326.6	204.5	158.4	17.6	41.5	13.3	674.0
144	49.7	117.9	2.9	291.0	19.4	140.7	364.2	227.4	172.9	20.0	24.2	21.6	1396.0
156	54.0	119.1	4.0	305.2	19.3	167.3	369.0	199.4	180.8	14.1	20.0	18.7	1199.0
160	49.7	104.8	3.8	244.2	17.0	151.9	316.5	168.1	179.5	15.7	32.4	17.1	1090.0
179	46.7	104.3	4.4	281.5	15.2	149.8	350.2	204.2	117.8	12.4	11.3	14.6	923.0
195	50.3	98.8	2.6	273.5	19.2	157.5	317.0	163.0	146.5	11.7	19.7	21.4	1384.0
200	45.0	103.5	3.4	240.6	18.3	132.0	332.9	204.5	104.8	15.5	14.7	18.8	1207.0
237	52.0	98.6	4.4	225.4	14.9	143.0	329.4	190.0	91.3	11.3	11.1	15.8	1003.0
238	60.6	116.7	2.7	236.9	16.3	143.0	331.7	192.3	118.7	16.3	22.5	37.4	2258.0
254	48.0	109.8	3.8	222.1	14.6	122.0	330.1	211.6	110.4	14.9	29.3	27.2	1670.0
267	59.0	105.3	4.2	261.7	17.2	155.0	350.2	199.1	85.3	18.9	31.9	17.7	1635.0
289	53.0	97.8	4.4	251.1	13.9	99.6	282.2	185.5	112.7	17.0	26.1	8.6	508.0
302	49.3	98.8	5.1	237.3	16.5	129.1	303.2	176.8	111.1	20.2	41.8	28.2	1846.0
362	57.0	107.3	4.0	286.1	17.6	154.6	336.1	185.2	165.0	13.8	15.1	26.9	1759.0
364	62.6	100.0	3.5	218.1	16.0	123.6	326.2	209.0	120.3	13.6	32.6	46.4	2437.0
375	57.7	86.8	1.6	167.7	16.7	109.0	307.1	201.3	75.4	24.1	56.7	22.8	1478.0
388	60.0	113.9	4.7	235.3	19.5	166.3	369.3	207.1	125.3	15.7	30.6	36.6	2204.0
398	55.3	111.6	1.8	243.2	15.5	124.9	348.6	227.4	116.7	20.2	18.7	34.1	2145.0
403	39.0	54.4	4.1	107.7	12.4	108.4	250.2	157.5	59.2	11.0	2.9	3.8	226.0
458	41.0	64.6	4.9	223.4	13.6	73.6	239.4	168.3	71.7	15.0	4.5	9.6	582.0
480	54.0	110.8	4.2	249.8	16.2	161.8	300.1	141.7	137.2	15.5	19.7	20.6	1329.0
507	54.3	94.7	4.0	240.6	16.3	123.9	331.3	211.0	125.3	17.5	22.0	16.4	1043.0
525	44.4	113.6	2.5	285.7	22.1	132.3	342.8	214.2	151.1	18.7	24.0	18.3	1170.0
663	54.7	118.3	5.4	230.3	14.9	145.3	299.7	157.8	125.3	16.8	19.0	9.9	602.0
710	53.7	104.3	4.8	244.8	15.7	156.6	300.4	147.2	127.3	14.9	22.0	18.9	1210.0
717	63.0	131.3	3.7	294.0	19.2	174.0	304.2	106.6	175.9	18.2	27.6	24.1	1587.0
719	43.0	110.0	4.7	232.6	15.0	121.6	330.7	212.6	126.6	16.7	4.8	8.6	508.0
735	50.0	93.3	1.5	241.2	17.1	139.4	274.5	138.2	136.5	16.3	28.9	11.3	712.0
745	50.7	96.4	1.5	211.9	17.8	129.4	312.5	178.1	158.7	15.8	16.6	28.2	1846.0
746	53.7	70.7	1.3	233.3	19.6	128.1	267.2	142.1	111.7	15.6	28.3	29.7	1853.0
748	97.9	119.3	5.4	379.4	22.2	149.5	265.9	119.5	250.6	15.2	41.8	28.2	1323.0
751	102.9	122.7	2.8	436.8	23.9	148.5	293.7	148.5	218.2	20.7	32.6	15.6	930.0
758	50.3	102.1	2.5	273.2	15.4	142.7	370.9	246.4	131.3	19.4	22.5	4.2	207.0
769	92.6	124.9	4.2	345.1	26.3	159.8	293.7	137.2	187.5	19.3	61.3	16.8	1298.0
771	58.3	102.9	4.4	235.4	13.4	138.5	239.1	103.4	126.0	20.7	18.0	18.4	1190.0
783	46.7	105.5	2.8	239.2	14.9	161.1	345.7	188.4	107.8	19.6	33.2	23.3	1511.0
785	50.0	101.4	3.5	250.5	15.1	140.1	330.7	194.2	120.7	16.6	25.6	17.7	529.0
792	48.4	80.5	1.3	223.4	16.3	115.5	357.8	246.1	129.9	16.3	12.4	21.1	1345.0
795	62.0	102.9	4.0	242.2	15.5	133.6	336.1	206.2	128.6	13.4	16.1	18.4	1177.0
796	59.7	119.2	2.7	257.4	16.9	142.0	283.4	144.6	154.4	15.6	27.3	18.4	1177.0
813	43.4	72.4	2.7	136.3	11.1	100.3	252.8	155.3	78.4	14.5	11.4	8.8	521.0
827	39.7	55.7	2.9	96.8	14.9	95.1	331.0	242.9	47.3	14.3	3.5	8.2	545.0
828	43.0	74.5	2.5	239.6	16.1	118.7	306.1	190.7	143.5	20.3	19.0	11.8	729.0
838	52.3	97.2	3.9	241.6	13.9	137.8	296.2	161.7	137.2	17.2	11.6	21.4	1342.0
840	62.0	88.9	3.8	254.4	15.8	144.9	320.2	178.8	120.0	11.0	15.1	17.6	1123.0
842	62.0	99.2	3.1	190.1	14.4	102.5	258.2	158.5	73.7	18.8	39.2	10.4	524.0
846	51.0	87.6	3.9	223.7	14.3	149.1	275.1	129.2	117.4	16.1	17.7	26.1	1705.0
869	59.7	112.9	3.6	264.6	14.9	157.9	369.3	215.5	132.2	16.5	30.4	8.6	580.0

Appendix 3. Cont..

ISe	DF[1]	PLHT	BT	FLBL	FLBW	FLSL	PEDL	PEX	INFL	INFW	W5P	SPY	PY
900	52.0	112.1	2.7	272.9	21.5	144.6	306.8	165.6	142.8	20.2	21.0	19.4	1250.0
907	53.3	98.0	2.9	236.6	15.6	117.8	292.4	177.8	112.7	15.8	19.7	12.2	755.0
909	48.0	105.2	3.5	237.6	15.3	150.4	348.6	202.0	126.6	16.5	22.7	21.0	1464.0
914	56.0	114.9	4.4	301.9	17.2	168.0	367.7	203.8	149.8	12.9	12.4	23.3	1403.0
931	56.7	100.9	4.1	235.3	13.4	138.8	279.9	144.3	134.9	14.7	16.9	23.3	1511.0
936	49.3	96.2	1.7	195.4	13.0	132.3	304.2	175.2	106.8	10.8	21.0	23.3	1511.0
946	47.7	127.1	4.6	268.9	19.3	161.4	370.9	213.6	133.9	22.4	15.1	22.2	1438.0
956	55.0	117.5	3.9	286.7	16.1	145.6	332.3	190.4	149.4	13.1	31.4	44.7	2597.0
963	60.3	115.1	4.1	265.0	17.8	141.7	326.6	188.4	139.2	16.7	18.7	34.9	2307.0
969	53.7	81.2	3.0	223.4	14.9	126.5	330.7	207.8	70.1	11.3	20.0	19.6	1368.0
983	63.3	108.3	1.1	261.7	18.7	154.3	314.7	164.0	152.4	20.2	29.6	14.4	909.0
985	52.3	92.5	4.5	241.2	14.6	135.5	328.5	196.5	122.3	17.5	17.1	24.7	1607.0
995	49.7	82.3	2.8	236.6	13.2	146.5	285.4	142.1	115.7	21.9	11.4	23.2	1641.0
999	53.3	137.0	5.3	285.1	17.8	148.2	323.4	178.8	154.7	18.7	13.1	23.9	1551.0
1000	58.3	115.0	5.7	279.1	17.6	156.1	327.2	174.7	138.9	14.4	22.3	27.8	1602.0
1009	43.4	68.4	6.2	197.4	14.6	126.5	321.1	198.1	57.2	10.8	2.9	6.8	422.0
1026	45.4	62.7	3.7	234.0	14.1	102.2	250.9	151.4	78.4	11.2	3.9	11.9	735.0
1037	43.4	68.8	4.1	165.4	14.6	87.0	275.5	191.3	69.1	12.8	4.5	14.6	923.0
1059	70.3	127.5	4.0	259.4	17.8	147.8	356.9	244.5	151.1	18.1	31.9	40.1	2662.0
1067	45.0	53.5	1.3	115.2	17.6	103.6	218.4	119.8	103.5	15.9	22.3	5.9	500.0
1118	44.4	49.2	3.2	89.8	11.8	73.8	228.5	157.2	47.0	10.3	3.9	3.1	172.0
1119	40.7	64.1	2.5	239.6	17.5	131.0	347.0	219.7	99.5	11.7	3.5	10.9	669.0
1129	39.4	52.1	5.6	143.9	10.7	94.8	240.7	148.5	60.5	11.5	2.5	3.8	150.0
1134	52.3	69.3	5.4	253.1	14.5	100.9	353.7	259.6	70.4	10.1	17.1	7.4	431.0
1136	45.4	70.4	3.4	204.3	11.5	106.5	249.6	145.9	67.1	10.1	10.8	9.1	541.0
1137	59.0	82.1	1.6	160.8	17.9	118.4	333.6	218.7	103.8	19.7	24.2	19.6	1371.0
1151	40.7	40.4	1.8	69.1	14.5	110.0	229.2	117.6	44.3	9.6	20.5	32.4	170.0
1161	41.4	70.2	2.7	184.5	13.8	113.5	273.9	245.1	50.6	12.8	4.5	4.4	506.0
1162	54.3	87.6	4.7	175.3	14.9	121.0	361.7	244.5	87.9	11.8	9.8	21.0	1727.0
1163	53.7	87.0	3.8	234.6	16.0	122.6	264.6	145.0	59.8	11.6	13.4	3.8	185.0
1177	49.3	73.4	3.3	287.1	14.9	101.9	231.7	132.4	123.0	11.5	7.8	12.4	769.0
1181	36.4	92.7	4.0	171.2	16.0	114.5	296.9	185.5	108.1	11.7	4.8	4.7	200.0
1187	44.4	74.0	2.1	178.6	16.7	134.6	352.7	221.9	85.0	12.7	7.8	7.5	373.0
1201	31.1	84.8	1.8	73.7	14.2	65.3	210.3	152.0	106.8	11.6	6.8	4.4	327.0
1204	40.7	66.7	1.9	142.3	15.2	101.9	267.2	161.4	68.1	15.1	22.3	6.1	374.0
1209	43.4	57.8	2.6	147.2	12.6	122.0	283.1	184.6	63.2	12.4	3.5	4.7	251.0
1227	50.0	56.5	3.7	236.3	15.2	111.9	272.9	164.0	125.3	18.3	9.5	11.1	682.0
1234	35.7	39.7	3.5	125.5	10.9	104.2	213.5	112.7	50.3	12.3	3.9	6.9	391.0
1251	47.7	116.5	1.1	235.3	19.9	172.4	355.0	186.5	134.6	19.7	58.0	35.0	1971.0
1254	41.4	55.5	1.1	82.3	11.7	78.6	293.7	192.9	40.0	10.5	2.5	3.8	181.0
1258	38.0	64.5	1.6	196.4	15.9	115.5	326.6	214.5	75.4	11.0	23.0	5.6	307.0
1269	58.0	106.9	6.1	228.0	15.5	153.0	321.1	171.7	145.8	14.2	21.4	19.0	1199.0
1286	39.4	66.6	3.8	129.4	11.7	98.3	295.6	194.9	53.2	11.3	3.9	3.4	164.0
1299	44.4	54.6	4.8	139.6	10.9	97.0	256.6	162.3	41.0	11.9	9.3	10.6	648.0
1302	45.4	61.4	4.6	214.5	14.7	104.8	264.9	163.0	81.0	11.4	5.8	5.0	282.0
1305	44.4	59.5	4.3	165.4	9.5	127.8	380.5	256.7	43.6	10.0	4.8	8.4	495.0
1312	35.4	54.3	3.6	104.7	12.3	127.8	277.1	152.4	69.8	9.6	3.5	4.4	189.0
1320	38.4	57.9	2.5	111.3	12.5	98.3	266.2	170.7	56.5	10.7	3.9	5.0	294.0
1332	44.0	65.4	3.8	120.5	14.1	96.1	293.3	195.5	83.3	10.6	7.8	15.4	1426.0
1335	38.0	35.6	3.0	115.9	16.3	114.2	280.9	169.8	38.0	9.9	15.7	4.0	206.0
1338	41.4	36.5	1.7	114.6	16.8	48.5	196.9	144.0	57.5	18.0	3.2	4.1	200.0
1354	56.0	100.3	3.3	244.5	16.7	143.3	338.4	198.7	135.6	15.0	17.1	30.6	1904.0
1387	83.3	118.9	4.3	391.3	22.2	174.0	351.1	181.0	179.9	19.9	28.9	6.5	364.0
1400	55.0	103.8	4.0	253.1	17.1	126.5	306.4	183.3	143.5	16.0	24.0	18.4	1177.0
1402	44.4	112.6	2.8	233.3	14.9	127.5	309.9	180.1	122.0	15.6	17.2	20.0	1291.0
1406	42.7	119.1	4.6	211.5	15.5	172.4	203.9	229.7	145.5	18.8	46.8	37.1	2128.0
1408	45.4	89.3	5.2	223.4	16.2	121.0	305.8	188.1	82.0	16.2	9.6	33.4	1871.0
1419	94.2	117.3	3.0	326.6	21.6	136.8	273.2	139.5	186.8	23.2	44.6	11.8	892.0

Appendix 3. Cont..

ISe	DF[1]	PLHT	BT	FLBL	FLBW	FLSL	PEDL	PEX	INFL	INFW	W5P	SPY	PY
1454	64.0	108.0	1.2	244.2	17.8	181.2	328.5	151.1	174.9	18.8	53.7	15.7	1104.0
1458	52.7	102.8	4.0	240.6	16.3	119.0	291.1	165.9	107.5	14.8	40.5	21.8	1411.0
1460	52.0	111.5	3.6	190.6	15.2	137.5	324.3	224.2	167.3	17.7	44.8	28.2	1846.0
1474	63.3	128.0	2.4	282.8	19.6	136.5	314.4	178.1	228.4	19.4	51.7	50.9	2527.0
1511	62.3	105.3	4.5	286.4	17.9	155.0	293.7	142.1	185.1	18.5	49.4	33.1	2072.0
1547	49.0	83.5	1.3	183.2	16.0	126.8	375.1	252.2	154.7	13.5	19.2	13.5	842.0
1563	35.1	64.0	1.7	141.3	15.4	106.1	314.2	211.4	79.4	10.1	3.5	4.7	240.0
1575	59.3	91.5	1.2	230.7	20.7	159.2	329.1	173.6	151.1	15.4	13.4	11.2	398.0
1581	45.0	76.0	1.5	221.4	19.1	126.5	318.6	195.5	87.6	20.0	25.3	11.7	724.0
1593	49.7	87.1	1.1	200.3	22.9	127.1	297.2	173.3	119.0	18.3	38.2	9.4	561.0
1597	82.3	114.9	1.9	399.8	27.9	112.6	345.4	214.5	243.3	20.2	58.0	42.9	2414.0
1605	54.0	120.7	3.4	265.0	17.8	144.9	327.5	186.2	174.6	19.0	32.6	20.3	1311.0
1610	61.6	103.3	2.9	233.3	18.3	133.9	344.8	214.5	98.5	24.7	18.4	19.1	1337.0
1629	50.3	88.9	4.2	233.6	16.5	137.5	278.0	120.8	156.0	15.1	5.5	23.7	1755.0
1638	39.0	64.7	1.1	173.0	14.4	119.0	327.8	212.3	94.6	13.6	5.2	7.4	277.0
1647	39.7	64.1	1.1	163.4	15.7	118.1	277.7	162.7	74.4	15.1	27.0	7.0	307.0
1655	37.4	115.9	3.7	253.4	15.7	160.1	416.0	246.7	157.4	19.9	14.7	9.2	548.0
1664	59.0	104.4	5.2	226.7	16.0	122.3	320.5	201.6	128.6	13.0	20.4	8.7	515.0
1666	53.3	104.6	3.7	259.7	16.4	129.7	369.7	243.8	159.0	18.3	72.9	23.5	1519.0
1674	46.4	102.4	4.0	262.3	16.2	108.4	259.2	153.6	114.1	16.7	25.3	27.4	1792.0
1685	90.6	107.1	2.8	289.4	19.9	114.5	211.9	100.2	216.9	22.5	35.9	43.9	2379.0
1687	70.6	116.5	3.1	280.8	20.8	143.0	252.5	97.6	167.3	18.2	44.8	46.7	2540.0
1704	50.3	81.5	3.9	208.2	14.9	138.5	276.1	140.8	95.2	12.9	6.5	29.7	1731.0
1725	51.0	106.4	1.2	222.1	15.3	144.9	309.6	168.1	163.0	19.6	32.1	28.2	1846.0
1736	79.3	121.4	2.8	271.2	20.5	168.9	346.7	181.7	194.7	19.9	49.8	33.8	2227.0
1745	60.0	116.4	2.9	259.0	18.1	155.6	340.6	188.8	137.2	16.2	33.2	25.6	1671.0
1762	57.7	107.2	3.2	270.2	15.9	128.8	292.7	167.2	143.2	12.8	16.1	23.3	1228.0
1767	51.3	113.4	4.3	280.1	18.5	141.4	389.5	252.2	154.4	15.4	24.2	35.1	2210.0
1773	49.7	99.1	4.0	249.1	17.4	126.8	327.8	204.5	85.6	19.4	36.9	32.6	2147.0
1780	52.0	101.9	2.8	259.0	20.2	153.7	372.9	223.2	144.8	19.4	19.0	34.3	2267.0
1789	42.0	78.3	2.9	123.8	17.5	116.1	228.5	115.0	97.9	19.7	22.0	16.4	1049.0
1805	49.7	106.3	5.0	254.1	15.3	149.8	306.8	160.4	135.6	17.7	32.9	33.1	2180.0
1806	53.3	81.6	3.1	264.3	15.0	137.2	310.6	176.8	130.3	16.3	18.0	25.9	1692.0
1808	54.0	107.9	3.8	258.4	17.0	158.5	345.1	190.4	139.5	19.9	23.5	29.8	1960.0
1820	54.7	96.7	4.7	238.3	16.0	145.9	333.9	191.7	130.9	13.6	15.6	28.2	1846.0
1846	50.7	101.0	3.9	235.3	14.7	140.7	301.3	140.4	140.5	14.4	28.9	41.9	2347.0
1851	51.0	121.1	3.7	302.6	17.8	160.5	337.7	181.0	170.9	18.5	19.4	16.0	1016.0
1858	48.7	76.5	2.5	201.0	16.2	128.4	307.7	182.6	93.6	16.8	31.3	19.3	1244.0
1859	47.7	100.7	3.5	220.1	15.2	134.3	351.5	221.0	137.9	16.5	21.0	27.2	1779.0
1881	60.3	116.1	2.2	249.5	14.6	168.9	310.9	145.6	172.9	15.9	38.9	55.5	2308.0
1888	49.3	98.9	3.1	225.1	17.3	136.5	263.9	130.5	120.3	17.6	18.4	37.0	2448.0
1892	69.3	96.9	4.4	259.0	14.9	155.3	345.7	194.2	130.3	16.7	15.2	18.4	1177.0
1900	61.0	112.7	3.5	268.9	17.2	134.6	363.9	211.9	130.6	14.9	24.2	22.6	1465.0
Control cultivars													
1468	59.3	108.0	3.1	285.1	15.2	131.7	361.7	233.9	117.7	20.0	31.3	34.5	2281.0
1541	79.6	110.5	3.1	310.5	18.0	128.8	230.4	92.8	168.6	32.3	52.7	46.4	2546.0
375	49.3	98.6	1.2	209.6	16.5	112.6	260.5	150.7	83.6	23.0	61.0	34.7	2294.0
376	59.7	99.9	1.1	287.4	22.9	119.7	288.6	172.0	109.8	22.5	56.4	30.3	1995.0

1= DF = Days to 50 per cent flowering, PLHT = Plant height (cm), BT = Basal tiller number, FLBL = Flag leaf blade length (mm), FLBW = Flag leaf blade width (mm), FLSL = Flag leaf sheath length (mm), PEDL = Peduncle length (mm), PEX = Panicle exertion (mm), INFL = Inflorescence length (mm), INFW = Inflorescence width (mm), W5P = Weight of five panicles (g), SPY = Single plant yield (g), PY = Grain yield per plot (Kg ha-1)

Appendix 4. Mean performance 155 accessions in foxtail millet core collection for 13 quantitative traits at ICRISAT, Patancheru (E3) during 2010 rainy season

ISe	DF[1]	PLHT	BT	FLBL	FLBW	FLSL	PEDL	PEX	INFL	INFW	W5P	SPY	PY
2	55.0	112.1	3.4	349.1	19.3	153.5	326.3	172.6	183.5	16.2	29.5	16.6	1087.4
18	50.7	106.4	2.4	335.5	19.8	130.0	313.0	183.8	159.8	20.1	35.1	17.5	1094.4
31	57.3	106.5	1.5	316.7	21.9	130.7	325.7	196.4	162.1	18.0	36.4	12.6	840.3
49	54.3	106.4	2.6	319.6	20.7	147.9	328.9	181.2	176.6	16.8	34.1	15.5	963.3
90	56.7	101.4	3.1	330.7	23.0	147.6	289.5	140.6	184.8	15.1	30.8	16.1	1040.5
96	56.7	102.3	1.5	295.4	22.8	134.4	296.5	162.0	178.2	14.6	29.0	12.6	953.2
132	53.3	118.1	1.9	399.3	21.3	175.7	368.2	192.4	220.9	16.6	35.2	17.6	1075.8
144	60.0	113.4	1.9	358.7	24.1	146.4	308.5	161.6	193.3	18.6	38.6	16.2	1068.7
156	61.0	109.5	3.3	327.2	21.6	168.3	297.4	126.7	192.3	15.3	28.1	15.4	1253.3
160	55.7	102.8	2.3	307.8	19.6	148.9	313.6	164.3	162.1	15.0	24.1	15.4	847.7
179	55.7	108.1	5.0	324.3	18.1	150.7	340.0	189.8	151.6	13.2	23.6	17.2	1076.8
195	58.3	111.7	3.1	260.8	20.7	164.9	351.4	186.5	165.7	13.6	24.1	16.3	1094.2
200	56.7	97.1	3.1	307.8	21.8	144.2	318.1	173.9	143.4	16.3	25.5	18.1	1172.7
237	56.0	96.2	4.0	281.8	17.5	145.2	283.5	136.9	136.5	13.7	18.7	11.6	1220.8
238	56.7	100.2	3.3	281.8	18.7	156.0	319.9	163.2	150.6	13.1	19.4	12.6	604.8
254	55.0	92.8	3.6	276.3	16.8	123.3	292.4	169.6	142.4	13.3	25.4	11.6	1217.6
267	53.3	102.5	2.5	330.7	19.7	135.3	294.9	159.4	162.1	16.4	28.7	12.2	1037.2
289	58.3	90.0	4.1	325.3	18.1	126.3	260.3	133.0	142.1	21.0	22.2	15.3	1283.7
302	54.3	105.7	1.9	319.3	20.7	128.5	319.3	192.1	161.1	17.3	27.6	13.0	1066.8
362	56.0	100.3	4.3	316.1	17.6	148.3	263.1	112.5	154.9	12.5	19.2	16.5	1385.9
364	58.0	104.2	3.5	267.1	18.7	125.4	310.8	186.5	144.4	13.6	23.1	15.7	1156.8
375	56.0	100.3	1.0	312.0	27.9	126.0	290.7	164.7	114.7	23.1	39.4	10.1	744.7
388	54.7	106.6	3.7	261.1	16.7	145.8	305.1	158.7	159.8	13.4	23.0	14.6	969.9
398	52.3	111.8	2.0	336.4	22.0	135.6	325.4	190.8	185.1	19.0	38.1	14.1	509.1
403	48.7	59.6	4.8	170.2	11.8	103.5	285.4	183.5	86.9	9.3	3.5	3.4	294.1
458	42.0	69.4	4.0	255.4	13.4	114.6	272.3	158.1	114.5	9.7	8.4	7.7	314.5
480	59.3	93.1	4.1	260.8	17.5	151.7	286.0	132.6	142.4	12.4	20.0	10.6	493.2
507	57.0	96.3	2.7	316.7	17.2	138.4	337.4	200.3	148.0	14.4	21.4	9.8	701.4
525	55.7	103.7	2.0	331.0	21.4	126.0	322.8	198.3	160.5	15.6	27.2	10.2	894.4
663	53.3	102.1	3.8	282.4	18.5	155.7	296.5	139.2	158.5	12.7	22.0	13.4	975.2
710	57.3	101.9	4.1	316.1	18.0	145.8	290.8	143.9	167.0	13.3	20.7	13.5	838.0
717	60.3	113.2	2.1	326.2	21.3	179.1	306.3	124.4	195.3	15.4	32.1	11.7	992.2
719	49.7	99.7	3.9	310.4	18.7	142.1	345.1	204.3	185.1	14.0	16.2	18.0	945.0
735	53.0	95.5	1.0	279.5	22.0	127.3	291.7	164.7	143.1	16.3	28.1	8.8	431.9
745	53.7	103.1	2.3	310.4	21.6	155.0	316.5	160.7	191.3	17.3	30.4	13.5	817.6
746	57.0	103.2	1.1	307.2	20.1	148.3	281.2	131.3	135.2	15.3	22.2	11.8	557.7
748	99.0	133.1	2.9	304.6	22.8	164.3	323.5	158.1	248.5	23.1	40.6	14.6	733.7
751	103.6	125.5	3.5	407.0	25.0	161.2	308.9	146.2	247.8	20.8	31.4	12.7	416.6
758	55.3	103.0	1.0	324.7	20.9	146.1	343.5	198.3	163.4	16.6	27.0	8.6	796.0
769	85.7	130.8	2.0	345.9	24.3	153.5	293.3	138.3	205.1	22.2	32.7	10.2	648.2
771	52.3	89.5	4.2	270.9	14.7	121.7	264.4	142.2	143.1	12.2	15.1	14.1	812.4
783	52.7	106.1	1.9	317.3	21.3	159.7	353.6	194.4	177.9	17.6	26.8	9.1	828.4
785	52.0	105.3	1.3	275.1	19.6	156.6	333.0	176.2	202.2	16.8	30.1	9.4	817.7
792	52.0	96.7	1.0	346.6	18.9	137.8	318.4	181.2	208.1	15.3	31.9	9.5	884.5
795	57.0	106.2	3.5	303.0	17.6	137.8	329.2	192.4	145.4	11.9	17.2	13.0	839.7
796	55.0	105.6	2.9	304.0	17.5	142.4	308.2	165.7	135.8	12.9	15.0	20.6	1080.5
813	53.3	109.3	1.5	335.1	22.2	158.4	312.7	153.1	199.9	19.1	38.4	12.8	1002.4
827	33.7	55.9	1.3	154.0	14.2	91.8	333.3	245.9	61.0	10.0	10.2	4.0	385.2
828	53.3	97.1	1.7	244.3	19.2	143.3	296.2	152.1	144.7	17.5	28.6	7.3	452.9
838	55.0	106.0	3.6	287.5	18.5	132.8	320.6	188.8	146.7	15.5	24.4	17.5	1138.5
840	57.3	103.5	3.4	323.1	16.9	138.1	287.6	148.8	157.2	17.0	20.0	16.1	1174.3
842	62.7	106.2	3.5	278.6	20.1	145.8	249.5	100.9	165.7	19.4	26.2	12.6	942.8
846	56.0	103.9	3.5	271.6	17.7	148.3	277.1	127.0	140.1	12.6	22.7	12.9	925.0
869	57.0	109.3	3.1	324.3	19.9	163.1	321.6	157.4	174.9	13.6	23.7	14.6	1460.5

Appendix 4. Cont..

ISe	DF[1]	PLHT	BT	FLBL	FLBW	FLSL	PEDL	PEX	INFL	INFW	W5P	SPY	PY
900	60.3	118.4	1.1	311.9	25.3	156.6	268.9	109.6	181.2	16.7	30.1	10.9	877.3
907	59.0	109.3	2.8	286.8	21.7	152.3	300.3	146.8	173.9	16.1	29.0	14.4	1087.7
909	56.7	101.4	3.5	279.5	18.2	142.7	286.6	142.9	151.9	14.8	27.7	18.7	1097.6
914	55.3	109.2	3.4	321.2	19.8	154.1	306.6	151.5	168.0	14.4	21.0	13.6	546.6
931	56.3	88.0	4.3	282.4	15.6	134.4	261.5	125.6	142.7	11.4	18.9	15.6	1183.1
936	56.0	104.3	4.1	274.8	18.0	152.6	318.1	165.0	161.1	14.7	19.9	18.0	1109.6
946	56.0	112.3	3.3	267.8	19.6	154.4	287.9	131.6	150.6	14.7	27.6	15.7	1222.7
956	56.0	106.4	2.1	272.2	16.8	139.0	313.9	175.2	142.4	13.6	30.9	14.1	722.5
963	57.3	103.0	2.7	284.3	19.0	148.9	308.9	159.4	148.0	14.0	20.4	10.9	696.0
969	55.0	101.7	3.3	296.4	19.3	137.1	313.6	176.9	126.6	13.7	16.9	14.3	795.5
983	60.3	117.4	1.8	343.4	21.1	162.5	327.0	163.7	184.8	20.1	40.2	8.7	804.1
985	55.7	113.2	3.7	281.8	19.6	140.5	282.8	141.2	159.2	16.1	27.8	22.6	1014.6
995	55.0	101.1	4.0	293.2	18.9	130.4	301.9	171.9	147.3	14.6	21.1	12.0	936.3
999	57.7	97.8	4.8	302.1	18.4	145.5	280.3	133.3	147.0	11.4	21.3	13.7	1299.4
1000	60.7	100.0	3.8	289.4	16.0	134.7	257.4	121.1	139.8	11.5	24.5	14.5	1149.8
1009	50.0	52.6	3.8	167.0	11.6	84.4	216.8	132.6	58.7	10.7	4.2	3.2	442.0
1026	47.7	68.9	4.1	268.2	16.6	109.4	262.5	153.4	98.4	12.0	11.3	12.5	692.0
1037	36.7	68.4	4.4	193.0	14.5	91.8	262.6	172.4	90.9	9.5	6.8	10.1	229.0
1059	61.3	122.7	1.1	358.0	24.3	155.7	290.4	133.0	186.1	19.0	30.0	12.9	538.4
1067	50.0	70.4	1.1	232.2	18.9	135.3	287.9	152.1	114.8	16.1	23.6	7.4	603.8
1118	48.3	48.9	4.6	131.7	12.5	88.7	209.8	120.8	45.9	8.7	4.1	3.3	264.3
1119	37.3	53.7	3.3	149.2	12.5	90.8	237.4	147.2	63.9	10.1	3.8	3.6	202.8
1129	42.3	44.4	4.9	139.4	12.4	64.0	210.1	147.5	50.8	9.9	4.9	4.0	154.7
1134	45.0	83.5	3.2	290.0	16.4	133.1	309.8	177.2	139.1	13.0	10.7	8.4	417.4
1136	44.3	71.3	5.1	257.0	13.5	106.6	235.2	128.0	115.8	12.0	11.8	3.5	168.0
1137	48.0	72.8	3.8	290.0	15.0	110.0	289.5	180.8	124.3	13.1	9.8	6.7	390.7
1151	33.7	103.0	2.8	297.0	16.6	150.1	315.2	164.7	158.4	14.9	20.8	7.1	174.5
1161	36.3	73.8	3.7	175.9	13.9	110.3	367.0	261.1	71.5	11.9	7.9	4.2	415.4
1162	57.7	90.8	4.3	272.9	17.1	135.9	280.6	143.9	207.8	12.0	12.6	11.9	637.3
1163	42.3	78.9	2.1	163.8	11.0	111.2	339.4	231.4	62.0	10.7	5.9	2.3	166.7
1177	50.3	70.2	3.1	268.4	16.0	102.9	271.7	169.9	100.0	12.7	12.5	9.5	639.5
1181	41.3	83.7	1.1	214.4	19.5	122.3	300.6	179.2	144.0	14.7	27.0	6.9	143.0
1187	41.0	68.2	2.6	187.0	18.9	128.2	335.9	209.6	97.7	13.6	10.4	6.4	687.6
1201	33.3	42.1	1.6	127.6	13.4	102.0	251.7	150.1	133.5	11.4	8.3	3.0	313.3
1204	45.0	74.5	1.3	202.9	17.0	130.7	297.8	167.3	89.2	15.8	39.8	8.0	446.0
1209	36.3	59.5	2.8	177.2	14.7	110.3	290.1	181.2	73.8	13.2	10.3	5.1	498.2
1227	34.0	37.7	3.0	141.3	13.0	86.5	220.3	134.0	51.0	8.3	3.8	3.7	439.9
1234	34.0	54.6	3.4	169.2	13.5	106.9	260.0	153.4	69.5	10.5	6.6	4.1	207.6
1251	53.7	101.0	2.2	264.8	19.9	136.6	280.6	143.1	153.5	18.1	28.5	7.8	203.6
1254	34.3	59.2	1.9	131.7	14.2	91.8	318.4	230.4	61.3	10.4	7.4	2.8	167.5
1258	38.0	69.3	1.5	195.9	18.0	119.2	288.5	169.9	116.8	14.9	7.6	4.8	378.0
1269	54.0	101.6	4.1	293.8	17.2	156.9	322.2	164.7	176.9	13.3	20.1	13.1	1112.5
1286	35.7	53.2	3.7	141.0	11.3	99.5	314.3	217.8	51.4	8.9	4.2	3.0	223.9
1299	39.3	54.8	4.0	191.5	16.1	97.6	245.7	148.5	74.1	9.1	9.9	3.1	1035.9
1302	43.3	74.4	3.9	198.5	14.5	114.9	317.1	204.3	101.0	10.3	8.7	9.8	204.7
1305	39.0	97.4	2.9	232.8	14.9	139.0	409.8	275.0	138.1	13.1	15.7	7.7	262.1
1312	32.7	42.1	4.1	119.0	9.0	83.4	238.0	155.8	33.0	8.2	3.9	2.5	269.1
1320	33.0	40.6	2.4	143.2	11.8	89.0	237.7	149.5	42.9	8.6	4.0	4.7	431.3
1332	49.0	56.2	5.1	171.8	14.7	91.8	241.2	150.1	74.1	8.9	4.0	4.3	179.2
1335	35.3	55.6	2.6	154.9	10.0	89.3	284.1	197.4	60.3	7.0	4.1	4.0	180.2
1338	47.7	39.6	1.7	126.0	18.8	50.9	189.3	139.8	57.1	10.3	4.2	10.0	495.3
1354	53.3	111.0	3.5	302.1	18.9	150.4	318.1	167.3	180.2	15.1	30.2	17.9	968.4
1387	75.3	138.8	3.3	364.4	26.1	166.2	308.2	140.2	220.2	21.5	28.9	10.0	614.0
1400	54.3	98.6	3.7	279.8	18.4	136.5	294.3	157.4	139.8	13.6	20.7	14.5	907.1
1402	53.0	97.0	2.8	290.0	16.5	143.3	321.6	178.5	149.0	14.5	20.3	11.7	753.9
1406	46.3	100.4	1.8	235.4	19.5	176.0	409.8	235.3	149.3	15.3	15.5	10.8	734.9
1408	56.3	88.2	4.0	249.3	16.3	135.3	266.3	129.7	120.4	12.0	16.6	10.0	982.9
1419	89.3	137.6	1.3	357.4	22.2	144.6	251.4	104.2	246.5	23.5	25.6	6.4	237.5

Appendix 4. Cont..

ISe	DF[1]	PLHT	BT	FLBL	FLBW	FLSL	PEDL	PEX	INFL	INFW	W5P	SPY	PY
1454	57.0	118.1	2.2	343.4	21.3	160.6	320.3	158.7	207.8	22.8	38.2	14.1	876.9
1458	55.0	107.9	4.5	274.1	17.7	148.6	300.9	151.5	156.2	14.9	27.3	14.3	797.5
1460	51.7	105.4	1.5	243.6	20.5	167.4	352.1	184.5	156.8	15.9	15.8	11.0	644.4
1474	51.0	105.3	1.1	252.8	21.5	130.4	339.4	210.9	140.1	17.1	20.6	10.8	571.1
1511	60.3	119.5	2.1	344.7	19.9	134.3	295.8	161.4	189.7	16.0	22.9	10.5	657.0
1547	43.3	91.9	1.1	241.4	21.3	129.7	409.2	284.2	109.9	16.5	25.1	7.2	513.3
1563	37.7	97.1	2.6	259.5	17.2	139.9	331.8	192.8	111.1	11.9	14.4	3.8	346.3
1575	47.7	86.0	1.7	259.2	21.1	120.5	325.4	206.9	134.9	18.8	31.2	5.4	530.0
1581	45.3	79.8	1.2	223.3	21.3	124.8	336.2	213.5	120.7	16.8	41.6	9.5	409.5
1593	51.3	87.3	1.1	287.2	25.7	129.4	319.3	191.1	151.9	21.2	16.2	11.2	455.9
1597	80.7	131.6	2.1	468.0	26.2	168.0	258.7	86.7	286.6	26.9	32.6	13.6	459.1
1605	56.0	104.4	2.7	288.7	21.6	139.0	282.2	142.2	181.8	16.6	27.4	18.3	866.0
1610	51.7	99.7	2.1	315.4	19.5	129.1	300.6	171.9	150.9	19.6	38.9	12.7	855.2
1629	56.3	82.3	3.8	277.6	16.8	137.1	276.8	138.6	126.6	11.8	13.1	9.7	829.1
1638	40.3	72.6	2.1	191.2	16.9	104.6	317.9	216.2	105.6	12.7	5.0	9.1	396.3
1647	42.0	77.5	1.1	201.0	16.0	133.5	293.7	160.0	121.4	19.0	24.2	4.8	718.4
1655	41.7	80.1	1.9	176.0	12.0	109.4	325.8	219.3	120.4	10.4	37.3	9.0	566.1
1664	59.7	98.2	3.9	309.7	18.4	136.8	311.7	175.2	155.2	13.2	18.8	9.7	763.1
1666	54.3	110.1	1.0	330.7	20.4	134.4	358.1	226.1	179.5	17.7	35.7	10.0	333.5
1674	56.0	91.6	1.4	279.2	22.3	144.6	302.5	157.4	133.2	15.8	24.9	14.2	791.1
1685	72.7	129.2	2.3	321.8	24.9	146.4	277.1	129.0	243.2	23.5	46.9	12.6	657.0
1687	61.3	120.2	1.3	360.6	26.8	138.4	263.8	123.7	197.2	22.8	44.2	15.0	690.0
1704	53.3	94.5	4.0	269.7	16.0	131.9	255.8	122.4	163.1	15.0	15.1	15.4	922.1
1725	55.3	112.5	1.5	311.0	20.8	154.7	309.5	153.8	202.8	16.5	27.3	12.8	723.3
1736	53.0	98.7	2.1	262.7	19.9	142.1	331.1	189.8	150.3	14.9	22.6	11.4	803.4
1745	55.3	106.2	1.3	317.3	23.0	151.3	342.5	191.7	180.5	15.9	26.1	9.8	707.2
1762	55.3	108.6	2.3	310.4	20.9	144.2	331.4	187.8	155.2	15.3	27.1	13.4	1278.7
1767	54.3	104.1	2.9	312.3	18.7	135.3	319.0	184.5	168.3	13.8	26.4	12.0	1056.4
1773	56.3	93.9	3.3	303.4	20.3	138.1	304.4	166.3	141.1	14.9	22.9	14.0	1046.9
1780	54.7	108.1	1.2	321.2	18.7	147.9	317.4	169.3	189.4	17.4	25.6	10.6	753.4
1789	45.3	80.0	1.1	275.1	20.9	103.3	239.1	135.6	132.9	14.9	15.9	3.5	400.6
1805	56.3	100.2	3.1	326.2	20.4	156.3	294.9	136.9	163.1	15.8	24.0	11.5	759.2
1806	54.3	95.3	2.9	311.6	18.3	147.3	322.2	174.9	163.1	15.0	25.8	14.1	801.6
1808	53.3	103.4	2.1	299.9	18.7	154.4	337.8	183.5	173.3	14.6	32.4	11.6	976.0
1820	52.3	96.0	2.5	293.8	18.4	145.8	298.7	152.1	155.9	15.1	20.9	11.8	714.9
1846	55.7	102.0	3.7	302.1	17.7	150.7	298.1	146.2	163.4	14.4	23.6	12.3	1044.5
1851	56.3	110.0	3.0	299.5	18.3	134.1	284.4	149.8	169.0	15.1	28.6	13.2	781.5
1858	57.0	108.4	3.5	350.1	20.7	157.2	315.2	157.1	177.2	17.5	26.6	17.7	1039.8
1859	54.7	108.2	3.2	304.0	17.4	139.6	315.5	176.2	157.8	13.9	23.6	16.3	1262.1
1881	55.3	111.4	2.5	314.8	17.8	159.4	319.0	158.7	192.0	14.6	26.8	14.0	1256.6
1888	54.3	92.1	3.6	278.6	18.7	146.1	265.0	116.8	167.7	13.4	25.5	17.8	945.8
1892	58.0	100.4	4.7	294.5	15.9	136.5	306.0	169.6	132.2	12.5	16.5	9.5	741.7
1900	54.7	110.2	3.4	310.4	19.4	149.8	331.7	182.2	170.3	14.9	20.8	12.5	1126.6
Control cultivars													
1468	51.0	103.6	2.6	305.9	21.3	121.6	293.5	172.6	157.2	20.2	43.0	12.7	841.8
1541	71.3	113.4	2.1	397.4	26.0	141.5	164.4	17.1	205.8	40.3	47.8	19.4	888.5
375	56.3	94.7	1.1	282.0	24.3	110.3	271.7	161.3	103.7	21.6	39.3	11.8	633.7
376	52.0	98.3	1.0	282.4	24.7	114.0	262.5	146.5	105.3	22.1	35.5	11.8	666.9

1= DF = Days to 50 per cent flowering, PLHT = Plant height (cm), BT = Basal tiller number, FLBL = Flag leaf blade length (mm), FLBW = Flag leaf blade width (mm), FLSL = Flag leaf sheath length (mm), PEDL = Peduncle length (mm), PEX = Panicle exertion (mm), INFL = Inflorescence length (mm), INFW = Inflorescence width (mm), W5P = Weight of five panicles (g), SPY = Single plant yield (g), PY = Grain yield per plot (Kg ha-1)

Appendix 5. Mean performance 155 accessions in foxtail millet core collection for 13 quantitative traits based on pooled BLUPs over the environments

ISE	DF	PLHT	BT	FLBL	FLBW	FLSL	PEDL	PEX	INFL	INFW	W5P	SPY	YKGPH
2	50.0	112.1	3.8	316.2	17.5	151.1	337.9	189.4	168.9	18.2	32.0	22.2	1416.0
18	48.3	108.5	3.6	282.7	17.6	121.0	331.3	213.3	137.0	22.6	35.9	20.0	1308.0
31	59.0	106.2	2.4	285.7	21.3	132.0	337.9	216.5	135.7	17.6	37.7	12.7	844.0
49	51.6	112.7	3.7	288.4	20.8	145.6	330.4	187.4	168.0	19.9	23.4	16.1	997.0
90	53.3	97.6	4.1	294.2	21.4	142.7	289.8	148.8	168.3	16.2	18.4	15.8	1049.0
96	58.0	105.8	1.7	283.0	21.8	142.0	315.8	176.3	172.3	15.7	32.6	21.7	1189.0
132	51.6	116.7	3.8	325.8	19.7	152.9	348.0	197.8	189.3	18.5	39.3	16.9	933.0
144	53.2	116.6	3.0	323.2	21.9	138.5	340.0	204.4	185.3	19.5	31.9	20.9	1330.0
156	57.8	118.9	4.6	294.8	21.3	168.7	321.9	153.3	191.1	14.1	25.4	22.0	1507.0
160	51.6	106.4	3.7	273.9	18.7	147.5	316.7	171.7	164.8	16.5	30.6	20.2	1292.0
179	50.1	108.3	4.6	287.9	16.5	141.7	318.8	179.7	139.7	12.5	15.5	17.8	1088.0
195	54.2	108.3	3.0	260.9	19.8	158.6	329.0	172.5	153.7	13.5	21.2	20.9	1324.0
200	49.6	100.3	3.7	262.3	19.2	133.6	308.3	177.2	131.9	16.4	20.7	19.6	1228.0
237	54.2	102.8	4.6	263.1	16.2	140.2	305.1	167.3	129.3	12.5	15.7	18.4	1352.0
238	60.1	114.0	3.6	273.2	19.1	165.2	335.7	174.5	153.5	16.0	22.5	31.4	1629.0
254	51.7	105.1	3.6	259.7	16.9	123.4	302.5	181.7	137.9	14.4	29.1	27.9	1779.0
267	58.4	105.9	4.3	294.4	18.8	147.1	326.9	182.4	135.8	18.8	32.6	26.5	1680.0
289	55.9	95.6	4.4	289.0	17.0	113.0	270.5	159.9	131.8	20.1	25.7	13.0	992.0
302	51.2	105.5	3.6	286.6	19.2	128.8	305.0	178.5	143.8	19.7	38.0	24.2	1643.0
362	57.4	106.3	5.0	299.6	18.2	156.4	306.0	151.7	164.8	13.4	18.2	24.9	1597.0
364	61.9	105.4	4.1	249.7	18.2	128.2	325.9	201.5	142.5	14.2	32.8	37.0	2084.0
375	58.0	96.0	1.7	250.2	22.3	122.1	275.7	156.8	103.9	25.4	53.7	19.9	1466.0
388	58.9	109.7	4.4	265.6	18.5	156.4	327.9	174.0	155.0	14.9	29.1	30.8	1971.0
398	55.7	110.4	2.5	285.6	19.1	129.3	336.6	210.3	155.4	19.8	28.8	28.5	1755.0
403	42.7	54.2	4.1	129.3	11.1	104.1	264.2	166.8	68.7	8.9	2.7	3.7	249.0
458	42.0	76.0	4.0	245.5	14.3	108.6	269.8	164.9	108.9	12.9	7.0	9.7	627.0
480	57.1	103.0	4.6	260.2	17.9	151.2	295.2	146.2	142.7	14.7	20.6	20.4	1306.0
507	56.0	103.8	3.9	279.1	17.9	126.9	313.9	189.6	146.0	17.5	23.2	14.3	1091.0
525	48.3	110.2	2.5	296.9	20.3	127.7	325.9	201.1	165.7	17.7	25.3	17.5	1322.0
663	54.4	111.8	4.4	271.4	17.7	157.5	302.5	147.2	158.9	15.3	23.8	13.9	902.0
710	54.9	102.5	5.4	280.9	17.4	151.9	284.3	134.4	153.1	14.3	22.2	18.8	1146.0
717	62.5	125.4	3.0	308.9	20.2	161.7	278.9	109.9	203.5	18.6	31.0	21.9	1668.0
719	44.9	98.8	4.3	246.6	16.3	126.7	341.7	218.0	144.5	16.3	9.8	14.2	894.0
735	52.2	94.3	1.2	268.9	20.9	133.5	290.2	159.0	141.4	16.6	29.3	10.2	646.0
745	51.2	101.4	2.5	268.2	21.5	150.9	314.5	163.2	168.2	16.6	23.1	24.7	1733.0
746	54.4	91.9	1.5	281.0	20.8	144.0	280.9	136.8	135.2	15.6	23.7	19.3	1166.0
748	97.5	128.8	5.0	349.2	25.8	159.2	306.4	153.9	255.1	22.3	43.0	21.2	902.0
751	103.1	125.7	3.6	425.3	25.4	164.4	306.6	144.4	241.2	21.9	34.1	16.4	853.0
758	52.0	102.5	2.5	299.1	20.2	145.0	365.1	227.9	162.5	18.0	25.2	8.9	676.0
769	89.9	136.7	3.8	360.4	27.2	166.4	304.4	137.2	212.1	23.1	47.2	16.9	1208.0
771	57.1	99.6	4.8	265.1	15.0	133.6	256.9	130.1	139.4	17.5	17.4	24.6	1595.0
783	48.9	106.3	2.8	275.3	17.5	160.2	343.0	185.4	147.7	19.1	32.9	20.5	1460.0
785	50.3	105.2	3.4	269.6	18.8	151.1	349.2	200.9	177.5	17.1	29.0	13.1	720.0
792	50.0	90.4	1.9	283.6	18.9	125.7	330.6	207.7	176.5	16.1	20.9	18.5	1343.0
795	61.1	104.5	4.3	261.8	16.6	138.2	322.0	186.4	133.5	13.1	16.6	17.9	1232.0
796	58.4	107.7	3.9	288.6	17.9	151.0	301.2	159.0	156.9	16.9	24.3	20.5	1385.0
813	47.2	89.6	2.7	234.5	16.6	129.4	279.6	152.5	138.0	15.9	20.4	11.9	862.0
827	36.9	57.0	2.7	111.2	14.6	92.6	341.4	253.4	46.3	11.3	5.2	4.8	386.0
828	47.8	83.0	2.5	238.3	19.7	123.7	280.6	159.2	145.7	20.1	23.7	12.8	722.0
838	54.4	102.7	4.0	271.0	17.1	135.9	308.0	174.6	146.1	17.0	16.2	20.1	1503.0
840	60.9	101.1	3.9	289.6	16.1	144.3	310.6	168.6	140.7	12.9	18.6	18.5	1348.0
842	63.1	107.1	3.9	242.2	18.3	128.1	269.3	135.4	138.2	19.9	35.6	11.2	738.0
846	53.8	103.6	4.1	246.8	16.9	152.7	281.4	130.2	140.8	14.7	22.2	23.8	1687.0
869	59.1	117.6	4.1	297.6	18.0	160.3	336.1	178.3	172.9	15.6	28.0	12.6	1039.0

Appendix 5. Cont..

ISE	DF	PLHT	BT	FLBL	FLBW	FLSL	PEDL	PEX	INFL	INFW	W5P	SPY	YKGPH
900	55.6	113.9	2.0	295.2	24.1	145.2	287.4	144.3	169.9	19.3	27.1	17.3	1238.0
907	55.6	111.1	3.5	259.8	18.9	142.8	308.8	168.4	148.8	16.6	23.8	14.4	1047.0
909	51.5	105.1	4.1	253.7	16.3	142.0	301.9	162.2	139.2	16.1	25.6	21.2	1395.0
914	56.4	113.7	5.0	305.0	18.3	152.3	310.7	165.0	163.5	12.8	17.7	22.3	1278.0
931	58.1	99.8	4.6	251.9	14.3	130.3	265.2	137.0	143.0	13.4	18.4	22.4	1608.0
936	51.9	99.8	3.2	228.6	16.6	140.6	308.5	169.3	132.6	12.9	21.2	23.4	1655.0
946	51.2	119.8	4.1	281.9	19.6	152.2	328.8	182.6	148.2	18.6	20.8	21.2	1541.0
956	56.8	117.6	3.4	278.8	17.5	145.7	339.2	196.3	152.7	13.8	31.0	37.4	2081.0
963	60.4	113.6	3.9	277.0	19.2	150.7	335.5	187.5	150.5	15.7	21.6	27.3	1902.0
969	55.6	97.5	3.4	261.6	17.0	138.5	323.8	188.0	113.0	12.2	21.2	19.9	1417.0
983	62.8	123.5	2.0	314.1	21.8	169.2	328.5	161.6	186.1	22.2	35.0	13.9	992.0
985	55.7	110.2	4.1	267.1	17.2	146.5	315.3	171.2	154.8	16.9	22.2	25.7	1560.0
995	51.8	97.3	3.5	277.1	17.5	148.0	302.0	156.3	150.1	18.1	16.9	23.3	1680.0
999	56.3	122.4	5.1	283.3	18.5	152.9	296.0	145.2	162.0	15.7	17.2	19.9	1496.0
1000	60.2	110.6	4.7	283.9	17.1	150.6	301.7	140.8	140.1	13.1	23.5	29.2	1946.0
1009	47.0	60.5	5.5	170.4	11.5	102.4	251.7	151.6	60.0	10.6	4.1	6.8	568.0
1026	46.8	64.4	3.7	245.9	14.9	99.9	246.3	148.6	88.1	11.3	8.0	14.0	932.0
1037	40.6	72.3	4.7	175.3	13.4	96.1	286.5	174.5	92.7	11.7	5.9	15.2	937.0
1059	66.5	131.2	2.9	315.9	23.6	150.1	325.9	195.4	194.9	21.1	35.6	31.0	1889.0
1067	47.9	57.2	1.9	157.5	19.2	121.7	277.1	132.2	108.6	16.1	23.2	5.9	483.0
1118	47.2	47.8	4.4	106.9	11.2	80.5	217.6	139.3	46.5	9.2	4.3	4.3	260.0
1119	39.9	53.2	3.2	155.1	14.7	105.0	277.0	174.6	72.4	10.8	3.2	9.4	516.0
1129	41.3	46.4	5.9	123.3	10.2	75.9	225.2	151.6	49.2	10.0	3.3	4.6	283.0
1134	50.0	78.8	4.8	267.7	15.5	122.1	340.5	222.5	140.4	11.0	15.5	9.0	525.0
1136	44.7	74.4	4.8	232.2	13.6	109.2	261.1	154.2	102.8	11.2	11.5	9.7	636.0
1137	55.6	81.6	3.2	215.6	18.2	111.8	307.5	207.6	125.2	17.1	19.4	17.2	1199.0
1151	37.8	62.3	2.7	143.2	15.5	106.7	233.9	134.5	78.0	11.3	20.9	14.2	196.0
1161	39.0	67.9	3.3	154.2	13.1	132.9	275.9	216.1	51.7	11.7	4.9	4.0	398.0
1162	55.4	93.6	6.0	235.3	15.9	132.1	319.6	186.3	138.9	11.8	12.4	22.3	1566.0
1163	50.3	78.4	4.2	217.8	14.5	114.5	285.2	174.3	75.5	10.7	11.4	6.5	414.0
1177	50.3	75.9	3.7	274.9	16.1	105.6	252.7	149.4	113.1	11.5	10.3	12.6	882.0
1181	38.7	80.1	2.5	174.3	17.8	113.2	294.2	183.6	107.8	12.3	13.8	5.6	211.0
1187	44.0	73.1	2.5	185.4	18.1	137.4	356.4	222.0	94.9	12.8	9.0	6.7	499.0
1201	31.8	51.0	2.0	86.6	11.5	71.7	221.9	152.5	95.6	10.6	7.4	4.1	360.0
1204	41.8	68.6	1.4	169.4	16.8	117.0	287.4	170.7	74.6	15.7	31.1	10.2	597.0
1209	42.1	54.9	2.6	141.5	13.8	106.8	271.6	174.4	57.2	12.5	7.5	7.4	518.0
1227	45.2	59.9	3.8	214.2	15.3	119.0	279.1	163.5	110.7	12.6	9.5	8.9	611.0
1234	36.2	44.5	3.6	140.9	11.4	102.3	227.1	127.1	54.4	11.0	5.6	6.9	443.0
1251	49.7	107.7	1.9	266.3	22.8	158.4	329.5	173.6	160.4	20.7	51.4	28.1	1141.0
1254	38.5	56.6	1.4	95.5	12.4	81.5	286.8	208.4	42.8	10.3	3.8	3.4	283.0
1258	37.8	67.6	1.4	191.9	19.0	113.6	308.8	198.0	108.4	13.0	17.2	6.0	413.0
1269	56.8	108.4	5.1	269.3	17.3	157.2	322.5	167.7	166.1	13.5	22.1	25.1	1744.0
1286	38.0	55.3	4.8	115.7	11.3	88.6	286.4	198.9	50.2	10.2	5.1	3.9	288.0
1299	43.2	59.7	4.8	157.3	12.2	96.6	250.8	156.6	61.2	10.6	9.5	9.0	878.0
1302	45.5	68.8	4.7	202.3	14.8	106.8	304.0	200.0	88.9	10.6	8.3	8.0	309.0
1305	42.7	70.6	5.0	155.0	10.1	116.8	361.1	247.8	70.8	10.7	10.3	9.2	537.0
1312	34.7	46.0	3.5	104.8	9.5	95.5	244.8	151.6	45.9	8.5	3.2	3.3	196.0
1320	35.7	48.7	2.5	129.4	11.9	96.3	251.1	156.7	52.5	9.8	4.5	7.0	533.0
1332	47.1	59.4	4.5	133.8	13.7	104.5	276.3	172.6	78.3	9.4	5.4	13.4	1087.0
1335	37.4	41.3	2.7	114.6	11.2	88.6	254.5	168.3	41.1	8.1	12.3	4.2	283.0
1338	44.1	37.9	1.6	115.9	18.2	47.4	186.8	142.1	57.1	15.9	3.8	6.9	342.0
1354	55.3	111.2	3.9	275.0	18.6	145.5	326.0	183.0	164.9	16.2	24.2	28.4	1848.0
1387	79.8	140.4	4.3	400.4	26.8	173.9	340.6	169.1	221.3	23.1	28.7	9.1	596.0
1400	55.4	110.3	4.2	269.8	18.1	135.6	293.6	160.4	148.8	14.9	23.3	18.3	1204.0
1402	48.1	107.8	3.6	262.5	17.0	141.2	324.2	183.6	146.6	16.6	20.3	18.2	1148.0
1406	45.0	119.4	3.4	240.4	16.8	158.3	272.3	195.5	112.8	17.3	36.6	35.1	1917.0
1408	49.9	89.1	5.9	243.6	16.1	131.7	289.7	160.3	111.6	13.8	13.6	27.1	1941.0
1419	90.1	131.6	2.9	359.7	21.2	138.0	256.1	120.0	231.9	25.9	39.6	7.8	560.0

Appendix 5. Cont..

ISE	DF	PLHT	BT	FLBL	FLBW	FLSL	PEDL	PEX	INFL	INFW	W5P	SPY	YKGPH
1454	61.7	115.1	1.8	297.0	20.8	175.3	341.7	168.8	209.7	21.0	54.5	15.8	1100.0
1458	53.6	105.6	3.9	248.8	17.9	133.9	294.9	161.9	140.1	14.8	37.2	18.8	1183.0
1460	52.3	108.8	3.0	245.5	19.4	163.5	357.5	206.0	174.4	17.2	34.7	19.4	1331.0
1474	59.3	127.8	2.7	285.3	21.0	128.9	292.9	174.4	211.1	19.5	42.5	37.1	1980.0
1511	62.2	124.5	3.4	323.3	19.2	146.9	295.1	147.8	197.7	19.3	41.5	27.1	1762.0
1547	46.8	89.0	1.2	214.1	20.2	128.5	403.9	279.0	121.3	15.0	22.4	14.7	1011.0
1563	36.3	75.4	1.9	169.4	14.4	114.5	329.6	218.1	80.9	10.8	7.2	4.7	361.0
1575	55.9	84.8	1.3	245.6	23.8	128.5	323.1	197.3	140.1	18.6	22.3	11.0	489.0
1581	44.8	76.7	1.5	220.3	21.0	126.8	328.2	204.3	97.5	18.0	35.1	12.9	795.0
1593	51.2	83.4	1.1	248.9	26.8	129.0	318.1	191.7	136.2	20.5	34.7	13.1	758.0
1597	80.9	122.2	2.6	423.4	26.7	130.9	283.3	147.4	257.1	23.7	52.6	34.8	1870.0
1605	54.8	114.7	3.3	273.7	20.2	138.1	297.9	162.1	181.4	18.5	33.9	21.8	1441.0
1610	58.0	102.7	2.5	270.6	19.9	130.0	321.3	194.0	130.6	21.7	28.3	18.3	1190.0
1629	51.9	85.9	4.7	258.4	16.3	127.2	258.3	125.5	140.8	13.8	9.7	21.8	1593.0
1638	39.4	68.9	1.4	180.1	15.4	111.0	324.1	216.1	96.2	13.3	5.8	7.1	359.0
1647	40.5	70.0	1.1	182.5	15.7	123.2	288.9	168.2	94.3	16.5	26.6	5.2	465.0
1655	38.5	97.0	3.3	220.6	15.2	140.5	359.8	217.7	143.3	18.4	23.5	10.5	634.0
1664	59.0	110.7	5.0	275.0	18.6	136.4	325.6	191.8	153.3	14.4	19.2	12.3	791.0
1666	54.1	110.4	2.5	309.2	19.8	128.5	342.3	216.7	178.9	20.7	58.4	21.2	1429.0
1674	50.3	95.7	2.7	275.9	21.2	120.8	272.9	154.7	126.1	16.8	27.6	25.3	1725.0
1685	84.0	119.1	2.5	305.7	24.3	125.1	232.9	109.7	247.6	25.9	44.5	34.4	1959.0
1687	68.3	122.1	3.3	329.4	24.7	147.8	258.9	107.4	201.4	23.1	46.4	38.0	2013.0
1704	51.2	91.6	4.2	238.4	15.4	138.1	270.5	134.4	144.4	14.7	10.3	26.8	1722.0
1725	53.2	120.9	1.7	286.1	20.0	139.4	301.6	161.2	208.4	20.1	32.6	26.3	1808.0
1736	69.7	121.1	3.4	280.9	21.5	165.3	337.9	175.0	192.1	19.2	41.6	27.5	1961.0
1745	58.5	114.0	2.2	286.5	22.5	159.1	337.8	181.2	170.1	17.5	33.0	21.7	1602.0
1762	56.3	111.6	3.1	288.6	19.2	141.5	310.6	171.8	151.7	14.2	20.4	27.6	1850.0
1767	52.1	110.7	4.1	304.6	17.8	137.3	344.8	210.4	169.3	15.0	27.3	28.8	1974.0
1773	53.7	99.7	3.4	288.4	19.4	136.4	320.3	186.5	139.0	18.9	35.4	27.0	1862.0
1780	53.6	114.2	2.9	278.6	20.3	143.8	334.9	193.9	179.5	20.3	23.0	26.7	1931.0
1789	42.4	69.8	1.8	177.2	16.8	100.3	226.0	127.2	91.1	15.1	20.3	8.1	647.0
1805	53.2	104.8	3.9	273.0	18.2	149.8	300.1	152.5	151.1	17.4	28.6	27.9	1928.0
1806	53.8	93.3	3.7	284.1	17.1	139.0	307.5	170.9	148.1	16.7	21.7	23.8	1681.0
1808	53.6	107.5	3.3	274.3	18.2	155.3	322.1	168.2	156.1	17.1	28.4	23.7	1710.0
1820	54.4	100.9	4.0	258.7	17.7	145.7	317.1	173.8	144.3	15.4	18.7	25.1	1747.0
1846	52.8	108.5	4.8	265.6	15.6	136.2	278.8	136.9	149.8	14.8	27.3	32.6	2080.0
1851	52.3	115.2	3.6	298.0	19.1	143.4	308.3	167.3	172.4	17.2	22.7	16.1	1104.0
1858	51.6	104.1	3.9	274.8	19.0	155.4	318.7	165.7	153.5	18.3	33.2	20.0	1369.0
1859	50.9	112.6	3.9	273.5	18.2	139.1	326.0	189.5	160.1	15.8	22.7	24.9	1878.0
1881	58.5	121.9	4.2	290.5	17.3	165.9	323.3	160.7	196.4	17.5	35.5	43.1	2225.0
1888	50.7	98.3	3.8	261.3	18.6	154.0	280.4	128.4	158.0	16.8	21.7	35.4	2240.0
1892	65.0	108.5	4.7	280.9	15.8	143.3	318.6	177.1	140.9	15.0	16.8	15.9	1204.0
1900	58.7	116.4	3.8	291.6	19.0	145.2	338.2	188.6	157.0	16.3	22.6	20.9	1540.0
Control cultivars													
1468	58.0	104.9	3.3	291.4	19.3	124.5	322.9	201.2	135.5	21.1	40.1	27.3	1914.0
1541	76.2	116.5	3.0	354.9	22.0	130.3	199.6	68.9	198.9	35.6	55.1	38.5	2077.0
375	52.9	100.5	1.4	261.8	21.7	113.1	259.9	149.0	100.5	25.2	59.6	28.4	1926.0
376	58.1	103.2	1.2	293.9	26.3	118.5	258.6	141.7	115.4	25.1	56.7	26.9	1794.0

1= DF = Days to 50 per cent flowering, PLHT = Plant height (cm), BT = Basal tiller number, FLBL = Flag leaf blade length (mm), FLBW = Flag leaf blade width (mm), FLSL = Flag leaf sheath length (mm), PEDL = Peduncle length (mm), PEX = Panicle exertion (mm), INFL = Inflorescence length (mm), INFW = Inflorescence width (mm), W5P = Weight of five panicles (g), SPY = Single plant yield (g), PY = Grain yield per plot (Kg ha-1)