PHENOTYPIC AND GENOTYPIC DIVERSITY OF GLOBAL FINGER MILLET (*Eleusine coracana* (L.) Gaertn.) COMPOSITE COLLECTION

Thesis submitted in part fulfillment of the requirements for the award of degree of
DOCTOR OF PHILOSOPHY IN PLANT BREEDING AND GENETICS

to the Tamil Nadu Agricultural University, Coimbatore

By

A. BHARATHI

(I.D. No. 04-810-003)

CENTRE FOR PLANT BREEDING AND GENETICS
TAMIL NADU AGRICULTURAL UNIVERSITY
COIMBATORE – 641003.

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CERTIFICATE

This is to certify that the thesis entitled **"PHENOTYPIC AND GENOTYPIC DIVERSITY OF GLOBAL FINGER MILLET (*Eleusine coracana* (L.) Gaertn.) COMPOSITE COLLECTION**" submitted in part fulfillment of the requirements for the degree of **Doctor of Philosophy in Plant Breeding and Genetics** to the Tamil Nadu Agricultural University, Coimbatore is a record of *bonafide* research work carried out by **Mrs. A. Bharathi** under my supervision and guidance and that no part of this thesis has been submitted for the award of any other degree, diploma, fellowship or other similar titles or prizes and that the work has not been published in part or full in any scientific or popular journal or magazine.

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(Dr. P. VEERABADHIRAN)
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Members : **(Dr. A. NIRMALA KUMARI)**

(Dr. B. RAJASEKARAN)

(Dr. S. KRISHNAVENI)

Date: **External examiner**

Abstract

ABSTRACT

PHENOTYPIC AND GENOTYPIC DIVERSITY OF GLOBAL FINGER MILLET COMPOSITE COLLECTION (*Eleusine coracana* (L.) Gaertn.)

BY

A. BHARATHI

Degree : DOCTOR OF PHILOSOPHY
(PLANT BREEDING AND GENETICS)

Chairman : Dr. P. VEERABADHIRAN
Professor and Head
Department of Millets
Center for Plant Breeding and Genetics
Tamil Nadu Agricultural University
Coimbatore – 641 003.

2011

A composite collection of 1000 accessions that included 622 core collection accessions was developed, to study diversity and population structure and develop a reference set of 300 genetically most diverse accessions using Simple Sequence Repeats (SSRs). The global composite collection of finger millet was evaluated in three environments v*iz.,* 2005/2006 post rainy season at Tamil Nadu Agricultural University (TNAU), Coimbatore (E1), in 2006 (E2) and 2007 rainy (E3) seasons at ICRISAT, Patancheru centre, Hyderabad for various morpho-agronomic traits under field conditions. For qualitative traits, the accessions of composite collection showed higher frequency for erect plant habit, green pigmentation, non lodging plant types, medium glume prominence, semi-compact inflorescence and light brown seed colour. High estimates of PCV, GCV and heritability in broad sense for most of the traits indicated that the yield attributes were stable with less environmental influence and variability could be exploited for selection of these traits. The traits such as number of basal tillers, ear head length, finger number, length of longest finger and flag leaf blade length exhibited a positive and significant phenotypic correlation and direct effect with grain yield in all the three or two environments indicating selection on these traits will simultaneously improve the yield. Stability analysis revealed wide range for linear regression (bi) which indicated variable responses of genotypes to environmental changes. Only 40 accessions

(days to 50 per cent flowering) and 7 accessions (plot yield) had b = 1 and $S^2d = 0$ were considered as stable genotypes. The mean and range of Shannon- Weaver diversity index (H`) was variable for different traits and environments. Accessions of races *elongata* and *compacta* and from East Africa, Southern Africa and South Asia regions showed higher mean H` for most of the traits in all three environments. Principal Component Analysis (PCA) (first seven PCs) indicated relative importance of the traits (days to 50 per cent flowering, plant height, peduncle length, ear head length and panicle exertion) to total divergence at lEast in two environments. The traits such as flag leaf blade width, width of longest finger, 1000 grain weight showed relatively low contribution towards divergence. Clustering analysis using Ward's method (1963) grouped biological races into three clusters: cultivated races *vulgaris*, *plana*, *elongata*, and *compacta* grouped in Cluster I and wild races *spontanea* in Cluster II and *africana* in Cluster III. Geographical regionwise there were four clusters: America and Europe grouped in Cluster I, South Asia, East Africa and Southern Africa grouped together in Cluster II., central Africa in Cluster III and west Africa in Cluster IV. The clustering pattern revealed highly diverse nature of composite collection based on racial and regional diversity.

Accessions for various important traits were selected for use in improvement programme: early flowering (24); high grain yield (36), fodder yield (17); more fingers (21); basal tiller number (19) and ear head length (20). Extensive evaluation of these accessions in different locations will be useful for identifying their agronomic potential and stability. The accessions with high iron (Fe) content (IEs 5941, 2572, 3475, 4545, 4734) and Zinc (Zn) content (IEs 5870, 2589, 5941, and 3045) were identified as a good source material for micronutrients content in grain.

The DNA was extracted by 96 well plate mini preparation method. Twenty polymorphic markers were identified. Using ABI 3700 automated sequencing platform at ICRISAT, 20,000 (1000 accessions x 20 SSR loci data) data points were generated. The data set of 20 SSR loci on 959 accessions after quality checking were used for statistical analysis using Power Marker V3.0 for estimating basic statistics such as PIC value, allelic richness as determined by a total number of the detected alleles and a number of alleles per locus, gene diversity (H_e), occurrence of unique allele, rare and common alleles, and percentage of multiple alleles. The composite collection showed rich allelic diversity (231 alleles, 11.6 alleles per locus, 121 common alleles and 110 rare alleles at

1%). The gene diversity varied from 0.200 to 0.850, with a mean of 0.560. The maximum gene diversity (0.611) was observed in wild *spontanea* race. The average multiple alleles were maximum (13.6%) in wild *spontanea* types and ranged from 1.7 to 9.5 per cent.

Markers UGEP81, UGEP10, UGEP102, UGEP26, and UGEP77 detected the large number of alleles (10-21). The large numbers of multiple alleles were detected in this study in few markers such as UGEP3, UGEP5, UGEP31 and UGEP104. Cultivated finger millet, being the tetraploid, has A and B genomes and marker UGEP3 was detected in both A and B genomes. The remaining markers are linked in the linkage groups were allocated to either the A or B genome supported by two or more loci, this explains occurrence of multiple alleles loci for these markers as well. Markers with high PIC values (>0.636) were UGEP15, UGEP5, UGEP18, UGEP102, UGEP12, and UGEP77. Unique alleles are those detected only in a group of accessions but absent in other groups. Race-specific unique alleles were 37 in *vulgaris*, 5 in *plana*, 4 in *africana*, and 2 in *compacta* while region-specific alleles were 29 in the accessions originating from East Africa, 12 in the accessions originating from South Asia, 11 from Southern Africa, and one each in Central Africa and Europe. The common alleles shared by two groups were 15 for East Africa and South Asia, 5 for East Africa and Southern Africa, and 3 for South Asia and Southern Africa. Unweighted neighbour-joining tree was constructed using simple matching pair wise dissimilarity matrix in DARwin 5.0. A reference set consisting of 300 genetically most diverse accessions have been formed, capturing 206 (89.2%) of the 231 alleles detected in the composite collection. The reference set captured diversity from the entire spectrum of composite collection and can be used for diverse applications in genomics and breeding in finger millet. Association analysis of markers with traits showed inconsistent QTL for many traits. However, QTL UGEP8 in LG3 and UGEP56 in LG6 for days to 50 per cent flowering were consistent at least in two environments indicating relative strong association between marker and traits. Extensive study of these markers in mapping population would be helpful for confirmation of QTL.

ABBREVIATIONS

% : per cent

b : regression coefficient

°C : degree Celsius

Ca : Calcium

Fe : Iron

μg : microgram

μl : microlitre

μM : micromolar

AAT : Asparate Amino Transferase

AFLP : Amplified Fragment Length Polymorphism

APS : Ammonoum Persulphate

bp : base pair

BLUP : Best Linear Unbiased Prediction

C : Chloroform

cDNA : complementary DNA

CGIAR : Consultative group of Agricultural Research

cM : centi Morgan

CTAB : Cetyl Trimethyl Ammonium Bromide

DAF : DNA Amplification Fingerprinting

DNA	: Deoxyribo Nucleic Acid
dNTP	: deoxy Nucleotide Tri-Phosphate
EDTA	: Ethylene Diamine Tetra Acetic acid
FAO	: Food and Agriculture Organization
g	: gram
GCV	: Genotypic Coefficient of Variance
IAA	: Iso-amylAlcohol
ICRISAT	: International Crop Research Institute for the Semi-Arid Tropics
IDH	: Isocitrate Dehydrogenase
ISSR	: Inter Simple Sequence Repeat
H^2	: Broad sense heritability
M	: Molar
MAB	: Marker-Assisted Breeding
MAS	: Marker-Assisted Selection
MDS	: Multi Dimensional Scaling
mg	: milligram
Mha	: Million hectares
ml	: millilitre
mm	: millimetre
mM	: millimolar
Mt	: Million tonnes
ng	: nanogram
QTL	: Quantitative Trait Loci

P : Phosphorus
PCA : Principal Component Analysis
PCoA : Principal Coordinate Analysis
PCR : Polymerase Chain Reaction
PCV : Phenotypic Coefficient of Variance
PHI : Phospho Hexose Isomerase
PIC : Polymorphism Information Content
Pmol : picomole
QTL : Quantitative trait Loci
r : cophenetic correlation coefficient
RAPD : Randomly Amplified Polymorphic DNA
RFLP : Restriction Fragment Length Polymorphism
REML : Restricted Maximum Likelihood
RNA : Ribo Nucleic Acid
RNase : Ribonuclease
rpm : revolutions per minute
SAT : Semi-Arid Tropic
S^2d : mean squared deviations
SE : Standard Error
SSR : Simple Sequence Repeat
STMS : Sequence Tagged Micro-Satellite
t/ha : tonnes per hectare
TBE : Tris Borate EDTA
TE : Tris EDTA

TE : Tris-EDTA

TEMED : N,N.N',N'- Tetra methyl Ethylene Diamine

TNAU : Tamil Nadu Agricultural University

UPGMA : Unweighed Pair Group Method based on Arithmatic Average

UV : Ultraviolet

v : volt

v/v : volume by volume

vol : volume

W : Watt

w/v : weight by volume

Zn : Zinc

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"Trust in the world with all your heart and lean not on your own understanding in all your ways acknowledge Him and He will make paths straight" - Proverbs 3: 5-6

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Coimbatore

(A. Bharathi)

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INTRODUCTION

Finger millet [*Eleusine coracana* (L.) Gaertn], also known as *ragi*, is cultivated for human consumption in Sub-Saharan Africa and South Asia. Precise data of area and production under finger millet is not known because the production statistics of this crop had often been clubbed with other millets. The Consultative Group on International Agricultural Research (CGIAR) has estimated that 10 per cent of the area under millets is with finger millet. Global area under finger millet is 3.38 million hectares with the production of 3.76 million tonnes (FAO, 2007).

Finger millet was domesticated about 5000 years ago in eastern Africa (possibly Ethiopia) and introduced into India, 3000 years ago (Hilu *et al.*, 1979). The closest wild relative of finger millet is *E. coracana* subsp. *africana* (Hilu *et al.*, 1979) which is native of Africa. Finger millet can perform better under adverse soil and weather conditions compared to other crops. Its climatic requirements match with upland paddy crop. The crop has a wide range of seasonal adaptation, and is grown in lands almost at sea level (in parts of Andhra Pradesh and Tamil Nadu, India) to about 2400m above mean sea level in hills of Uttranchal (India), in Uganda, Kenya and Ethiopia. In a trial of nine summer cereal species (rice, job's tears, pearl millet, sorghum, maize, common millet, barnyard millet, foxtail millet, and finger millet) in Japan, finger millet was most resistant to water logging, except rice (Kono *et al.*, 1988). Its reported yield potential is 4265 kg ha^{-1} in Uganda (Odelle, 1993), 6060 kg ha^{-1} in Zimbabwe (Mushonga *et al.,* 1993), 3700 kg ha^{-1} in Ethiopia (Mulatu and Kebebe, 1993) and 4789 kg ha^{-1} in India (Bondale, 1993).

Finger millet seeds are consumed in variety of forms, such as unleavened bread (roti), thin or thick porridge, and fermented porridge, and also used in brewing. Finger millet food has high biological value. Seed protein content is about 7.4 per cent, which is comparable to that of rice. However, some lines with 14.2 per cent protein are reported (Iyengar *et al.*, 1945). Finger millet seeds are particularly rich in tryptophan, cystine, methionine, and total aromatic amino acids compared to other cereals (Kurien *et al.,* 1959). The seeds are exceptionally rich in calcium containing about 0.34 per cent in whole seed compared with 0.01–0.06 per cent in most cereals (Kurien *et al.,* 1959). The seeds are also rich in iron (46 mg kg^{-1}) (Serna-Saldivar and Rooney, 1995), which is much higher compared to wheat and rice. Despite of so many merits, finger millet has remained neglected crop compared to other cereals such as maize, rice, and wheat.

Plant breeders have successfully improved the yield potential of most of the crops, which has resulted in higher production in last four decades, and further progress is not very significant. One of the main reasons for such a situation is that plant breeders tend to use their working collection of highly adapted material (Evans, 1983).

The major genebank holding germplasm of finger millet in the world are ICRISAT (5949 accessions), All India Coordinated Small Millets Improvement Programme (AICSMIP), University of Agricultural Science, Bangalore (6000 accessions), National genebanks of Uganda (1231 accessions), Ethiopia (1989 accessions), Kenya (1500 accessions), Malawi (1000 accessions) and Nepal (869 accessions). The ICRISAT genebank has major holding of finger millet accessions from 23 countries. These accessions have been characterized for a various morpho- agronomic traits. However, a small fraction of these accessions has been used in various national programmes including India (Ramakrishna *et al.,* 1996). This is mainly due to lack of economic importance.

Thus, the large pool of variability instead of prompting more use has created a situation of not knowing where to begin (Upadhyaya *et al.,* 2005). To overcome this problem, Frankel (1984) proposed sampling of the collection to a manageable sample or ‘core collection’. A core collection contains a subset of accessions (10 per cent of entire collection) from entire collection that captures most of available diversity of species (Brown, 1989a). The core collection thus formed can be evaluated extensively and the information derived could be used to guide more efficient utilization of the entire collection (Brown 1989b). Core collections have been established in number of crops, namely, wheat (Zeuli and Qualset, 1993), maize (Taba *et al.,* 1994), barley (Knupffer and van Hintum, 1995), sorghum (Prasada Rao and Ramanatha Rao, 1995; Grenier *et al.,* 2001), quinoa (Ortiz *et al.,* 1998), pearl millet (Bhattacharjee, 2000; Upadhyaya *et al.,* 2009), and finger millet (Upadhyaya *et al.*, 2006a).

The DNA markers have been used to evaluate genetic diversity in different crop species (Cooke, 1995). Various molecular markers are being used for fingerprinting such as Restriction Fragment Length Polymorphism (RFLP) (Dubrail and Charcosset, 1998), Random Amplified Polymorphic DNA (RAPD) (Williams *et al.*, 1990), microsatellites (Smith *et al.*, 2000) and Amplified Fragment Length Polymorphism (AFLP) (Agarwal *et al.,* 1999). Some of these techniques are robust and reliable (e.g., RFLP and AFLP), while some are quick, e.g., RAPD and some others are quick and reliable e.g., microsatellites also known as Simple Sequence Repeats (SSR). The main limitation in the use of RFLP and AFLP markers is that it is time consuming (Kochert, 1994), and requires large amount of DNA (Vos *et al.*, 1995). The PCR based markers such as microsatellites and RAPD have been used in genetic diversity analysis, but microsatellite markers need prior sequence information. The SSR markers offer many advantages such as higher frequency of polymorphism, rapidity, technical simplicity, use of fluorescence, requirement of only a few nanograms of DNA, compatible for high throughput genotyping and feasibility of automation (Semang *et al.*, 2006). Therefore, SSRs has been used to analyze the genetic relatedness in several crop species (Varshney *et al.*, 2001).

The development of gene-based markers based on information derived from model plant is a key component. An important goal of the GCP is extensive genetic characterization, using molecular markers, of the genetic resources held by the participating institutions. Upadhyaya *et al*, (2006b) has developed a global composite collection of finger millet consisting 1000 accessions consisting of 622 accessions of core collection (Upadhyaya *et al.,* 2006a), 222 accessions for various agronomic traits, and 50 accessions from Indian national programme collection, 85 accessions for various stress resistances, 12 accessions for grain nutrition traits, and 9 accessions possessing most genetic diversity in the ICRISAT collection. Further assessment of genetic diversity and dissection of population structure, based on morpho-agronomic characters only might be biased because distinct morpho-types can result from few mutations and share a common genetic background. Therefore, molecular markers are essential for explaining whether existing genetic variability, assessed by measuring morpho-agronomic characters, is related to genetic diversity. Measuring alleleic frequencies using molecular markers may assess this. Thus, the present study was undertaken with the following objectives:

1. To assess the phenotypic diversity of global composite collection of finger millet based on morpho-agronomic characters.
2. Identification trait specific accessions for desirable agronomic traits.
3. To assess the genotypic diversity and determine population structure of global composite collection using 20 polymorphic SSR markers.
4. Development of genotype based reference set with 300 most diverse accessions from composite collection.
5. Identification of marker association for quantitative trait loci (QTL) in global composite collection and reference set using 20 SSR markers.

Review of Literature

CHAPTER II

REVIEW OF LITERATURE

Finger millet is highly self-fertilized allotetraploid (2n = 36) derived from the wild tetraploid progenitor *E. coracana* subsp. *africana*. At present 55 to 60 per cent of the finger millet crop is grown in southern and Central Africa, and remaining is produced in India (Rao and Mushonga, 1985).

Finger millet belongs to *Poaceae* family, *Chloridoideae* subfamily, and *Eleusine* genus. Common names in different language are *tailabon* (in Arabic); *cănzi* and *pinyin* (Chinese); *eleusine cultivee, coracan, koracan* (French); *fingerhirse* (German); ragi (Kannada, Telugu); *kelvaragu, aariyam* (Tamil); *maduva* (in some parts of north India) *nachani* (Marathi); *wimbi* (Kiswahili); *kurakkan* (Singala) and *koddo* (Nepali). In several African countries where it is cultivated known by names, *kal dholuo, ugimbi, Kikuyu* (Kenya); *ceyut, bari* (Sudan); *mwimbi, mbege* (Tanzania); *bulo* (Uganda); *ambale, lupoko, mawele, majolothi, amale, bule* (Zambia) and *apoko, zviyo, njera, rukweza, mazhovole, uphoko, poho* (Zimbabwe).

2.1.1 Origin, Evolution and Distribution

Domestication of *E. coracana* started around 5,000 years BC in Western Uganda and Ethiopian highlands and the crop has reached the western ghats of India around 3,000 BC (Mehra, 1963a; Hilu and De Wet, 1976a; Hilu *et al.*, 1979). Cytogenetically, *E. coracana* is reported to be an allotetraploid, from a cross between two wild diploid species. It is suggested that the two genome donors might be from a group of diploid species, *E. indica*, *E. floccifolia*, *E. intermedia, E. tristachya* and *E. verticillata,* all with chromosome number 2n = 18 (Mehra, 1963b; Chennaveeraiah and Hiremath, 1974; Hilu and De Wet, 1976b and Hiremath and Salimath, 1992). The genomic notation of AABB is proposed for *E. coracana* and *E. africana* (Chennaveeraiah and Hiremath, 1974). The diploid species are considered to be potential sources of genome contributors to these polyploid species (Mehra, 1963b; Hilu, 1988; Hiremath and Salimath, 1992). Cytogenetical analysis of the hybrids and chloroplast DNA restriction analysis of diploid and polyploid species have shown that *E. indica* is the donor of A genome to *E. coracana*

Figure:2. 1. origin of finger millet

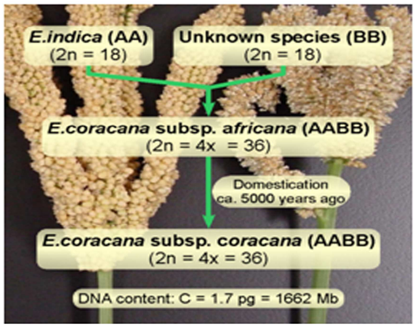
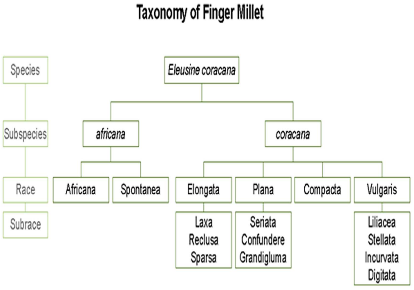


Figure 2.2. Classification of finger millet



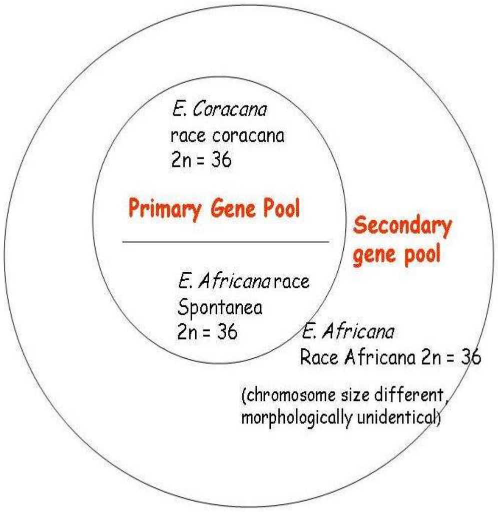


Figure: 2.1 origin, Taxonomy, gene pool of finger millet

(Hilu, 1988 and Hiremath and Salimath, 1992), whereas the B genome donor could be either E. *floccifolia* or *E. tristachya* (Hilu and De Wet, 1976a). The earlier reports of a genetic relationship between *E. coracana* and the diploid species were mainly based on breeding and cytogenetical studies of hybrids and a few molecular studies (Chennaveeraiah and Hiremath, 1974; Hiremath and Chennaveeraiah, 1982; Hilu, 1988; Hilu and Johnson, 1992; Hiremath and Salimath, 1992) (Figure 2.1)

History of finger millet

The genus *Eleusine* comprises of ten annual or perennial grasses. These are commonly occur in the warm regions of the old world, particularly in southern Asia and Eastern and Central Africa. However, *E. indica* has wide distribution in Europe and also in the new world. The term *Eleusine* is derived from Eluesis, an old epic city sacred to Demeter, the Greek deity presiding over agriculture. The term coracana is derived from kurukkan, the Sinhalese name for this grain. Early botanists (De Candolle, 1986: Watt, 1908) and later botonists (Mann, 1946, 1950; Narayanaswami, 1952) suggested a probable Indian origin of finger millet. The earlier authors mentioned that the ancient monuments of Egypt bear no trace of its cultivation in earlier times; and early Greece- Roman authors did not refer to it. In India, finger millet is mentioned by Sanskrit writers and referred as ragi or rajika. Burkhill (1935) suggested that *E. coracana* is the cultigen of the wild species *E. indica (L) Gaertn*, and that its early selection by man appears to have taken place in India since (a) it has been cultivated for a very long time there; (b) it has a Sanskrit name, ragi; (c) it was probably in India when the Aryans reached there; and (d) its spread in Africa from East to West suggests its introduction from the East. Werth, (1937) opinioned E. *coracana* originated in India from where it spread through Arabia, Abyssinia and to the rest of Africa.

2.1.2 Taxonomy

Based on inflorescence compactness and shape, finger millet germplasm is classified into races and subraces. Species *E. coracana* consists of two subspecies *africana* and *coracana*. Subspecies *africana* consists of two wild races a*fricana* and s*pontanea*; and subspecies *coracana* consists of four cultivated races namely e*longata*, *plana*, *compacta*, and *vulgaris*. Each of these races is further classified into subraces. The race e*longata* has three subraces; *laxa, reclusa* and *sparsa;* race *plana* also consists of three subraces; *seriata, confundere* and *grandigluma*; race *compacta* has no subrace*,* while the race *vulgaris* has four subraces, *liliacea, stellata, incurvata* and *digitata* (Prasada Rao *et al.,* 1993). (Figure 2.2)

Subspecies *africana*:

It is a tufted annual, with slender and geniculately ascending culms that branch at the lower nodes. Flowering culms are up to 135cm tall, with leaf blades up to 36 cm long and 10 mm wide. Inflorescence branches are 8- 17cm long and rarely more than 5 mm wide, with the Spikelets arranged in two rows on one side of the rachis. Spikelets have four to nine flowers and are 5-8 mm long. Glumes are shorter than spikelet, lanceolate - oblong in profiles, rarely over 5 mm long and narrowly winged along the keel.

E. coracana is predominately self- fertilized. Subspecies *africana*, however, crosses occasionally with subsp. *coracana* to produce fully fertile hybrids. Derivatives of such crosses are aggressive colonizers and are grouped under the race s*pontanea* (De Wet *et al.,* 1984a).

Subspecies *coracana:*

It includes all cultivated finger millets. Plants are annual, tufted, and erect or with geneiculately ascending culms that are up to 165 cm high and sometimes root from the lower nodes.

Race *vulgaris*: This race is commonly found in Africa and Asia. The inflorescence fingers are reflexed in subrace *liliacea*, twisted in subrace *stellata*, incurved in subrace *incurvata* giving fist-like appearance, and top curved in subrace *digitata* (Figure 2.2).

Race *plana*: This race is characterized by large spikelets that are arranged in two, almost even rows along the rachis, giving the inflorescence branch a flat ribbon-like appearance. In the subrace *seriata*, the spikelets are serially arranged giving a typical ribbon-like appearance, in confundere, the fertile florets are numerous and almost surround the rachis at maturity thus giving a compact appearance to the panicle and in *grandigluma* are characterized by large pointed glumes, which are several times longer than the spikelets (Figure 2.3a).

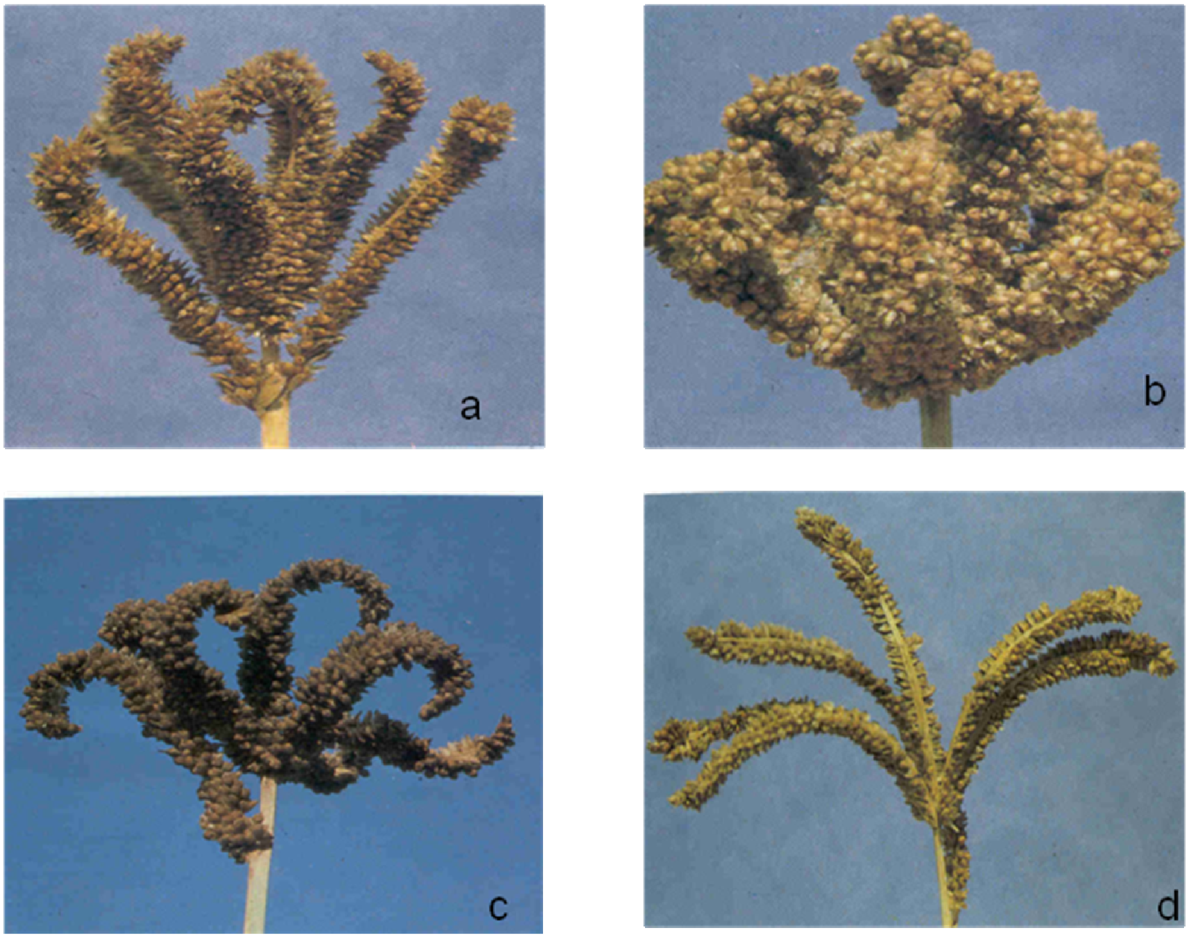


Figure 2.2. Subraces of race Vulgaris
a. Incurvata (Inflorescence branches incurved)
b. Digitata (Inflorescence branches top curved)
c. Liliacea (inflorescence branches reflexed)

d. Stellata (inflorescence branches twisted

Figure 2.3 Subraces of race Plana and Elongata of finger millet

a. Plana 1 Confundere (Spikelets numerous and clustered)
  2 Grandigluma (large pointed glumes)
  3 Seriata (spikelets serially arranged)

b. Elongata
  1 Sparsa (spikelets in clusters)
  2 Laxa (long open fingers, spikelets in rows)
  3 Reclusa (short open fingers spikelets in rows)

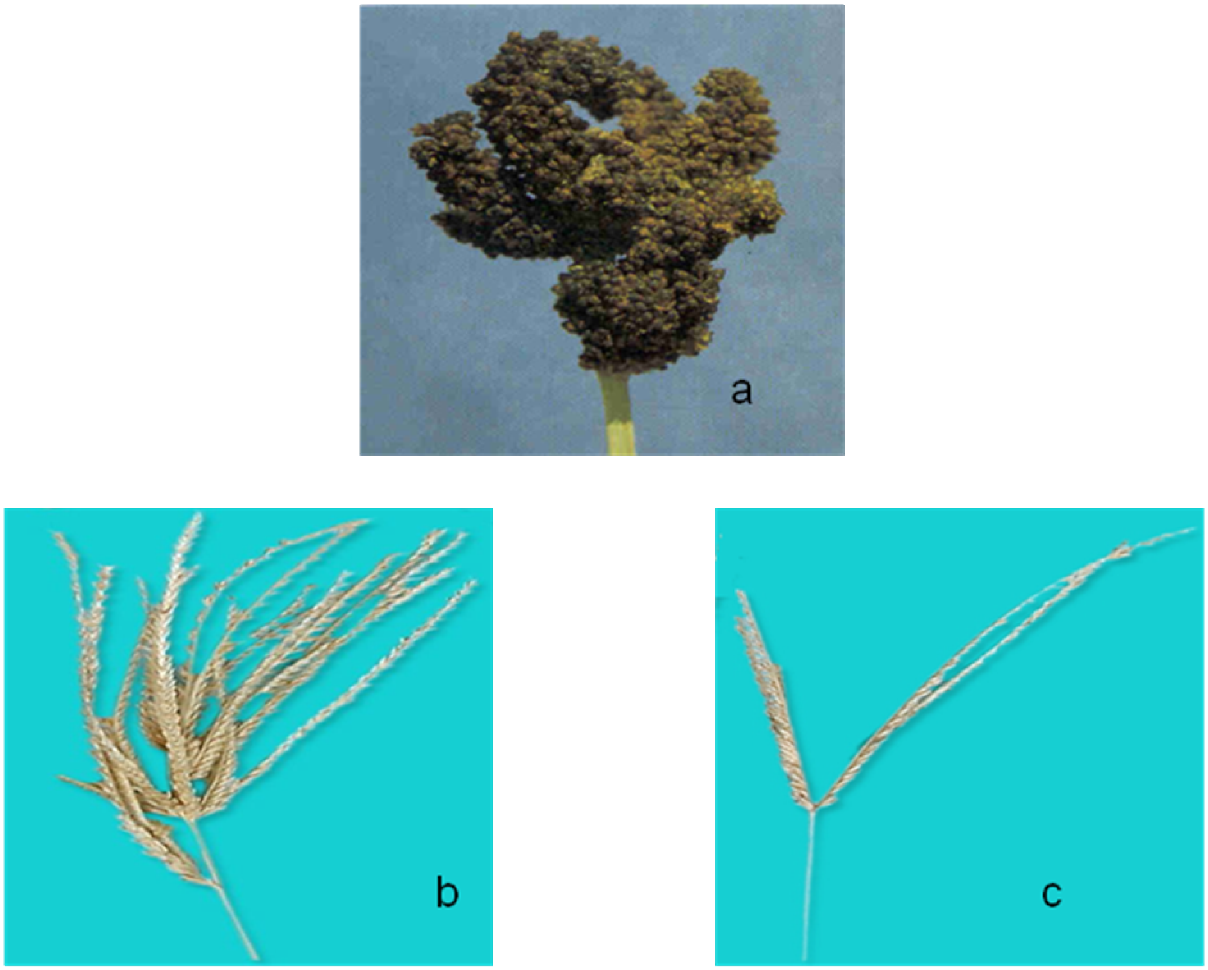


Figure 2.4 Finger millet races

a. **Compacta**

b. **Spontanea**

c. **Africana**

Race *compacta*: Members of this race are commonly referred to as cockscomb finger millets in both Africa and India. Spikelets are composed of nine or more florets, sometimes with the inflorescence axis divided at the base, ascending and incurved at the tip to form a fist-like inflorescence (Figure 2.4).

Race e*longata*: This race is morphologically the most distinct of the four races of finger millet (Prasada Rao *et al.,* 1993). It is characterized by long slender inflorescence branches, digitately arranged, spreading and curved outward at the time of maturity. Subrace *laxa* has long open fingers with spikelets arranged in narrow rows on inflorescence branches, closely resembling wild *africana*, while subrace *reclusa* has short open fingers without any curving out of finger branches. Subrace *sparsa* also has open fingers but spikelets are arranged in clusters on the inflorescence branch with naked space in between (Figure 2.3b).

2.1.3 Finger millet micronutrients

According to recent estimate more than 3 billion people globally suffer from Zn and Fe deficiency (Shankar *et al.*, 2006). There is growing evidence and reorganization that a staggering burden of disease and death is posed by chronic micronutrient-deficiencies even in seemingly healthy people. Deficiency of vitamin A, iron and zinc, are major contributing causes to several health hazards in children and adult people. Among trace elements iron and zinc in edible parts of plants are much lower than the required level for human nutrition. Attempts have been made to improve iron status in some crops, but as such very limited attempts made with regard to zinc. Nearly 49 per cent of global population does not meet their recommended dose, making zinc deficiency. The processing of finger millet (malting, grinding, sprouting, and puffing) reduces anti-nutritional factors, there by resulting in better availability of micronutrients (Sankara Rao and Deosthale, 1983).

Among millets, finger millet was reported to contain high amounts of iron (Ramachandra *et al.*, 1977) ranging from 4.2 - 8.47 per cent. Poor availability (represented by low ionizable iron) in brown varieties is due to their high tannin content which adversely affect nutritional quality of the grains (Udayasekhara *et al.*, 1988). Premavalli *et al.* (2003) have reported 4 - 8 per cent of iron in finger millet based convenience mixes. Mallo *et al.* (1998) reported the range of 2.70 - 5.57 per cent of iron on 12 finger millet varieties. Kadkol and Swaminathan (1954) reported that the proximate analysis of Fe of eight finger millet varieties such as RO862, RO870, RO871, RO883, K1, RCO2 (all brown colored), EC4310 and Majjige (both white) ranged from 5.9 to 6.9 mg/100g. Kamalanathan *et al.* (1971) reported the mean of 12 mg/100g in white seeded finger millet, whereas brown seeded recorded a mean of 17 mg/100g. The iron (3 – 20 mg/100g) were reported for 15 finger millet genotypes (Balakrishna Rao *et al.,* 1973). Indira and Naik (1971) reported the mean of Fe (13 mg/100g) content on five finger millet genotypes.

Zinc is an important constituent of several enzymes. Various studies were conducted and it was reported that a wide range of Zn content depending upon use of genotypes. Madibela and Modiakgolta (2004) reported a mean of 20.5 ppm in forage finger millet and 29.1 ppm in straw of finger millet. Yamuna Rani and Shankar (2006) reported a 27 fold range of Zn content of 1 mg/100g to as high as 27 mg/100g, in 333 genotypes of finger millet. However, Shankar *et al.* (2006) reported a narrow range of 1.5 - 6.5 mg/ 100g zinc on 35 finger millet genotypes.

2.2.1 Germplasm collection and its uses

Genetic diversity in crop plants is continuously being lost in farmer's field and in nature. In this context, genebanks assume paramount importance as reservoirs of biodiversity and source of alleles that can be easily retrieved for genetic enhancement of crop plants. Increasingly, efforts are being made to collect threatened landraces, obsolete cultivars, genetic stocks and wild relatives of cultivated species (Ortiz and Engels, 2004). All these materials are important for crop improvement because breeding gains rely largely on access to the genetic variation in the respective gene pool. International germplasm collections play a major role in securing genetic diversity and promoting its use. This has resulted in assemblage of large collections in national and international genebanks. The finger millet germplasm collection had not been used extensively due to lack of proper evaluation data.

2.2.2 Core collection

Core collections (Frankel and Brown, 1984; Brown 1989a and 1989b), which represent the genetic diversity of crop species and its wild relatives, were proposed to enhance the use of germplasm held in the collections. The core collection should contain about 10 per cent of the total number of accessions, such as that it represents the possible diversity in the collection.

Using sampling theory of selectively neutral alleles, Brown (1989a) suggested the about 10 per cent sample size of the entire collection with an upper limit of 3000 per species would effectively retain about 70 per cent of the alleles in the sample. However, Crossa (1989) suggested a slightly different approach for cross-pollinated crops. He proposed the use of probability models and determined optimal sample size with 95 per cent probability of including at least one copy of alleles with a given frequency. For example, if there are 50 loci with four alleles each, 156 individuals are required to retain at least one copy of alleles with 95 per cent probability and with a frequency of 0.05. Although finger millet is highly self-pollinated crop, with lack of information on number of loci and alleles per locus has not allowed use of this method in developing the core collection.

Ever since the concept of core collection is developed, a number of core collections have already been established for many crop species including perennial glycine (Brown *et al.,* 1987), peanut (Holbrook *et al.*, 1993), perennial medicago species (Diwan *et al.,* 1994, Basigulp *et al.,* 1995), sorghum (Prasda Rao and Ramanath Rao, 1995), common bean (Tohme *et al.,* 1995), okra (Mahajan *et al.,* 1996), quinoa (Ortiz *et al.,* 1998), alfalfa (Skinner *et al.,* 1999), sweet potato (Huaman *et al.,* 1999) and safflower (Dwivedi *et al.,* 2005).

2.3. Phenotypic diversity

Finger millet has not been extensively investigated for the purpose of understanding of diversity, taxonomic relations and evolution of the crop. Traditionally, diversity studies and inter- relationship in finger millet have been undertaken using morphological and cytogenetical traits and methods of numerical taxonomy. As such these studies have been of limited help to plant breeding programmeme. The research on finger millet was initiated as early as 1910 by Coleman, and later in 1930 by Ayyangar and his group. Ayyangar (1931) described variability in inflorescence. Mehra (1963a) studied rachis width, stem width, raceme width, spikelet length, glume length, by metroglyph analysis and differentiated four taxa such as *E.indica*, *E.africana* (wild types), *E.coracana* (Afro-Asiatic type) and *E.coracana* (African highland type). Kempanna and Govindu (1969a) reported the variation of plant habit, maturity structure and composition of the ear and glume and grain colour in 78 African collections.

Goud and Laxmi (1977) reported the wide phenotypic and genotypic variations for tiller number, ear number and ear weight in 33 cultivars. Suyambulingam and Jebarani (1977) grouped 50 collections of finger millet into 6 clusters consisting major cluster of 34 genotypes.

Kempanna and Govindu (1969a) reported the range and pattern of variations in leaf sheath, plant height, maturity and ear morphology in 541 Indian collections. Kempanna (1969) reported the results of 617 world collections and discussed the wide range of variations in plant height and maturity. Hussaini (1973) reported the diversity of 640 germplasm lines from the world collection and found highly significant differences among the germplasm lines for the 18 characters studied. Mallana *et al.* (1978) reported variability pattern of 1064 accessions from diverse geographic origins and reported wide variability among the accessions.

The phenotypic variability of finger millet was reported by several workers (Prabhakar and Prasad, 1983, Goswami and Asthana, 1984, Abraham *et al.,* 1989, Verma, 1989, Rao, 1991, Naik *et al.,* 1993, Dhanakodi, 1994, Ravikumar and Seetharam, 1994, Ramasamy *et al.,* 1994, Thakur and Saini, 1995, Chunilal *et al.,* 1996, Ravishankar *et al.,* 1997, Bandyopadhyay, 1998, Mahto *et al.,* 2000, Anantharaju, 2001, Yazhini, 2006).

Rao *et al.* (2005) studied the variability among F_2 generation of three crosses (Indaf 5 x GE1462, PR 202 x GE1409 and Indaf 9 x GE1409) and reported high variability, heritability and genetic advance for the traits grain yield, number of tillers and plant height. It indicated that the predominance of additive gene action controlling these traits (Prabhakar and Prasad, 1983). The similar kind of results was reported by Sivagurunathan *et al.* (2006a).

Genetic diversity of 185 finger millet accessions were reported in two locations ICRISAT, Patancheru and MS Swaminathan Research Foundation (MSSRF), Chennai (Geetharani, 2005), reported that mean diversity (H') 0.022 of minimum diversity (0.032) between IE3101 and IE3220, and maximum diversity (0.464) between IE588 and IE2790 at ICRISAT location, and mean diversity of 0.149, minimum diversity (0.019) between IE3196 and IE3952, maximum diversity (0.337) between IE2689 and IE3101 at MSSRF location.

Upadhyaya *et al.* (2006a) has developed a set of core collection in finger millet which constituted 622 accessions (10.47%) form the entire collection 5940 accessions conserved in ICRISAT gene bank. This core collection was developed based on agro morphological diversity, and the core collection represented the entire collection. Upadhyaya *et al.* (2006b) developed a set of composite collection consisting of 1000 accessions.

Upadhyaya *et al.* (2007a) reported that the diversity pattern of 909 finger millet accessions introduced from southern and eastern African region from ICRISAT gene bank and observed large variability for days to 50 per cent flowering, plant height and inflorescence length. Bedis *et al.* (2006) reported the phenotypic diversity among thirty seven finger millet accessions and identified significant variability for days to flowering, days to maturity, plant height ear length, number of fingers, fodder yield and grain yield.

Table: 2.1 List of literature on genetic diversity in finger millet

Number of genotypes studied	Number of characters studied	Number of clusters observed	Maximum contributing traits to total divergence	Authour(S)
64	18	12	NR	Hussaini *et al.* (1977)
50	6	6	Number of tillers	Suyambulingam and Jebarani (1977)
175	15	21	NR	Swaminathan (1979)
60	11	20	Straw yield and days to 50 per cent flowering	Xavier (1979)
30	12	13	NR	Jain *et al.* (1981
150	NR	2	NR	Shigeta (1985)
120	6	10	NR	Patel (1989)
100	13	18	NR	Singh and Singh (1991)
20	9	4 (rainfed) 11 (irrigated)	Days to 50 per cent flowering, plant height, ear length, ear weight and grain weight	Sheriff (1992)
50	11	12	Days to 50per cent flowering	Reddy *et al.* (1993)
46	8	5	Number of days to maturity, followed by ear length, number of finger per ear and harvest index	Jaylal and Haider (1994)
48	1	6	Grain yield	Ramasamy *et al.* (1996)
50	11	14	Seed yield	Gupta and Srivastava (1997)
36	7	7	NR	Kailash Kumar *et al.* (1997)
57	6	7	Days to maturity, seed yield per plant and productive tillers per plant	Hanumanaram *et al.* (1997)
48	6	10	NR	Ramasamy *et al.* (1997)
99	7	10	NR	Suryakumar *et al.* (1997)
36	2	8	NR	Vadivoo *et al.* (1998)
50	10	14	Days to 50 per cent flowering	Anantharaju (2001)

NR- Not reported

2.4 Molecular diversity

Traditionally, genetic variation is inferred by morphological/ phenotypic variation or the growth response of the organism. Many researchers have also used cytological tools for such studies. Classical methods of establishing genetic diversity and / or relatedness among groups of plants relied upon phenotypic (observable) traits. However, these had two disadvantages: quantitative traits were subject to environmental influences; secondly the levels of polymorphism (allelic variation) that could be looked at were limited. These limitations were significantly overcome by deployment of environment–neutral biochemical makers (Isozymes) and protein electrophoresis and molecular markers that focus directly on the variation controlled by genes or on the genetic material (DNA). The higher resolution of molecular markers makes them a valuable tool for finger printing and protection of breeder’s rights, facilitating appropriate choice of parents for breeding programmemes, analyzing quantitative traits and detection of Quantitative Trait Loci (QTLs), gene mapping, marker assisted selection and gene transfer, understanding evolutionary pathways and for the assessment of genetic diversity. Hills (1987) recommended that morphological work on large samples combined with molecular analyses on smaller samples maximizes both information and usefulness. Kresovich and McPherson (1992) reported that molecular markers could resolve biological, operational and logistical questions dealing with four broad areas of germplasm characterization: Determination of the correct identity of an individual (whether it i.e. true to type, duplicate etc,), Estimation of the degree of similarity among individuals, Understanding of the hierarchical structure and partitioning of variation among individuals, accessions, populations and species, Identification and detection of the presence of particular alleles in individuals, accessions, populations, chromosomes or cloned DNA segments.

Genotyping of complete or a significant proportion of the genebank collections provides information to improve the management of plant genetics resources in manifold ways. In this context, storing and managing genotyping data of genebank materials obtained by using molecular markers is important.

The range of molecular markers that can be used on most plant germplasm is quite extensive (Mohan *et al.,* 1997, Gupta and Varshney, 2002). Techniques vary from identifying the polymorphism in the actual DNA sequence to the use of DNA hybridization methods used to identify RFLPs (Restriction Fragment Length Polymorphisms) or the use of PCR based (Polymerase Chain Reaction) technology to find polymorphism using RAPD (Random Amplified Polymorphic DNA), microsatellites such as SSR (Simple Sequence Repeat) or combination techniques such as AFLP (Amplified Fragment Length polymorphism). The different methods differ in their cost, ease of application, type of data generated (whether it provides dominant or co-dominant markers) the degree of polymorphism they reveal, the way they resolve genetic difference, and in the taxonomic levels at which they can be most appropriately used (Karp *et al.,* 1997).

2.4.1 Microsatellite markers

The genomes of higher organisms contain three types of multiple copies of simple repetitive DNA sequences (satellite DNAs, minisatellites, and microsatellites) arranged in arrays of vastly differing sizes (Armour *et al.,* 1999). Microsatellites (Litt and Luty, 1989), also known as SSRs (Tautz *et al.,* 1986), short tandem repeats or simple sequence length polymorphisms (Mc Donald and Potts, 1977), are the smallest classes of simple repetitive DNA sequences. Some authors (e.g. Armour *et al.,* 1999) define microsatellites as 2-8 bp repeats, others like Goldstein and Pollock (1997) as 1-6 bp or even 1-5 bp repeats (Schlotterer, 1998). Chambers and MacAvoy (2000) suggested following a strict definition of 2-6 bp repeats, in line with the descriptions of the original authors. Microsatellites are born from regions in which variants of simple repetitive DNA sequence motifs are already over represented (Tautz *et al.,* 1986). These markers often present high levels of inter and intra specific polymorphism, particularly when tandem repeat number is ten or greater (Queller *et al.,* 1993)

The SSRs are now the marker of choice in molecular genetics as they are highly polymorphic, require low amount of DNA, can be easily automated for high throughput screening, can be exchanged between laboratories, and are highly transferable between populations (Gupta *et al.,* 1999). The SSRs are mostly co-dominant markers, and are indeed excellent for studies of population genetics and mapping (Jarne and Lagoda, 1996, Goldstein and Schlotterer, 1999). The SSR based primers have been used successfully to generate distinct banding patterns that are resolvable on low- resolution agarose gels using ethidium bromide staining (Gupta *et al.,* 1994: Weising *et al.,* 1995), on high resolution polyacrylamide gels by silver staining (Buscot *et al.,* 1996), through primer radio active labeling followed by autoradiography (Gupta *et al.,* 1994), or through primer labeling with fluorescent dyes and automated high resolution visualization of PCR products separated by PAGE (Poly Acrylaminde Gel Electrophresis) or capillary electrophoresis (Kresovich *et al.,* 1992). Further automated high resolution visualization of dye – labeled PCR products allows effective allele size discrimination of 1bp. Post PCR multiplexing involving the simultaneous separation of PCR amplification products of several SSR loci in a single gel lane or capillary reduces the time and money required in SSR based assays (Masi *et al.,* 2003). The fluorescent primers in combination with automatic capillary or gel based DNA sequencers are now used in most advanced laboratories and SSRs are excellent markers for fluorescent techniques, multiplexing and high throughput analysis. Other considerations include obtaining products from various loci with non-overlapping ranges of allele sizes, which can be amplified with similar efficiency under a standard set of conditions and enables multiplexing for high throughput analysis (Schlotterer, 1998)

2.4.2 Applications of DNA markers in genetic diversity studies

Genetic diversity refers the variations within the individual gene loci / among alleles of a gene, or gene combinations, between individual plants or between plant populations. Genetic diversity has several ‘indicators’, which are measured using various tools such as classical or Mendelian genetic analysis, that can be employed to evaluate variation in single known gene (qualitative traits), such as resistance to disease (Smale and Mc Bride, 1996). The classical methods of diversity studies are based on morphological characters, which are influenced by various environmental factors. However, the molecular markers, which are unrestricted in number and not influenced by the environment, have the ability of sampling diversity directly at the genome level. The molecular biology tools provide detailed information about the genetic structure of natural population, which was not available in the past (Statkin, 1987).

2.4.3 Genotypic diversity studies in finger millet

A few studies on phenotypic diversity of finger millet are reported, but there are very limited studies at molecular level. Earlier reports of genetic relationship between *E. coracana* and the diploid species were mainly based on breeding and cytogenetical studies of hybrids and a few molecular studies. Cytogenetical studies (Chennaveeraiah and Hiremath, 1974, Hiremath and Chennaveeraiah, 1982) suggested that finger millet is an allopolyploid, derived directly from the wild tetraploid *E. coracana subsp. africana* (Kennedy-O'Byrne, 1957; Hilu and De Wet, 1976). Evidence from chloroplast DNA (cp DNA) nucleotide sequence similarities further substantiates the direct origin of the crop from sub sp *africana* (Hilu *et al.,* 1979; Hilu, 1988).

Evolutionary divergence among species or other related taxa, accompanied by quantitative changes in nuclear DNA content, is well documented. (Price, 1976, 1988a, Raina, 1990). This variation in genome size could be due to several mechanisms, such as environmental and/ or genetically induced genomic rearrangements (Price, 1988b), transposition (Doolittle, 1985, Dyson and Sherratt, 1985), gene duplication (Maclean, 1973), salutatory amplification (Britten and Kohne, 1968), unusual crossing over and errors in DNA replication (Dyson and Sherratt, 1985).

Differences in nuclear genome size with in the genus *Eleusine* have been investigated using Felugen microdensiometery by Hiremath and Salimath (1991). These authors determined the nuclear DNA amount in accessions of all the *Eleusine* species and reported a 2 to 2.5-fold variation in DNA content. The DNA amount in the diploid species ranged from 2.5 pg (*E. verticullata*, 2n=18) to 3.35 pg (*E. inermediata*, 2n=18). The tetraploid species showed a range from 4.95 pg (*E. coracana subsp africana,* 2n= 36) to 6.13 pg (tetraploid accessions of *E. floccifolia,* 2n=36). Mysore and Baird, (1997) reported nuclear DNA content of six to seven species that were 15 to 50 per cent less than previously reported. Hilu and Johnson (1992) studied the ribosomal DNA variation in finger millet and wild species of *Eleusine*.

Salimath *et al* (1995) experimented with three different DNA marker techniques, *viz.,* RFLP (8 probe-3-enzyme combination), RAPD (18 primers) and ISSR (6 primers) to analyze the diversity of 22 accessions belonging to 5 species of *Eleusine*. The results revealed 14, 10, and 26 per cent polymorphisms in 17 accessions of *E. coracana* from

Africa and Asia and very low level of DNA sequence variability in finger millet. They suggested that the ISSR marker was good as compared to RFLP and RAPD in terms of the quantity and quality of data output.

Muza *et al.* (1995) reported diversity of 26 germplasm lines of finger millet from Africa and India based on the southern blot hybridization patterns obtained with maize and sorghum mitochondrial cloned gene probes with five restriction endonuclease enzymes. A total of 20 enzyme/probe combinations observed a low level of polymorphism/ with identical RFLP banding patterns in 23 of the 26 lines. Based on this data, 26 germplasm lines were classified into 3 cluster groups**.**

Salimath *et al.* (1995) reported molecular diversity of 20 finger millet accessions by using isozyme, RFLP and RAPD. Sixteen isozyme loci and 15 RFLP loci showed uniformity among the accessions indicating less genetic diversity among the accessions.

Wang *et al.* (2005) made an attempt to identify the transferability of 210 SSR markers from major cereal crops (wheat, rice, maize, and sorghum) to *E. coracana* and *more* than half (57%) of the SSR primers screened, generated reproducible cross-species or cross-genus amplicons. They described that the transfer rate of SSR markers was correlated with the phylogenetic relationship or genetic relatedness.

Babu *et al.* (2007) reported the diversity of 32 finger millet genotypes, using 50 RAPD markers and reported a total 529 loci of which 479 loci (91%) were polymorphic and informative to differentiate the accessions and do cluster analysis. They grouped the 32 finger millet accessions into two major clusters, and genotypes GEC 182 and CO 12 were distantly related with a low similarity index of 0.315 and also differed considerably in days to flowering and grain weight.

Diversity of 30 finger millet genotypes by using 13 RAPD primers was reported by Das *et al.,* (2007). A total of 124 distinct DNA fragments ranging from 300 to3000 bp were reported. The genetic similarity and cluster analysis based on similarity coefficient indicated two major clusters, first major cluster had one genotype and a second major cluster contained 29 genotypes.

Dida *et al.*, (2007) developed a first genetic map of finger millet by using RFLP, AFLP, EST and SSR markers. The map span was 721 cM on the A genome and 787 cM on the B genome and cover all 18 finger millet chromosomes. They developed a set of 82 SSR markers specific for finger millet by small-insert genomic libraries generated using methylation-sensitive restriction enzymes and among them, 31SSRs were mapped. Comparative analysis of this map with rice genetic map (International rice genome sequencing project, 2005) was a novel attempt reported high level of conserved co-linearity between the finger millet and rice genomic (Srinivasachary *et al.,* 2007).

Recently, Dida *et al.* (2008) reported the population structure of 79 finger millet accessions with 45 SSR markers and identified significant difference of plant architecture and yield in Asian and African subpopulation.

Materials and Methods

CHAPTER-III

MATERIALS AND METHODS

The present investigation was undertaken to assess phenotypic and genotypic diversity in the global finger millet composite collection developed at the International Crops Research Institute for the Semi Arid Tropics (ICRISAT), Patancheru. The second component involved was identifying the trait specific accessions including yield and grain nutritional traits such as zinc and iron. The finger millet germplasm collection conserved in the ICRISAT genebank, Patancheru holds 5949 accessions (consists of 5658 land laces, 136 advanced cultivars, 50 breeding lines, and 105 wild species) is one of the largest collection of finger millet in the world. These collections have been characterized at ICRISAT, Patancheru research farm over the years from 1974 to 2005.

3.1. Phenotypic diversity

3.1.1 Genetic materials

The genetic material for the study was the global composite collection was developed at ICRISAT in collaboration with the Generation Challenge Programmeme (GCP) consisting of 1000 diverse finger millet (Upadhyaya *et al.*, 2006b). It included 622 accessions of core collection (Upadhyaya *et al.*, 2006a), 222 accessions for various agronomic traits, and 50 accessions from Indian national programme core collection, 85 accessions for various stress resistances, 12 accessions for grain nutrition traits, and 9 accessions possessing most genetic diversity in the ICRISAT collection. Race wise, the composite collection consisted of 579 accessions from race v*ulgaris* [subraces *incurvata* (249 accessions), *digitata* (230), *stellata* (64) and *lilacae* (36)], 207 accessions from *plana* [subraces *confundere* (183), *seriata* (14) and *grandigluma* (10)], 132 accessions from *compacta,* 71 accessions from *elongata* [subraces *reclusa* (31), *sparsa* (20) and *laxa* (20)] and 7 from *spontanea* and 3 from *africana*. Geographical origin wise, composite collection included accessions from South Asia (328 accessions), East Africa (362), southern Africa (261), West Africa (7), Central Africa (3), Europe 7, America (5) and unknown origin (27) (Table 3.1 and Figure 3.1.a).

Table: 3. 1 Composition of global finger millet composite collection according to the country of origin, races and sub races

Country of Origin	**Biological races**													**Total**
	vulgaris				***plana***			***elongata***			***compacta***	***africana***	***spontanea***	
	Sub race				**Sub race**			**Subrace**						
	digitata	***liliacea***	***stellata***	***incurvata***	***confundere***	***grandigluma***	***seriata***	***laxa***	***reclusa***	***sparsa***				
America (5)														
Mexico	1	-	-	-	-	-	-	-	-	-	-	-	-	1
USA	1	-	-	-	2	-	1	-	-	-	-	-	-	4
Central Africa (3)														
Cameroon	-	-	-	-	-	-	-	-	-	-	-	-	3	3
East Africa (362)														
Burundi	-	-	-	2	-	-	-	-	-	-	-	2	1	5
Ethiopia	-	-	-	1	-	-	-	1	2	-	-	-	-	4
Kenya	31	2	6	12	53	2	2		1		28	-	-	137
Tanzania	6	-	1	-	2	-	-	1	-	-	1	-	-	11
Uganda	30	-	7	55	69	-	1		5	-	37	1	-	205
Europe (7)														
Germany	-	1	-	-	-	-	-	-	-	-	-	-	-	1
Italy	2	-	-	-	1	-	-	-	-	-	-	-	-	3
United Kingdom	1	-	1	1	-	-	-	-	-	-	-	-	-	3
South Asia (328)														
India	42	27	34	90	17	2	4	3	13	2	15	-	-	249
Maldives	-	1	-	1	-	-	-	-	-	-	-	-	-	2
Nepal	11	4	13	20	2	-	-	-	-	16	8	-	-	74
Pakistan	-	-	-	1	-	-	-	-	-	-	-	-	-	1
Sri Lanka	-	-	-	1	-	-	-	-	-	-	1	-	-	2
Southern Africa (261)														
Malawi	24	-	-	13	13	5	2	14	7	-	7	-	2	87
Mozambique	-	-	-	-	-	-	1	-	-	-	-	-	-	1
Zambia	13	-	-	7	5	-	-	-	-	-	13	-	-	38
Zimbabwe	59	-	-	34	11	1	3	-	4	1	21	-	1	135
West Africa (7)														
Nigeria	-	1	-	3	-	-	-	1	-	1	-	-	-	6
Senegal	-	-	-	1	-	-	-	-	-	-	-	-	-	1
Unknown (27)	9	-	2	7	8	-	-	-	-	-	1	-	-	27
Total	230	36	64	249	183	10	14	20	32	20	132	3	7	1000
Numbers in parenthesis are number of accessions to particular region														

This composite collection was developed based on morpho-agronomic traits including 18 quantitative and 6 qualitative traits (Upadhyaya *et al.*, 2006). The passport, origin and characterization details are given in the appendix 1.

3.1.2 Evaluation of finger millet germplasm:

The finger millet composite collection was evaluated during 2005/2006) post rainy (E1) at Coimbatore, 2006 rainy (E2) and 2007 rainy (E3) seasons at ICRISAT Centre, Patancheru, thus constituting three environments (E1, E2 and E3 respectively) (Figure 3.1.b). Agro-climatic conditions of the two locations and mean sea level (MSL) are given in table 3.2 and the map illustrates the location where the germplasm was evaluated.

The experiments were conducted in alfisol fields in all three environments on ridges spaced 60 cm apart. Plant to plant spacing was 10 cm and the length of each row was 4 meters. so as to accommodate 40 plants. An augmented design with four check cultivars (VR708, VL149, PR202 and RAU8) were used and repeated after every nine test accessions. Normal agronomic practices were followed to raise the crop.

Table: 3.2 Meteorological details of evaluation locations of finger millet composite collection

Environ -ments	Location	Season	Temperature (°C) range	Average annual rainfall (mm)	Attitude (m)	Latitude	Longitude
E1	Millet Breeding station, TNAU, Coimbatore	Post rainy (February to June, 2006)	21-42	700	426	11°02" N	76°57" E
E2	Red Campus East, 23 North, ICRISAT Centre, Patancheru	Rainy (June to December, 2006)	19-38	1700	545	17º 32' N	78º 16' E
E3	Red Campus East 23 South, ICRISAT Centre, Patancheru	Rainy (June to December, 2007)	18-36	1550	545	17º 32' N	78º 16' E

3.1.3.1 Observations recorded

Observations on selected morphological characters were recorded during all the three seasons according to finger millet descriptors (IBPGR, 1985). The data on all the six qualitative traits and days to 50 per cent flowering and days to maturity were recorded

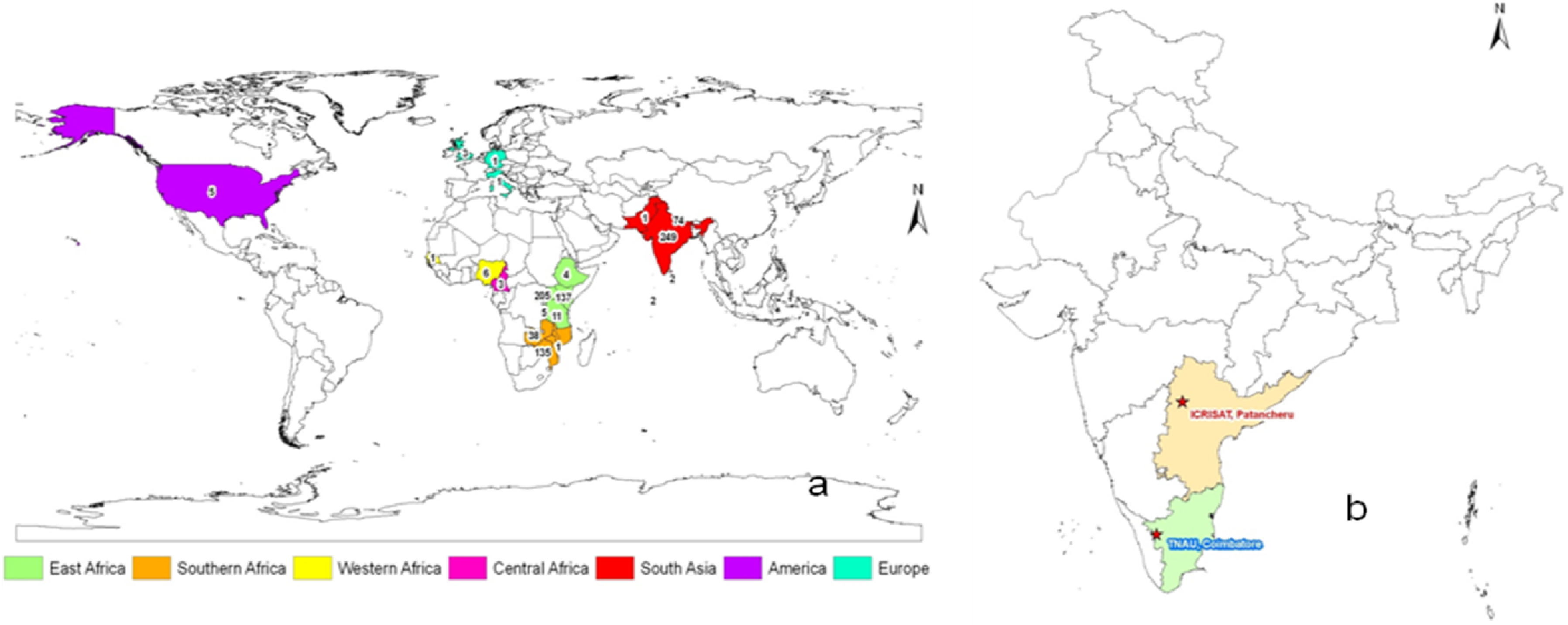


Figure: 3.1. a. Accessions represents respective geographical region of origin
3.1.b. Sites of characterization fields of finger millet composite collection

on row basis. Data for the remaining quantitative traits were recorded on five representative plants from each row.

Table: 3.3 List of qualitative characters studied

S No	Trait	Description
1	Growth habit	Decumbent Erect Prostrate
2	Plant pigmentation	Non pigmented Pigmented
3	Inflorescence compactness and shape	Long open Compact Fisty Top curved Pendulous Short open Incurved Laxa
4	Glume prominence	No prominence Low prominence Medium prominence High prominence
5	Grain colour	Ragi brown Dark brown Light brown Reddish brown White
6	Lodging	No lodging Slightly lodging Medium lodging Mostly lodging Completely lodging

Table: 3. 4 List of quantitative characters studied

S. No	Trait	Description
1	Days to 50 per cent flowering (days)	From sowing to stage when ears have emerged from 50 per cent of main tillers
2	Plant height (cm)	From the ground level to tip of inflorescence at dough stage
3	Basal tillers (numbers)	Number of basal tillers which bears mature ears
4	Culm branching (numbers) (recorded only on E1 and E2)	Number of culm branches at maturity
5	Flag leaf blade length (mm)	Measured from ligule to tip of fourth blade from top at flowering
6	Flag leaf blade width (mm)	Measured across centre of fourth leaf from top at flowering
7	Flag leaf sheath length (mm)	Measured from node to ligule of flag top at flowering
8	Peduncle length (mm)	From top most node to base of the thumb finger
9	Panicle exsertion (cm) (recorded only on E2 and E3)	From top of leaf sheath to base of inflorescence at dough stage
10	Ear head length (mm)	From base tip of inflorescence to top of inflorescence at dough stage
11	Ear head width (mm)	Measured across the inflorescence at dough stage
12	Length of longest finger (mm) (recorded only on E2 and E3)	From the base tip of longest spike from main tiller at dough stage
13	Width of longest finger (mm) (recorded only on E2 and E3)	Measured across centre of longest finger at dough stage
14	Finger per inflorescence (number)	The number of fingers present in the main ear head at dough stage was counted
15	Days to maturity (days) (recorded only on E1)	From sowing to stage when 50per cent of main tillers have mature ears.
16	Single panicle weight (g) (recorded only on E3)	The average weight of single panicle
17	1000 grain weight (g) (recorded only on E2)	The weight of random sample of 1000 seeds from the total harvest of an accession was expressed in grams.
18	Grain yield per hectare (t ha^{-1})	The total yield potential observed in the accessions in post harvest

3.1.4 Statistical analysis

Data on all quantitative traits were analyzed following Residual Maximum Likelihood (REML) method for the three environments separately on Genstat 8.1. Homogeneity of variance was tested by using Bartlett's test of homogeneity (Snedecor and Cochran, 1980). Variance was not homogeneous for 14 out of 18 traits and therefore, Meta analysis was performed for the data of three environments together. Environment/season was considered as fixed and genotypes and blocks as random. Variance components due to genotype (δ^2g) and genotype x environment influence (δ^2ge) their standard errors (SE) were estimated. Significance of variance components was tested against their respective standard errors and environments/seasons by Wald statistics.

Mean and range of all quantitative traits in individual environment and pooled were calculated. Means of group of races and regions were compared using Newman-Keuls (Newman 1939; Keuls, 1952) procedure. The homogeneity of variances among the groups was tested using Levene's test (Levene 1960). Phenotypic and genotypic coefficients of variations were calculated based on the method advocated by Burton (1952)

Heritability in broad sense was estimated from the phenotypic and genotypic components of variance using the formula suggested by Lush (1940) for each character as given below:

Heritability broad sense (h^2) =genotypic variance (σ^2g)/ phenotypic variance (σ^2p) where $\sigma^2 p = \sigma^2 g + \sigma^2 ge / n_e + \sigma^2 e / (n_r \text{ x } n_e)$

where n_e - the number of environments

n_r - the number of blocks.

The association between yield and component traits and among themselves was computed based on phenotypic correlation co-efficients (Goulden, 1952). Referring to the standard table given by Snedecor (1961) the significance of phenotypic and genotypic correlation co-efficients were tested.

Path co-efficient analysis was used to partition the correlation coefficient into components of direct and indirect effects. By keeping yield as a dependent variable and the other traits as independent variables, simultaneous equation, which express the basic relationship between path coefficients were solved to estimate the direct and indirect effects. The direct and indirect effects were classified as follows based on the scale given by Lenka and Misra (1973). Eberhart and Russell (1966) method was followed to estimate the three parameters of stability *viz.,* mean, regression coefficient (bi) and mean squared deviations (S^2d) for each genotype.

The mean observations for all traits for each season were standardized by subtracting the mean value of the character from each observation and subsequently dividing by its respective standard deviation. These standardized values, with average 0 and standard deviation of 1, were used for Principal Component Analysis (PCA) on Genstat 8.1 to know the importance of different traits in explaining multivariate polymorphism. Cluster analysis was performed based on geographical origin and biological races group using the scores of first four PCs following Ward (1963).

3.1.5 Identification of trait specific accessions for high micronutrient content (Iron and Zinc)

Estimation of Iron and Zinc

The 65 accessions from composite collection were used to estimate iron (Fe) and zinc (Zn) along with 2 check cultivars (VL149 and PR202). The method of estimation of both elements is given below.

Grain samples from single plants of the 65 accessions raised during the 2006 rainy season were analyzed for Iron and Zinc in Central Analytical Laboratory, ICRISAT Centre Patancheru. Finger millet grain Fe and Zn content was determined by triacid mixture method (Sahrawat *et al.,* 2002). The grain samples were finely ground (< 60 mesh for grain samples) using cyclone mill then oven dried at 60°C for 48 h before analysis.

Ground and dried grain samples of 0.5 g were transferred to 125 ml conical flasks. Twelve ml of tri-acid mixture of nitric acid, sulfuric acid and perchloric acid (9:2:1(v/v)) were added to the flasks. The flour samples were digested in a room temperature for 3 h followed by digestion for 2 – 3 hours on a hot plate, until the digest was clear or colorless. The flasks were allowed to cool and contents were diluted to an appropriate volume. The digests were used for Fe and Zn determination using Atomic Absorption Spectrophotometry (AAS). The mean content of iron and zinc was calculated.

3.2 Molecular Diversity

Although the global finger millet composite collection was developed based on phenotypic data for several morphological and agronomic traits, the current study is the first effort to assess genetic diversity at DNA level. The composite collection of finger millet was planted at ICRISAT, Patancheru in the 2nd week of June 2006 and DNA was extracted from single representative plant in each accession.

3.2.1 Genomic DNA isolation

Total genomic DNA was isolated from newly expanded leaves by using a modified CTAB method (Saghai-Maroof *et al.*, 1984). DNA was further purified by RNAse digestion followed by isophenol/ chloroform/ iso-amylalcohol extraction and ethanol precipitation in 96- well plate high throughput (Mace *et al.*, (2004) (Figure 3. 2).

Reagents required were:

1. 3% CTAB (cetyl trimethyl ammonium bromide) buffer having 10 mM Tris, 1.4 M NaCl, 20 mM EDTA and 3% CTAB, and pH 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 10 mM Tris (pH 7.5) and 15 mM NaCl stored at –20°C; working stocks 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% ethanol)
8. $T_1E_{0.1}$ buffer (10 mM Tris and 1 mM EDTA)
9. $T_{10}E1$ buffer (0.5 M Tris and 0.5 M EDTA)

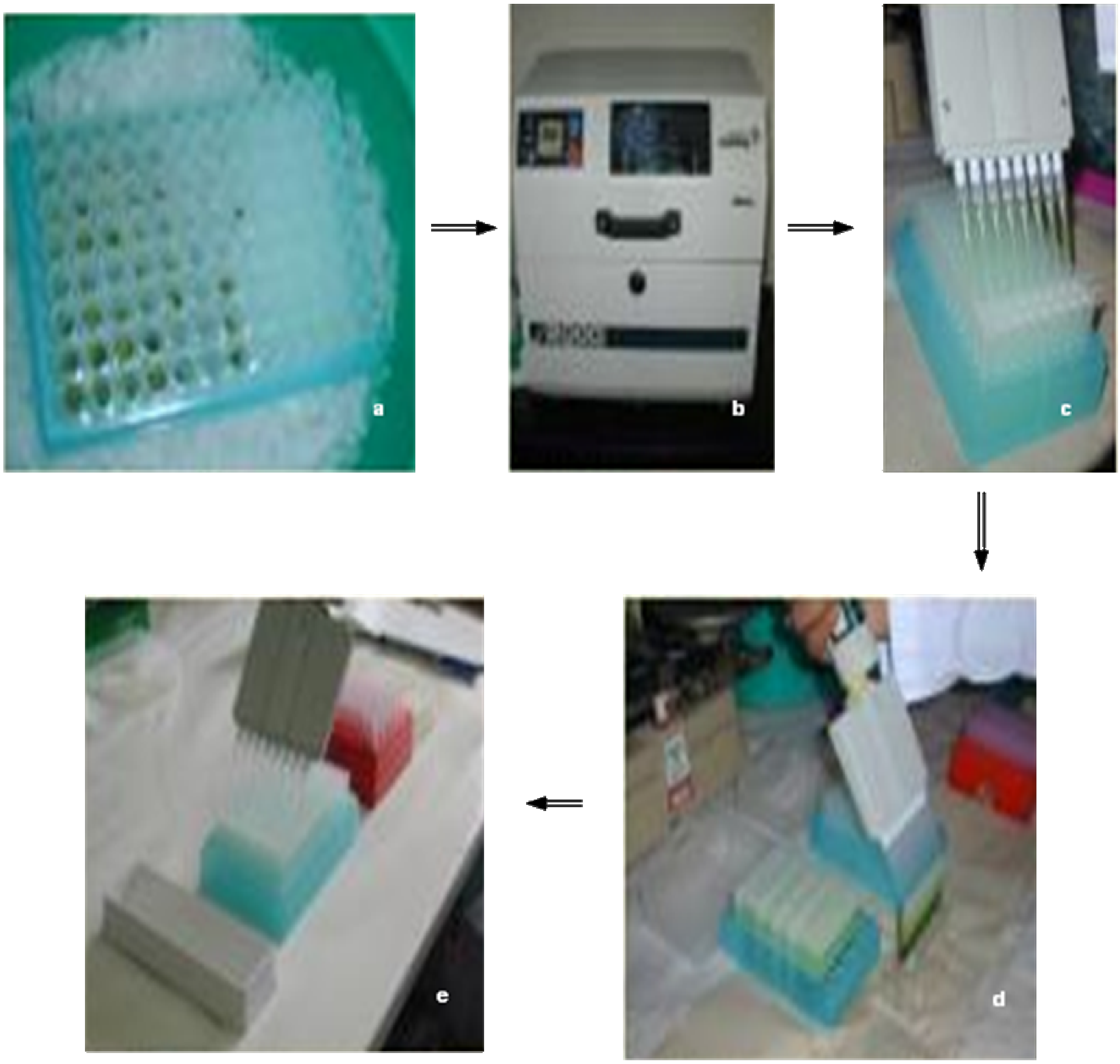


Figure: 3.2. 96–well plate high throughput DNA extraction
Steps as per order:

- **a. Leaf sample collection**
- **b. Grinding in Sigma Geno/Grinder**
- **c. Solvent extraction**
- **d. Separation of aqueous phase**
- **e. DNA precipitation**

3.2.1.1 Protocol

(i) Preparation

1. Steel balls (4-mm in diameter and 2 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. CTAB buffer was pre-heated in 65ºC water bath before start of DNA extraction
3. Leaf samples (Final weight of 30-40 mg) were cut into pieces (1 mm in length). These cut leaves were transferred to the extraction tubes, which were fitted into a 96-tube box

(ii) Grinding and extraction

1. 450 µl of pre-heated CTAB buffer was added to each extraction tube containing a leaf sample
2. 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
3. Grinding of leaf tissues was repeated until the color of the buffer solution became pale green and the cut leaf bits were sufficiently macerated
4. After grinding, the tube box was fixed in a locking device and incubated at 65ºC in a water bath for 10 minutes with occasional shaking

(iii) Solvent extraction

1. 450 µl 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 × 1120g SW)
2. After centrifugation the aqueous layer (approximately 300 µl) was transferred to a fresh strip tube (Marsh Biomarket)

(iv) Initial DNA preparation

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

2. The samples were centrifuged at 6200 rpm for 15 minutes
3. The supernatant was decanted under a fume-hood and pellets were allowed to air dry (minimum 20 minutes)

(v) RNase-A treatment

1. In order to remove co-isolated RNA, 200 µl of low salt TE buffer ($T_1E_{0.1}$) and 3 µl of RNase-A (stock 10 mg/µl) were added to the each tube containing dry pellet and mixed properly
2. The solution was incubated at 37ºC for 30 minutes

(vi) Solvent extraction

1. After incubation, 200 µl of phenol-chloroform-isoamyl alcohol mixture (25:24:1) was added to each tube, carefully mixed and centrifuged at 5000 rpm for 10 minutes
2. The aqueous layer was transferred to fresh tubes and the above solvent extraction step was repeated with the chloroform-isoamyl alcohol mixture

(vii) DNA precipitation

1. To the tubes containing aqueous layer, 15 µl (approximately 1/10th volume) of 3 M sodium acetate (pH 5.2) and 300 µl (2 vol) of absolute ethanol (kept at –20ºC) were added and the tubes subsequently placed in a freezer (–20ºC) for 5 minutes
2. Following incubation, the box containing tubes was centrifuged at 6200 rpm for 15 minutes

(viii) Ethanol wash

1. After centrifugation, supernatant was carefully decanted from each tube in order to ensure that the pellets remained inside the tubes and 200 µl of 70% ethanol was added to the tubes followed by centrifugation at 5000 rpm for 5 minutes

(ix) Final re-suspension

1. Pellets were obtained by carefully decanting the supernatant from each tube and then allowed to air dry for one hour
2. Completely dried pellets were re-suspended in 100 µl of $T_{10}E1$ buffer and incubated overnight at room temperature to allow them to dissolve completely

3. Dissolved DNA samples were stored in 4ºC

3.2.1.2 DNA quantification and quality check

The DNA concentration of each dissolved sample was measured by fluorescence estimation using a Spectraflour Plus® (Tecan, Switzerland) plate reader. The DNA was stained with Picogreen™ (1/200 dilution) (Juru supply Gmbh, Switzerland). The Relative Fluorescence Units (RFU) values obtained from Spectraflour Plus were converted into ng scale (DNA concentration in ng = –2.78273 + 0.002019 * RFU). The conversion factor was determined using a calibration curve produced from samples of known DNA concentration. The final concentration of DNA was normalized to 5 ng/µl for all of the working samples to be used in PCR reactions.

DNA quality check : The quality of DNA was checked by agarose gel electrophoresis as described below:

Reagents required were:

1. Agarose

2. 1X TBE buffer

   For 10X TBE buffer, 109 g of Tris and 55 g of boric acid were dissolved one by one in 800 ml distilled water; then 40 ml of 0.5 M EDTA (pH 8.0) was added. The volume was made up to 1 litre 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)

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

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

Procedure

A 0.8 g of agarose was added to 100 ml 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, 5 µl 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 of the 0.8 per cent agarose gel was loaded with 5 µl of sample aliquot having 3 µl distilled water, 1 µl Orange dye and 1 µl of DNA sample. The DNA samples of known concentration (lambda DNA of 50 ng/µl, 100 ng/µl and 200 ng/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.

3.2.2 Optimization of SSR primers

DNA amplification parameters (viz., specificity, efficiency and fidelity) are strongly influenced by the several components of the PCR reaction and by thermal cycling conditions (Caetano-Anolles, 1991). Therefore, the careful optimization of reaction components and conditions will ultimately result in more reproducible and efficient amplification. PCR condition (the concentrations of primers, template DNA, Mg^{++}, dNTP, enzyme, and annealing temperature) was optimized on eight diverse accessions (IE4709, IE6082, IE2921, IE5177, IE4057, IE4443, IE2564 and IE3025) (Table 3.5) for 31 SSR markers (Dida *et al.*, 2007) by modified Taguchi method (Cobb and Clarkson, 1994). Twenty polymorphic markers were identified as good for genotyping.

The DNA of eight diverse genotypes was used as template for SSR polymorphism analysis. Generally, a diverse population shows high diversity and wide allelic range. Considering this situation, the available 31 finger millet SSR primer pairs were tested for their ability to produce amplification profiles (in terms of differences in the peak, number of peak and peak height in the chromatogram). The SSR primer pairs which produce polymorphic allele amplification were chosen to genotype the entire set of composite collection. The height of the chromatogram peaks (representing the alleles) obtained through capillary electrophoresis is direct by proportional to the signal strength, which in turn is decided by the amount of amplified products in the sample.

Table : 3.5 Most diverse accessions with their species and country of origin

Accessions	Sub species	Race	Country of origin	Geographical Region
IE4709	*E. africana* (wild)	*africana*	Burundi	Eastern Africa
IE6082	*E .spontanea* (wild)	*plana*	Nepal	Southern Asia
IE4443	*E. spontanea* (wild)	*spontanea*	Cameroon	Southern Africa
IE2921	*E.coracana* (cultivated)	*spontanea*	Malawi	Southern Africa
IE5177	*E.coracana* (cultivated)	*vulgaris*	Nepal	South Asia
IE4057	*E.coracana* (cultivated)	*plana*	Uganda	Eastern Africa
IE2564	*E.coracana* (cultivated)	*compacta*	Kenya	Eastern Africa
IE3025	*E.coracana* (cultivated)	*elongata*	Ethiopia	Eastern Africa

Markers for genotyping

The 20 SSR markers used for genotyping were mapped on 9 chromosomes. Marker UGEP3 was mapped on chromosome IIIA genome and Chromosome IIIB genome. Most of the markers (UGEP8, UGEP15, UGEP31, UGEP3 and UGEP104) were mapped on chromosome III. Among 20 SSRs, 19 contained dinucleotide repeat motifs while the remaining one contained trinucleotide repeat motifs. The markers and the respective chromosome number, position and primer sequence are given in 3.6 and figure 3.3

Table: 3.6 Marker, chromosome number and position repeat motif, forward and reverse primer sequence.

Marker name	Chromosome no	Position _cm	Repeat motif	Forward Primer	Reverse Primer
UGEP56	9A	7.4	(GT)12	CTCCGATACAGGCGTAAAGG	ACCATAATAGGGCCGCTTG
UGEP8	3B	65.2	(GA)13	ATTTCCGCCATCACTCCAC	AGACGCAAATGGGTAAATGTC
UGEP11	5Ab	63.5	(CT)12	CCTCGAGTGGGGATCCAG	AAGACGCTGGTGGAAATAGC
UGEP15	3 A	6.5	(CT)22	AAGGCAATCTCGAATGCAAC	AAGCCATGGATCCTTCCTTC
UGEP3	3A & 3B	IIIA(75.8),IIIB(64)	(CA)7N12(GA)15	CCACGAGGCCATACTGAATAG	GATGGCCACTAGGGATGTTG
UGEP81	6B	2.9	(GT)12	AAGGGCCATACCAACACTCC	CACTCGAGAACCGACCTTTG
UGEP5	9B	29.1	(TC)12AC(TC)4	TGTACACAACACCACACTGATG	TTGTTTGGACGTTGGATGTG
UGEP107	1A	9.5	(GA)15	TCATGCTCCATGAAGAGTGTG	TGTCAAAAACCGGATCCAAG
UGEP31	3A	75.8	(GA)12	ATGTTGATAGCCGGAAATGG	CCGTGAGCCTCGAGTTTTAG
UGEP104	3B	124.7	(CT)11	TCAGCACCACCTGAATAGG	AATAGGGAGGGCGAAGACTC
UGEP90	6B	23.3	(CT)11/(CT)8	GGCCTTTGCAGTCATGTGAG	CGACTCCAGGTGTTGTTGG
UGEP18	1B	70.3	(CT)12	TTGCATGTGTTGCTTTTTGC	TGTTCTTGATTGCAAACTGATG
UGEP68	9B	0.0	(CT)14	CGGTCAGCATATAACGAATGG	TCATTGATGAATCCGACGTG
UGEP65	8A	31.6	(CT)19	AGTGCTAGCTTCCCATCAGC	ACCGAAACCCTTGTCAGTTC
UGEP1	5Ab	25.9	(TC)11	TTCAGTGGTGACGGAAGTTCT	GGCTCCATGAAGAGCTTGAC
UGEP10	8A	52.2	(GA)19	AAACGCGATGAATTTTAAGCTC	CTATGTCGTGTCCCATGTCG
UGEP102	10	3.7	(TG)17	ATGCAGCCTTTGTCATCTCC	GATGCCTTCCTTCCCTTCTC
UGEP26	5B	121.1	(CGG)7	ATGGGGTTAGGGTTCGAGTC	TGTCCCTCACTCGTCTCCTC
UGEP77	4B	4.8	(CT)19	TTCGCGCGAAATATAGGC	CTCGTAAGCACCCACCTTTC
UGEP12	8B	50.8	(CT)22	ATCCCCACCTACGAGATGC	TCAAAGTGATGCGTCAGGTC

3.2.3 Amplification of SSR markers

PCR reactions were conducted in 96-well and 384-well micro-titer plates in a GeneAmp PCR system 9700 (Applied Biosystems, USA) thermocycler. PCR reactions were performed in 5 µl volume in 384-well PCR plates. The reaction mixtures contained 10 pmol of primer, 25 mM $MgCl_2$, 2mM dNTP, 0.3 unit of Taq polymerase (Qiagen, PE-Applied Biosystems, Foster City, California) and 1 x PCR buffer (PE- Applied Biosystems, Foster City, California) was used. The touch down PCR protocol was used

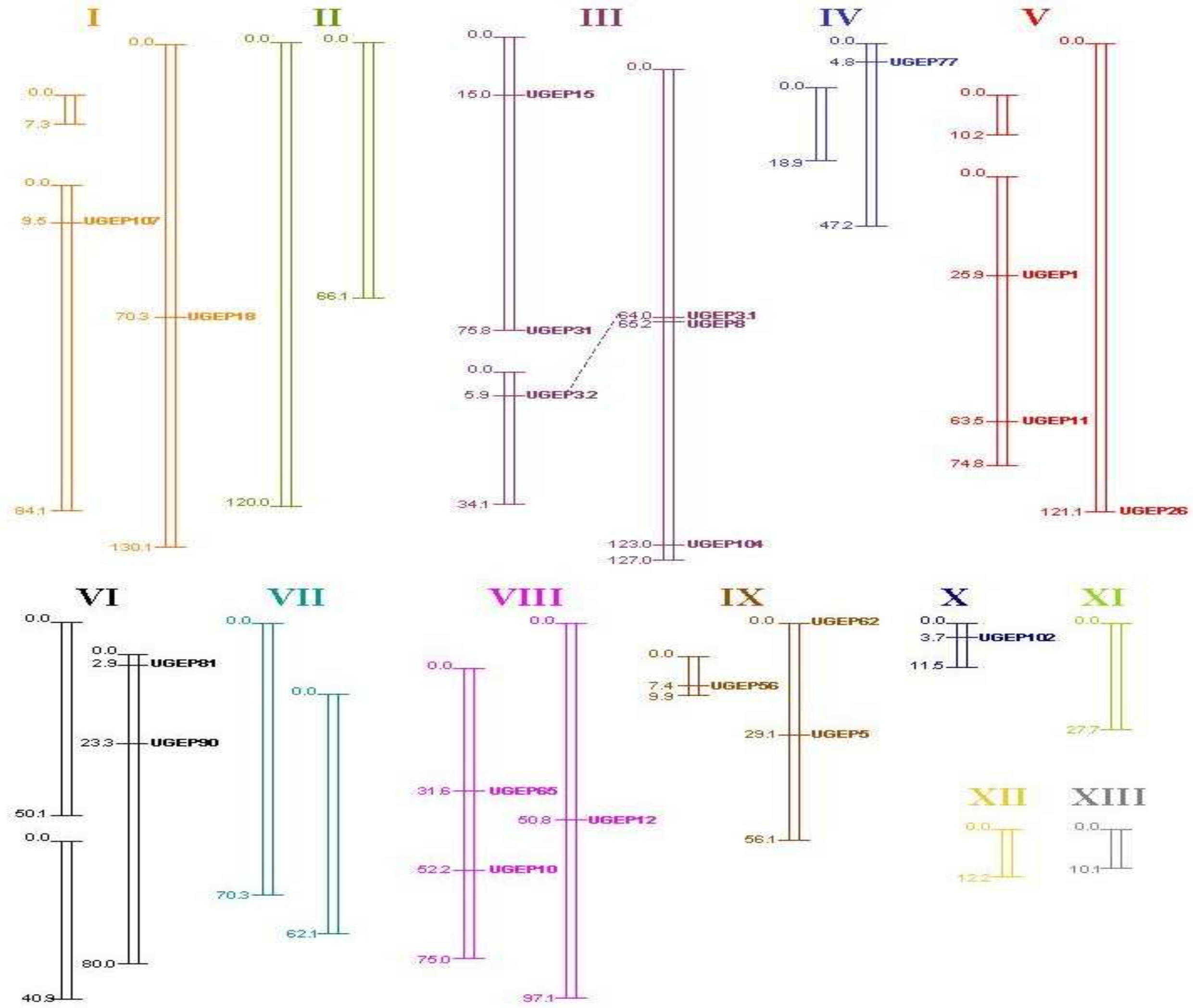


Figure: 3.3 Markers selected for genotyping of global composite collection and its position in finger millet genetic map (Dida *et al.*, 2007)

for the reaction as following: one three-minutes denaturation cycle, followed by first five cycles of 94°C for 20 seconds, 60 °C for 20 seconds and 72 °C for 30 seconds, then by 30 cycles of 94 °C for 20 seconds. After completion of the 30 cycles, a final extension of 20 min at 72 °C to ensure amplification to equal lengths of both DNA strands (Smith *et al*., 1995). The amplified products were tested on 1.2 per cent agarose gel to check for the amplification of the products.

3.2.4 Capillary electrophoresis

(i) Sample preparation

The PCR products were size-separated by capillary electrophoresis using an ABI Prism 3700 DNA analyzer (Applied Biosystems Inc.). For this purpose, forward primers were labeled with 6-FAM™ (Blue), VIC™ (Green), NED™ (Yellow) and PET™ (Red) fluorophores (Applied Biosystems). PCR products of 4 primer pairs labeled with different dyes could be pooled (post-PCR), because of the different signal spectra of the fluorophores used. The products of the same fluorophore-labeled primers were also pooled, when they had non-overlapping amplicons in terms of size. The products of different fluorophore-labeled primers were pooled in different proportions (1.0 µl of 6-FAM-labeled product, 1.0 µl of VIC-labeled product, 1.5 µl of NED-labeled product and 1.5 µl of PET-labeled product). The pooled PCR products were mixed with 0.25 µl of the GeneScan 500™ LIZ® internal size standard (Applied Biosystems) and 7 µl of Hi-Di™ Formamide (Applied Biosystems). The final volume was made up to 12 µl with sterile double-distilled water. This mixture was denatured for 5 minutes at 95°C and cooled immediately on ice.

(ii) Fragment size fractionation

After denaturation, the plate with samples was placed into the sequencer machine (ABI Prism 3700 DNA analyzer). The capillary run was performed using the "Genescan2_POP6 Default" run module and "G5" filter-set. The analysis module used was "GS500 analysis". The fragments were separated in a 50 cm capillary array using POP6 (Performance Optimized Polymer, Applied Biosystems) as the separation matrix (Figure 3. 4)

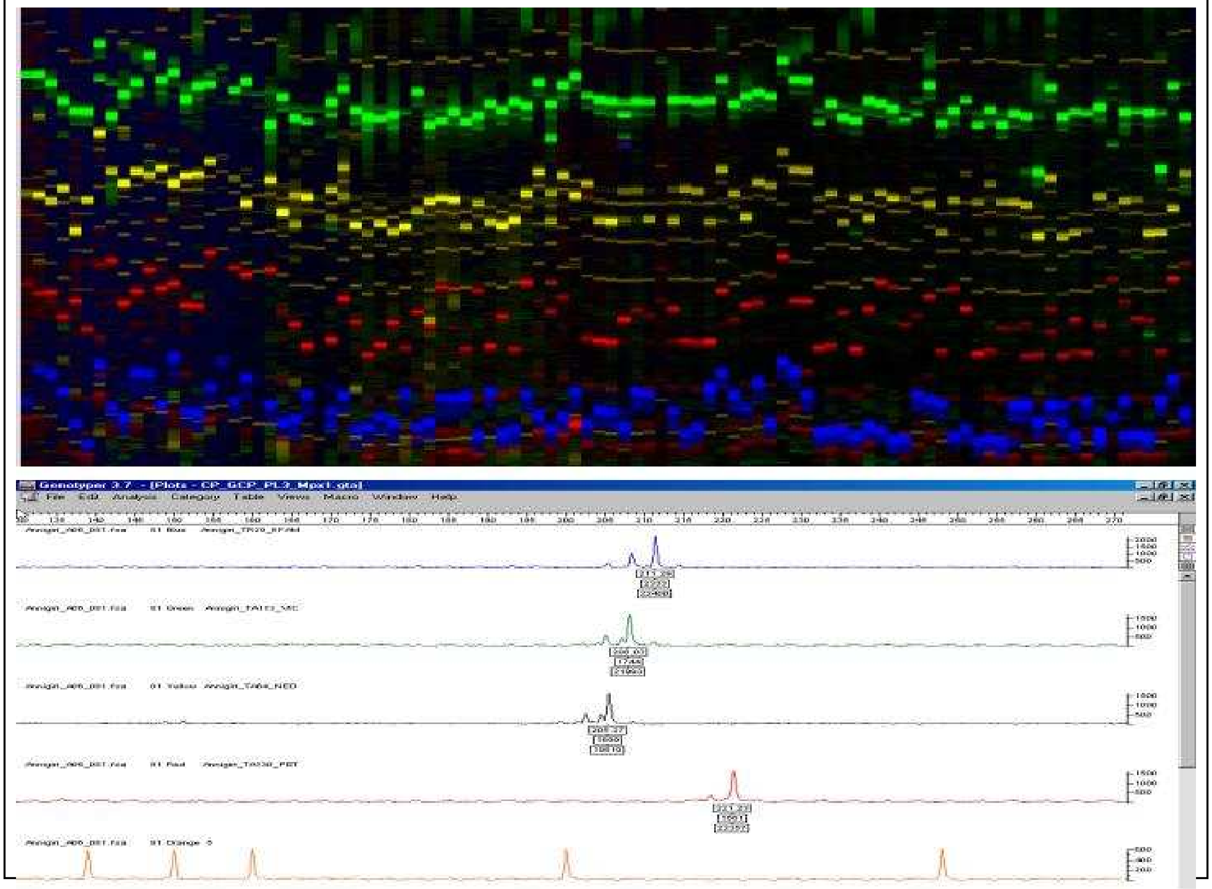


Figure 3.4. Polymorphic of the alleles at SSR locus UGEP10 in eight diverse genotypes

3.2.5 Data processing

After the capillary runs were over, the raw data were processed with Genescan 3.1 software (Applied Biosystems) to size the peak patterns in relation to the internal size standard GeneScan 500™ LIZ® (Figure 3. 4) The principle behind this is that standards are run in the same lane or capillary injection as the samples, which contain fragments of unknown sizes labeled with different fluorophores. Genescan® analysis software automatically calculates the size of the unknown DNA sample fragments by generating a calibration sizing curve based upon the migration times of the known fragments in the standard. The unknown fragments are mapped onto the curve and the sample data is converted from migration times to fragment size. Genotyper 3.7 (Applied Biosystems) was used for allele calling. The peaks were displayed with base pair values and height (amplitude) in a chromatogram and the allelic data were exported in to Excel spread sheet for further analysis.

3.2.6 Quality index of allelic drift

Using ABI 3700 automated sequencing platform at ICRISAT, 20,000 (1000 accessions x 20 SSR loci data) data points were generated. The quality assessment using Allelobin for binning the raw data (Idury and Cardon. 1997) gave the idea of the quality of markers.

Quality index - Binning quality

0.00 - 0.30 - Accurate binning

0.31 - 0.40 - Binning likely

> 0.40 - Binning and size unacceptable

3.2.7 Data analysis

The binned data were subjected to diversity analysis in DARwin5 (Perrier *et al.*, 2003). The 19180 data points (959 accessions x 20 SSR loci data) validated for final diversity analysis and the population structure. The accessions with more than 5per cent missing data were excluded for the analysis.

The data set of 20 SSR loci on 959 accessions were used for statistical analysis using PowerMarker V3.0 (Liu and Muse 2005) for estimating basic statistics (PIC value, allelic richeness as determined by a total number of the detected alleles and a number of alleles per locus, gene diversity (H_e), occurrence of unique allele, rare and common alleles, and multiple allele percentage (%). Unweighted neighbour-joining tree using the simple- matching pair wise dissimilarity matrix were produced.

3.2.7.1 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

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

where the inbreeding coefficient, f, is estimated from the data using the method of moments. The user can also request the common biased estimator of the gene

3.2.7.2 Polymorphism Information Content (PIC)

A closely related diversity measure is the polymorphism information content (PIC) (Botstein *et al.*, 1980). It is estimated as

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

3.2.7.3 Multiple allele percentage

DNA was extracted from individual plant, so there is very small or no chance of heterozygosity in a self pollinated crop like finger millet. But two alleles were observed for some SSR markers (which are mapped in both chromosomes of A and B genome III) in the population. This may be due to Tetraploid nature of the finger millet. A proportion of the accessions possessing multiple alleles in the entire population is called multiple allele percentage.

3.2.7.4 Bootstrap across loci

For all of these summary statistics, the overall estimates are calculated as the average across all loci, whereas variances and confidence intervals are estimated by non-parametric bootstrapping across different loci.

3.2.7.5 Allele and genotype frequencies

The sample allele frequencies are calculated as

$$\tilde{p}_u = n_u /(2n)$$

With the variance estimated as,

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

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.

3.2.7.6 Principle coordinate analysis

The Principal Co-ordinate analysis (PCoA) was carried out with similarity matrix using DARwin5 version 5.0 programmeme (Perrier *et al.,* 2003) and similarity matrix for the phenotypic data was calculated by using the option dissimilarity for interval data from NTsys PC2 (Rholf, 1997).

3.2.7.7 Population Structure Analysis

Analysis of the population structure and of gene flow between *E. coracana* subsp. *coracana* and subsp. a*fricana* and based on geographical origin was carried out using a model-based clustering method as implemented in the software programme STRUCTURE v. 2.1. In this method, it is assumed that a number of subpopulations exist in the sample analyzed. Each accession can have membership in different subgroups (admixture model; ALPHAPROPSD=0.20). The number of subgroups (K) in the population was determined by running the programme at different K values with K varying from 2 to 6. Three independent runs were assessed for each K value. We used a burn-in period of 1,00,000 and 10,00,000 replications. Biological race and geographic origin information was used to assist with the clustering.

3.2.8. Development of reference set

Unweighted neighbour-joining tree was constructed using simple matching pair wise dissimilarity matrix in DARwin-5.0 (Perrier *et al.,* 2003) to develop a reference set consisting of 300 genetically most diverse accessions.

3.2.9 Association of markers with phenotypic data

All the accessions of composite collection were considered as a single unit and used for association analysis. Association analysis was done by using phenotypic data of composite collection and reference set of each environment separately and overall, using 20 SSR marker data and population structure data (Q matrix) by using software TASSEL (Bradbury *et al.,* 2007) by simple linear regression markers.

3.2.10 Cophenetic correlation

A binary matrix was constructed using the SSR results, from which the GDs of each hybrid were calculated using the Roger modified distance (Wright, 1978), with the NTSYS-PC 2.1 program (Rohlf, 1997). The distance matrix was grouped by the UPGMA and then the dendrogram was obtained that was an indication of kinship among the germplasm analyzed. The cophenotypic correlation was calculated between the GD matrix and the cophenotypic value matrix to verify the consistency of the grouping. The significance of the associations among matrices (r) was tested by the Mantel (1967).

Experimental Results

CHAPTER IV

EXPERIMENTAL RESULTS

The global composite collection of finger millet developed at International Crop Research Institute for the Semi-Arid Tropics (ICRISAT) was evaluated in three environments *Viz.,* 2005/2006 post rainy season at Tamil Nadu Agricultural University (TNAU), Coimbatore (E1), in 2006 (E2) and 2007 rainy season (E3) at ICRISAT, Patancheru, Andhra Pradesh for morpho-agronomic traits under field conditions. The global composite collection was also molecularly profiled by using 20 polymorphic SSR markers. The results of the investigation are presented under three main topics given below.

1. Phenotypic diversity of global finger millet composite collection based on multi-location evaluation for morphological and agronomical characteristics.
2. Genotypic diversity and population structure of global finger millet composite collection based on 20 SSR markers and development of genotype based reference set with 300 most diverse accessions.
3. Identification of desirable trait-specific accessions for agronomic traits including grain yield and high nutrient content.

4.1. Phenotypic diversity of global finger millet composite collection based on morphological and agronomical characteristics

4.1.1 Qualitative Characters

4.1.1.1 Growth habit

Based on the growth habit, finger millet composite collection accessions were grouped into three types *Viz.,* erect, decumbent and prostrate. A larger number of accessions were erect type (58.5%), followed by decumbent (41.2%). The prostrate type was very less (0.3%). All the prostrate types were *Spontanea* accessions (IE2921, IE4476 and IE 4442). This was because of spreading morphological nature of plants. The large number of accessions from race *Vulgaris* were erect (348 accessions) and decumbent (226 accessions) out of 576 accessions, followed by race *Plana* (126 accessions of erect

Table: 4. 1 Number of accessions and frequency percentage (%) of different groups of qualitative traits based on biological races and geographical origins in the global finger millet composite collection across three environments.

Trait	Total	Biological races						Geographical origin							
		africana	*compacta*	*elongata*	*plana*	*spontanea*	*vulgaris*	America	Central Africa	East Africa	Europe	South Asia	Southern Africa	Unknown	Western Africa
Growth habit															
Decumbent	412 (41.2%)	3	49	45	81	5	229	5	3	113	2	159	117	13	-
Erect	585 (58.5%)	-	83	27	126	1	348	-	-	249	4	169	143	13	7
Prostrate	3 (0.3%)	-	-	-	-	1	2	-	-	-	1	-	1	1	-
Plant pigmentation															
Green	713 (71.3%)	3	97	60	150	6	397	5	3	237	5	241	201	15	6
Purple pigmented	287 (28.7%)	-	35	12	57	1	182	-	-	125	2	87	60	12	1
Inflorescence shape															
Long open	37 (3.7%)	3	-	32	-	2	-	-	-	7	-	9	20	-	1
Compact	16 (1.6%)	-	16	-	-	-	-	-	-	3	-	4	9	-	-
Fisty	117 (11.7%)	-	115	-	-	-	1	-	-	61	-	20	35	1	-
Top curved	426 (42.6%)	-	1	-	201	-	224	5	-	192	4	81	126	17	1
Pendulous	21 (2.1%)	-	-	21	-	-	-	-	-	1	-	18	-	-	2
Short open	56 (5.6%)	-	-	19	4	-	33	-	-	9	1	38	8	-	-
Incurved	322 (32.2%)	-	-	-	1	-	321	-	-	87	2	158	63	9	3
Laxa	5 (0.5%)	-	-	-	-	5		-	3	2	-	-	-	-	-
Glume prominence															
No prominence	207 (20.7%)	-	48	2	60	-	97	4	-	93	2	45	50	12	1
Low prominence	215 (21.5%)	-	23	7	47	-	138	-	-	145	2	29	39	-	-
Medium prominence	382 (38.2%)	-	49	22	76	-	235	1	1	91	2	157	116	12	2
High prominence	196 (19.6%)	3	12	41	24	7	109	-	2	33	1	97	56	3	4
Seed colour															
Ragi brown	94 (9.4%)	3	2	16	15	5	53	-	3	26	3	52	7	1	2
Dark brown	66 (6.6%)	-	3	9	9	2	43	1	-	55	2	1	5	1	1
Light brown	545 (54.5%)	-	96	28	129	-	292	-	-	203	-	141	191	8	2
Reddish brown	265 (26.5%)	-	23	19	54	-	169	4	-	77	2	127	36	17	2
White	30 (3%)	-	8	-	-	-	22	-	-	1	-	7	22	-	-
Lodging*															
No lodging	318 (31.8%)	3	53	21	57	1	183	-	2	142	-	54	110	4	6
Slightly lodging	111 (11.1%)	-	22	3	33	-	53	1	-	17	1	50	35	7	-
Medium lodging	311 (31.1%)	-	44	16	77	1	173	1	-	129	1	111	60	9	-
Mostly lodging	89 (8.9%)	-	7	8	11	2	61	2	-	19	2	38	23	5	-
Completely lodging	171 (17.1%)	-	6	24	29	3	109	1	1	55	3	75	33	2	1

Numbers in parenthesis indicate percentage of accessions in each group

*Data based on E2 (2006 rainy season) at ICRISAT Centre, Patancheru and 81 accessions of decumbent) out of 208 accessions. Regionwise, East African region had more number of erect (249 accessions) followed by South Asia (169 accessions). Decumbent type was more in South Asia (159 accessions), southern Africa (117 accessions) and East Africa (113 accessions) (Table 4.1).

4.1.1.2 Plant pigmentation

Purple colour pigmentation was observed at internodes, leaf sheath and flag leaf of 287 accessions in the composite collection and classified as pigmented. Remaining 713 accessions had green colour and classified as non-pigmented (Table 4.1). The frequency of purple pigmentation was predominant in accessions of race *Vulgaris* (182 accessions) and from East Africa region (125 accessions).

4.1.1.3 Inflorescence compactness and shape

The composite collection was divided into eight classes based on inflorescence shape. Composite collection was predominant with top curved (42.6%) followed by incurved (32.2%), fisty (11.7%), short open (5.6%), long open (3.7%), pendulous (2.1%), compact (1.6%) and laxa (0.5%) (Table 4.1). Most of the accessions belonging to race *Compacta* have fisty inflorescence (115 accessions), whereas *Vulgaris* accessions were both incurved (321 accessions) and top curved (224 accessions), and *Plana* accessions were top curved (201 accessions). Accessions from East Africa and southern Africa (except laxa and pendulous) and South Asia (except laxa) had all types of inflorescences (Table 4.1)

4.1.1.4 Glume prominence

Glume prominence was grouped into four categories. Medium glume prominence was observed predominately in 38.2% of accessions, followed by low glume prominence (21.5 % of accessions), non prominence (20.7 %) and high prominence (19.6 %). All accessions of wild races, *Africana* (3 accessions) and *Spontanea* (7 accessions) had high glume prominence, whereas the accessions of cultivated race accessions had all four types of glume prominence (Table 4.1). Similarly, accessions originated from major regions like East Africa, South Asia, southern Africa and Europe had all type of glume prominence.

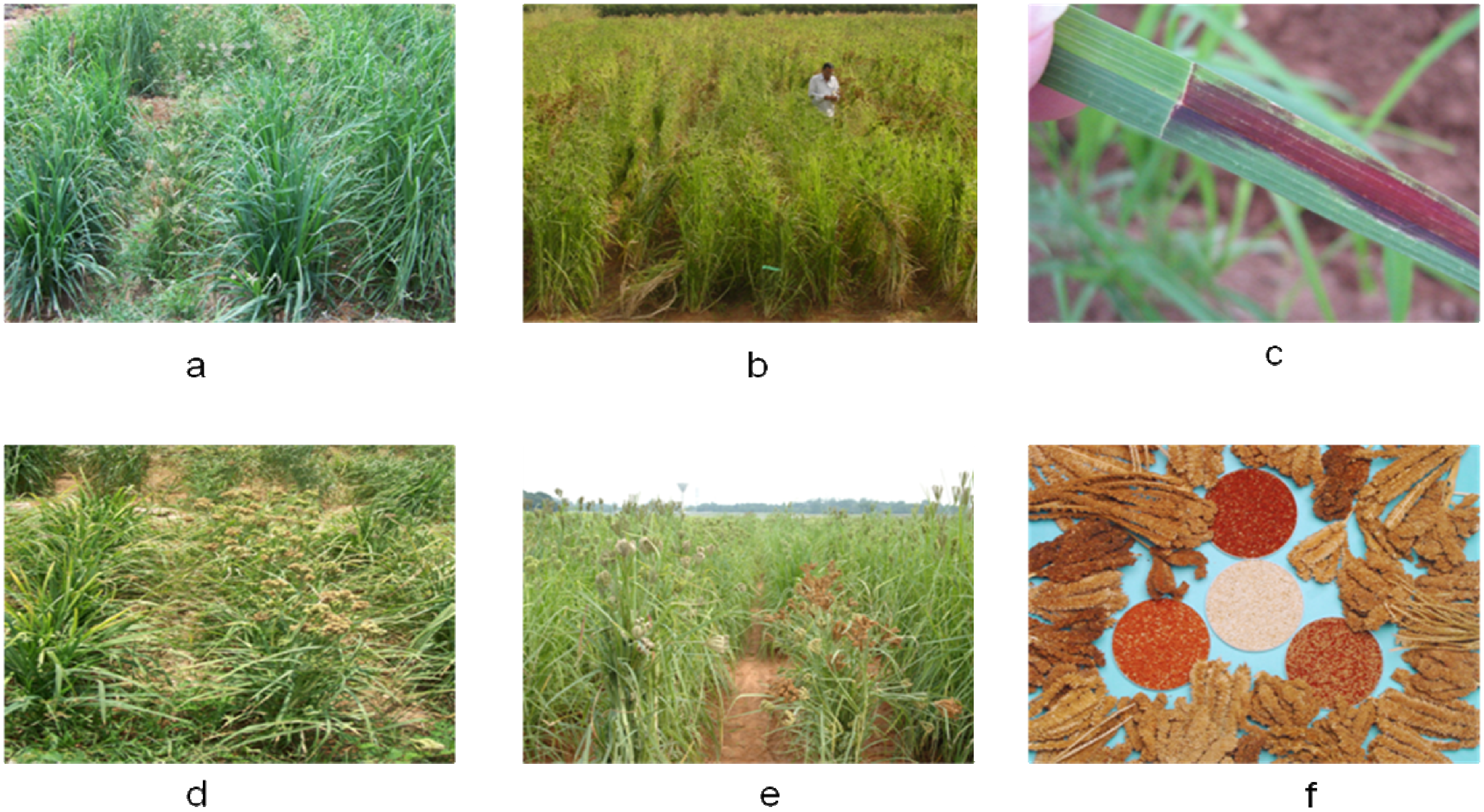


Figure: 4.1 Phenotypic variation observed in global finger millet composite collection

a. Variation in flowering
b. Field view
c. Variation for leaf
d. Variation for maturity
e. Variation for plant height
f. Variation for finger size, shape and grain colour

4.1.1.5 Seed colour

A wide range of grain colour (ragi brown, dark brown, light brown, reddish brown and white) was observed. More than half of the accessions (54.5 % of accessions) were light brown, followed by reddish brown (26.5 %), ragi brown (9.4 %), dark brown (6.6 %) and white (3.0 %) (Table 4.1). Accessions from races *Compacta* and *Vulgaris* and East Africa, South Asia and southern Africa regions had all the five seed colors. Thirty white colored accessions were from races *Vulgaris* (22 accessions) and *Compacta* (8 accessions) and from southern Africa (22 accessions), South Asia (7 accessions) and East Africa (1 accession) regions.

4.1.1.6 Lodging

Lodging was evaluated in both the rainy seasons at ICRISAT center (E2 and E3). Data were quite contradictory in both the seasons. The main reason for this could be that this trait depends on the intensity of the rainfall received during the season. However, based on the overall performance in E2, accessions were grouped into no lodging (31.8% of accessions), slightly lodging (11.1 % of accessions), medium lodging (31.1 % of accessions), mostly lodging (8.9 % of accessions) and completely lodging (17.1 % of accessions) (Table 4.1).

4.1.2 Quantitative characters

4.1.2.1 Variance components

The REML analysis of data for individual environment revealed significant genotypic variance for 12 out of the 13 traits in E1, 15 out of the 16 traits in E2 all the 15 traits in E3. However the combined analysis showed significant genotypic variance for 14 traits (days to 50% flowering, plant height, basal tiller number, culm branching, flag leaf blade length, flag leaf blade width, flag leaf sheath length, peduncle length, panicle excertion, ear head length, ear head width, length of longest finger, width of longest finger and number of fingers) out of 15 traits (Table 4.2). Significant variance in most of the traits in individual and combined analysis showed that the genotypes in the composite collection were diverse and had sufficient scope for selection and utilization in crop improvement program. The variances due to genotype x environment were significant for all the traits except grain yield per hectare in the combined analysis. This indicated that

Table: 4.2 Variance components due to genotypes (σ^2g) and genotype x environment (σ^2ge) their standard errors (SE) estimated in the global finger millet composite collection across three environments and pooled analysis.

Traits	E1		E2		E3		Pooled		Pooled	
	σ^2 g	SE	σ^2 g	SE	σ^2 g	SE	σ^2 g	SE	σ^2 g x e	SE
# Days to 50 per cent flowering (days)	111.3**	5.31	94.1**	5.76	69.2**	3.38	95.9**	18.77	44.2**	5.82
# Plant height (cm)	149.5**	24.9	171.2**	24.9	120.7**	14.59	129.7**	15.13	86.8**	11.78
# Basal tiller number (numbers)	1.4**	0.07	1.9**	0.29	1.9**	0.05	1.5**	0.05	0.12**	0.07
# Culm branching (numbers)	1.5**	0.3	2.7**	0.24	a	a	2.5**	0.83	1.9**	0.02
# Flag leaf blade length (mm)	1227.0**	551	2764.0**	326	2270.0**	372	2217.6**	393.23	2499.0**	335.21
# Flag leaf blade width (mm)	11.8**	0.24	15.7**	0.75	12.5**	0.23	13.4*	0.58	4.5**	0.55
# Flag leaf sheath length (mm)	122.9**	38.1	156.6**	45.1	84.0**	7.06	89.0**	6.21	1212.0**	95.23
# Peduncle length (mm)	2188.1**	180.7	1917.6**	115.2	1416.0**	71	1730.0**	333	1694.0**	318.12
# Panicle exertion (mm)	a	a	91.3**	24.7	109.0**	15	98.3*	4.06	8.01**	2.75
# Ear head length(mm)	503.0**	37.1	446.2**	58.8	266.5**	74.9	441.0**	89.21	538.5**	72.82
# Ear head width (mm)	57.2**	9.79	143.8**	14.67	71.2**	33.56	75.6**	6.73	7.0**	7.03
# Number of fingers (numbers)	32.8**	0.24	48.1**	30.19	47.5**	29.4	41.7**	3.43	42.1**	0.28
# Length of longest finger (mm)	a	a	45.5**	2.18	61.51*	0.61	48.0**	16.23	35.0**	15.23
# Width of longest finger (mm)	a	a	8.1**	0.65	1.2**	0.33	1.7**	0.17	1.4**	0.04
Days to maturity (days)	215.6**	41.3	a	a	a	a	b	b	b	b
Panicle weight (g)	a	a	a	a	15.7**	0.75	b	b	b	b
1000 grain weight (g)	a	a	0.4*	0.2	a	a	b	b	b	b
Grain yield per hectare (tha^{-1})	<0.001	0.01	<0.001	0.01	4.8**	0.47	<0.001	0.01	<0.001	0.01

a – data not recorded

b – data recorded only in one season

trait significant in all environment and pooled

performance of genotypes differed in different environments. Phenotypic variation observed for various traits was illustrated in Figure 4.1.

4.1.2.2 Mean performance of the global finger millet composite collection accessions for phenotypic traits in different environments

Mean and Range

Mean and range are simple and important measure of variability (Singh, 1983). Performance of the accessions in different environment was assessed by comparing the values of mean and range for particular traits.

4.1.2.2.1 Days to 50% flowering

The mean days to 50% flowering was lower in E3 (70.0 ± 2.17 days) and E1 (71.3 ± 2.44 days) than E2 (75.1 ± 4.15 days). However, the combined analysis revealed a mean of 72.1 ± 3.15 days for days to 50% flowering. The highest range for days to 50% flowering was observed in E3 (41 - 164 days) followed by E1 (43 - 128 days) and E2 (42 - 110 days). The range of days to 50% flowering was almost equal in three environments except E3, where few wild accessions (IE4443, IE4446 and IE4711) that took more than 150 days to flower.

Considering the earliest flowering control cultivar in each environment, the top 10 accessions (IE 2822, IE 2870, IE 5896, IE 2911, IE 4817, IE 2586, IE 5875, IE 2957, IE 4759, IE 413) with the range of 43 to 46 days in E1 (earliest control VR 708 recorded 46.1 ± 2.44 days), 7 accessions (IE 4708, IE 4442, IE 3537, IE 588, IE 4759, IE 4755, IE 2158) with the range of 42 to 47 days in E2 (earliest control VR 708 recorded 47.8 ± 4.15 days), 9 accessions (IE 6013, IE 2158, IE 4431, IE 2322, IE 600, IE 641, IE 196, IE 501, IE 2093) with the range of 41 to 45 days in E3 (earliest control PR 202 recorded 45.1 ± 2.17 days) were identified as promising early flowering accessions. These could provide useful genes for early flowering and used in improvement programme for early maturity.

4.1.2.2.2 Plant height

Plant height is the important trait related to biological yield and fodder yield. Wide variation for plant height was observed among the accessions in composite collection.

Table: 4.3 Mean (± standard error) and range for quantitative traits of global finger millet composite collection evaluated across three environments and pooled analysis

Traits	Mean ± SE				Range			
	E1	E2	E3	pooled	E1	E2	E3	pooled
Days to 50 per cent flowering (days)	71.3 ± 2.44	75.1 ± 4.15	70.0 ± 2.17	72.1 ± 3.15	43 - 128	42 - 110	41 - 164	41 - 164
Plant height (cm)	90.7 ± 6.33	115.6 ± 8.97	114.5 ± 7.06	103.7 ± 5.31	45 - 162	50 - 180	50 - 155	45 - 180
Basal tiller numbers (number)	3.7 ± 0.43	4.1 ± 0.84	3.7 ± 0.81	3.8 ± 0.32	1- 18	1 -19	1 - 18	1- 19
Culm branching (number)	2.4 ± 0.36	2.5 ± 0.93	A	2.4 ± 0.36	1- 10	1 -13	a	1- 13
Flag leaf blade length (mm)	341.0 ± 31.01	343.7 ± 32.22	333.2 ± 33.97	340.2 ± 28.03	100 - 550	50 - 660	100 - 600	50 - 660
Flag leaf blade width (mm)	10.3 ± 0.90	9.6 ± 0.96	9.6 ± 0.51	9.8 ± 0.57	5 - 20	3 - 20	4 -15	3 - 20
Flag leaf sheath length (mm)	100.4 ± 9.21	99.2 ± 11.12	78.5 ± 8.75	92.6 ± 5.61	0 - 255	0 - 300	0 - 300	0 - 300
Peduncle length (mm)	159.9 ± 25.02	200.0 ± 17.88	192.9 ± 18.97	184.2 ± 14.86	0 - 290	0 - 360	0 - 360	0 - 360
Panicle exertion (mm)	a	106.7 ± 20.26	98.0 ± 15.74	102.1 ± 10.96	a	0 - 400	0 - 400	0 - 400
Ear head length(mm)	78.4 ± 11.12	78.2 ±14.03	87.7 ± 13.30	81.5 ± 8.57	10 - 250	10 - 230	10 - 200	10 - 250
Ear head width (mm)	43.0 ± 5.46	48.8 ± 7.18	54.2 ± 0.51	46.3 ± 0.51	10 - 150	15 - 135	12 - 150	10 - 150
Length of longest finger (mm)	a	71.0 ± 8.41	71.3 ± 10.11	71.1± 9.38	a	10 - 180	10 - 200	10 - 200
Width of longest finger (mm)	a	9.8 ± 1.59	11.1 ± 1.07	10.2 ± 1.12	a	5 - 15	5 - 15	5 - 15
Finger number per inflorescence (Number)	7.1 ± 0.93	7.5 ± 1.49	7.9 ± 0.89	7.4 ± 0.79	2 - 16	2 - 20	2 - 22	2 - 22
Days to maturity (days)	94.1 ± 10.95	a	a	b	96 - 165	a	a	b
Single panicle weight (g)	a	a	10.1 ± 1.29	b	a	a	0.63 – 13.1	b
1000-grain weight (g)	a	4.2 ± 0.75	a	b	a	0.6 – 7.5	a	b
Grain yield per hectare (t ha^{-1})	0.9 ± 0.01	0.9 ± 0.01	0.9 ± 0.81	0.9 ± 0.01	0.05 - 2.7	0.06 - 2.4	0.02 – 2.6	0.02 - 2.7

a- data not recorded

b- data recorded only in one season

The mean plant height was higher in E2 (115.6 ± 8.97 cm) and E3 (114.5 ± 7.06 cm) than E1 (90.7 ± 6.33 cm) (Table 4.3). A wide range for plant height was observed in the composite collection in different environments; in E1 (45-162 cm), in E2 (50 - 180 cm), E3 (50 – 155 cm) and pooled (45- 180 cm). Interestingly all the accessions from different geographical origins grew taller in the E2 and E3 (rainy seasons at Patancheru) than in E1 (post rainy season at Coimbatore).

The accessions were grouped based on plant height as dwarf or short (<85 cm), tall (>130 cm) and medium tall (85 to 130 cm). Using these criterion 36 accessions was considered as short, 760 accessions as medium tall and 204 accessions as tall based on the mean height over three environments. The 11 accessions (IE 2055, IE 2502, IE 6491, IE 2546, IE 2589, IE 2957, IE 3104, IE 3450, IE 518, IE 5343, IE 4017) were dwarf, whereas 8 accessions (IE2737, IE3973, IE3533, IE2713, IE6435, IE6451, IE3825, IE2772) were tall in all the three environments. The wild accessions belonging to races *Africana* and *Spontanea* were considered as short and attained a height of < 50 cm in all the three environments.

4.1.2.2.3 Number of basal tillers

The mean basal tiller numbers was higher in E2 (4.1 ± 0.84) than E3 (3.7 ± 0.81) and E1 (3.7 ± 0.43) (Table 4.3). Overall the mean basal tiller number was 3.8 ± 0.32. The range was almost equal in all environments (1 - 18 in E1, 1 - 19 in E2, 1 -18 in E3) (Table 4.3). Most of the accessions (83.25%) in the composite collection had good tillering ability (5 – 10 tillers). The 12 accessions (IE3070, IE2921, IE2180, IE3070, IE96, IE2296, IE2868, IE5281, IE6451, IE797, IE120, and IE2034) had consistently high (13 - 19) basal tiller numbers than the control VR708 (> 9 tillers) in all the environments individually and pooled. Eventhough, finger millet is a tillering plant, 8 accessions (IE 2540, IE 2561, IE 4296, IE 3935, IE 3317, IE 4677, IE 3120 and IE 6033) had no tillers (mono tiller) in any three environments.

4.1.2.2.4 Culm branching

The mean number of culm branching was similar in two environments (2.4 ± 0.36 in E1, 2.5 ± 0.93 in E2) and in pooled analysis (2.4 ± 0.36). However, a wide range was observed for this trait in two environments (1 - 10 in E1, 1 - 13 in E2) and overall (1-13). Wild accessions of races *Spontanea* and *Africana* had more number of culm branching (6 -13 numbers) than the accessions of cultivated races (1 – 6 umbers).

4.1.2.2.5 Flag leaf blade length

Mean flag leaf blade length was higher in E2 (343.7 ± 32.33 mm) and E1 (341.0 ± 31.01 mm) than E3 (333.2 ± 33.97 mm). Overall it was 340.2 ± 28.03 mm. A wide range (50 – 660 mm in E2, 100 – 600 mm in E3, 100 – 550 mm in E1 and in combined (50 – 660 mm) was observed for this trait (Table 4.3).

4.1.2.2.6 Flag leaf blade width

The slight difference were observed for mean flag leaf blade width in the three environments (10.3 ± 0.90 mm in E1, 9.6 ± 0.96 mm in E2, 9.6 ± 0.51 mm in E3) and overall (9.8 ± 0.57 mm). A wide range of 3 – 20 mm in E2, 5 – 20 mm in E1, and 4 – 15 mm in E3 and 3 – 20 mm in over all was observed for flag leaf blade width (Table 4.3).

4.1.2.2. 7 Flag leaf sheath length

The mean flag leaf sheath length was highest in E1 (100.4 ± 9.21 mm) followed by E2 (99.2 ± 11.12 mm). The mean length of flag leaf sheath was lowest in E3 (78.5 ± 8.75 mm). Over all the three environments, the mean flag leaf sheath length was 92.6 ± 5.61mm. (Table 4.3). The range was almost similar in E2 and E3 (0 - 300 mm) but greater than E1 (0-255mm).

4.1.2.2. 8 Peduncle length

The mean peduncle length was higher in E2 (200.0 ± 17.88 mm) followed by E3 (192.9 ± 18.97 mm). E1 recorded lowest mean peduncle length (159.9 ± 25.02 mm) (Table 4.3). The range of peduncle length was equal in E2 and E3 (0 – 360 mm), whereas post rainy season (E1) recorded low range of 0 – 290 mm. The combined analysis revealed the overall mean of 184.2 ± 14.86 mm with a range from 0 to 360 mm.

4.1.2.2. 9 Panicle excertion

The mean panicle excertion was higher in E2 (106.7 ± 20.26 mm) than in E3 (98.0 ± 15.74 mm). However, the range in the two environments (E2 and E3) was similar (0 – 400 mm). The range of overall two environments was 0 – 400 mm with a mean of 102.1 ± 10.96 mm (Table 4.3).

4.1.2.2. 10 Ear head length

The mean ear head length was highest in E3 (87.7 ± 13.30 mm), whereas E1 and E2 recorded similar mean (78.4 ± 11.12 mm and 78.2 ± 14.03 mm respectively) (Table 4.3). Over all the three environments the length of ear head was 81.5 ± 8.57 mm. The range of ear head length was almost similar in all the environments (10 - 250 mm in E1, 10 -230 mm in E2 and 10 – 200 mm in E3) (Table 4.3).

4.1.2.2. 11 Ear head width

The environment E3 recorded high mean ear head width of 54.2 ± 0.51 mm followed by E2 (48.8 ± 7.18 mm) and E1 (43.0 ± 5.46 mm). However the range for this trait was higher in E1 (10 - 150 mm) than E3 (12 – 150 mm) and E2 (15 – 135cm) (Table 4.3).

4.1.2.2. 12 Length of longest finger

The mean length of longest finger was observed similar in the environments (71.0 ± 8.41 mm in E2, 71.3 ± 10.11 mm in E3 and 71.1 ± 9.38 in pooled). However, wide range (10 – 200 mm in E3 and 10-180 mm in E2) was observed for this trait.

4.1.2.2. 13 Width of longest finger

The mean width of longest finger was higher in E3 (11.1 ± 1.07 mm) followed by E2 (9.8 ± 1.59 mm). However, the equal range of width of longest finger (5 – 15 mm) was observed in all the environments and in pooled analysis (Table 4.3).

4.1.2.2. 14 Finger number per inflorescence

The mean number of fingers per inflorescence was similar in all the three environments (7.1 ± 0.93 in E1, 7.5 ± 1.49 in E2, 7.9 ± 0.89 in E3). However, wide range was observed in E3 (2 - 22), E2 (2 - 20), and E1 (2- 16) (Table 4.3).

4.1.2.2. 15 Days to maturity

This trait was recorded only in E1. The mean days to maturity was observed as 94.1 ± 10.95 days with range of 96-165 days in E1. Based on days to maturity, the accessions were grouped into early maturing (<50 days) (32.45 % of accessions), medium maturing (51 – 80 days) (47.64 %) and late maturing (>80 days) (19.91 %) (Table 4.3).

4.1.2.2. 16 Single panicle weight

The mean single panicle weight was 10.1 ± 1.29 g with a range of 0.63 to 13.1 g in E3 (Table 4.3). In other two environments this trait was not recorded.

4.1.2.2.17 1000 -grain weight

The mean 1000-grain weight was 4.2 ± 0.75 g with a range of 0.6 to 7.5 g in E2 (Table 4.3). This trait was not recorded in E1 and E3.

4.1.2.2. 18 Grain yield per hectare

The mean grain yield per hectare was about 1.0 t ha^{-1} in all three environments (0.98 t ha^{-1} in E1 and E3, 0.99 t ha^{-1} in E2) and overall. However, a wide range was observed for this trait in all the three environments (0.05 to 2.7 t ha^{-1} in E1, 0.06 to 2.4 to ha^{-1} in E2 and 0.02 to 2.61 t ha^{-1} in E3 (Table 4.3). Average mean yield observed by different maturity groups were short duration (0.8 t ha^{-1} in E1, 0.9 t ha^{-1} in E2, 0.8 t ha^{-1} in E3 and 0.8 t ha^{-1} in pooled), medium duration (0.8 t ha^{-1}in E1, 1.2 t ha^{-1}in E2, 1.3 t ha^{-1} in E3 and 1.2 t ha^{-1} in pooled) and long duration (0.9 t ha^{-1} in all environments and pooled).

Seven accessions, IE6149, IE2890, IE642, IE3825, IE4699, IE5499 and IE4220 produced > 2. t ha^{-1} in all the three environments, and they were considered as high yielding accessions. Eight accessions, IE4443, IE4709, IE4446, IE4711, IE581, IE3612, IE712 and IE3547 yielded <0.35 t ha^{-1} in all the environments and were considered as poor yielding. The short duration accessions (<80 days) recorded 0.06statured early maturing accessions from *Compacta* and *Vulgaris* produced higher grain yield (1.5 – 2.7 t ha^{-1}).

4.1.2.2. 19 Mean performance of the accessions according to their biological races.

The mean values of cultivated races did not differ significantly for any of the traits and wild races *Africana* and *Spontanea* differed significantly for days to 50% flowering, plant height, basal tiller number, ear head length, ear head width and grain yield per hectare in all environments and over all in combined analysis, and for number of fingers in E1 and in combined as revealed by Newman-Keuls test (Table 4.4). According to Accessions from wild *Spontanea* race had higher mean number of days to 50% flowering (82.42 days in E1, 83.03 days in E2, 84.85 days in E3 and 71.51 days in overall) than other cultivated races. Contrastingly, another wild *Africana* race recorded lower mean number of days to 50% flowering (67.27 days in E1, 68.27 days in E2, and 67.54 days in E3 and 66.23 days in overall).

Accessions of *Spontanea* (52.06, 52.48, 51.97 and 56.52 cm) and *Africana* (54.18, 55.10, 57.49 and 53.45 cm) in E1, E2, E3 and pooled, respectively recorded low plant height compared to cultivated races. The mean basal tiller number was high in wild *Africana* (7.98 in E1, 9.98 in E2, 7.67 in E3 and 7.92 pooled) and *Spontanea* (14.56 in E1, 17.06 in E2, 13.69 in E3 and 14.10 in pooled), whereas cultivated races recorded lower (< 4.7) in all the environments. The four cultivated races recorded almost similar mean value for most of the traits such as days to 50 % flowering, plant height, flag leaf blade length, flag leaf blade width, flag leaf sheath length, ear head length, ear head width and panicle excertion. High mean yield was observed in cultivated accessions (0.96 – 2.03 t ha^{-1}), whereas low yield (0.32 to 0.35 t ha^{-1}) was recorded by accessions of wild races in all the environments (Table 4.4).

The variances of the cultivated and wild races were homogenous for most of the trait except days to 50% flowering ($P = 0.001$) and ear head width $P = 0.001$) in E1, days to 50% flowering ($P = 0.002$), ear head length ($P = 0.001$) and length of longest finger ($P = 0.001$) in E2, flag leaf blade length ($P = 0.005$), ear head length ($P = 0.001$) , width oflongest finger ($P = 0.001$), and number of fingers ($P = 0.001$) in E3, days to 50%

Table: 4.4 Means and variance for quantitative traits in different biological races of global finger millet composite collection evaluated across three environments and pooled analysis.

Traits	DF (days)	PH (cm)	BTN (no)	CB (no)	FLBL (mm)	FLBW (mm)	FLSL (mm)	PL (mm)	PE (mm)	EHL (mm)	EHW (mm)	LLF (mm)	WLF (mm)	NF (no)	PY (t/ha)
E1 (2005/ 2006 post rainy)															
africana (3)	67.27^{ab}	54.18^{ab}	7.98^{ab}	2.71^{a}	350.96^{a}	11.07^{a}	93.59^{a}	196.84^{a}	a	67.91^{a}	9.79^{ab}	a	a	4.56^{ab}	0.30^{ab}
compacta (132)	71.97^{a}	81.426^{a}	3.76^{a}	2.54^{a}	342.14^{a}	10.21^{a}	99.99^{a}	158.32^{a}	a	53.50^{a}	47.19^{a}	a	a	5.23^{a}	1.04^{a}
elongata (72)	71.94^{a}	80.01^{a}	3.79^{a}	2.14^{a}	341.69^{a}	10.17^{a}	99.61^{a}	163.41^{a}	a	93.09^{a}	37.07^{a}	a	a	4.35^{a}	1.03^{a}
plana (207)	72.55^{a}	80.69^{a}	3.78^{a}	2.24^{a}	339.98^{a}	10.33^{a}	100.03^{a}	156.62^{a}	a	92.75^{a}	56.97^{a}	a	a	6.76^{a}	0.99^{a}
spontanea (7)	82.42^{ab}	52.01^{ab}	14.56^{ab}	2.67^{a}	363.82^{a}	10.75^{a}	93.52^{a}	133.15^{a}	a	64.02^{a}	15.78^{ab}	a	a	9.43^{ab}	0.33^{ab}
vulgaris (579)	70.71^{a}	80.64^{a}	3.72^{a}	2.46^{a}	340.92^{a}	10.36^{a}	100.72^{a}	160.69^{a}	a	73.16^{a}	37.18^{a}	a	a	5.68^{a}	0.95^{a}
Variance	111.32	149.52	1.44	1.53	1227.05	11.83	122.96	2188.18	a	503.08	57.21	a	a	1.25	1.56
F value	4.422	0.473	0.644	0.284	1.115	1.415	1.185	0.156	a	5.524	0.583	a	a	0.273	1.393
P	0.001	0.760	0.635	0.892	0.351	0.228	0.318	0.960	a	0.001	0.677	a	a	0.894	0.234
E2 (2006 rainy)															
africana (3)	68.27^{ab}	55.10^{ab}	9.98^{ab}	2.31^{a}	351.96^{a}	9.07^{a}	94.59^{a}	197.84^{a}	100.43^{a}	68.91^{ab}	10.79^{ab}	55.45^{ab}	5.67^{ab}	3.52	0.35^{ab}
compacta (132)	72.97^{a}	82.426^{a}	4.76^{a}	2.34^{a}	343.14^{a}	11.21^{a}	100.99^{a}	159.31^{a}	105.46^{a}	64.53^{a}	38.19^{a}	45.67^{a}	13.24^{a}	9.23^{a}	1.04^{a}
elongata (72)	72.94^{a}	81.01^{a}	4.79^{a}	2.43^{a}	342.69^{a}	11.17^{a}	100.61^{a}	164.41^{a}	101.45^{a}	94.09^{a}	38.07^{a}	66.32^{a}	15.23^{a}	4.95^{a}	2.03
plana (207)	77.82^{a}	117.15^{a}	4.09^{a}	2.56^{a}	355.51^{a}	9.84^{a}	96.04^{a}	195.45^{a}	103.45^{a}	98.83^{a}	50.06^{a}	72.43^{a}	15.32^{a}	6.23^{a}	0.99^{a}
spontanea (7)	83.03^{a}	52.48^{ab}	17.06^{ab}	2.47^{a}	309.05^{a}	9.69^{a}	105.65^{a}	196.42^{a}	106.78^{a}	62.11^{ab}	15.96^{ab}	71.45^{a}	6.75	9.73^{a}	0.32^{ab}
vulgaris (579)	73.84^{a}	114.71^{a}	4.19^{a}	2.45^{a}	337.63^{a}	9.63^{a}	100.45^{a}	203.25^{a}	96.78^{a}	77.32^{a}	48.16^{a}	68.12^{a}	14.28^{a}	5.68^{a}	0.98^{a}
Variance	94.15	171.24	1.92	2.77	2764.05	15.73	156.63	1917.65	91.33	446.23	143.83	45.55	8.12	2.12	1.23
F value	4.116	0.288	1.763	2.015	2.398	0.527	0.134	0.145	0.434	8.448	1.018	10.558	0.586	0.215	0.464
P	0.002	0.887	0.134	0.091	0.049	0.722	0.971	0.983	0.806	0.001	0.398	0.001	0.674	0.933	0.761
E3 (2007 rainy)															
africana (3)	67.54^{a}	57.49^{ab}	7.67^{ab}	a	345.98^{a}	7.54^{a}	96.12^{a}	193.45^{a}	102.34^{a}	58.04^{ab}	10.34^{ab}	44.45^{ab}	5.34^{ab}	4.23^{ab}	0.32^{ab}
compacta (132)	71.85^{a}	114.13^{a}	3.73^{a}	a	336.14^{a}	9.64^{a}	78.32^{a}	191.89^{a}	96.45^{a}	74.16^{a}	49.82^{a}	76.43^{a}	13.56^{a}	9.67^{a}	1.46^{a}
elongata (72)	70.93^{a}	114.77^{a}	3.75^{a}	a	332.63^{a}	9.67^{a}	78.63^{a}	191.45^{a}	104.36^{a}	95.24^{a}	49.38^{a}	67.54^{a}	15.56^{a}	4.15^{a}	0.97^{a}
plana (207)	71.84^{a}	115.79^{a}	3.73^{a}	a	336.61^{a}	9.65^{a}	78.21^{a}	191.93^{a}	94.56^{a}	89.45^{a}	50.06^{a}	74.32^{a}	15.38^{a}	6.45^{a}	1.04^{a}
spontanea (7)	84.85^{ab}	51.97^{ab}	13.69^{ab}	a	277.82^{a}	9.65^{a}	77.82^{a}	190.49^{a}	105.45^{a}	78.74^{a}	14.96^{ab}	77.23^{a}	6.71^{ab}	9 .83^{a}	0.35^{ab}
vulgaris (579)	69.01^{a}	114.19^{a}	3.74^{a}	a	331.98^{a}	9.63^{a}	78.66^{a}	193.71^{a}	101.23^{a}	87.05^{a}	48.18^{a}	67.98^{a}	14.34^{a}	5.28^{a}	0.98^{a}
Variance	69.24	120.75	1.92	a	2270.06	12.45	84.07	1416.08	109.04	266.53	71.27	61.51	1.25	47.53	4.86
F value	11.134	1.065	1.575	a	5.087	0.694	0.297	0.239	3.723	13.525	43.253	0.796	0.857	30.259	11.212
P	0.005	0.375	0.179	a	0.001	0.595	0.887	0.919	0.005	0.001	0.001	0.533	0.494	0.000	0.012
Pooled															
africana (3)	66.23^{ab}	53.45^{ab}	7.92^{ab}	2.45^{a}	319.8^{a}	10.45^{a}	89.41^{a}	189.67^{a}	107.45^{a}	73.01^{a}	15.79^{ab}	74.78^{a}	5.67^{ab}	4.56^{ab}	0.35^{ab}
compacta (132)	73.47^{a}	104.13^{a}	3.79^{a}	2.41^{a}	343.82^{a}	9.82^{a}	92.24^{a}	182.61^{a}	104.65^{a}	68.16^{a}	45.36^{a}	69.35^{a}	13.56^{a}	9.23^{a}	1.01^{a}
elongata (72)	72.97^{a}	103.7^{a}	3.95^{a}	2.45^{a}	336.87^{a}	9.66^{a}	93.04^{a}	184.82^{a}	104.56^{a}	85.06^{a}	45.48^{a}	72.34^{a}	15.56^{a}	4.35^{a}	0.98^{a}
plana (207)	74.08^{a}	104.72^{a}	3.87^{a}	2.32^{a}	344.42^{a}	9.98^{a}	91.35^{a}	180.66^{a}	103.45^{a}	90.34^{a}	50.94^{a}	73.45^{a}	15.38^{a}	6.76^{a}	1.04^{a}
spontanea (7)	71.51^{a}	56.52^{ab}	14.10^{ab}	2.56^{a}	335.27^{a}	9.16^{a}	98.59^{a}	197.85^{a}	107.89^{a}	64.89^{a}	17.19^{ab}	76.78^{a}	6.56^{ab}	9.43^{ab}	0.33^{ab}
vulgaris (579)	71.16^{a}	103.06^{a}	3.88^{a}	2.34^{a}	336.83^{a}	9.88^{a}	93.26^{a}	185.85^{a}	98.56^{a}	79.06^{a}	44.33^{a}	75.56^{a}	14.34^{a}	5.68^{a}	0.97^{a}
Variance	95.93	129.74	1.56	2.52	2217.67	13.43	89.07	1730.04	98.33	441.02	75.67	41.72	48.08	1.72	1.34
F value	15.072	3.224	0.001	2.398	0.377	3.604	3.642	0.024	7.61	0.828	16.525	0.824	7.636	0.07	3.224
P	0.002	0.073	0.981	0.122	0.539	0.058	0.056	0.878	0.024	0.355	0.001	0.362	0.005	0.792	0.073

Numbers in parenthesis indicate number of accessions in each biological race

Letter arranged in subsequent letter are differed significantly from different races were tested by Newman-Keuls test

* Variance homogeneity was tested by Levene's test.

a- data not recorded.

DF (days to 50% flowering), PH (plant height), BTN (basal tiller number), CB (culm branching), FLBL (flag leaf blade length), FLBW (flag leaf blade width), FLSH (flag leaf sheath length), PL (peduncle length), PE (panicle exsertion), EHL (ear head length), EHW (ear head width), LLF (length of longest fingers), WLF (width of longest fingers), NF(number of fingers) and PY (Grain yield per hectare).

flowering (*P* = 0.002), width of longest finger (*P* = 0.005), ear head length (*P* = 0.005), ear head width (*P* = 0.001) in combined as detected by Levene's test (Table 4.4).

4.1.2.2. 20 Mean performances of the accessions according to their geographical regions

According to Newman- Keuls test, means were not significantly different for most of the traits of the accessions from different regions except for days to 50% flowering (West Africa), peduncle length (America), ear head width (Central Africa) and (East Africa) and number of fingers (Central Africa) in E1, days to 50% flowering (Southern Africa and West Africa) in E2, width of longest finger (East Africa) in combined analysis (Table 4.5). The accessions from West Africa (57.36, 62.93, 73.89 and 71.66 days) and Central Africa (68.17, 73.91, 64.33 and 65.96 days) flowered earlier, whereas accessions from Southern Africa (82.41, 83.51, 77.49 and 75.54 days) flowered late in E1, E2, E3 and pooled analysis overall, respectively. The accessions from different region recorded almost similar mean value for traits such as flag leaf blade length, flag leaf blade width, flag leaf sheath length, ear head length, ear head width and panicle excertion. The East African accessions had high mean yield (1.20, 0.99, 1.02 and 1.01 t ha^{-1}) followed by southern African accessions (1.03, 1.0, 1.07 and 1.01 t ha^{-1}) in E1, $E2_,$ E3, and combined respectively.

The variance of the accessions from different regions were homogeneous for all traits except for days to 50% flowering in E1, flag leaf blade length in E2, days to 50% flowering and basal tiller number in E3 and flag leaf blade length in combined analysis (*P* = 0.001) according to Levene's test (Table 4.5).

4.1.2.3 Phenotypic and genotypic coefficients of variation

In general, for all the traits, the phenotypic coefficient of variation was higher than the genotypic coefficient of variation. The values were grouped into high (> 20%), medium (10 – 20%) and low (< 10%). The PCV was high for basal tiller numbers (33.14 % in E1 , 34.99 % in E2, 28.49 % in combined), culm branching (32.14 % in E1 and 33.45 % in E2), flag leaf blade width (68.42 % in E1, 70.21 % in E2, 64.96 % in E3 and 24.6 % in combined), flag leaf sheath length (30.47 % in E1, 40.87 % in E2, 55.16 % in E3 and 21.20 % in combined), peduncle length (34.56 % in E1, 32.56% in E2 and 29.20

Traits	DF (days)	PH (cm)	BTN (no)	CB (no)	FLBL (mm)	FLBW (mm)	FLSL (mm)	PL (mm)	PE (mm)	EHL (mm)	EHW (mm)	LLF (mm)	WLF (mm)	NF (no)	PY (t/ ha)
E1 (2005 -2006 post rainy)															
America (5)	78.54^{a}	78.89^{a}	3.11^{a}	2.34^{a}	334.04^{a}	10.95^{a}	97.35^{a}	154.56^{a}	a	75.84^{a}	47.14^{a}	a	a	7.45^{a}	0.92^{a}
Central Africa (3)	68.17*	82.61^{a}	4.04^{a}	2.24^{a}	349.66^{a}	11.31^{a}	97.16^{a}	179.53^{ab}	a	74.96^{a}	7.94^{ab}	a	a	6.45^{ab}	0.88^{a}
East Africa (362)	71.42^{a}	81.26^{a}	3.69^{a}	2.71^{a}	341.53^{a}	10.34^{a}	100.51^{a}	159.08^{a}	a	72.74^{a}	6.99^{ab}	a	a	8.54^{a}	1.20^{a}
Europe (7)	78.53^{a}	98.28^{a}	3.55^{a}	2.54^{a}	337.34^{a}	9.86^{a}	101.31^{a}	154.37^{a}	a	76.24^{a}	57.27^{a}	a	a	7.86^{a}	0.82^{a}
South Asia (328)	69.11^{a}	80.35^{a}	3.64^{a}	2.67^{a}	340.54^{a}	10.38^{a}	100.42^{a}	162.43^{a}	a	83.25^{a}	47.18^{a}	a	a	7.81^{a}	0.95^{a}
Southern Africa (261)	82.41^{ab}	90.12^{a}	3.85^{a}	2.46^{a}	340.14^{a}	10.12^{a}	100.77^{a}	155.91^{a}	a	72.98^{a}	47.27^{a}	a	a	8.34^{a}	1.03^{a}
West Africa (7)	57.36^{ab}	99.94^{a}	4.33^{a}	2.14^{a}	337.04^{a}	10.54^{a}	100.48^{a}	162.92^{a}	a	75.57^{a}	56.5^{a}	a	a	6.89^{a}	1.01^{a}
Unknown (27)	75.74^{a}	91.63^{a}	4.12^{a}	2.34^{a}	342.58^{a}	10.49^{a}	99.73^{a}	202.84	a	82.66^{a}	47.28^{a}	a	a	8.45^{a}	0.95^{a}
Variance	111.32	149.52	1.44	1.53	1227.05	11.83	122.96	2188.18	a	503.08	57.21	a	a	1.25	1.56
F value	20.840	0.380	0.640	0.410	1.340	0.590	0.380	0.330	a	1.500	1.800	a	a	0.680	0.770
P	0.001	0.913	0.724	0.898	0.230	0.761	0.914	0.939	a	0.162	0.084	a	a	0.689	0.612
E2 (2006 rainy)															
America (5)	73.68^{a}	117.32^{a}	4.47^{a}	2.71^{a}	337.93^{a}	10.92^{a}	96.75^{a}	205.62^{a}	100.43^{a}	81.13^{a}	48.64^{a}	72.13^{a}	15.67^{a}	7.32^{a}	0.97^{a}
Central Africa (3)	73.91^{a}	116.45^{a}	4.07^{a}	2.54^{a}	340.87^{a}	9.63^{a}	113.31^{a}	216.21^{a}	105.46^{a}	81.92^{a}	50.43^{a}	65.67^{a}	13.24^{a}	6.34^{a}	0.98^{a}
East Africa (362)	76.36^{a}	117.17^{a}	4.61^{a}	2.24^{a}	362.06^{a}	9.94^{a}	95.67^{a}	199.98^{a}	113.45^{a}	77.22^{a}	48.82^{a}	72.43^{a}	8.32^{a}	8.43^{a}	0.99^{a}
Europe (7)	78.68^{a}	121.72^{a}	4.44^{a}	2.67^{a}	346.86^{a}	8.71^{a}	99.33^{a}	191.49^{a}	106.78^{a}	72.37^{a}	54.32^{a}	71.45^{a}	9.75^{a}	7.45^{a}	1.01^{a}
South Asia (328)	70.95^{a}	112.96^{a}	4.28^{a}	2.14^{a}	330.38^{a}	9.69^{a}	103.52^{a}	207.82^{a}	110.45^{a}	77.63^{a}	48.22^{a}	66.32^{a}	9.23^{a}	7.12^{a}	0.98^{a}
Southern Africa (261)	83.51^{ab}	120.83^{a}	4.28^{a}	2.45^{a}	339.68^{a}	9.03^{a}	91.86^{a}	185.37^{a}	102.34^{a}	86.95^{a}	50.34^{a}	66.34^{a}	13.45^{a}	6.78^{a}	1.02^{a}
West Africa (7)	62.93^{ab}	104.74^{a}	3.77^{a}	2.46^{a}	340.06^{a}	8.39^{a}	99.29^{a}	175.05^{a}	100.78^{a}	89.83^{a}	55.33^{a}	68.12^{a}	8.28^{a}	7.56^{a}	0.95^{a}
Unknown (27)	71.17^{a}	115.82^{a}	4.17^{a}	2.34^{a}	368.85^{a}	10.39^{a}	102.73^{a}	196.14^{a}	105.32^{a}	80.51^{a}	46.63^{a}	65.23^{a}	14.56^{a}	8.56^{a}	1.04^{a}
Variance	94.15	171.24	1.92	1.54	2764.05	15.73	156.63	1917.65	91.33	446.23	143.83	45.55	8.12	2.12	1.23
F value	1.100	1.060	1.570	0.876	5.080	0.690	0.290	0.230	0.340	1.950	1.330	1.820	0.220	0.400	0.360
P	0.356	0.375	0.179	0.013	0.001	0.596	0.888	0.919	0.937	0.058	0.232	0.081	0.980	0.901	0.926
traits	**DF (days)**	**PH (cm)**	**BTN (no)**	**CB (no)**	**FLBL (mm)**	**FLBW (mm)**	**FLSL (mm)**	**PL (mm)**	**PE (mm)**	**EHL (mm)**	**EHW (mm)**	**LLF (mm)**	**WLF (mm)**	**NF (no)**	**PY (t/ ha)**
E3 (2007 rainy)															
America (5)	68.94^{a}	117.84^{a}	3.71^{a}	a	349.75^{a}	9.74^{a}	78.46^{a}	197.67^{a}	113.45^{a}	92.95^{a}	48.64^{a}	55.45^{a}	5.67^{a}	7.45^{a}	0.85^{a}
Central Africa (3)	64.33^{a}	104.76^{a}	3.71^{a}	a	294.36^{a}	9.66^{a}	77.19^{a}	191.17^{a}	106.78^{a}	78.95^{a}	50.43^{a}	55.67^{a}	13.24^{a}	6.45^{a}	0.93^{a}

East Africa (362)	71.23^{a}	117.35^{a}	3.73^{a}	a	339.73^{a}	9.66^{a}	78.29^{a}	192.83^{a}	96.46^{a}	88.17^{a}	48.82^{a}	72.43^{a}	15.32^{a}	8.51^{a}	1.02^{a}
Europe (7)	67.72^{a}	119.79^{a}	3.74^{a}	a	333.02^{a}	9.69^{a}	81.19^{a}	192.13^{a}	105.45^{a}	87.42^{a}	54.32^{a}	71.45^{a}	11.75^{a}	7.85^{a}	0.98^{a}
South Asia (328)	66.14^{a}	112.75^{a}	3.75^{a}	a	328.43^{a}	9.62^{a}	79.05^{a}	194.11^{a}	100.78^{a}	87.21^{a}	48.22^{a}	56.32^{a}	15.23^{a}	7.81^{a}	0.94^{a}
Southern Africa (261)	77.49^{a}	112.59^{a}	3.75^{a}	a	328.38^{a}	9.64^{a}	77.67^{a}	189.71^{a}	97.32^{a}	89.14^{a}	50.34^{a}	76.43^{a}	10.56^{a}	8.65^{a}	1.07^{a}
West Africa (7)	73.89^{a}	114.32^{a}	3.73^{a}	a	339.11^{a}	8.72^{a}	77.78^{a}	191.34^{a}	104.34^{a}	97.15^{a}	55.33^{a}	68.12^{a}	14.28^{a}	6.89^{a}	0.95^{a}
Unknown (27)	67.86^{a}	118.88^{a}	3.74^{a}	a	346.82^{a}	9.74^{a}	79.42^{a}	155.62^{a}	105.45^{a}	89.32^{a}	46.63^{a}	62.34^{a}	14.23^{a}	8.21^{a}	1.09^{a}
Variance	69.24	120.75	1.92	a	2270.06	12.45	84.07	1416.08	109.04	266.53	71.27	61.51	1.25	47.53	4.86
F value	15.340	0.210	4.460	a	2.070	0.800	0.780	0.840	0.340	1.950	1.330	1.820	0.220	0.400	0.360
P	0.001	0.984	0.001	a	0.044	0.592	0.602	0.557	0.937	0.058	0.232	0.081	0.980	0.901	0.926
Pooled															
America (5)	73.72^{a}	104.69^{a}	3.76^{a}	2.67^{a}	340.57^{a}	10.54^{a}	90.85^{a}	185.95^{a}	113.45^{a}	73.35^{a}	34.93^{a}	71.45^{a}	16.75^{a}	7.45^{a}	0.92^{a}
Central Africa (3)	65.96*	101.27^{a}	3.93^{a}	2.24^{a}	328.32^{a}	10.24^{a}	95.88^{a}	195.64^{a}	103.78^{a}	88.61^{a}	36.27^{a}	68.12^{a}	14.28^{a}	6.45^{a}	0.94^{a}
East Africa (362)	72.82^{a}	106.23^{a}	3.83^{a}	2.71^{a}	348.32^{a}	9.96^{a}	91.27^{a}	184.61^{a}	106.46^{a}	70.11^{a}	35.64^{a}	56.32^{a}	9.23^{ab}	8.54^{a}	1.01^{a}
Europe (7)	74.97^{a}	106.64^{a}	3.91^{a}	2.54^{a}	339.07^{a}	9.42^{a}	93.94^{a}	179.33^{a}	110.45^{a}	68.65^{a}	38.63^{a}	66.43^{a}	10.56^{a}	7.86^{a}	0.94^{a}
South Asia (328)	68.82^{a}	102.02^{a}	3.89^{a}	2.67^{a}	333.14^{a}	9.94^{a}	94.31^{a}	187.96^{a}	106.78^{a}	69.36^{a}	54.53^{a}	82.34^{a}	14.23	7.81^{a}	0.96^{a}
Southern Africa (261)	75.54^{a}	103.32^{a}	3.91^{a}	2.46^{a}	334.29^{a}	9.72^{a}	92.24^{a}	180.03^{a}	102.32^{a}	90.18^{a}	45.59^{a}	64.34^{a}	10.45^{a}	8.34^{a}	1.01^{a}
West Africa (7)	71.66*	105.39^{a}	4.03^{a}	2.14^{a}	352.09^{a}	10.17^{a}	93.91^{a}	184.77^{a}	102.34^{a}	70.77^{a}	33.63^{a}	63.42^{a}	14.56^{a}	6.89^{a}	1.02^{a}
Unknown (27)	73.76^{a}	99.67^{a}	3.94^{a}	2.54^{a}	338.74^{a}	9.55^{a}	92.52^{a}	176.35^{a}	105.45	77.52^{a}	39.05^{a}	85.23^{a}	15.67^{a}	8.45^{a}	0.93^{a}
Variance	95.93	129.74	1.56	2.52	2217.67	13.43	89.07	1730.04	98.33	441.02	75.67	41.72	48.08	1.72	1.34
F value	1.100	1.060	1.570	1.980	5.080	0.690	0.290	0.230	3.700	3.520	3.56	3.250	0.790	0.850	0.910
P	0.356	0.375	0.179	0.055	0.001	0.596	0.888	0.919	0.005	0.012	0.035	0.021	0.534	0.494	0.459

Numbers in parenthesis indicates number of accessions in each region

Letter arranged in subsequent letter are differed significantly from different races were tested by Newman-Keuls test

Variance homogeneity was tested by Levene’s test.

DF (days to 50% flowering), PH (plant height), BTN (basal tiller number), CB (culm branching), FLBL (flag leaf blade length), FLBW (flag leaf blade width), FLSH (flag leaf sheath length), PL (peduncle length), PE (panicle exsertion), EHL (ear head length), EHW (ear head width), LLF (length of longest fingers), WLF (width of longest fingers), NF (number of fingers) and PY (Grain yield per hectare).

% in E3), panicle excertion (31.21 % in E1, 35.22 % in E2 and 34.20 % in combined), ear head length (35.32 % in E1, 29.56 % in E3 and 22.15 % in overall), ear head width (34.58 % in E1, 28.85 % in E2, 35.25 % in E3 and 25.3 % in pooled), finger number (43.40 % in E1, 23.05 % in E2, 29.68 % in pooled), length of longest finger (38.86 % in E2, 37.6 % in E3, 48.84 % in combined analysis), width of longest finger (39.22 % in E2, 39.39 % in E3, 23.91 % in pooled), grain yield per hectare (34.56 % in E1, 62.12 % in E2, 40.51 % in E3, 33.76 % in pooled), days to maturity (38.15 % in E1), 1000- grain weight (73.81 % in E2) and single panicle weight (26.42 % in E3). Medium PCV was exhibited for days to 50% flowering (14.95 % in E1, 13.57 % in E2, 12.09 % in E3 and 12.44 % in pooled) and plant height (15.43 % in E1, 13.68 % in E2, 11.14 % in E3and 11.83 % in combined analysis) (Table 4.6).

The GCV was highest for flag leaf blade width (32.43 % in E1, 55.33 % in E2 and 57.13 % in E3), flag leaf sheath length (25.86 % in E1, 39.51 % in E2 and 37.87 % in E3), panicle excertion (27.79 % in E2, 33.01 % in E3 and 29.66 % in pooled), ear head width (31.47 % in E1, 23.36 % in E2 and 33.61 % in E3), length of longest finger (21.21 % in E2, 26.14 % in E3 and 39.48 % in combined and number of fingers (36.91 % in E1 and 21.19 % in E2), grain yield per hectare (30.27 % in E1, 50.18 % in E2, 35.25 % in E3 and 24.04 % in pooled), days to maturity (29.64 % in E1) and 1000-grain weight (71.37 % in E2) . Medium GCV value was observed for days 50 % to flowering (14.78 % in E1, 13.57 % in E2, 12.09 % in E3 and 12.44 % in pooled) and plant height (15.14 % in E1, 11.32 % in E2) and low for plant height (9.59 in E3 and 5.91 % in pooled) (Table 4.6).

4.1.2.4 Heritability

The estimates of broad sense heritability in the global finger millet composite were high (> 80 %) for most of the traits such as, days to 50 % flowering (98.86 % in E1, 95.06 % in E2 and 98.34 % in E3), plant height (98.12 % in E1, 82.74 % in E2 and 86.04 % in E3), flag leaf blade length (90.96 % in E1, 93.66 % in E2, 80.88 % in E3) , flag leaf sheathlength (84.87 % in E1, 96.67 % in E2), peduncle length(87.22 % in E3), panicle excertion (89.04 % in E2, 93.72 % in E3 rainy), ear head length (90.93 % in E1, 88.43 % in E3), ear head width ((91.06 % in E1, 80.97 % in E2, 95.34 % in E3), finger number (85.04

Table: 4.6 Genotypic and phenotypic coefficients of variance and heritability of the global finger millet composite collection evaluated across three environments and pooled analysis

Traits	GCV (%)				PCV (%)				h^2 (%)			
	E1	**E2**	**E3**	**pooled**	**E1**	**E2**	**E3**	**pooled**	**E1**	**E2**	**E3**	**pooled**
Days to 50 per cent flowering (days)	14.78	12.9	11.89	8.93	14.95	13.57	12.09	12.44	98.86	95.06	98.34	91.78
Plant height (cm)	15.14	11.32	9.59	9.91	15.43	13.68	11.14	11.83	98.12	82.74	86.04	83.77
Basal tiller numbers (number)	31.81	24.92	14.63	18.73	33.14	34.99	20.18	28.49	95.98	71.22	72.49	75.42
Culm branching (number)	29.67	26.45	a	14.95	32.14	33.45	a	15.81	62.31	79.07	a	31.30
Flag leaf blade length (mm)	10.27	20.12	14.30	13.00	11.29	21.48	17.68	19.00	90.96	93.66	80.88	68.42
Flag leaf blade width (mm)	32.43	55.33	57.13	13.80	68.24	70.21	64.96	24.6	47.52	78.89	87.94	56.09
Flag leaf sheath length (mm)	25.86	39.51	37.87	16.34	30.47	40.87	55.16	21.2	84.87	96.67	68.65	77.05
Peduncle length (mm)	28.59	22.88	25.47	18.85	34.56	32.56	29.2	21.38	74.04	70.27	87.22	88.16
Panicle exertion (mm)	a	27.79	33.01	29.66	a	31.21	35.22	34.20	a	89.04	93.72	86.72
Ear head length (mm)	32.12	11.42	26.14	17.21	35.32	16.58	29.56	22.15	90.93	68.87	88.43	77.69
Ear head width (mm)	31.47	23.36	33.61	16.08	34.58	28.85	35.25	25.3	91.06	80.97	95.34	63.55
Length of longest finger (mm)	a	21.21	26.14	39.48	a	38.86	37.6	48.84	a	54.58	69.52	80.83
Width of longest finger (mm)	a	38.71	22.14	15.25	a	39.22	26.42	23.91	a	83.80	91.34	63.68
Finger number per inflorescence (Number)	36.91	21.19	9.96	25.41	43.4	23.05	12.85	29.68	85.04	91.93	77.5	85.60
Days to maturity (days)	29.64	a	a	b	38.15	a	a	b	77.63		a	b
1000-grain weight (g)	a	71.37	a	b	a	73.81	a	b	a	98.69	a	b
Single panicle weight (g)	a	a	35.98	b	a	a	26.42	b	a		87.01	b
Grain yield per hectare (t ha^{-1})	30.27	50.18	35.25	24.04	34.56	62.12	40.51	33.76	87.58	80.77	96.69	71.20

a- data not recorded

b- data recorded only in one season

% in E1, 91.06 % in E2), single panicle weight (83.80 % in E3) and grain yield per hectare (87.58 % in E1, 80.77 % in E2, 96.09 % in E3) (Table 4.6).

The estimates were medium (50 – 80 %) for basal tiller number (71.22 % in E2 and 72.49% in E3), peduncle length (74.04 % in E1), ear head length (68.87 % in E2), length of longest finger (54.58 % in E2 and 69.52 % in E3) and lag leaf blade width (47.52 % in E1) (Table 4.6).

Considering all the three environments together the estimates of heritability were high for plant height (83.77%), peduncle length (88.16%), panicle excertion (86.72%), length of longest finger (80.83%), number of fingers (85.60%) and low for culm branching (31.30%) and basal number of tiller (65.42%). High heritability observed in the present study in different environments as well as overall indicates high reliability of estimates of between-entry difference and potential of selection for these traits. The low estimate of heritability of some traits indicates less reliability of selection for these traits.

4.1.2.5 Phenotypic correlation coefficient between different traits

Correlation coefficient helps to estimate the degree of association among the different traits using phenotypic values obtained in different environments. Phenotypic correlation coefficients were calculated for the global composite collection to estimate the nature of associations between different quantitative traits in all the three environments separately and overall in the three environments. Any correlation coefficient for global finger millet composite (998 degrees of freedom) with an absolute value greater than 0.05 will be significant at $P = 0.05$ and greater than 0.09 will be significant at $P = 0.01$

In total, 352 correlations were estimated in the E1, E2, E3 and combined analysis. At probability 0.05 or less, 19 out of 78 correlations were significant in E1 (Table 4.7), 68 out of 91 in E2 (Table 4.8), 83 out of 105 in E3 (Table 4.9) and 33 out of 78 in the combined analysis of data (Table 4.10).

4.1.2.5.1 Days to 50 % flowering

Days to 50 % flowering was significantly and positively correlated with plant height (0.981 in E1, 0.412 in E2, 0.542 in E3, and 0.231 in overall), days to maturity (0.135 in E1), ear head length (0.118 in E2 and 0.056 in E3), ear head width (0.196 in E2 and 0.095 in pooled), length of longest finger (0.127 in E2, 0.198 in E3 and 0.101 in pooled), grain yield per hectare (0.371 in E2, and 0.240 in E3), flag leaf blade width (0.801 in E3) and panicle weight (0.299 in E3), whereas significantly negatively correlated with flag leaf blade width (-0.056 in E1), culm branching (-0.074 in E2), flag leaf sheath length (-0.192 in E2), peduncle length (- 0.287 in E2), panicle excertion (-0.308 in E2 and -0.197in E3) and finger numbers (-0.101 in E3) (Table 4.7 to 4. 10).

4.1.2.5.2 Plant height

Plant height was significantly and positively correlated with basal tiller number (0.770 in E1), flag leaf blade length (0.134 in E1, 0.109 in E2, 0.245 in E3 and 0.844 in pooled), ear head length (0.255 in E2, 0.184 in E3, 0.150 in pooled), grain yield per hectare (0.371 in E2, 0.550 in E3), flag leaf blade width (0.132 in E3), flag leaf sheath length (0.129 in E3) and panicle excertion (0.081 in E3), whereas significantly negatively correlated with finger number (-0.056 in E1 and -0.058 in E3), basal tiller number (-0.089 in E3) and flag leaf blade length (-0.065 in pooled) (Table 4.7 to 4. 10).

4.1.2.5.3 Basal tiller number

Basal tiller number was significantly and positively correlated with flag leaf blade length (0.054 in E1), peduncle length (0.430 in E1, 0.127 in E2 and 0.079 in pooled), culm branching (0.470 in E2), panicle excertion (0.123 in E2) and grain yield per hectare (0.111 in E2), whereas significantly negatively correlated with flag leaf blade width (-0.090 in E2), ear head width (-0.092 in E2), width of longest finger (-0.091 in E2 and -0.090 in E3), panicle weight (-0.127 in E3) (Table 4.7 to 4. 10).

4.1.2.5.4 Clum branching

Culm branching was not significantly correlated either positively or negatively with any of the character in E1 and combined analysis. However, in E2, culm branching was positively correlated with peduncle length (0.096), panicle excertion (0.151) and grain yield per hectare (0.072) and negatively correlated with flag leaf blade width (-0.105), ear head length (-0.263), length of longest finger (-0.189), width of longest finger (-0.107) and flag leaf sheath length (-0.055).

4.1.2.5.5 Flag leaf blade length

Flag leaf blade length was significantly and positively correlated with ear head length (0.100 in E1, 0.244 in E2, 0.166 in E3 and 0.117 in overall), flag leaf blade width (0.237 in E2, 0.143 in E3 and 0.066 in combined), peduncle length (0.061 in E2 and 0.051 in E3), panicle excertion (0.064 in E2 and 0.064 in E3), ear head width (0.083 in E2 and 0.068 in E3), length of longest finger (0.245 in E2 and 0.230 in E3), width of longest finger (0.101 in E2 and 0.108 in E3) and grain yield per hectare (0.357 in E2 and 0.188 in E3), whereas significantly negatively correlated with flag leaf blade width (-0.050 in E1 and -0.081 in E3) (Table 4. 7 to 4. 10).

4.1.2.5.6 Flag leaf blade width

Flag leaf blade width was significantly and positively correlated with peduncle length (0.064 in E1), ear head length (0.141 in E2, 0.210 in E3 and 0.770 in combined), ear head width (0.249 in E2, 0.051 in E3 and 0.060 in pooled), length of longest finger (0.245 in E2 and 0.051 in E3), width of longest finger (0.205 in E2 and 0.221 in E3), an grain yield per hectare (0.298 in E2 and 0.366 in E3) and significantly, negatively correlated with peduncle length (-0.069 in E2), flag leaf sheath length (-0.081in E3), panicle excertion (-0.070 in E3) (Table 4. 7 to 4. 10).

4.1.2.5.7 Flag leaf sheath length

Flag leaf sheath length was not significantly correlated with any of the traits in E1, whereas positively correlated with peduncle length (0.277 in E2, 0.230 in E3, 0.091 in pooled), ear head length (0.089 in E2), length of longest finger (0.111 in E2, 0.097 in E3, 0.064 in pooled) and grain yield per hectare (0.366 in E2) and significantly negatively correlated with width of longest finger(-0.181), panicle weight (-0.088) and grain yield per hectare (-0.179) in E3 and width of longest finger (-0.007) in pooled.

Table: 4.7 Phenotypic correlation coefficients between 13 quantitative traits in the global finger millet composite collection estimated in 2005- 2006 post rainy (E1) season at TNAU, Coimbatore.

Traits	DF	PH	BTN	CB	FLBL	FLBW	***FLSL***	PL	EHL	EHW	FN	DM	PY
DF	-												
PH	0.981**	-											
BTN	0.018	0.770**	-										
CB	-0.006	0.011	-0.004	-									
FLBL	0.043	0.134*	0.054**	0.004	-								
FLBW	-0.056*	0.006	0.024	0.015	-0.059*	-							
FLSL	-0.018	-0.014	-0.034	-0.007	-0.017	-0.032	-						
PL	0.046	0.028	0.43**	-0.031	0.002	0.064*	0.011	-					
EHL	0.031	-0.016	0.023	-0.018	0.100*	0.0201	0.002	0.203**	-				
EHW	0.004	-0.016	-0.031	-0.024	-0.020	-0.004	0.016	0.092**	0.040	-			
FN	-0.030	-0.056*	-0.000	0.029	0.011	-0.003	0.004	-0.006	0.131**	0.017	-		
DM	0.135**	0.036	-0.051*	-0.008	0.035	-0.044	0.042	-0.006	0.180*	0.330*	0.002	-	
PY	-0.036	-0.006	0.029	-0.041	0.003	0.025	0.030	-0.007	0.012	-0.016	0.507**	0.038	-

* and ** significant at $P = 0.05$ and 0.01 respectively

DF (days to 50% flowering), PH (plant height), BTN (basal tiller number), CB (culm branching), FLBL (flag leaf blade length), FLBW (flag leaf blade width), FLSH (flag leaf sheath length), PL (peduncle length), EHL (ear head length), EHW (ear head width), NF (number of fingers), DM (days to maturity) and PY (Grain yield per hectare).

Table: 4.8 Phenotypic correlation coefficients between 16 quantitative traits in the global finger millet composite collection estimated in 2006 rainy (E2) season at ICRISAT Centre , Patancheru, India

Traits	DF	PH	BTN	CB	FLBL	FLBW	FLSL	PL	PE	EHL	EHW	LLF	WLF	NF	TGW	PY
DF	-															
PH	0.412**	-														
BTN	-0.036	-0.033	-													
CB	-0.074**	-0.082*	0.407*	-												
FLBL	0.002	0.109**	-0.006	-0.046	-											
FLBW	-0.01	-0.011	-0.090**	-0.105**	0.273**	-										
FLSL	-0.192**	-0.024	0.005	-0.055*	-0.097**	-0.026	-									
PL	--0.287**	0.053*	0.127**	0.096**	0.061*	-0.069*	0.277**	-								
PE	-0.308**	-0.017	0.123**	0.151**	0.064*	-0.033	0.009	0.656**	-							
EHL	0.118**	0.255**	-0.034	-0.263**	0.244**	0.141**	0.089**	-0.01	-0.170**	-						
EHW	0.196**	0.099**	-0.092**	-0.222**	0.083**	0.249**	0.026	-0.136**	-0.153**	0.266**	-					
LLF	0.127**	0.189	-0.028	-0.189**	0.245**	0.099**	0.111**	-0.04	-0.171**	0.817**	0.258**	-				
WLF	0.053*	0.044	-0.091**	-0.107**	0.101**	0.205**	-0.006	-0.064*	-0.043	0.108**	0.331**	0.013	-			
NF	0.002	0.004	0.001	0.002	0.006	0.002	0.004	0.003	0.001	0.002	0.002	0.001	0.002	-		
TGW	0.01	0.002	0.018	0.03	0.005	0.006	0.012	0.004	0.001	0.002	0.001	0.003	0.003	0.001	-	
PY	0.371**	0.228**	0.111**	0.072*	0.357**	0.298**	0.366**	-0.179**	-0.133**	0.186**	0.102**	0.774**	0.250**	0.002	0.002	-

* and ** significant at $P = 0.05$ and 0.01 respectively

DF (days to 50% flowering), PH (plant height), BTN (basal tiller number), CB (culm branching), FLBL (flag leaf blade length), FLBW (flag leaf blade width), FLSH (flag leaf sheath length), PL (peduncle length), PE (panicle exertion), EHL (ear head length), EHW (ear head width), LLF (length of longest fingers), WLF (width of longest fingers), FN (finger number), PY (Grain yield per hectare).

Table: 4.9 Phenotypic correlation coefficients between 15 quantitative traits in the global finger millet composite collection observed in 2007 rainy (E3) season at ICRISAT Centre, Patancheru, India

Traits	DF	PH	BTN	FLBL	FLBW	FLSL	*PL*	***PE***	EHL	EHW	LLF	WLF	NF	PW	PY
DF	-														
PH	0.542**	-													
BTN	-0.105**	-0.089**	-												
FLBL	0.044	0.245**	-0.059*	-											
FLBW	0.801**	0.132**	-0.031	0.143**	-										
FLSL	-0.218**	0.129**	0.0207	0.044	-0.081**	-									
PL	-0.309**	0.097**	-0.036	0.051*	-0.073*	0.230**	-								
PE	-0.197**	0.081**	-0.021	0.064*	-0.070*	0.112**	0.662**	-							
EHL	0.056*	0.184**	-0.042	0.166**	0.142**	-0.042	0.015	-0.082**	-						
EHW	0.028	0.064*	0.027	0.068**	0.210**	0.026	0.014	0.003	0.132**	-					
LLF	0.198**	0.199**	-0.051*	0.230**	0.051*	0.097**	-0.070	-0.062*	0.716**	0.066*	-				
WLF	0.203**	-0.019	-0.090**	0.108**	0.221**	-0.181**	0.090	-0.129**	0.060*	0.214**	0.032	-			
NF	-0.101**	-0.058*	0.083**	-0.005	0.084**	0.003	0.034	0.019	0.100**	0.304**	-0.049	-0.112**	-		
PW	0.299**	0.112**	-0.127**	0.053*	0.095**	-0.088**	-0.174**	-0.095**	0.102**	0.183**	0.147**	0.203**	0.066*	-	
PY	0.240**	0.550**	0.077*	0.188**	0.366**	-0.179**	-0.210**	-0.342**	0.337**	0.233**	0.583**	0.720**	0.025	0.575**	-

* and ** significant at $P = 0.05$ and 0.01 respectively

DF (days to 50% flowering), PH (plant height), BTN (basal tiller number), FLBL (flag leaf blade length), FLBW (flag leaf blade width), FLSL (flag leaf sheath length),PL (peduncle length), PE (panicle exertion), EHL (ear head length), EHW (ear head width), LLF(length of longest fingers), WLF(width of longest fingers), NF(number of fingers), PW (Panicle weight) and PY (Grain yield per hectare).

Table: 4.10 Phenotypic correlation coefficient s between 15 quantitative traits in the global finger millet composite collection observed in pooled analysis

Trait	DF	PH	BTN	CB	FLBL	FLBW	FLSL	PL	EHL	EHW	LLF	WLF	NF	PY
DF	-													
PH	0.231**	-												
BTN	-0.035	0.044	-											
CB	0.001	0.004	0.001	-										
FLBL	0.026	0.844**	-0.015	0.003	-									
FLBW	-0.019	0650*	-0.042	0.001	0.066*	-								
FLSL	-0.071*	-0.097**	0.043	0.001	0.024	-0.01	-							
PL	-0.107**	0.257**	0.079**	0.003	0.032	-0.062*	0.091**	-						
EHL	0.026	0.150**	-0.006	0.002	0.117**	0.077**	-0.048	0.072**	-					
EHW	0.095**	0.188**	-0.019	0.002	0.061*	0.060*	0.005	0.062*	0.180**	-				
LLF	0.101**	0.090**	0.019	0.002	0.152**	0.045	0.064*	-0.019	0.502**	0.116	-			
WLF	0.043	0.035	-0.023	0.001	0.015	0.041	-0.067*	-0.004	0.034	0.062*	0.012	-		
NF	-0.008	0.062*	0.024	0.001	-0.058*	0.01	-0.031	0.023	0.789**	0.092**	-0.013	0.016	-	
PY	0.011	0.013	0.002	0.001	0.005	0.008	0.014	-0.006	0.011	0.044	0.013	-0.003	-0.001	-

* and ** significant at $P = 0.05$ and 0.01 respectively

DF (days to 50% flowering), PH (plant height), BTN (basal tiller number), FLBL (flag leaf blade length), FLBW (flag leaf blade width), FLSH (flag leaf sheath length), PL (peduncle length), EHL (ear head length), EHW (ear head width), LLF (length of longest fingers), WLF (width of longest fingers), NF (number of fingers) and PY (Grain yield per hectare).

4.1.2.5. 8 Peduncle length

Peduncle length was significantly positively correlated with ear head length (0.203 in E1 and 0.072 in pooled), ear head width (0.092 in E1) and significantly, negatively correlated with ear head width (0.136 in E2), and grain yield per hectare (-0.210 in E3).

4.1.2.5.9 Panicle excertion

It was significantly negatively correlated with ear head length (-0.170 in E2 and 0.082 in E3), ear head width (-0.153 in E2), length of longest finger (-0.171 in E2 and -0.062 in E3), width of longest finger (-0.129 in E3), panicle weight (-0.095 in E3) and grain yield per hectare (-0.133 in E2 and -0.342 in E3).

4.1.2.5.10 Ear head length

This trait was positively correlated with days to maturity in (0.180 in E1), ear head width (0.066 in E2 and 0.132 in E3), number of fingers (0.789 in pooled), length of longest finger (0.817 in E2, 0.716 in E3 and 0.502 in pooled), grain yield per hectare (0.186 in E2, 0.337 in E3).

4.1.2.5.11 Ear head width

Ear head width was significantly correlated with days to maturity (0.330 in E1), length of longest finger (0.258 in E2 and 0.266 in E3), width of longest finger (0.331 in E2 and E3) and grain yield per hectare (0.102 in E2 and 0.233 in E3).

4.1.2.5.12 Grain yield per hectare

Grain yield per hectare was correlated only with finger number (0.507) in E1 and with most of the traits in (E2 and E3 (rainy seasons) except number of fingers in E3. Whereas, negatively correlated with peduncle length (-0.179) in E2 and flag leaf sheath length (0.179), peduncle length (-0.210), panicle excertion (-0.342) in E3. In the combined analysis revealed the positive correlation with plant height (0.130) for this trait.

4.1.2.5.13 Pairs of characters showing meaningful correlation

The numbers of significant correlations were large (203 out of 352 correlations) in the present study and some of them may not be biologically meaningful. Skinner *et al,*

(1999) suggested that only those correlations, which are greater than 0.707 or less than –0.707 are biologically meaningful, so that 50 % of the variation in one trait is predicted by the other trait (Snedecor and Cochran, 1980). However with 998 degrees of freedom, the character pairs showing correlation greater than 0.700 or lesser than –0.700 is biologically meaningful and 8 pairs of characters were found that they showed meaningful. The correlations for all the 8 pairs of the characters were positive; Viz., days to 50% flowering and plant height in E1 (0.981); days to 50% flowering and flag leaf blade width in E3 (0.801); plant height and basal tiller number in E1 (0.770); plant height and flag leaf blade length in pooled (0.844); ear head length and length of longest finger in E2 (0.817) and E3 (0.716); grain yield per hectare and length of longest finger in E2 (0.774); grain yield per hectare and width of longest finger in E3 (0.720), and grain yield per hectare and panicle weight in E3 (0.789) showed significantly higher and biologically meaningful correlation (Table 4.11).

However the seven pairs of traits, Viz., days to 50% flowering and plant height in E3 (0.542); plant height and flag leaf blade width in combined (0.650); plant height and grain yield per hectare in E3 (0.550); peduncle length and panicle excertion in E2 (0.656) and E3 (0.662); ear head length and length of longest finger in pooled (0.502); grain yield per hectare and length of longest finger in E3 (0.583) and grain yield per hectare with finger number(0.507 in E1 and 0.575 in E3) showed high correlation (r = 0.50 or more) (Table 4.11).

4.1.2.6 Path coefficient analysis

The direct and indirect effects of all the traits on grain yield were partitioned from the genotypic correlation matrix by path analysis and are presented in Table 4.12 to 4.15. A residual value of 0.099 in E1, 0.097 in E2, 0.097 in E3 and 0.099 in combined analysis indicated the adequacy of the traits chosen for path analysis. The direct and indirect effects of different traits on grain yield per plant were as follows.

4.1.2.6.1 Direct effect

Several traits exhibited positive direct effect on grain yield per hectare in different environments. Thus 7 out of 12 in E1, 5 out of 15 in E2, 5 out of 14 in E3, 9 out of 14 in combined analysis. The direct effect of flag leaf blade length (0.67) was found to be very high

Table: 4.11 Meaningful correlation (r > 0.500) for quantitative traits of global finger millet evaluated across three environments and combined analysis.

Pair of traits	Environment	Correlation coefficient
Days to 50% flowering Vs. plant height	E1	0.981**
Days to 50% Flowering Vs. flag leaf blade width	E3	0.801**
Plant height Vs. Basal tiller numbers	E2	0.770**
Plant height Vs. Flag leaf blade length	Pooled	0.844**
Ear head length Vs. length of longest finger	E2	0.817**
	E3	0.716**
Length of longest finger Vs. Grain yield per hectare	E2	0.774**
Width of longest finger Vs. Grain yield per hectare	E3	0.720*
panicle weight Vs. Grain yield per hectare	E3	0.789**
Traits showed high correlation (r = 0.5 or more)		
Days to 50% flowering Vs. plant height	E3	0.543**
Plant height Vs. flag leaf blade width	Pooled	0.650**
Plant height Vs. Grain yield per hectare	E3	0.550**
Peduncle length Vs. Panicle exsertion	E2	0.656**
	E3	0.662**
Ear head length Vs. length of longest finger	Pooled	0.502**
Length of longest finger Vs. Grain yield per hectare	E3	0.583**
Number of fingers Vs. Grain yield per hectare	E1	0.507**
	E3	0.575

**** significant at $P = 0.05$**

Table: 4.12 Direct and indirect contribution of various traits to Grain yield per hectare in global finger millet composite collection estimated in 2005 – 2006 post rainy (E1) at TNAU, Coimbatore, India

Traits	DF	PH	BTN	CB	FLBL	FLBW	FLSL	PL	EE	EHL	EHW	DM	PY
DF	-0.39**	-0.02**	0.00	0.00	0.00	-0.04**	0.01*	0.01*	-0.01*	0.00	0.00	0.00	-0.45**
PH	0.03**	0.29**	-0.01*	0.01*	0.00	0.00	0.00	0.01*	0.00	0.00	0.00	0.02**	0.34**
BNT	-0.01*	0.02**	-0.15**	0.01*	0.00	0.02**	0.01*	0.01*	-0.01	0.00	0.00	-0.01*	-0.11**
CB	0.00	0.01*	0.00	0.02**	0.00	0.00	0.00	-0.01*	0.00	0.00	0.00	-0.01*	0.18**
FLBL	-0.02**	0.00	0.00	0.00	-0.01*	-0.05**	0.01*	0.00	0.00	0.00	0.00	0.02**	-0.14*
FLBW	0.03**	0.00	0.00	0.00	0.01*	0.63**	0.00	0.02*	0.00	0.00	0.00	-0.01*	0.67**
FLSL	0.01*	-0.01*	0.00	0.00	0.00	-0.01*	-0.23**	0.00	0.00	0.00	0.00	0.01*	-0.22**
PL	-0.02**	0.01*	-0.01*	0.00	0.00	0.04**	0.00	0.26**	-0.04**	-0.01*	0.00	-0.01*	0.22**
EE	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
EHL	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02***	0.00	-0.12**	0.00	-0.01*	-0.11**
EHW	0.01*	-0.01*	0.00	0.01*	0.00	0.01*	0.00	0.00	-0.03**	0.00	-0.03*	0.00	-0.05**
DM	0.00	0.02**	0.01*	-0.01*	-0.01*	-0.02**	0.00	-0.01*	0.00	0.00	0.00	0.25**	0.23**
NF	-0.01*	0.00	-0.01*	0.00	0.00	0.01*	0.00	0.05**	-0.23**	0.00	0.00	0.00	-0.02*

Residual value = 0.099

DF (days to 50% flowering), PH (plant height), BTN (basal tiller number), FLBL (flag leaf blade length), FLBW (flag leaf blade width), FLSH (flag leaf sheath length), PL (peduncle length), EE (Ear exsertion) EHL (ear head length), EHW (ear head width), LLF (length of longest fingers), WLF (width of longest fingers), NF (number of fingers) and PY (Grain yield per hectare).

** and * significant at $P = 0.05$ and $P=0.01$

Table: 4.13 Direct and indirect contribution of various traits to Grain yield per hectare in global finger millet composite collection estimated in 2006 rainy (E2) at ICRISAT Centre, Patancheru, India

Traits	**DF**	**PH**	**BTN**	**CB**	**FLBL**	**FLBW**	**FLSL**	**PL**	**PE**	**EHL**	**EHW**	**LLF**	**WLF**	**TGW**	**PY**
DF	**0.19****	**0.32****	0.03**	0.01*	-0.01*	0.01	0.05	0.08	-0.05	0.04	0.05	-0.02	0.00	0.01	**0.69**
PH	0.07 **	0.93**	0.01*	0.00	-0.04**	0.01	0.00	-0.03	0.01	0.09	0.06	-0.04	0.00	0.00	0.16
BTN	-0.02**	-0.01*	**-0.35****	-0.03**	0.00	0.02	-0.02	-0.05	0.03	0.01	-0.02	-0.01	0.00	0.00	**-0.44**
CB	-0.02**	-0.05**	-0.16**	-0.07**	0.01*	0.02	-0.01	-0.04	0.04	-0.04	-0.05	0.01	0.00	0.00	-0.03
FLBL	0.01*	0.18**	0.01*	0.00	-0.02	-0.03	0.01	-0.02	0.02	0.07	0.04	-0.04	0.00	-0.02	0.02
FLBW	0.00	-0.02**	0.02**	0.00	-0.02	-0.35	0.01	0.02	-0.02	0.04	0.03	-0.01	0.00	0.00	-0.03
FLSL	-0.02**	0.00	-0.02**	0.00	0.00	0.00	**-0.41**	-0.05	-0.01	0.02	0.03	-0.02	0.00	0.00	**-0.47**
PL	0.01*	0.00	0.02**	0.00	0.00	0.02	0.01	0.00	0.00	0.02	0.02	0.00	0.00	0.00	0.10
PE	-0.03**	0.04**	-0.05**	-0.01*	-0.02	0.02	0.02	-0.23	0.26	-0.04	-0.04	0.02	0.00	-0.01	-0.06
EHL	0.02**	0.22**	-0.01*	0.01*	-0.04	-0.03	-0.03	0.01	-0.03	**0.37**	0.12	-0.14	0.00	0.00	**0.47**
EHW	0.02**	0.14**	0.02**	0.01*	-0.02	-0.03	-0.03	0.04	-0.03	0.12	**0.37**	-0.04	0.00	0.02	**0.58**
LLF	0.02**	0.02**	-0.02**	0.00	-0.04	-0.03	-0.04	0.01	-0.03	0.03	0.09	**-0.18**	0.00	0.00	**0.30**
WLF	0.01*	0.01*	-0.01*	0.00	-0.01	-0.02	0.01	0.02	0.00	0.01	0.03	0.00	-0.04	0.00	0.01
NF	0.01*	0.01*	0.00	0.00	0.02	0.00	0.00	0.02	-0.01	0.00	0.03	0.00	0.00	0.19	**0.29**
TGW	-0.02**	-0.05**	0.03***	0.01*	-0.02	-0.01	0.02	-0.01	0.01	-0.04	-0.03	-0.03	0.01	-0.03	**0.27**

Residual Value = 0.097

DF (days to 50% flowering), PH (plant height), BTN (basal tiller number), FLBL (flag leaf blade length), FLBW (flag leaf blade width), FLSH (flag leaf sheath length), PL (peduncle length), EHL (ear head length), EHW (ear head width), LLF (length of longest fingers), WLF (width of longest fingers), NF (number of fingers), TGW (Thousand grain weight) And PY (Grain yield per hectare).

Table: 4.14 Direct and indirect contribution of various traits to Grain yield per hectare in global finger millet composite collection estimated in 2007 rainy (E3) at ICRISAT Centre, Patancheru, India

Traits	DF	PH	BTN	CB	FLBL	FLBW	FLSL	PL	PE	EHL	EHW	LLF	WLF	TGW	PY
DF	**0.46**	0.13	0.01	0.00	-0.03	-0.05	-0.05	-0.22	0.09	0.01	0.00	0.03	0.08	-0.04	**0.51**
PH	0.06	**0.90**	0.01	0.00	-0.14	-0.08	0.03	0.07	-0.04	0.04	-0.03	0.03	-0.01	-0.03	**0.83**
BTN	-0.05	-0.08	-0.06	-0.01	0.03	0.02	0.00	-0.03	0.01	-0.01	0.01	-0.01	-0.03	0.04	-0.16
FLBL	0.02	0.22	0.00	0.01	**-0.57**	-0.08	0.01	0.04	-0.03	0.04	-0.03	0.03	0.04	0.00	**-0.30**
FLBW	0.04	0.12	0.00	0.01	-0.08	**-0.59**	-0.02	-0.05	0.03	0.03	-0.06	0.01	0.08	0.04	**-0.43**
FLSL	-0.1	0.12	0.00	-0.01	-0.03	0.05	**0.21**	0.17	-0.05	-0.01	0.02	0.01	-0.07	0.00	**0.31**
PL	-0.14	0.09	0.00	0.00	-0.03	0.04	0.05	**0.72**	-0.30	0.00	-0.03	-0.01	-0.03	0.02	**0.38**
PE	-0.09	0.07	0.00	0.01	-0.04	0.04	0.02	0.48	-0.45	-0.02	0.00	-0.01	-0.05	0.01	-0.01
EHL	0.03	0.17	0.00	0.01	-0.09	-0.09	-0.01	0.01	0.04	**0.23**	-0.04	0.09	0.02	0.04	**0.41**
EHW	0.00	0.06	0.00	0.00	-0.04	-0.09	-0.01	0.05	0.00	0.03	-0.38	0.00	0.05	0.07	-0.27
LLF	0.09	0.18	0.00	0.00	**-0.13**	-0.03	0.02	-0.05	0.03	0.14	-0.01	**0.15**	0.01	-0.02	**0..37**
WLF	0.09	-0.02	0.01	0.00	-0.06	-0.13	-0.04	-0.07	0.06	0.01	-0.05	0.00	0.37	-0.05	0.14
NF	-0.05	-0.05	0.00	0.00	0.00	-0.05	0.00	0.02	-0.01	0.02	-0.06	-0.01	-0.04	0.44	**0.22**

Residual value = 0.097

DF (days to 50% flowering), PH (plant height), BTN (basal tiller number), FLBL (flag leaf blade length), FLBW (flag leaf blade width), FLSH (flag leaf sheath length),

PL (peduncle length), EHL (ear head length), EHW (ear head width), LLF (length of longest fingers), WLF (width of longest fingers), NF (number of fingers), PY (Grain yield per hectare).

Table: 4.15 Direct and indirect contribution of various traits to Grain yield per hectare in global finger millet composite collection estimated in pooled analysis

Traits	**DF**	**PH**	**BTN**	**CB**	**FLBL**	**FLBW**	**FLSL**	**PL**	**PE**	**EHW**	**EHW**	**LLF**	**WLF**	**NF**	**PY**
DF	0.17	-0.01	0.01	0.01	-0.01	0.00	-0.01	-0.01	0.02	0.00	0.02	-0.01	-0.01	0.00	0.16
PH	0.04	-0.02	-0.01	0.00	-0.04	-0.01	-0.02	0.01	0.00	-0.01	0.04	-0.01	-0.01	0.01	-0.04
BTN	-0.01	0.00	-0.34	-0.02	0.01	-0.01	0.01	0.00	0.01	0.00	0.00	0.00	0.01	0.00	-0.34
CB	-0.02	0.00	-0.11	-0.06	0.01	-0.01	0.00	0.00	0.01	0.00	-0.02	0.01	0.01	0.00	-0.16
FLBL	0.00	0.00	0.00	0.00	-0.51	0.01	0.01	0.00	-0.01	-0.01	0.01	-0.02	0.00	-0.01	-0.51
FLBW	0.00	0.00	0.01	0.00	-0.03	0.22	0.00	0.00	0.00	0.00	0.01	0.00	-0.01	0.00	0.19
FLSL	-0.01	0.00	-0.01	0.00	-0.01	0.00	0.21	0.00	-0.02	0.00	0.00	-0.01	0.02	0.00	0.17
PL	-0.02	-0.01	-0.03	0.00	-0.02	-0.01	0.02	0.05	-0.06	0.00	0.01	0.00	0.00	0.00	-0.06
PE	-0.02	0.00	0.01	0.00	-0.03	0.00	0.02	0.02	-0.21	0.00	-0.01	0.01	0.02	0.00	-0.18
EHL	0.00	0.00	0.00	0.00	-0.06	0.02	-0.01	0.00	0.01	-0.06	0.04	-0.05	-0.01	0.01	-0.10
EHW	0.02	0.00	0.01	0.01	-0.03	0.01	0.00	0.00	0.01	-0.01	0.22	-0.01	-0.02	0.01	0.21
LLF	0.02	0.00	-0.01	0.00	-0.08	0.01	0.01	0.00	0.02	-0.03	0.03	-0.1	0.00	0.00	-0.14
WLF	0.01	0.00	0.01	0.00	-0.01	0.01	-0.01	0.00	0.01	0.00	0.01	0.00	-0.31	0.00	-0.29
NF	0.00	0.00	-0.01	0.00	0.03	0.00	-0.01	0.00	0.01	0.00	0.02	0.00	0.00	0.11	0.14

Residual Value = 0.099

DF (days to 50% flowering), PH (plant height), BTN (basal tiller number), FLBL (flag leaf blade length), FLBW (flag leaf blade width), FLSH (flag leaf sheath length),

PL (peduncle length), EHL (ear head length), EHW (ear head width), LLF (length of longest fingers), WLF (width of longest fingers), NF (number of fingers) and PY (Grain yield per hectare).

and positive followed by plant height (0.34), days to maturity (0.23) in E1, and days to 50 % flowering (0.69), followed by ear head width (0.58), ear head length (0.47) and length of longest finger (0.30) in E2, and plant height (0.83) followed by days to 50% flowering (0.51), ear head length (0.41), peduncle length (0.38) and length of longest finger (0.37) in E3 (Table 4. 12 – 4.15).

Among the remaining traits, negative direct effects exhibited towards yield per plot, were days to 50 % flowering (-0.45 in E1), basal tiller number (-0.44 in E2), flag leaf blade length (-0.30 in E3), flag leaf blade width (-0.43 in E3), flag leaf sheath length (-0.47 in E2) and width of longest finger (-0.29 in pooled) (Table 4. 12 – 4.15).

4.1.2.6.2 Indirect effect

Regarding the indirect effect of component traits on grain yield, flag leaf blade length had high indirect effect on grain yield through plant height, number of tillers. Culm branching exhibited high indirect effect on yield through basal tiller numbers, days to 50 % flowering and peduncle length. The indirect effect of all the other traits was low.

4.1.2.7 Stability analysis

Both linear (b_i) and non-linear (S^2d_i) components of GE interactions are important for judging the stability of genotypes (Eberhart and Russell, 1966). A regression coefficient (b_i) approximately 1.0 coupled with an S^2d_i equal to Zero indicates good stability of the genotype. A regression value above 1.0 describes the genotypes with higher sensitivity to environmental changes and below 1.0 provides a measurement of greater resistance to environmental change.

In the present study, 468 accessions for days to 50% flowering and 495 accessions for grain yield per hectare recorded b_i value below 1.0 indicating the stable nature of accessions over environments. Linear regression ranged from -11.45 to 7.91 for days to 50% flowering, and from -146.01 to 210.96 for grain yield. This large variation in regression coefficients indicates different response of genotypes to environmental changes (Appendix II). Only 40 accessions for days to 50 % flowering and 7 accessions for grain yield per hectare (Appendix II) recorded a regression coefficient equal to unity ($b = 1$)

and small deviations from regression ($S^2d = 0$) are considered as stable genotypes over environments.

4.1.2.8 Phenotypic diversity

The Shannon-Weaver diversity index (H`) was calculated to compare phenotypic diversity among traits in each environment separately and also over all environments. The index is used as a measure of allelic richness and evenness; a low H` indicates an extremely unbalanced frequency class for an individual and lack of genetic diversity.

Out of six morphological traits studied, plant pigmentation showed lowest H` (0.217) in all environments followed by lodging (0.241 in E2 and E3). However, inflorescence shape (0.571 in E1 and E2 and 0.573 in E3) showed high H`. Among the quantitative traits studied, lowest mean H` was observed for flag leaf blade width (0.447 in E1, 0.343 in E2 and 0.446 in E3).

The traits such as, number of basal tiller (0.648), flag leaf sheath length (0.623), ear head width (0.607), number of fingers (0.611) in E1, days to 50% flowering (0.619), culm branching (0.615), panicle length (0.627), panicle excertion (0.626), length of longest finger (0.603) in E2, plant height (0.623), flag leaf blade length (0.624), ear head length (0.603), width of longest finger (0.616) and grain yield per hectare (0.634) in E3 showed high H` compared to other two environments. The combined analysis revealed low H` for flag leaf blade width (0.412) and high H` for panicle excertion (0.618). Among the environments, E3 (0.591 ± 0.0480) revealed high H` for the quantitative traits followed by E1 (0.590 ± 0.0380) and E2
(0.560 ± 0.0892) (Table 4.16).

4.1.2.8.2 Phenotypic diversity of global finger millet composite collection according to their biological race and geographical origin

4.1.2.8.2.1 Qualitative traits

The high H` was observed for the accessions from race *Elongata* for growth habit (0.463), inflorescent shape (0.681) and seed colour (0.685), accessions from race *Compacta* for glume prominence (0.612) and from *Plana* for plant pigmentation (0.287), whereas accessions of race *Spontanea* recorded low H` for all traits except plant

Table: 4.17 Shannon –Weaver diversity index (H`) observed for qualitative traits in different biological race and geographical origin 2006 rainy (E2) at ICRISAT Centre Patancheru, India

Trait/ Race/ Origin	Growth habit	Plant pigmentation	Inflorescence shape	Glume prominence	Seed colour	Lodging
Biological race						
africana	0.452	0.070	0.602	0.565	0.386	0.215
compacta	0.459	0.274	0.628	0.612	0.38	0.248
elongata	0.463	0.268	0.681	0.468	0.685	0.244
plana	0.459	0.287	0.606	0.468	0.453	0.231
spontanea	0.269	0.123	0.285	0.185	0.079	0.175
vulgaris	0.427	0.281	0.628	0.415	0.314	0.334
Mean	0.422	0.217	0.571	0.452	0.382	0.241
Min	0.269	0.070	0.285	0.185	0.079	0.175
Max	0.463	0.287	0.681	0.612	0.685	0.334
Geographical origin						
America	0.395	0.244	0.445	0.276	0.314	0.201
Central Africa	0.376	0.001	0.524	0.295	0.415	0.214
East Africa	0.453	0.270	0.589	0.503	0.415	0.218
Europe	0.432	0.178	0.515	0.510	0.328	0.276
South Asia	0.433	0.278	0.656	0.514	0.355	0.268
Southern Africa	0.453	0.248	0.646	0.509	0.415	0.234
Unknown	0.434	0.258	0.550	0.505	0.345	0.241
West Africa	0.396	0.259	0.641	0.51	0.468	0.280
Mean	0.422	0.217	0.571	0.452	0.382	0.241
Min	0.376	0.001	0.445	0.276	0.314	0.201
Max	0.453	0.278	0.656	0.514	0.468	0.280

Table: 4.18 Shannon –Weaver diversity index (H`) for quantitative traits in the global finger millet composite collection based on biological races estimated across three environments and pooled analysis.

Race	Season	DF	PH	BTN	CB	FLBL	FLBW	FLSL	PL	PE	EHL	EHW	LLF	WLF	NF	DM	TGW	PW	PY	Min	Max	Mean
africana	E1	0.456	0.451	0.31	0.456	0.456	0.451	0.301	0.456	a	0.245	0.456	A	a	0.451	0.456	a	a	0.451	0.245	0.456	0.414±0.08
	E2	0.451	0.451	0.451	0.244	0.451	0.451	0.451	0.451	0.451	0.455	0.451	0.452	0.451	0.244	a	0.452	a	0.451	0.244	0.455	0.425±0.07
	E3	0.301	0.301	0.303	a	0.301	0.301	0.31	0.301	0.301	0.301	0.301	0.301	0.311	0.302	a	a	0.301	0.301	0.301	0.311	0.302±0.03
	Pooled	0.445	0.423	0.345	0.312	0.407	0.345	0.345	0.403	0.378	0.378	0.423	0.333	0.434	0.312	b	b	b	0.401	0.312	0.445	0.379±0.03
compacta	E1	0.582	0.581	0.492	0.517	0.627	0.602	0.618	0.612	a	0.615	0.617	a	a	0.572	0.602	a	a	0.606	0.492	0.627	0.587±0.05
	E2	0.607	0.539	0.572	0.611	0.603	0.532	0.602	0.680	0.614	0.578	0.526	0.603	0.569	0.605	a	0.482	a	0.583	0.482	0.680	0.577±0.04
	E3	0.597	0.621	0.614	a	0.627	0.482	0.533	0.614	0.622	0.624	0.526	0.6	0.58	0.594	a	a	0.582	0.606	0.482	0.627	0.588±0.05
	Pooled	0.545	0.584	0.559	0.545	0.617	0.523	0.584	0.645	0.616	0.616	0.545	0.601	0.568	0.595	b	b	b	0.598	0.523	0.645	0.582±0.04
elongata	E1	0.488	0.599	0.534	0.55	0.586	0.534	0.619	0.601	a	0.585	0.51	a	a	0.607	0.573	a	a	0.568	0.488	0.619	0.565±0.04
	E2	0.601	0.613	0.567	0.548	0.633	0.542	0.588	0.596	0.598	0.581	0.489	0.573	0.54	0.541	a	0.5	a	0.602	0.489	0.633	0.569±0.04
	E3	0.537	0.617	0.601	A	0.606	0.547	0.549	0.651	0.524	0.568	0.489	0.571	0.542	0.558	a	a	0.593	0.589	0.489	0.651	0.569±0.04
	Pooled	0.532	0.614	0.545	0.523	0.648	0.544	0.583	0.618	0.543	0.574	0.498	0.574	0.549	0.561	b	b	b	0.546	0.498	0.648	0.563±0.03
plana	E1	0.586	0.615	0.660	0.495	0.624	0.54	0.617	0.611	a	0.601	0.597	a	a	0.607	0.605	a	a	0.612	0.495	0.660	0.597±0.05
	E2	0.606	0.597	0.602	0.582	0.614	0.543	0.524	0.624	0.618	0.568	0.571	0.59	0.4	0.574	a	0.464	a	0.545	0.400	0.624	0.563±0.06
	E3	0.653	0.618	0.598	A	0.624	0.474	0.554	0.606	0.619	0.613	0.567	0.605	0.558	0.598	a	a	0.619	0.622	0.474	0.653	0.595±0.05
	Pooled	0.615	0.618	0.624	0.553	0.621	0.519	0.565	0.614	0.618	0.594	0.568	0.634	0.545	0.593	b	b	b	0.593	0.519	0.634	0.591±0.01
vulgaris	E1	0.614	0.614	0.637	0.527	0.601	0.578	0.607	0.509	a	0.599	0.582	a	a	0.629	0.603	a	a	0.617	0.509	0.637	0.593±0.05
	E2	0.642	0.599	0.579	0.627	0.627	0.34	0.55	0.626	0.609	0.602	0.558	0.614	0.179	0.345	a	0.471	a	0.615	0.179	0.642	0.536±0.01
	E3	0.562	0.624	0.595	A	0.625	0.471	0.549	0.624	0.613	0.616	0.562	0.611	0.639	0.595	a	a	0.603	0.635	0.471	0.639	0.594±0.05
	Pooled	0.616	0.612	0.604	0.554	0.618	0.463	0.569	0.576	0.616	0.606	0.567	0.642	0.485	0.556	b	b	b	0.645	0.463	0.645	0.58 ±0 .05
spontanea	E1	0.261	0.261	0.261	0.261	0.261	0.261	0.261	0.261	a	0.261	0.261	a	a	0.261	0.261	a	a	0.261	0.261	0.261	0.261±0.05
	E2	.0.261	.0.261	.0.261	.0.261	.0.261	.0.261	.0.261	.0.261	.0.261	.0.261	.0.261	.0.261	.0.261	.0.261	a	.0.261	a	.0.261	.0.261	.0.261	0.261±0.05
	E3	0..261	0..261	0..261	0..261	0..261	0..261	0..261	0..261	0..261	0..261	0..261	0..261	0..261	0..261	a	a	0..261	0..261	0..261	0..261	0.261±0.05
	Pooled	0..261	0..261	0..261	0..261	0..261	0..261	0..261	0..261	0..261	0..261	0..261	0..261	0..261	0..261	b	b	b	0..261	0..261	0..261	0.261±0.05

a- data not recorded

b- data recorded only in one season

FL (days to 50% flowering), PH (plant height), BTN (basal tiller number), CB (culm branching), FLBL (flag leaf blade length), FLBW (flag leaf blade width), FLSH (flag leaf sheath length), PL (peduncle length), PE (panicle exsertion), EHL (ear head length), EHW (ear head width), LLF (length of longest fingers), WLF (width of longest fingers), NF (number of fingers), PY (Grain yield per hectare).

Table: 4.19 Shannon –Weaver diversity index (H`) for quantitative traits in the global finger millet composite collection based on geographical origin estimated across three environments and pooled analysis.

Region	Season	DF	PH	BTN	CB	FLBL	FLBW	FLSL	PL	PE	EHL	ELW	LLF	WLF	NF	DM	TGW	PW	PY	Min	Max	Mean
America	E1	0.451	0.244	0.301	0.451	0.451	0.451	0.452	0.244	0.452	0.451	0.451	a	a	0.451	0.452	a	a	0.452	0.244	0.452	0.411 ± 0.01
	E2	0.244	0.244	0.451	0.244	0.451	0.451	0.451	0.452	0.451	0.244	0.244	0.301	0.451	0.301	a	0.451	a	0.451	0.244	0.452	0.367 ± 0.01
	E3	0.456	0.301	0.244	a	0.244	0.244	0.244	0.452	0.451	0.244	0.244	0.244	0.244	0.244	a	a	0.244	0.451	0.244	0.456	0.303 ± 0.09
	Pooled	0.382	0.264	0.336	0.313	0.388	0.386	0.38	0.385	0.453	0.316	0.314	0.265	0.313	0.334	b	b	b	0.45	0.264	0.453	0.351 ± 0.07
Central Africa	E1	0.285	0.285	0.285	0.285	0.285	0.285	0.285	0.285	0.285	0.285	0.285	A	a	0.285	0.285	a	a	0.285	0.285	0.285	0.285 ± 0.08
	E2	0.285	0.285	0.285	0.285	0.285	0.285	0.285	0.285	0.285	0.285	0.285	0.285	0.285	0.285	a	0.285	a	0.285	0.285	0.285	0.285 ± 0.18
	E3	0.285	0.285	0.285	0.285	0.285	0.285	0.285	0.285	0.285	0.285	0.285	0.285	0.285	0.285	a	a	0.285	0.285	0.285	0.285	0.285 ± 0.08
	Pooled	0.285	0.285	0.285	0.285	0.285	0.285	0.285	0.285	0.285	0.285	0.285	0.285	0.285	0.285	b	b	b	0.285	0.285	0.285	0.285 ± 0.08
East Africa	E1	0.553	0.618	0.649	0.537	0.607	0.588	0.615	0.616	0.631	0.607	0.556	A	a	0.599	0.622	a	a	0.636	0.537	0.649	0.602 ± 0.04
	E2	0.641	0.587	0.588	0.612	0.613	0.548	0.538	0.62	0.631	0.594	0.563	0.596	0.357	0.584	a	0.491	a	0.589	0.357	0.641	0.572 ± 0.06
	E3	0.547	0.621	0.59	a	0.623	0.314	0.583	0.622	0.624	0.609	0.563	0.61	0.598	0.62	a	a	0.61	0.623	0.314	0.624	0.583 ± 0.07
	Pooled	0.581	0.613	0.614	0.592	0.616	0.482	0.584	0.625	0.634	0.645	0.516	0.612	0.52	0.609	b	b	b	0.642	0.482	0.645	0.592 ± 0.04
Europe	E1	0.436	0.554	0.296	0.436	0.436	0.468	0.468	0.415	0.415	0.345	0.468	A	a	0.468	0.436	a	a	0.554	0.296	0.554	0.442 ± 0.06
	E2	0.415	0.415	0.468	0.468	0.415	0.468	0.468	0.468	0.415	0.468	0.178	0.259	0.415	0.296	a	0.415	a	0.345	0.178	0.468	0.398 ± 0.06
	E3	0.178	0.415	0.415	a	0.415	0.178	0.178	0.436	0.468	0.501	0.178	0.415	0.468	0.178	a	a	0.349	0.415	0.178	0.501	0.345 ± 0.02
	Pooled	0.313	0.467	0.345	0.456	0.423	0.345	0.384	0.445	0.467	0.434	0.245	0.356	0.457	0.323	b	b	b	0.458	0.245	0.467	0.394 ± 0.05
South Asia	E1	0.581	0.615	0.635	0.517	0.606	0.584	0.62	0.612	0.602	0.579	0.561	A	a	0.616	0.606	a	a	0.598	0.517	0.635	0.595 ± 0.03
	E2	0.645	0.620	0.578	0.558	0.629	0.152	0.593	0.598	0.602	0.597	0.558	0.605	0.159	0.582	a	0.52	a	0.615	0.152	0.645	0.538 ± 0.04
	E3	0.593	0.629	0.589	a	0.638	0.466	0.548	0.617	0.614	0.577	0.558	0.598	0.548	0.603	a	a	0.624	0.593	0.466	0.638	0.586 ± 0.04
	Pooled	0.612	0.625	0.634	0.549	0.623	0.445	0.589	0.623	0.606	0.534	0.555	0.623	0.41	0.623	b	b	b	0.622	0.41	0.625	0.579 ± 0.06
Southern Africa	E1	0.569	0.59	0.659	0.522	0.628	0.592	0.616	0.415	0.561	0.595	0.619	A	a	0.611	0.606	a	a	0.621	0.415	0.659	0.586 ± 0.06
	E2	0.588	0.591	0.605	0.565	0.599	0.569	0.584	0.624	0.561	0.548	0.547	0.547	0.432	0.327	a	0.475	a	0.609	0.327	0.624	0.548 ± 0.07
	E3	0.525	0.617	0.597	a	0.606	0.512	0.584	0.628	0.592	0.589	0.546	0.537	0.616	0.608	a	a	0.596	0.612	0.512	0.628	0.584 ± 0.04
	Pooled	0.523	0.534	0.625	0.565	0.612	0.557	0.557	0.523	0.571	0.575	0.561	0.545	0.534	0.543	b	b	b	0.61	0.523	0.625	0.562 ± 0.03
West Africa	E1	0.178	0.415	0.415	0.345	0.415	0.501	0.345	0.436	0.178	0.345	0.468	A	a	0.415	0.554	a	a	0.468	0.178	0.554	0.391 ± 0.09
	E2	0.297	0.415	0.415	0.436	0.178	0.415	0.415	0.469	0.178	0.469	0.346	0.555	0.415	0.415	a	0.415	a	0.469	0.178	0.555	0.393 ± 0.10
	E3	0.297	0.415	0.468	0.436	0.469	0.178	0.555	0.415	0.415	0.469	0.346	0.469	0.415	0.435	a	a	0.415	0.415	0.178	0.555	0.413 ± 0.08
	Pooled	0.267	0.435	0.333	0.486	0.344	0.395	0.448	0.445	0.256	0.42	0.386	0.461	0.413	0.423	b	b	b	0.451	0.256	0.486	0.397 ± 0.07
unknown	E1	0.463	0.573	0.504	0.476	0.527	0.562	0.542	0.552	0.579	0.547	0.483	a	a	0.552	0.537	a	a	0.552	0.463	0.579	0.532 ± 0.03
	E2	0.6	0.559	0.576	0.562	0.552	0.514	0.313	0.539	0.579	0.58	0.561	0.617	0.525	0.598	a	0.561	a	0.505	0.313	0.617	0.546 ± 0.06
	E3	0.477	0.589	0.588	a	0.472	0.346	0.359	0.608	0.538	0.452	0.566	0.582	0.541	0.626	a	a	0.549	0.624	0.346	0.626	0.527 ± 0.08
	Pooled	0.512	0.554	0.565	0.523	0.516	0.444	0.435	0.566	0.556	0.526	0.507	0.593	0.523	0.595	b	b	b	0.56	0.435	0.595	0.531 ± 0.04

a- data not recorded

b- data recorded only in one season

FL (days to 50% flowering), PH (plant height), BTN (basal tiller number), CB (culm branching), FLBL (flag leaf blade length), FLBW (flag leaf blade width), FLSH (flag leaf sheath length), PL (peduncle length), PE (panicle exsertion), EHL (ear head length), EHW (ear head width), LLF (length of longest fingers), WLF (width of longest fingers), NF (number of fingers), PY (Grain yield per hectare).

pigmentation in E2 (Table 4. 17). Regionwise, the accessions from South Asia for inflorescence shape (0.656), glume prominence (0.514) and plant pigmentation (0.278), accessions from West Africa for seed colour (0.468) and lodging (0.280) and accessions from East Africa for growth habit (0.453) had high H` in E2, whereas accessions from America had low H` for all traits except growth habit (Table 4.17).

4.1.2.8.2.2 Quantitative traits

The cultivated race accessions had more diversity than wild race accessions. The race *Plana* accessions showed higher diversity (0.597 ± 0.05 in E1, 0.595 ±0.05 in E3 and 0.595 ± 0.05 in overall), whereas *Compacta* accessions had high mean H` in E2 (0.577 ± 0.04). Accessions of wild race *Africana* (0.414 ± 0.08 in E1, 0.425 ± 0.07 in E2, 0.302 ± 0.03 in E3 and 0.379± 0.03 in overall) and *Spontanea* (0.261 ± 0.05 in all environments and pooled) showed low H` (Table 4. 18). The traits such flag leaf blade length in accessions of *Compacta* (0.627 E1 and E3) and *Elongata* (0.633 in E1 and 0.648 in overall), panicle length in the accessions *Compacta* (0.680 in E2 and 0.645 in overall), *Elongata* (0.651 in E3) and *Plana* (0.624 in E2), days to 50% flowering in the accessions of *Plana* (0.653 in E2) and *Vulgaris* (0.642 in E3) had more H`.

Region wise, the accessions from East Africa (0.602 ± 0.04 in E1, 0.572 ± 0.06 in E2 and 0.592 ± 0.04 in pooled) and South Asia (0.586 ± 0.04 in E3) recorded high H`, whereas Central Africa accessions showed low H` (0.285 ± 08 in all environments and overall) (Table 4.23). The traits such as, days to 50% flowering in the accessions of East Africa (0.641 in E2) and South Asia (0.645 in E2), basal tiller number to the accessions from East Africa (0.649 in E1), South Asia (0.635 in E2) and southern Africa (0.659 in E1),panicle length to southern Africa (0.624 in E2 and 0.628 in E3) and panicle excertion to East Africa (0.624 in E1) had high H` in different environments (Table 4. 19).

4.1.2.9 Principal components analysis

Principal component analysis is used to provide reduced dimension model that would indicate measured differences among groups. In all the three environments and also in the combined analysis, a large proportion of the total variation was explained by the first seven Principal Components (PCs). The first seven PCs explained 59.63%

variation in E1, 62.50% in E2, 68.29% in E3 variation was explained by first seven PCs (Table 4.20, 4.21, 4.22). In the pooled analysis 88.90% variation was accounted by first seven PCs and reduced the original 10 traits to 9 traits (Table 4. 23). The PC1 separated the accessions on peduncle length, days to 50% flowering and ear head length in the three environments and combined analysis, whereas length of longest finger was important trait in E2, E3 and in the combined analysis. PC2 separated the accessions on basal tiller number and peduncle length in E1, E2 and in combined analysis, while in E3 plant height was main trait. The PC3 separated the accessions based on basal tiller number in all the three environments and plant height and days to maturity in E1, ear head length in E3. PC4 separated the accessions on days to flowering and flag leaf blade width (E2), ear head width and basal tiller numbers (E1) and number of finger and grain yield per hectare (E3). The PC5 separated the accessions on flag leaf sheath length (E1) ear head length and width and 1000- grain weight (E2). Similarly PC6 separated the accessions on basal number of tillers in all the environments and in combined analysis. PC7 also separated on basal number of tillers in all environments and finger numbers and grain yield per hectare in E2 and E3.

Table: 4.20 Percentage of variation explained (%) and vector loading explained by first ten Principle component estimated for 14 quantitative traits of the global finger millet composite collection in 2005/2006 post rainy season at TNAU, Coimbatore (E1), India.

Percentage of variation explained (%)	Principle components									
	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
	9.84	**9.11**	**8.69**	**8.25**	**8.08**	**7.92**	**7.74**	**7.42**	**7.04**	**6.98**
Latent vectors	**1.279**	**1.184**	**1.13**	**1.072**	**1.05**	**1.03**	**1.006**	**0.965**	**0.916**	**0.908**
Days to 50% flowering	20.089	0.531	0.131	20.257	20.036	0.001	0.229	0.298	20.466	0.055
Plant height	20.033	20.235	20.599	20.007	0.070	20.365	20.193	20.100	20.242	20.194
Basal number of tillers	20.259	20.039	20.236	20.391	20.317	20.246	20.349	0.116	0.107	0.538
Culm branching	20.055	20.089	0.108	0.260	20.089	20.715	0.297	0.383	0.047	20.256
Flag leaf blade length	0.072	0.4319	20.372	0.011	20.000	20.007	0.284	0.107	0.717	0.061
Flag leaf blade width	20.23	20.498	0.088	20.129	20.033	0.296	0.085	0.165	0.306	20.264
Flag leaf sheath length	0.055	20.009	0.139	0.327	0.497	0.016	20.457	0.544	0.085	0.274
Peduncle length	20.591	0.045	20.158	20.156	0.342	0.100	0.039	0.120	0.001	20.163
Ear head length	20.190	0.005	0.161	20.027	0.578	20.303	0.215	20.526	0.071	0.288
Ear head width	20.287	0.020	0.144	0.594	20.399	20.019	20.036	20.227	0.034	0.277
Days to maturity	0.205	0.114	20.51	0.362	0.137	0.222	0.017	20.043	20.186	20.018
Number of fingers	0.004	0.005	0.108	0.534	0.214	0.421	0.023	0.005	0.021	0.543
Grain yield per hectare	20.026	20.393	20.200	0.071	0.015	0.177	0.590	0.244	20.210	0.491

Table: 4.21 Percentage of variation explained (%) and vector loading explained by first ten principle component estimated for 16 quantitative traits of the global finger millet composite collection in 2006 rainy (E2) season at ICRISAT Centre, Patancheru.

Percentage variation explained (%)	**Principle components**									
	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
	15.34	**11.55**	**8.86**	**7.38**	**6.89**	**6.49**	**6.08**	**5.99**	**5.66**	**5.46**
Latent vectors	**2.455**	**1.848**	**1.417**	**1.18**	**1.102**	**1.039**	**0.973**	**0.959**	**0.906**	**0.874**
Days to 50 per cent flowering	0.303	0.227	0.285	20.360	20.017	20.173	0.114	20.110	20.091	20.258
Plant height	0.297	20.141	0.381	20.340	20.088	20.041	0.067	20.096	20.005	20.357
Basal number of tillers	20.059	20.285	20.385	20.369	0.242	20.224	0.019	0.129	0.174	20.023
Culm branching	20.174	20.256	20.343	0.114	0.233	20.177	20.047	0.053	20.011	20.316
Flag leaf blade length	0.244	20.200	0.226	0.252	0.183	20.121	20.064	20.053	20.084	20.202
Flag leaf blade width	0.112	0.040	20.039	0.488	0.308	20.053	20.357	0.048	0.397	20.469
Flag leaf sheath length	0.021	20.194	20.250	0.116	20.181	0.539	0.527	20.227	0.197	20.290
Peduncle length	20.194	20.558	0.244	0.065	20.119	0.055	20.010	20.148	0.044	0.044
Panicle exertion	20.221	20.497	0.331	0.047	20.030	20.114	20.144	20.124	0.005	0.116
Ear head length	0.485	20.249	20.226	0.097	20.089	20.048	20.080	0.114	20.183	0.194
Ear head width	0.350	20.046	20.080	20.070	20.000	0.008	0.090	20.216	0.337	0.016
Length of longest finger	0.487	20.255	20.216	0.108	20.098	20.017	20.045	0.131	20.188	0.183
Width of longest finger	0.071	0.033	0.083	0.120	0.580	20.253	0.453	20.357	0.111	0.376
Number of fingers	0.062	0.064	20.147	20.219	0.150	0.355	20.547	20.652	20.103	0.120
Thousand grain weight	0.005	20.082	0.137	20.021	0.554	0.487	0.092	0.283	20.475	20.110
Grain yield per hectare	0.145	20.026	0.262	20.277	0.127	0.361	20.136	0.391	0.567	0.320

Table 4.22 Percentage of variation explained (%) and vector loading explained by first ten principle component for 15 quantitative traits of the global finger millet composite collection in 2007 rainy (E3) season at ICRISAT Centre, Patancheru.

Percentage of variation explained (%)	Principle components									
	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
	16.11	**13.41**	**9.52**	**7.77**	**7.44**	**7.17**	**6.87**	**6.56**	**6.33**	**5.2**
Latent vectors	**2.256**	**1.878**	**1.333**	**1.087**	**1.041**	**1.004**	**0.962**	**0.918**	**0.886**	**0.727**
Days to 50 per cent flowering	0.393	20.116	20.212	20.073	20.025	20.207	0.151	20.154	20.420	0.238
Plant height	0.163	0.391	20.189	20.232	0.286	0.060	0.127	20.144	20.405	0.211
Basal number of tillers	20.113	20.037	0.351	0.117	0.337	20.414	0.539	0.291	20.212	20.363
Flag leaf blade length	0.179	0.318	20.135	0.017	0.303	0.016	0.035	0.614	0.227	0.424
Flag leaf blade width	0.227	0.141	20.251	0.268	0.417	0.352	20.289	0.034	20.109	20.598
Flag leaf sheath length	20.146	0.257	0.178	20.208	0.408	0.144	0.260	20.522	0.429	0.047
Panicle length	20.366	0.445	20.229	0.050	20.154	20.221	20.046	20.068	0.033	20.058
Panicle exertion	20.347	0.398	20.281	0.122	20.193	20.268	20.030	0.004	20.160	20.111
Ear head length	0.356	0.361	0.336	20.02o	20.322	20.040	20.151	0.053	0.067	20.172
Ear head width	0.045	0.342	0.023	0.234	0.453	0.214	0.234	0.342	0.234	0.123
Length of longest finger	0.393	0.337	0.322	20.191	20.198	20.134	20.006	20.011	0.093	20.148
Width of longest finger	0.224	20.123	20.44	0.027	20.040	20.277	0.178	0.111	0.564	20.127
Number of finger	20.005	0.136	0.265	0.782	20.009	0.122	0.033	20.065	0.013	0.351
Panicle weight	0.332	20.002	20.213	0.375	20.084	20.157	0.290	20.399	0.062	20.054
Grain yield per hectare	0.055	20.010	20.148	0.044	0.044	20.119	0.055	20.010	0.567	0.320

Table: 4.23 Percentage of variation explained (%) and vector loading explained by first ten for 14 quantitative traits of the global finger millet composite collection in the pooled analysis.

Percentage of variation explained (%)	**Principle components**									
	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
	38.92	**22.60**	**14.14**	**5.26**	**4.74**	**1.81**	**1.43**	**0.98**	**0.10**	**0.010**
Latent vectors	**6.130**	**5.135**	**2.227**	**1.280**	**1.462**	**1.855**	**1.249**	**1.548**	**1.575**	**1.646**
Plant height	-0.296	0.061	0.336	-0.152	-0.041	-0.315	0.129	0.809	0.019	-0.002
Days to 50% flowering	-0.008	-0.013	0.040	-0.065	-0.013	-0.748	-0.620	-0.224	0.003	-0.002
Basal number of tillers	-0.003	0.001	-0.001	-0.006	0.002	-0.003	0.001	0.000	-0.004	1.000
Flag leaf blade length	-0.241	-0.970	-0.002	0.031	-0.005	0.002	0.021	-0.011	-0.005	0.000
Flag leaf blade width	0.005	-0.007	-0.002	0.003	-0.005	0.013	-0.006	-0.014	1.000	0.004
Flag leaf sheath length	0.070	-0.047	-0.301	-0.941	-0.095	0.084	-0.025	0.009	-0.001	-0.005
Peduncle length	-0.711	0.185	-0.600	0.155	-0.275	-0.029	-0.003	-0.021	0.002	-0.001
Panicle exertion	-0.333	0.073	-0.034	-0.100	0.922	0.093	-0.109	-0.031	0.005	-0.003
Ear head length	-0.343	0.073	0.493	-0.102	-0.241	0.515	-0.543	-0.080	-0.009	0.001
Ear head width	-0.340	0.095	0.437	-0.204	-0.066	-0.243	0.540	-0.536	0.003	-0.003
Length of longest finger	0.321	0.034	0.032	0.345	0.023	0.123	0.145	0.432	0.024	0.023
Width of longest finger	0.456	0.004	0.045	0.423	0.034	0.765	0.231	0.321	0.112	0.032
Number of fingers	0.213	0.087	0.032	0.325	0.045	0.356	0.432	0.467	0.324	0.034
Grain yield per hectare	0.000	0.000	0.000	0.000	-0.001	0.000	0.000	-0.001	0.002	-0.003

4.1.2.10 Cluster analysis

Clustering analysis using Ward's (1963) method was performed using score of first four PCs (68.29% variation) on the pooled data based on biological race and geographical origin.

According to the biological races, the four cultivated races (*Elongata*, *Plana*, *Vulgaris* and *Compacta*) were delineated in to Cluster I, whereas accessions of wild races were grouped separately in two clusters Viz., Cluster II (wild *Spontanea*) and Cluster III (wild *Africana*) (Figure 4.2).

Grouping of geographical regions resulted in to four clusters. Accessions from America and Europe were grouped in to Cluster I, whereas the major finger millet growing regions such as East Africa, southern Africa, South Asia and unknown origin in Cluster II. The West Africa was grouped together in Cluster III and from Central Africa grouped separately in cluster IV (Figure 4.3).

4.1.2.11 Identification of accessions with high micro nutrient (Zinc and Iron) content

The diverse 65 accessions (selected from composite collection) with two check cultivars (VL 149 and PR 202) were used to estimate Fe and Zn content by Atomic Spectra Photometric Meter (ASPM). The genotypic variances for Fe and Zn were highly differed significantly. The mean Fe content was 17.9 mg/g. The accessions with high Fe content were IE 5941 (63.4 mg/g), IE 2572 (54.5 mg/g), IE 3475 (39.8 mg/g), IE 4545 (38.1 mg/g) and IE 4734 (35.5 mg/g), whereas the control VL 149 recorded 29.5 ± 0.86 mg/g. The mean Zn content was 23.56mg/g with the range of 17.5 – 31.7 mg/g compared to control VL 149 recorded 29.5 ± 0.40 mg/g. The accessions IE 5870 (31.7 mg/g), IE 2589 (30.7 mg/g), IE 5941 (29.9 mg/g), IE3045 (29.3 mg/g) recorded higher Zn content than the control. The accessions showed low Zn content were, IE 4795 (17.5 mg/g), IE 2790 (19.0 mg/g), IE 4570 (19.1 mg/g), IE 5066 (18.7 mg/g), IE 6326 (19.1 mg/g), IE 6337 (19.2 mg/g) and IE 6421 (19.4 mg/g) (Table 4. 24).

Most of the *Vulgaris* and *Plana* race accessions showed high Fe and Zn content compared to other races. The white seed finger millet accessions such as IE 2872 (35.9

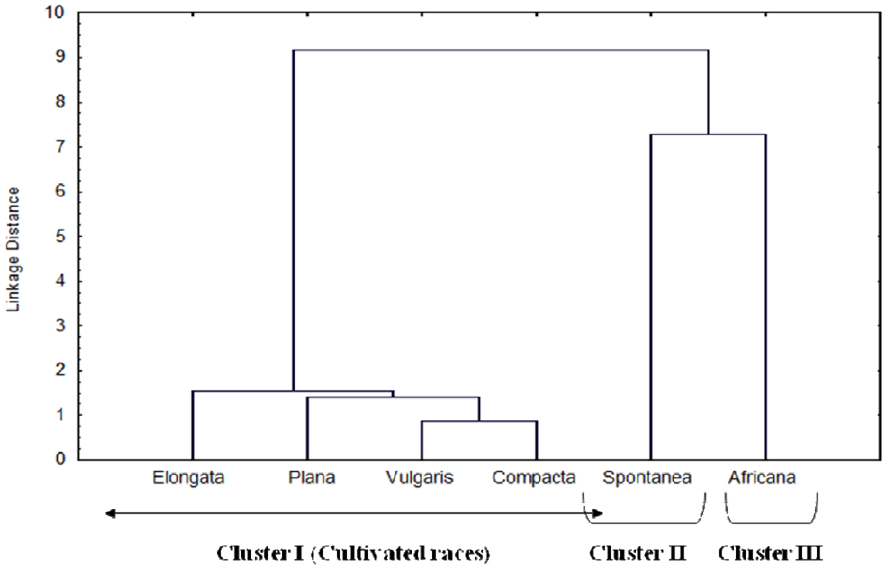


Figure 4.2. Ward's clustering of finger millet races in composite collection based on scores of first four PCs

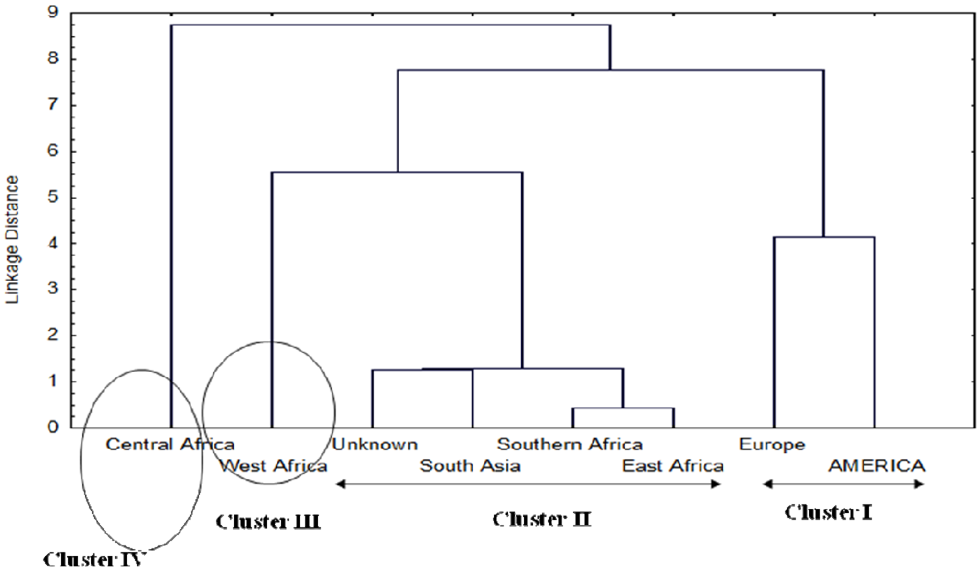


Figure 4.4. Ward's clustering of finger millet geographic origins in composite collection based scores of first four PCs

Table: 4.24 Mean iron and zinc content estimated in the 65 selected accessions from global finger millet composite collection in E2 (2006 rainy season) at ICRISAT Centre, Patancheru, India

Accession No	Fe (mg/g)	Zn (mg/g)	Accession No	Fe (mg/g)	Zn (mg/g)	Accession No	Fe (mg/g)	Zn (mg/g)
IE518	29.6	23.8	IE4816	34.7	23.9	IE3719	27.1	26.2
IE1055	26.2	20.4	IE2606	26.4	27.8	IE3945	22.6	23.1
IE2296	29.7	23.1	IE5066	27.9	18.7	IE4671	32.3	26.1
IE2790	20.9	19.21	IE5091	26.4	21.2	IE4057	31.6	28.2
IE2871	25.6	22.2	IE5106	30.8	25.9	IE4073	28.2	25.4
IE2957	21.2	25.4	IE5306	20.6	22.5	IE4491	32.4	24.8
IE2872	35.9	27.1	IE5367	33.6	24.7	IE4545	**38.1**	27.5
IE3077	36.1	22.5	IE6154	20.7	22.5	IE4757	29.1	23.9
IE3317	23.9	20.7	IE6165	34.7	27.2	IE5870	29.4	31.7
IE3391	25.7	22.9	IE6240	23.4	23.4	IE6082	26.8	25.6
IE3392	26.0	24.4	IE6294	36.9	24.8	IE2572	**54.5**	26.8
IE3475	39.8	22.6	IE6326	22.3	19.1	IE2589	30.9	**30.7**
IE3614	27.2	24.5	IE6337	21.5	19.2	IE2619	27.6	25.3
IE3952	25.2	22.7	IE6421	30.1	19.4	IE2710	31.3	26.3
IE3973	31.6	25.3	IE6473	26.9	21.8	IE2821	27.9	27.2
IE6350	30.3	26.4	IE6537	29.4	25.3	IE3045	30.4	**29.3**
IE4329	23.7	20.2	IE2430	**34.9**	27.3	IE3470	31.5	26.4
IE4497	23.9	26.6	IE5201	17.9	17.9	IE2437	28.2	27.7
IE4570	24.2	19.1	IE5941	**63.4**	**29.9**	IE2457	27.2	26.7
IE4734	37.5	19.8	IE2034	34.3	27.5	VL149 (Control)	26.2	**29.5**
IE4028	29.3	23.2	IE2217	**35.2**	26.6	PR202 (Control)	27.3	23.3
IE4121	30.6	20.9	IE2312	30.2	**28.4**			
IE4795	22.7	17.5	IE4797	25.4	22.9			

Minimum: Fe: 17.9 mg/g (IE5201) and Zn: 17.5 mg/g (IE4795)
Maximum: Fe : 63.4 mg/g (IE5941) and Zn : 31.7 mg/g, (IE5870)
Mean: Fe : 29.4 ± 0.80 mg/g and Zn: 24.2 ± 0.40 mg/g
Correlation coefficient (Fe Vs. Zn): 0.446** (*P* = <0.001)

mg/g and 27.1 mg/g), IE 2296 (29.7 mg/g and 23.1 mg/g) and IE 5367 (33.0 mg/g and 24.7 mg/g) showed high Fe and medium Zn content which is quite higher than brown seeded accessions (Table 4. 24). The Fe and Zn contents were and correlated positively (r = 0.446, p = 0.01).

4.1.2.12 Identification of trait specific accessions

By evaluating the global finger millet composite collection over three seasons 2005/2006 post-rainy (E1), 2006 rainy (E2), 2007 rainy (E3), we could identify few accessions performed repeatedly better than the best control cultivar for the particular trait(s) in all environments. The number of accessions identified specific for traits, were 35 for early flowering, 28 for high grain yield, 25 for more fingers, 25 for basal tiller number and 28 for ear head length (Table 4. 25). Extensive evaluation of these accessions in different locations may be useful to reconfirm this genetic worth and use in crop improvement.

4.2 Molecular diversity in finger millet

In the present study, genotypic diversity and population structure of finger millet composite collection was dissected by using 20 polymorphic SSR markers allelic data. The experiment was carried out in different steps and the results are briefly described in the following sub titles,

1. Protocol optimization and marker selection
2. Genotyping and quality index of markers
3. Molecular diversity and population structure of global finger millet composite collection
4. Development of genotype based reference set with 300 most diverse accessions

4.2.1 Protocol optimization and marker selection

A total of 31 SSR markers mapped on 9 finger millet chromosome (Dida *et al.,* 2007) were used for screening and PCR protocol optimization. Eventhough the markers were mapped in finger millet genetic map, genotypic pattern of these markers have not

Table 4:25 Trait specific accessions identified from the evaluation of composite collection in three environments Viz., 2005/2006 post rainy at TNAU, Coimbatore (E1), 2006 rainy (E2) and 2007 rainy (E3) at ICRISAT Centre, Patancheru, and Hyderabad.

Early flowering (<50 days)	IEs 49, 120, 189, 196, 234, 501, 509, 581, 588, 600, 641, 694, 847, 2030, 2093, 2158, 2275, 2293, 2322, 2323, 2957, 3104, 3537, 3543, 4425, 4431, 4432, 4442, 4711, 4734, 4755, 4759, 6013, 6550
More basal tillers (< 13)	IEs 2296,2034, 4711, 2293, 2299, 2608, 2619, 5145, 6553, 847, 2408, 2534, 3987, 1013, 120, 2042, 2091, 2106, 2139, 2146, 2233, 2288, 2367, 2410, 2504, 2645, 2657, 2674
High number of fingers (<10)	IEs 6033, 3790, 4586, 6059, 3111, 4476,3106, 2914, 4677,5733, 5875, 5877, 4257,5105, 5563, 6510, 4297,2957, 5689, 5956, 4563,3120, 2816, 6013, 2303, 2591, 6252, 6241, 4866
High ear head length (<150 mm)	IEs 2223, 2621, 2789, 6553, 3581, 3431, 3722, 6512, 2108, 2781, 3046, 2486, 5321, 3704, 798, 3489, 5022,2591, 2608, 4476, 2611, 3531, 2336,4125, 4658, 6546
High forage yield (<10 t ha^{-1})	IEs 2117,24, 2568, 2651,2753, 2796, 2811, 2880, 2942, 2979, 3789, 50, 672, 715, 860, 908, 916, 96, 99
High grain yield (<2 t ha^{-1})	IEs 94,2340, 2498,2578,2587,2683,2773, 2903, 2983, 2992, 3194, 3790, 3802, 4600, 4974, 5198, 5472, 5862, 6142, 6236, 667, 1010, 2299, 2590, 2678, 2684, 2698, 2712, 2756, 2827, 2872, 3135, 3136,3270, 3663, 3693, 3744,4121, 4310, 4679
Blast susceptible lines (infestation > 10%)	IEs 633,2293, 2322, 2384, 2589, 2622, 5960, 4005, 5875, 4491, 2957, 5367, 860, 2811, 4220, 5620, 4554, 3157, 413, 6229

been studied thoroughly in large population. So to get the basic idea of allele range, markers productivity and marker efficiency in genotyping in the global composite collection, these markers were optimized initially by Modified Taguchi method (Cobb and Clarkson, 1994). The optimization PCR protocol was carried out with eight most diverse finger millet accessions (IEs 2569, 2921, 3025, 4057, 4443, 4709, 5177 and 6082) (Table 3. 5) identified from composite collection at ICRISAT genebank.

Among the 31 markers, 25 markers produced strong and easily scorable band in all eight genotypes. The PCR products for these markers were analyzed through ABI 3700 Gene Analyzer and produced first hand information about the range of the alleles present in the eight genotypes. In these genotypes, alleles close in size could be distinguished using different fluorescent dye labels. Equimolar primer concentrations in multiplex PCRs showed uneven amplification in some markers. Similar levels of amplification of each marker was obtained by decreasing the quantity of primer for the strongly amplified fragments, increasing the amount of primers for the poorly amplified fragments and adjusting the concentration of the remaining PCR reagents accordingly. To increase the efficiency of the genotyping the markers with different labels and different allelic range were grouped as a set of multiplex and six post PCR multiplex were made (Table 4. 26). Some of the markers (UGEP3, UGEP5, UGEP31 and UGEP104) produced multiple alleles and were highly polymorphic also. From these 25 markers, based on high polymorphism and amplification rate, 20 SSR markers were selected and six multiplex were made to increase the efficiency of genotyping of entire composite collection. The details of SSR markers screened and optimized protocols for genotyping are given in Table 4. 26.

4.2.2 Quality index of the markers

Raw allelic data was binned through AlleloBin (Indury and Cardon, 1997) to get perfect allele calls based on the repeat length of the marker. A good marker is the one that has quality index < 0.40 and a zero allelic drift. The quality index and allelic drift of these markers are listed in the Table 4. 27. All selected markers had less than 0.40 quality index. The good quality index of 0.19 was observed for the marker UGEP18 with 0 allelic drift, the maximum quality index was 0.38 (UGEP11).

Table:4.26 Optimized PCR protocol, temperature, allele range, gene diversity and PIC of the markers on eight diverse genotypes (IEs 2569, 2921, 3025, 4057, 4443, 4709, 5177 and 6082)

Marker	PCR protocol optimized	Temp (°C)	Allele size range (bp)	Gene diversity	PIC
UGEP56	1	60 - 55	162 - 199	0.531	0.468
UGEP8	1	60 - 55	292 – 294	0.406	0.371
UGEP106	2	60 - 55	162 – 171	0.312	0.455
UGEP24	1	60 - 55	177 – 182	0.512	0.345
UGEP11	2	60 - 55	142 – 154	0.656	0.605
UGEP15	1	65 - 60	172 – 178	0.719	0.667
UGEP3	2	65 - 60	181 – 200	0.813	0.786
UGEP81	1	65 - 60	188 – 192	0.539	0.482
UGEP5	2	60 - 55	210 – 210	0.719	0.667
UGEP107	1	60 - 55	160 – 229	0.219	0.195
UGEP31	2	60 - 55	238 – 142	0.734	0.693
UGEP53	1	60 - 55	218 – 220	0.345	0.43
UGEP104	2	65 - 60	169 - 192	0.656	0.605
UGEP90	1	65 - 60	230 – 234	0.492	0.458
UGEP18	2	60 - 55	310 – 318	0.750	0.712
UGEP68	1	60 - 55	230 - 234	0.452	0.412
UGEP65	2	65 - 60	190 – 197	0.406	0.371
UGEP1	1	65 - 60	232 – 236	0.492	0.458
UGEP10	2	60 - 55	375 – 396	0.656	0.605
UGEP102	2	65 - 60	177 – 184	0.633	0.599
UGEP26	2	60 - 55	215-230	0.32	0.294
UGEP77	2	65 - 60	240-275	0.477	0.427
UGEP12	2	65 - 60	210-240	0.719	0.667
UGEP108	1	60 - 55	150 – 156	0.656	0.605
UGEP106	1	60 - 55	175 - 178	0.375	0.305
UGEP53	2	65 - 60	218 - 228	0.406	0.371
UGEP68	1	65 - 60	231 - 238	0.75	0.712
UGEP78	1	65 - 60	215 - 248	0.594	0.511
UGEP52	2	65 - 60	192 - 212	0.734	0.693
Mean	-	-	-	0.578	0.533
Min	-	-	-	0.219	0.195
Max	-	-	-	0.813	0.786
Cultivated	-	-	-	0.480	0.423
Wild	-	-	-	0.488	0.412

Protocol 1: (0.1 (primer 10pm/ul), 0.5 (2mMdNTP), 0.1(25mM Mg++), 0.05 (10x Buffer), 0.06 (5U/ul Quigen Taq), 2.7 (H20), 1(DNA template) ul of PCR components for each reaction

Protocol 2 : (0.1 (primer 10pm/ul), 0.25 (2mMdNTP), 0 (25mM Mg++),0.5(10X Buffer), 0.04 (5U/ul Quigen Taq), 3.1 (H20), 1(DNA template) ul of PCR components for each reaction

4.2.3 Molecular diversity of global finger millet composite collection

4.2.3.1 Allelic richness and diversity in composite collection

The quality of data on 41 accessions of composite collection was not to the desired level and hence those were excluded from analysis. The twenty SSR markers detected a total of 231 alleles in 959 finger millet accessions. The number of alleles per locus ranged from 7 (UGEP11) to 21 (UGEP5), with an average of 11.55 alleles per locus (Table 4.27). The polymorphic information content (PIC) values ranged from 0.196 (UGEP107) to 0.834 (UGEP12), with an average of 0.530. Most of the markers had high PIC (< 4), whereas markers UGEP107 (0.196), UGEP56 (0.313), UGEP11 (0.316), UGEP65 (0.369) and UGEP81 (0.388) showed low polymorphism. Gene diversity is defined as the probability that two randomly chosen alleles from the population are different. It varied from 0.200 (UGEP31) to 0.850 (UGEP26) with an average of 0.560 in the composite collection.

Correlation analysis revealed that allele size range was significantly associated with alleles per locus ($r = 0.470$) and common allele ($r = 0.580$, $P < 0.01$); alleles per locus with rare allele ($r = 0.890$, $P < 0.01$); common alleles ($r = 0.808$, $P < 0.01$) and PIC value ($r = 0.595$, $P < 0.01$); common alleles with PIC ($r = 0.833$, $P < 0.01$) and gene diversity with multiple allele percentage ($r = 0.437$, $P < 0.01$). Significant and positive relationships were observed between allele size range and the amount of variation at SSR loci (as measured by alleles per locus and gene diversity) indicate that SSR loci with large allele range (resulting from large number of SSR units) show greater variation, and agree with the idea that replication slippage plays an important role in the generation of new alleles at SSR loci.

4.2.3.2 Heterozygosity in germplasm accessions

Finger millet is a self pollinated crop. Moreover, in this study, a single plant from each accession was harvested and parts of the seeds obtained from such plants were sown in field to raise seedlings for DNA extraction. Extreme care was taken to avoid inadvertent seed mixtures. In spite of this, a wide range of heterozygosity (%) was detected in the investigated materials, from 0.00 % to 19.00 %, with an average of 9.00 %. One SSR loci (UGEP18) detected no heterozygosity, while the markers UGEP3 and

Table: 4.27 Quality index, allele range, allelic richness, Polymorphic Information Content (PIC), gene diversity and multiple allele percentage in the 959 accessions of global finger millet composite collection by using 20 SSR markers.

Marker	Quality index	Allele size range (bp)	Total alleles	Rare allele	Common allele	Major allele frequency (%)	PIC value	Gene diversity	Multiple allele percentage (%)
UGEP56	0.31	160 - 168	8	5	3	78.11	0.313	0.360	1.00
UGEP8	0.19	285 - 305	10	5	5	51.90	0.452	0.350	13.00
UGEP11	0.38	145 - 165	7	4	3	77.33	0.316	0.550	14.00
UGEP15	0.32	165 - 185	11	2	9	32.12	0.753	0.780	10.00
UGEP3	0.35	195 - 205	10	5	5	50.01	0.568	0.620	12.00
UGEP81	0.33	225 - 230	10	5	5	74.30	0.388	0.670	19.00
UGEP5	0.35	205 - 215	21	13	8	52.44	0.636	0.420	4.00
UGEP107	0.32	225 - 240	9	5	4	89.22	0.196	0.390	2.00
UGEP31	0.35	235 - 245	10	3	7	55.20	0.522	0.200	4.00
UGEP104	0.29	189 - 201	8	4	4	77.03	0.564	0.590	10.00
UGEP90	0.34	225 - 235	8	3	5	57.65	0.593	0.720	17.00
UGEP18	0.32	310 - 340	12	4	8	41.30	0.669	0.420	0.00
UGEP68	0.38	225 - 240	8	3	5	57.47	0.543	0.590	2.00
UGEP65	0.31	195 - 205	10	5	5	73.11	0.369	0.590	2.00
UGEP1	0.23	180 - 186	8	3	5	44.41	0.559	0.630	2.00
UGEP10	0.24	295 - 405	16	9	7	60.15	0.571	0.600	12.00
UGEP102	0.32	180 - 190	16	9	7	50.02	0.630	0.670	17.00
UGEP26	0.31	215 - 230	12	6	6	67.06	0.497	0.850	9.00
UGEP77	0.34	240 - 275	17	8	9	58.37	0.644	0.520	16.00
UGEP12	0.34	210 - 240	20	9	11	27.07	0.834	0.680	9.00
Mean	-	-	11.55	5.50	6.05	0.58	0.530	0.560	9.00
Min	0.19	-	7	2	3	0.27	0.196	0.200	0.00
Max	0.38	-	21	13	11	0.89	0.834	0.850	19.00
Total	-	-	231	110	121	-	-	-	-

Table 4.28 Correlation coefficients between the genotypic parameters for genotypic diversity in 959 accessions global finger millet composite collection by using 20 SSR markers

Parameter	Allele size	Allele per locus	Rare allele	Common allele	Allele frequency (%)	PIC value	Gene diversity	Hetrozygosity
Allele size	-							
Allele per locus	0.470	-						
Rare allele	0.259	0.890	-					
Common allele	0.586	0.808	0.450	-				
Allele frequency	-0.269	-0.470	-0.115	-0.770	-			
PIC value	0.321	0.595	0.257	0.833	-0.882	-		
Gene diversity	-0.019	0.064	-0.025	0.157	-0.210	0.349	-	
Heterozygosity	0.091	0.140	0.152	0.077	-0.023	0.162	0.437	-

UGEP10 (12%), UGEP8 (13%), UGEP11 (14%), UGEP77 (16%), UGEP90 and UGEP102 (17%) detected >10% in 959 accessions. A large collection of landraces was involved in this study and it is possible that these accessions still possess some residual heterozygosity at least at some SSR loci reported. A landrace is defined as an autochthonous (primitive) variety with a high capacity to tolerate biotic and abiotic stresses, resulting in high yield stability and an intermediate yield level under a low input agricultural system (Zeven, 1998). As finger millet is a tetraploid, having A and B genomes, loci UGEP3 was mapped in both the chromosome could be the reason for occurring two alleles and high heterozygozity for this loci. The heterozygosity observed at some of the loci could also be due to high mutational rate and mutational bias at SSR loci. The loci with large number of repeat units (SSR units) tend to show high mutational rate. As a result, any mutations in any one of the alleles may create a heterozygous condition. Many of the loci which displayed heterozygous status have a large number of SSR units. Wild *Spontanea* accessions as a group were more heterozygous (13.50%) than cultivated races *Compacta* (9.40%), *Elongata* (7.70%), *Plana* (7.30%) and *Vulgaris* (8.90%), whereas other wild *Africana* accessions had very low (1.60%) heterozygosity (Table 4.31). This may be due to the minimum number of accessions in this group. Central Africa (12.80%) and American accessions (11.60%) were more heterozygous than the accessions from rest of the geographic regions (4.50% to 9.00%) (Table 4. 32).

4.2.3.3 Biological and geographical diversity in the composite collection

Biologically, the 959 accessions could be grouped into different cultivated (*Compacta*, *Elongata*, *Plana* and *Vulgaris*) and wild races (*Africana* and *Spontanea*). Geographically also they can be assigned to seven geographical regions (America, Central Africa, East Africa, Europe, South Asia, southern Africa and West Africa) and another group of accessions of unknown origin. Though cultivated race accessions showed similar mean gene diversity, the *Vulgaris* accessions as a group were genetically more diverse (high range of gene diversity, 0.182 - 0.854) than other cultivated races (Table 4. 31). Interestingly, accessions from southern Africa (0.167 – 0.841), South Asia

(0.158 – 0.823) and East Africa (0.022 – 0.831) were genetically more diverse (high range in mean gene diversity) than other regions.

Table: 4.31 **Allelic richness, number of accessions, Polymorphic Information Content (PIC), gene diversity and multiple allele percentage (%) in accessions from different biological races in the 959 accessions of global finger millet composite collection by using 20 SSR markers.**

Biological races	Allele frequency	Number of accessions	Allele No	PIC	Gene diversity	Hetrozygosity (%)
compacta	58.74	127	7.4	0.509 (0.153 - 0.810)	0.553 (0.156 - 0.829)	9.40
elongata	60.22	69	6.5	0.501 (0.191 - 0.816)	0.542 (0.197 - 0.834)	7.70
plana	58.08	201	8.0	0.521 (0.259 - 0.805)	0.563 (0.267 - 0.825)	7.30
vulgaris	59.00	551	10.3	0.509 (0.177 - 0.840)	0.552 (0.182 - 0.854)	8.90
spontanea	51.61	7	4.0	0.566 (0.214 - 0.811)	0.611 (0.244 - 0.833)	13.50
africana	63.33	3	2.1	0.349 (0.000 - 0.592)	0.422 (0.000 - 0.666)	1.60
Minimum	51.61	3	2.1	0.349	0.422	1.60
Maximum	63.33	551	10.3	0.566	0.611	13.50
Mean	58.40	-	6.3	0.429	0.540	8.30
Total	-	959	38.3	2.957	3.245	4.87

Values in parenthesis indicate the range for particular group

Table: 4. 32 Allelic richness, number of accessions, Polymorphic Information Content (PIC), gene diversity and multiple allele percentage (%) in the accessions from different geographical origins in the 959 accessions of global finger millet composite collection by using 20 SSR markers.

Geographical origin	Allele Frequency (%)	Number of accessions	Allele No	PIC	Gene Diversity	Hetrozygosity (%)
Central Africa	55.13	8	3.7	0.517 (0.214 - 0.778)	0.568 (0.244 - 0.806)	12.80
East Africa	57.77	429	9.9	0.523 (0.222 - 0.831)	0.564 (0.229 - 0.846)	8.60
Southern Africa	61.89	164	8.1	0.484 (0.163 - 0.823)	0.524 (0.167 - 0.841)	9.00
West Africa	68.15	7	2.6	0.370 (0.00 - 0.671)	0.419 (0.000 - 0.722)	5.80
South Asia	61.50	316	8.8	0.496 (0.158 - 0.823)	0.537 (0.160 - 0.841)	8.30
Europe	60.21	4	2.2	0.359 (0.00 - 0.703)	0.435 (0.000 - 0.750)	4.50
America	59.83	4	2.6	0.427 (0.00 - 0.745)	0.496 (0.000 - 0.781)	11.60
Unknown	60.12	27	5.3	0.525 (0.211- 0.816)	0.572 (0.240 - 0.834)	8.40
Minimum	55.13	4	2.2	0.359	0.419	4.50
Maximum	68.15	429	9.9	0.525	0.572	12.80
Mean	60.00	0	5.4	0.462	0.514	8.60
Total	--	959	-	3.703	4.119	69.40

Values in parenthesis indicate the range for particular group

This study detected many rare, common, and unique alleles within each group. In the cultivated group, *Vulgaris* accessions contained the largest number of unique alleles (37) followed by *Plana* (5), *Africana* (4) and *Compacta* (2). Surprisingly, the wild *Spontanea* race had no unique allele. Region wise, East Africa (29), South Asia (12), southern Africa (11) and each one in accessions from Central Africa and Europe had total 54 unique alleles. Shared alleles are those detected in two groups but absent in other groups. The common alleles shared by two biological races were 2 for *Vulgaris* and *Africana*, and 26 for *Vulgaris* and *Plana*. Region wise, shared alleles were 15 for East Africa and South Asia, 5 for East Africa and southern Africa, and 3 for South Asia and southern Africa.

The mean PIC was lower in accessions of *Africana* (0.349) whereas higher PIC was observed in accessions of *Spontanea* (0.566). The other cultivated races, which recorded high PIC value were *Plana* (0.521 with range of 0.259 - 0.805) followed by *Compacta* (0.509 with range of 0.153 - 0.810), *Vulgaris* (0.509 with range of 0.177 - 0.840) and *Elongata* (0.501 with range of 0.191 - 0.816) (Table 4. 31).

The mean PIC was higher in the accessions from unknown origin (0.525) followed East Africa (0.523), whereas low PIC was observed in the accessions from Europe (0.359). The other regions, with mean PIC value were Central Africa with 0.517 (range of 0.215 - 0.779), East Africa with 0.523 (0.223 - 0.831), South Africa with 0.484 (0.163 - 0.823) and South Asia with 0.496 (0.158 - 0.824) (Table 4. 32).

4.2.3.5 Rare alleles in composite collection and the reference set

Alleles were considered as rare alleles, when the frequency is less than 1% in the population. These rare alleles may possess genes responsible for specific traits like pest and disease resistance and tolerant to drought. In the composite collection 110 rare alleles were observed in 104 accessions from 20 SSR markers. It ranged from 3.0 to 13.0 in composite collection. The markers UGEP12 (9 alleles), UGEP5 (13 alleles), UGEP77 (8 alleles) showed high number of rare alleles, whereas markers UGEP90, UGEP65 (each 3 rare alleles in 3 accessions) and UGEP15 (2 alleles in 4 accessions) showed low number of rare alleles. The rare allele loci, number of rare alleles, observed frequency of

Table: 4 .29 Allele loci, no of alleles, frequency of alleles and status of alleles in the 959 accessions of global finger millet composite collection by using 20 SSR markers

Allele	Count	Freq	Status	Allele	Count	Freq	Status	Allele	Count	Freq	Status	Allele	Count	Freq	Status
UGEP1				**UGEP11**				**UGEP65**				**UGEP5**			
178	2	0.0011	R	163	1	0.0005	R	182	2	0.0011	R	177	2	0.0012	R
190	7	0.004	R	147	2	0.0011	R	188	2	0.0011	R	179	2	0.0012	R
192	14	0.0079	R	159	4	0.0021	R	204	2	0.0011	R	187	2	0.0012	R
180	19	0.0107	C	157	14	0.0075	R	190	6	0.0032	R	195	2	0.0012	R
188	30	0.0169	C	151	35	0.0187	C	202	8	0.0043	R	227	2	0.0012	R
182	211	0.1192	C	153	368	0.1968	C	194	20	0.0106	C	245	2	0.0012	R
186	701	0.396	C	155	1446	0.7733	C	192	30	0.0159	C	225	4	0.0023	R
184	786	0.4441	C	**UGEP104**				196	32	0.017	C	233	4	0.0023	R
UGEP10				185	2	0.0011	R	200	404	0.2147	C	209	6	0.0035	R
378	2	0.0011	R	193	5	0.0028	R	198	1376	0.7311	C	229	7	0.0041	R
382	2	0.0011	R	183	6	0.0033	R	**UGEP77**				205	10	0.0058	R
390	2	0.0011	R	187	9	0.005	R	241	2	0.0012	R	203	14	0.0081	R
394	2	0.0011	R	197	80	0.0445	C	245	2	0.0012	R	207	16	0.0093	R
392	6	0.0032	R	195	94	0.0523	C	267	2	0.0012	R	221	18	0.0104	C
408	7	0.0037	R	191	217	0.1207	C	271	2	0.0012	R	217	21	0.0122	C
376	9	0.0048	R	189	1385	0.7703	C	247	3	0.0018	R	199	30	0.0174	C
384	13	0.0069	R	222	1	0.0005	R	249	3	0.0018	R	219	56	0.0325	C
386	13	0.0069	R	226	5	0.0027	R	227	4	0.0024	R	201	115	0.0667	C
406	19	0.0101	C	236	5	0.0027	R	223	16	0.0095	R	215	149	0.0864	C
396	23	0.0122	C	238	7	0.0038	R	265	18	0.0107	C	213	358	0.2077	C
388	79	0.042	C	240	8	0.0043	R	255	24	0.0143	C	211	904	0.5244	C
404	128	0.068	C	228	48	0.026	C	253	28	0.0167	C	**UGEP56**			
398	139	0.0739	C	234	59	0.032	C	251	30	0.0179	C	167	1	0.0005	R
402	306	0.1626	C	232	66	0.0358	C	263	76	0.0452	C	165	2	0.0011	R
400	1132	0.6015	C	230	1647	0.8922	C	261	116	0.069	C	155	4	0.0022	R
UGEP102				**UGEP15**				225	130	0.0774	C	159	10	0.0054	R
136	1	0.0005	R	165	4	0.0022	R	257	364	0.2167	C	153	14	0.0076	R
146	1	0.0005	R	167	4	0.0022	R	259	860	0.5119	C	161	47	0.0254	C
192	1	0.0005	R	185	24	0.0134	C	**UGEP68**				157	314	0.1697	C
196	1	0.0005	R	171	46	0.0257	C	229	2	0.0011	R	163	1458	0.7881	C
140	2	0.0011	R	173	52	0.0291	C	245	2	0.0011	R	**UGEP8**			
148	2	0.0011	R	183	64	0.0358	C	241	6	0.0032	R	322	1	0.0006	R
174	3	0.0016	R	181	96	0.0536	C	239	30	0.0162	C	312	2	0.0011	R
176	7	0.0038	R	163	178	0.0994	C	231	118	0.0639	C	302	3	0.0017	R
190	9	0.0049	R	179	237	0.1324	C	237	164	0.0887	C	304	4	0.0022	R
Allele	**Count**	**Freq**	**Status**	**Allele**	**Count**	**Freq**	**Status**	**Allele**	**Count**	**Freq**	**Status**	**Allele**	**Count**	**Freq**	**Status**
UGEP1				**UGEP11**				**UGEP65**				**UGEP5**			
188	21	0.0114	C	177	510	0.2849	C	235	464	0.2511	C	300	10	0.0056	R
178	23	0.0125	C	175	575	0.3212	C	233	1062	0.5747	C	290	23	0.0128	C
180	78	0.0425	C	**UGEP18**				**UGEP3**				298	28	0.0156	C
142	126	0.0686	C	337	2	0.0011	R	193	2	0.0011	R	292	30	0.0167	C
182	192	0.1046	C	311	3	0.0016	R	211	2	0.0011	R	296	762	0.4247	C
186	450	0.2451	C	315	5	0.0027	R	195	4	0.0021	R	294	931	0.519	C
184	919	0.5005	C	309	8	0.0043	R	191	5	0.0027	R	**UGEP12**			
UGEP26				313	21	0.0112	C	207	11	0.0059	R	206	1	0.0006	R
194	2	0.0011	R	329	28	0.015	C	197	49	0.0262	C	212	1	0.0006	R
197	4	0.0023	R	325	35	0.0187	C	205	93	0.0498	C	240	1	0.0006	R
227	4	0.0023	R	321	36	0.0192	C	199	122	0.0653	C	188	2	0.0012	R
215	6	0.0034	R	317	80	0.0427	C	201	646	0.3458	C	190	2	0.0012	R
185	7	0.004	R	323	400	0.2137	C	203	934	0.5	C	198	2	0.0012	R
221	16	0.0091	R	319	486	0.2596	C	**UGEP31**				216	6	0.0037	R

200	53	0.0301	C
203	54	0.0307	C
206	63	0.0358	C
191	125	0.0711	C
218	245	0.1394	C
224	1179	0.6706	C
UGEP81			
204	1	0.0005	R
182	2	0.0011	R
200	2	0.0011	R
184	5	0.0027	R
202	6	0.0032	R
190	21	0.0112	C
194	61	0.0327	C
186	87	0.0466	C
188	295	0.1579	C
192	1388	0.743	C

327	768	0.4103	C
UGEP90			
229	2	0.0011	R
245	2	0.0011	R
241	4	0.0022	R
239	28	0.0151	C
231	120	0.0647	C
237	158	0.0851	C
235	472	0.2543	C
233	1070	0.5765	C

245	2	0.0011	R
227	3	0.0016	R
229	5	0.0027	R
231	25	0.0135	C
235	29	0.0156	C
237	37	0.02	C
243	51	0.0275	C
233	82	0.0442	C
239	600	0.3236	C
241	1020	0.5502	C

238	6	0.0037	R
214	11	0.0068	R
236	17	0.0105	C
192	20	0.0123	C
232	40	0.0247	C
234	83	0.0512	C
230	92	0.0567	C
228	118	0.0727	C
220	144	0.0888	C
222	159	0.098	C
226	162	0.0999	C
224	316	0.1948	C
218	439	0.2707	C

each rare allele of composite collection and reference set were presented in the Table 4.30.

A wild *Spontanea* accessions, IE4708 from Burundi, had maximum number of 3 rare alleles. IE2921 (*Spontanea* accession); IE2609 (*Vulgaris* accession) from Malawi and IE6451 (*Africana* accession) from Uganda recorded 2 rare alleles. Interestingly, among the accessions, 64 accessions (61.53%) were originated from East African region (Uganda, Kenya and Malawi), which is believed to the origin of finger millet. Thirty three accessions from India recorded rare alleles and the most of remaining accessions were from southern and Central Africa.

4.2.3.6 Clustering of the accessions of global finger millet composite collection

Neighbour-joining tree based on simple matching dissimilarity matrix between 959 accessions of the composite collection grouped into two major groups (Group I and Group II), broadly representing Asian accessions (*coracana)* in group I and African accessions (*coracana* and *africana*) in group II.

Group I again clustered in into three clusters (cluster I, cluster II and cluster III) and group II subdivided into three clusters (cluster IV, cluster V and cluster VI). The diversity pattern of the composite collection is represented in a scatter diagram based on biological status, biological race and geographical origin.

4.2.3.6.1 Biological descriptors diversity (Figure 4.4a)

The numbers of landraces present in the global finger millet composite collection were originated from diverse origins and they were from different races also. So these landraces clustered in all the clusters.

Table: 4.30 Rare allele loci and the accessions having rare alleles in the global finger millet composite collection by using 20 SSR marker

Marker/ Rare allele Loci	Accessions possess rare alleles	Marker/ Rare allele Loci	Accessions possess rare alleles	Marker/ Rare allele Loci	Accessions possess rare alleles
UGEP1		198	IE3746	UGEP12	
178	IE4708	216	IE2332, IE2540, IE2441	206	IE5105
190	IE4053, IE3484, IE4091, IE3661, IE4134	238	IE2627, IE2416, IE5374	212	IE4232
192	IE2609	214	IE3543, IE2367, IE5345, IE4916, IE4245, IE5295	240	IE2921
UGEP10		UGEP15		188	IE1008, IE2093, IE2223, IE2327, IE2340, IE2551, IE2669, IE2743, IE2911, IE406, IE4725, IE4817, IE6416, IE905, IE2851, IE3693
378	IE5591	165	IE1022, IE4431	190	IE5037, IE2503, IE3614, IE5782, IE2037, IE2238, IE2296, IE3046, IE3942, IE4192, IE4991, IE5133, IE5248, IE5321, IE610, IE947
382	IE6421, IE3489	167	IE4492, IE5105	155	IE3727, IE3705, IE4699, IE5384, IE955
390	IE3745	UGEP18		159	IE2549, IE2861, IE3656, IE4222, IE4554, IE5231, IE5245, IE6443, IE897, IE906
394	IE4120	337	IE6229, IE2921	153	IE2055, IE2627, IE2728, IE3127, IE3329, IE3676, IE4647, IE5087, IE5124, IE5545, IE5578, IE5896, IE5968, IE6149
392	IE2561, IE2179, IE4975, IE6255	311	IE2525	UGEP65	
408	IE6020, IE6227, IE817, IE4826, IE3364	315	IE4218, IE5198, IE5349	182	IE2729
376	IE4711, IE6175, IE24, IE5733, IE3022	309	IE2698, IE3600, IE4909, IE6240	188	IE927
384	IE2534, IE2729, IE2393, IE2367, IE2370, IE2536, IE2364, IE6421	UGEP26		204	IE6025
386	IE2425, IE3746, IE6088, IE3531, IE4386, IE5354, IE968, IE2536	194	IE2656	UGEP8	
UGEP102		197	IE2678, IE3746	322	IE5782
136	IE563	227	IE5845, IE6451, IE2372	312	IE6451
146	IE24	215	IE3238, IE3766, IE5494, IE2551	302	IE5107, IE4220, IE6528, IE5537
192	IE2609	185	IE2158, IE2653, IE3169, IE3207, IE3910, IE829	304	IE4296, IE3413, IE2684, IE5090
196	IE4231	221	IE4957, IE5112, IE5525, IE2299, IE3543, IE4680, IE5023, IE6484, IE4476, IE6435	300	IE5106, IE2732, IE3094, IE5182, IE6537, IE6549, IE3120, IE2938, IE4383
140	IE4060	UGEP3		UGEP81	
148	IE2818, IE4594	193	IE2921	204	IE3581, IE4431, IE6387
174	IE5161, IE4231	211	IE3581,	182	IE2331, IE2395, IE2416, IE2293, IE6033, IE182
176	IE4339, IE3443, IE4671, IE5992, IE4130, IE5945	195	IE3028, IE3400, IE899	200	IE2684
190	IE5421, IE6280, IE3484, IE4091, IE3817, IE4053	191	IE2062, IE2487, IE4115	184	IE4992, IE4600

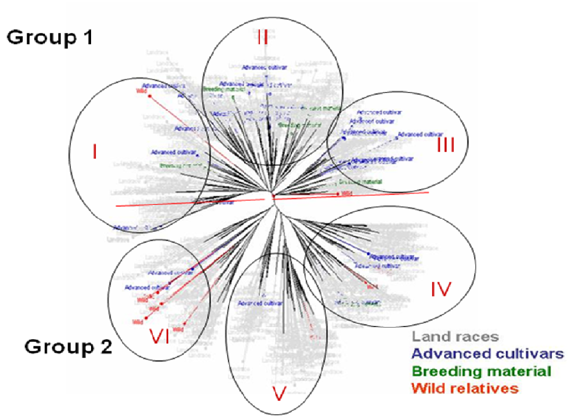
Marker/ Rare allele Loci	Accessions possess rare alleles	Marker/ Rare allele Loci	Accessions possess rare alleles	Marker/ Rare allele Loci	Accessions possess rare alleles
UGEP104		207	IE6082, IE2675, IE2861,IE4130, IE886, IE2769	202	IE4220
185	IE3022	UGEP31		UGEP90	
193	IE2636, IE3698, IE4232, IE5877	245	IE600	229	IE3157
183	IE4476, IE2921, IE5129	227	IE4116, IE5232	245	IE413
187	IE5292, IE5736, IE2395, IE3529, IE4116, IE5367	229	IE4368, IE3157, IE4232	241	IE3270
UGEP68		UGEP107		UGEP5	
229	IE6510	222	IE4147	177	IE2169, IE2858, IE3255, IE3901, IE4245, IE4570, IE4688, IE5457, IE6420, IE4073
245	IE6451	226	IE4708	179	IE2030, IE2356, IE2108, IE2235, IE2587, IE2312, IE2322, IE641, IE2742, IE2413, IE2836, IE2573
241	IE4476, IE2333, IE3223	236	IE4145	187	IE4127
UGEP77		238	IE3128	195	IE2921
241	IE2329	240	IE5519	227	IE4091
245	IE5620	UGEP11		245	IE3225
267	IE5672, IE4297	163	IE3485	225	IE2633, IE886, IE2638
271	IE4554	147	IE2816, IE2956	233	IE1011, IE6426
247	IE4671, IE2728	159	IE4709, IE5873	209	IE413, IE2329, IE2772, IE4826
249	IE3129, IE6443	157	IE2517, IE2489, IE2339, IE5231, IE3046	229	IE3270, IE4525, IE5315
227	IE2921, IE2613	UGEP56		205	IE2227, IE2549, IE3581, IE4431, IE2355
223	IE2386, IE2440, IE5419, IE4145, IE4383, IE6240, IE872, IE972	167	IE3449	203	IE3510, IE4023, IE4059, IE4145, IE6479, IE2586, IE2851
		165	IE5260	207	IE5198, IE1022, IE2769, IE2861, IE3656, IE4130, IE886, IE3207, IE5120
		190	IE4711, IE971, IE4443		
		202	IE895, IE678, IE2366, IE5165		

Cluster I consisted of 148 accessions, of which were 143 landraces, three advanced cultivars, and one each of breeding material and wild.

Cluster II consisted of 164 accessions, of which 150 landraces, 11 advanced cultivars and 3 breeding materials.

Cluster III consisted of 103 accessions, of which 91 landraces, 10 advanced cultivars and each one breeding line and wild accession.

Cluster IV consisted of 125 accessions, of which 118 landraces, 4 advanced cultivars, 2 wild and one breeding line.



Biological diversity of finger millet composite collection

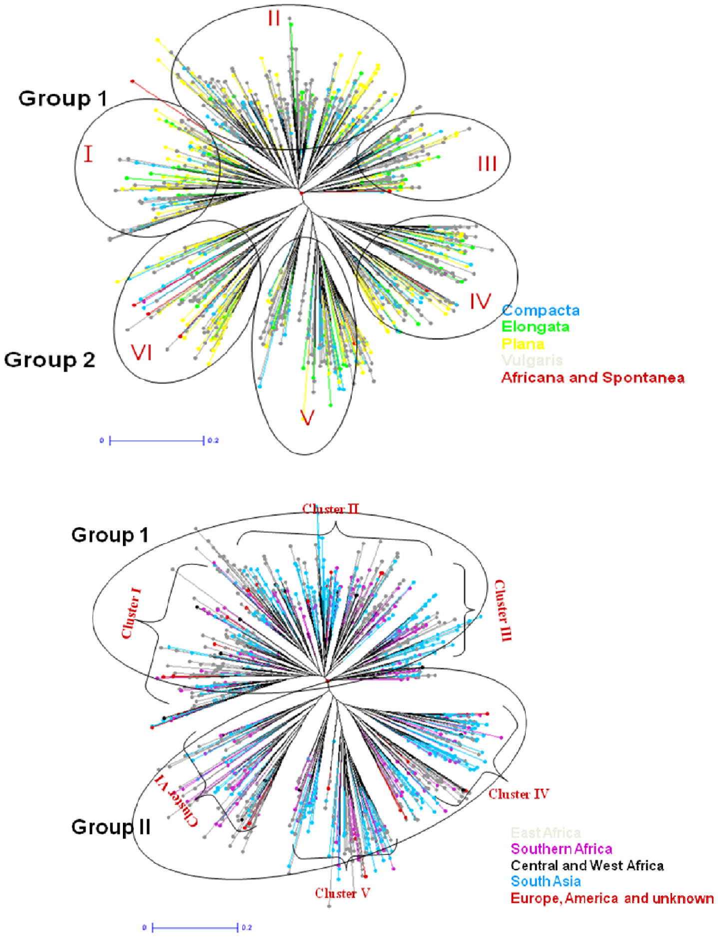


Figure 4.5. Unweighted neighbour-joining tree based on the simple matching dissimilarity matrix of 20 SSR markers diagram genotyped across the finger millet composite collection (959 accessions)

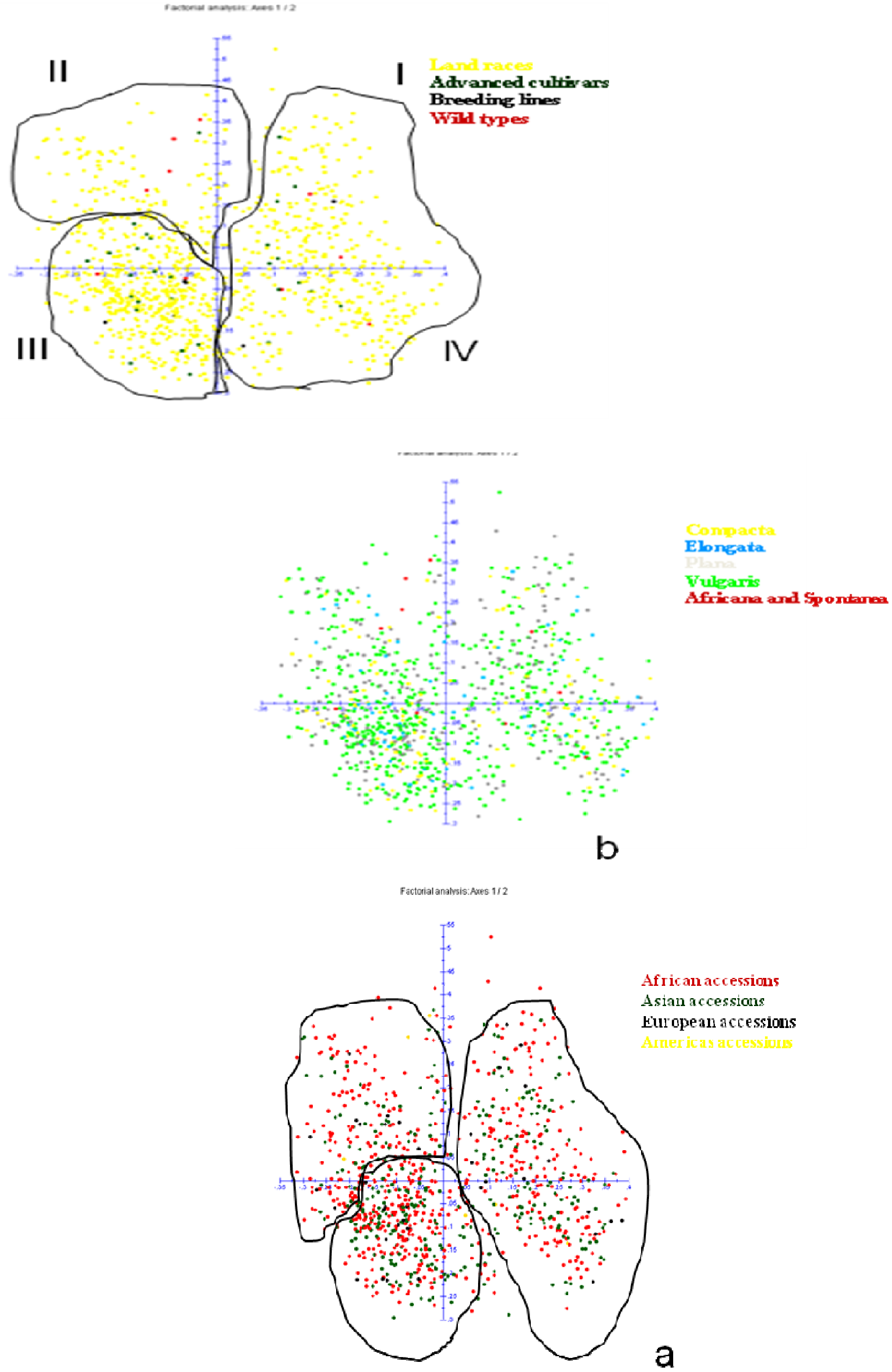


Figure 4. 6. Factorial analysis of global finger millet composite collection based on a. Biological descriptors b. Biological race c. geographical origin

Cluster V consisted of 330 accessions, of which 321 landraces, each two advanced cultivar and wild accession.

Cluster VI consisted of 89 accessions, of which 84 landraces along with 5 wild accessions.

4.2.3.6.2 Biological race diversity (Figure 4.4b)

There was no considerable grouping based on the biological race. Most of the accessions were cultivated *coracana* types and showed less diversity among the races. The accessions from different races were spread over into the entire spectrum of dendrogram except *Spontanea* (grouped together in cluster VI).

Cluster I: The 148 accessions consisted of accessions of 75 of *Vulgaris*, 39 of *Plana*, 21 of *Compacta*, 12 of *Elongata* and one of *Africana*.

Cluster II: The 164 accessions consisted of accessions of 56 of *Vulgaris*, 49 of *Plana*, 43 of *Compacta* and 12 of *Elongata*.

Cluster III: The 103 accessions consisted of accessions 63 of *Vulgaris*, 19 of *Plana*, 11 of *Compacta* and 10 of *Elongata*.

Cluster VI: The 330 accessions consisted of accessions of 83 of *Vulgaris*, 32 of *Plana*, 23 of *Compacta*, 11 of *Elongata* and one of *Africana*.

Cluster V: The 127 accessions consisted of accessions of 74 of *Vulgaris*, 24 of *Plana*, 20 of *Compacta* and 8 of *Elongata* and one *Spontanea* accession.

Cluster VI: The 89 accessions consisted of accessions of 26 of *Vulgaris*, 35 of *Plana*, 17 of *Compacta*, 6 of *Elongata* and 5 of *Spontanea*.

4.2.3.6.3 Geographical regional diversity (Figure 4.4c)

Majority of the accessions in the composite collection were from African and Asian accessions. Clustering did not follow the country of origin clearly. But in some clusters accessions from some particular origin were predominant.

Group I (clusters I, II and III) constituted predominantly with South Asian accessions (167 accessions) followed by East African (134 accessions) southern African (95 accessions) and. The limited number of accessions from Europe (2 accessions), America (1 accession), West Africa (5 accession) and unknown origin (9 accessions) were spread over in all clusters.

Group II (clusters IV, V and VI) constituted predominately with East African accessions (217 accessions), followed by South Asia (189 accessions) and southern Africa (125 accessions), unknown (10 accessions), each three accessions from America and West Africa.

4.2.3.7 Factorial analysis (Figure 4.5)

The factorial analysis based on biological status, biological race and geographical origin has been given in Figure 4.6. It illustrates the high divergence among genotypes of the composite collection based on biological status. The advanced cultivars and breeding lines were clustered together (quadrant III) and wild were in another cluster (quadrant II). The landraces both from Asia and Africa were distributed in overall the four quadrants.

All the wild races were clustered together in first quadrant and maximum number of *Vulgaris* accessions were grouped in quadrant III followed by quadrant II. Other cultivated races were grouped in all quadrants and similar pattern of distribution among quadrants was observed.

4.2.3.8 Population Structure analysis

In the present study, population structure was dissected for 959 accessions by using 20 SSR markers allelic data by using the software program STRUCTURE. The composite collection was grouped in to four subpopulations: subpopulation 1, subpopulation 2, subpopulation 3 and subpopulation 4 (Figure 4.6).

The subpopulation 1 contained with 252 accessions (96, East Africa; 83, South Asia; 62, southern Africa; 8, unknown origin; 1, America; 1, East Africa; 1, Europe)

The subpopulation 2 contained with 280 accessions (106, East Africa; 72, South Asia; 17, southern Africa; 17, unknown origin; 3, Europe; 1, America; 1, Central Africa.

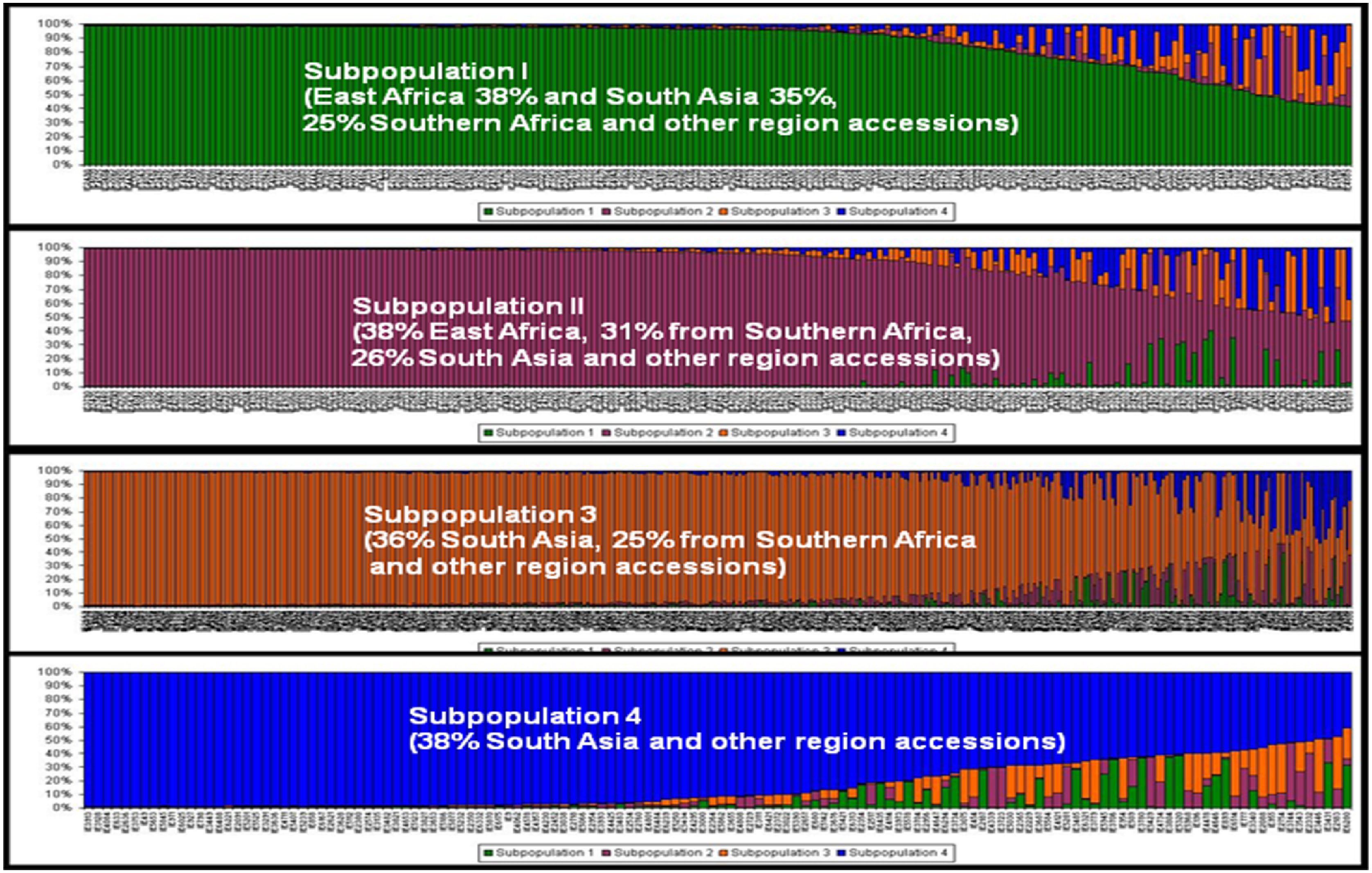


Figure 4. 7. Classification of finger millet composite collection based on 4 major geographical origin and accessions with mixture colour were % admixture from the respective population

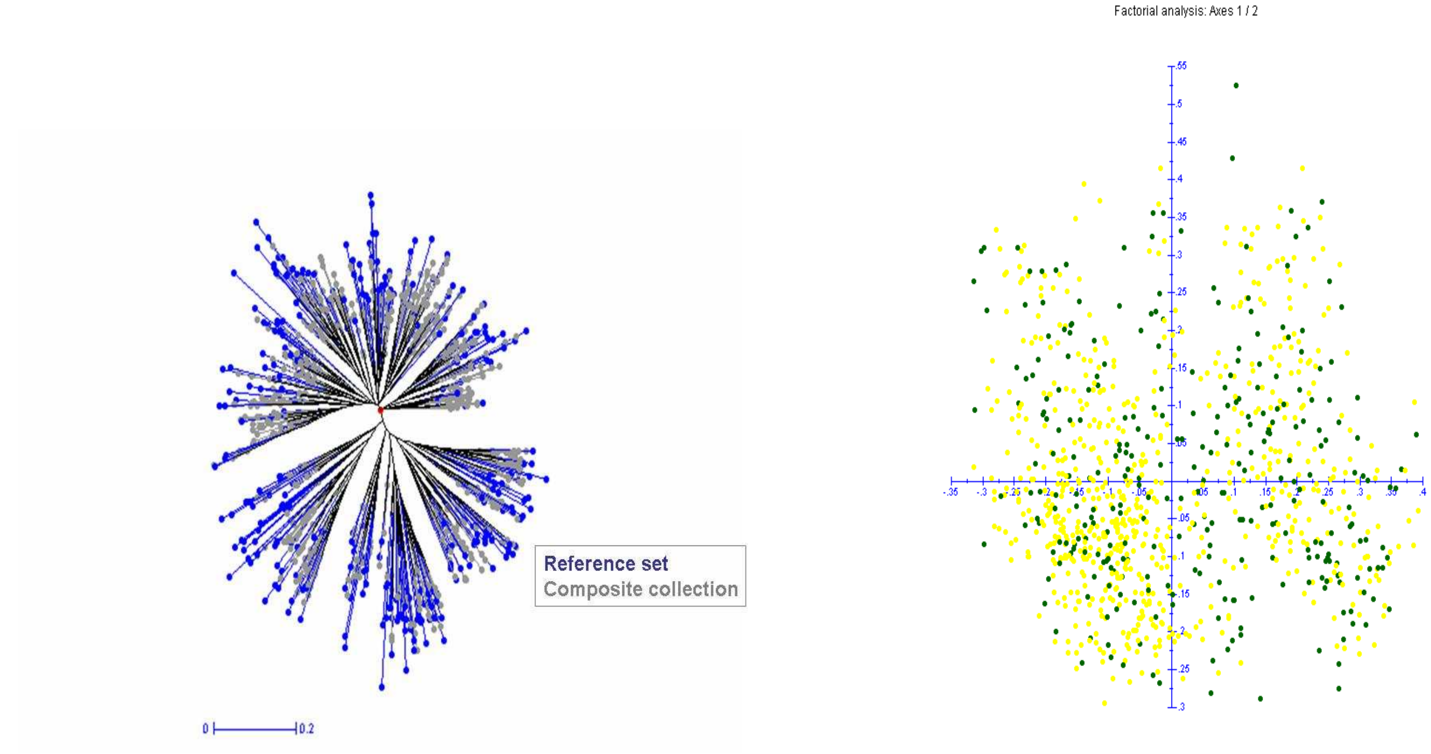


Figure: 4. 8. A reference set representing diversity in the entire spectrum of global finger millet

a. **DARwin dendogram**

b. **Factorial analysis**

The subpopulation 3 contained with 286 accessions (152, South Asia; 105, southern Africa; 14, East Africa; 10, unknown origin; 3, America; 2, Europe; 1, Central Africa).The subpopulation 4 contained with 141 accessions (50, East Africa; 51, South Asia, 30, southern Africa; 5, West Africa; 2, unknown origin; 1, Europe; 1, West Africa).

4.2.4 Development of global finger millet reference set

A global finger millet reference set consisting of 300 genetically most diverse accessions was drawn based on simple matching distance matrix. The reference set captured 206 (89.20%) of the 231 alleles detected in the composite collection and possessing high PIC (0.297 – 0.838), gene diversity (0.310 - 0.850) and mean multiple allele percentage 9.18% (Figure 4.7)

4.2.4.1 Molecular diversity of global finger millet reference set

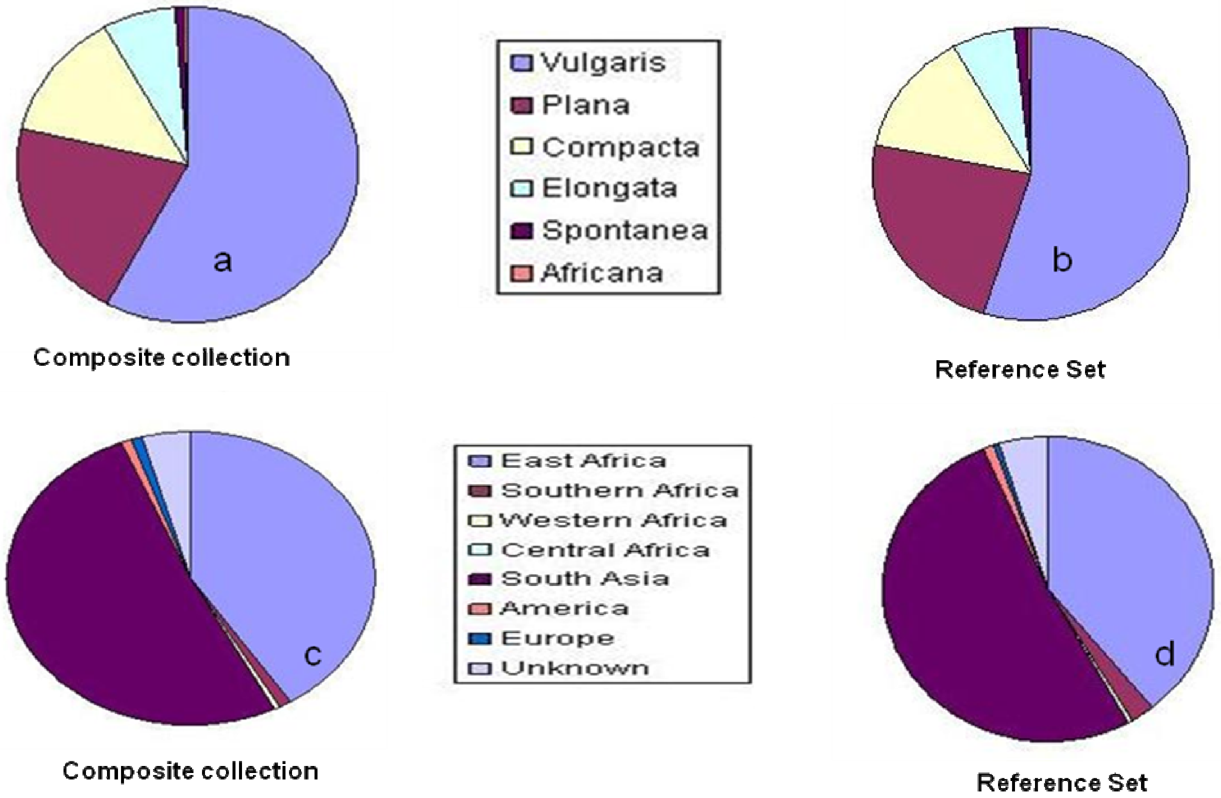
The 20 SSR loci generated a total 206 alleles ranging from 7 (UGEP11, UGEP56, UGEP104, UGEP) to 18 (UGEP5) with mean of 10.3 alleles per locus in reference collection (Table 4.33). Allele frequency of the composite collection was proportionally present on reference set also. The common alleles ranged from 3 (UGEP56) to 12 (UGEP12) in reference set. UGEP12 (12 alleles), UGEP5 (9 alleles), UGEP77 (10 alleles) showed high common allele numbers. The rare alleles ranged from 1 to 9 in reference set. The markers UGEP107 (5 alleles) and UGEP5 (9 alleles) showed high rare allele numbers.Gene diversity of the reference set was observed highest of 0.852 (UGEP26) and lowest of 0.307 (UGEP31) with a mean of 0.616 (Table 4.33). The high gene diversity was recorded and the markers UGEP15 (0.801), UGEP90 (0.728), UGEP12 (0.717), UGEP68 (0.709), UGEP102 (0.708) and UGEP10 (0.704) (Table 4. 33). The percentage of multiple alleles of reference set ranged between 0.34 and 17.69 % and mean was 9.08 %. The multiple allele was observed higher in UGEP81 (17.69 %) followed by in UGEP3 (16.67%), UGEP102 (16.55 %), UGEP77 (16.43 %) and UGEP11 (14.44 %). The low multiple alleles were observed for some markers like UGEP18 (0.34 %), UGEP6 (2.06 %), UGEP65 (2.74 %) and UGEP68 (2.75 %) (Table 4. 33).The PIC value of reference set ranged from 0.297 (UGEP31) to 0.837 (UGEP26), with the mean of 0.574. Markers with high PIC values (> 0.630) were UGEP12 (0.837), UGEP15 (0.774), UGEP18 (0.683), UGEP77 (0.688), UGEP102 (0.669) and UGEP26

Table:4.33 **Quality index, allele range, allelic richness, Polymorphic Information Content (PIC), gene diversity and multiple allele percentage in the 300 accessions of finger millet reference set by using 20 SSR markers.**

Marker	Quality index	Allele range (bp)	Rare allele	Common allele	Major allele frequency (%)	PIC value	Gene diversity	Multiple allele percentage (%)
UGEP56	0.31	160 - 168	4	3	69.55	0.402	0.458	2.08
UGEP8	0.19	285 - 305	3	5	77.26	0.336	0.372	12.50
UGEP11	0.38	145 - 165	3	4	49.32	0.464	0.560	14.44
UGEP15	0.32	165 - 185	3	8	30.53	0.774	0.800	8.07
UGEP3	0.35	195 - 205	3	6	45.07	0.612	0.667	16.67
UGEP81	0.33	225 - 230	4	5	48.56	0.66	0.699	17.69
UGEP5	0.35	205 - 215	9	9	65.77	0.482	0.522	4.44
UGEP107	0.32	225 - 240	5	4	73.94	0.404	0.430	1.06
UGEP31	0.35	235 - 245	3	7	82.75	0.297	0.307	7.39
UGEP104	0.29	189 - 201	1	6	49.14	0.586	0.643	15.86
UGEP90	0.34	225 - 235	3	5	38.55	0.683	0.728	1.56
UGEP18	0.32	310 - 340	4	8	62.29	0.462	0.528	0.34
UGEP68	0.38	225 - 240	2	6	42.61	0.665	0.709	2.75
UGEP65	0.31	195 - 205	4	6	43.84	0.653	0.700	2.74
UGEP1	0.23	180 - 186	3	5	43.04	0.558	0.631	17.9
UGEP10	0.24	295 - 405	5	9	48.49	0.674	0.704	13.09
UGEP102	0.32	180 - 190	6	6	45.17	0.669	0.708	16.55
UGEP26	0.31	215 - 230	4	7	26.49	0.837	0.852	8.58
UGEP77	0.34	240 - 275	3	10	61.79	0.567	0.589	16.43
UGEP12	0.34	210 - 240	3	12	47.05	0.688	0.717	5.90
Mean	-	-	3.75	6.55	52.55	0.574	0.616	9.18
Min	0.19	-	1	3	26.49	0.297	0.307	0.34
Max	-	-	9	12	82.75	0.837	0.852	17.69
Total	-	-	75	131	-	-	-	-

Table: 4. 34 Allele loci, no of alleles, frequency of alleles and status of alleles in the 300 accessions of finger millet reference set by using 20 SSR markers

Allele	Count	Freq	Status
UGEP1			
178	2	0.0036	R
192	2	0.0036	R
190	4	0.0071	R
180	6	0.0107	C
188	8	0.0143	C
182	67	0.1196	C
186	230	0.4107	C
184	241	0.4304	C
UGEP10			
382	1	0.0017	R
376	2	0.0034	R
378	2	0.0034	R
390	2	0.0034	R
408	4	0.0067	R
384	9	0.0151	C
386	9	0.0151	C
406	9	0.0151	C
396	17	0.0285	C
388	25	0.0419	C
404	51	0.0856	C
398	55	0.0923	C
402	121	0.203	C
400	289	0.4849	C
UGEP102			
146	1	0.0017	R
148	1	0.0017	R
174	2	0.0034	R
190	4	0.0069	R
176	5	0.0086	R
188	5	0.0086	R
178	9	0.0155	C
180	33	0.0569	C
142	40	0.069	C
182	71	0.1224	C
186	147	0.2534	C
184	262	0.4517	C
UGEP104			
193	2	0.0035	R
183	6	0.0106	C
187	7	0.0124	C
195	26	0.0461	C
197	30	0.0532	C
191	76	0.1348	C
189	417	0.7394	C
UGEP68			
229	2	0.0034	R
245	2	0.0034	R
241	6	0.0103	C
239	26	0.0447	C
231	56	0.0962	C
237	78	0.134	C
235	164	0.2818	C
233	248	0.4261	C
UGEP107			
222	1	0.0018	R
226	2	0.0035	R
240	3	0.0053	R
238	4	0.007	R
236	5	0.0088	R
228	20	0.0352	C
232	31	0.0546	C
234	32	0.0563	C
230	470	0.8275	C
UGEP11			
147	1	0.0017	R
163	1	0.0017	R
159	4	0.0069	R
157	12	0.0208	C
151	21	0.0363	C
153	137	0.237	C
155	402	0.6955	C
UGEP12			
212	1	0.0019	R
216	2	0.0037	R
238	2	0.0037	R
214	6	0.0112	C
192	7	0.0131	C
236	8	0.0149	C
232	16	0.0299	C
234	22	0.041	C
230	30	0.056	C
228	33	0.0616	C
220	49	0.0914	C
222	57	0.1063	C
226	63	0.1175	C
224	98	0.1828	C
218	142	0.2649	C
UGEP15			
165	2	0.0035	R
167	2	0.0035	R
185	5	0.0088	R
171	19	0.0333	C
173	22	0.0386	C
183	23	0.0404	C
181	39	0.0684	C
179	59	0.1035	C
163	74	0.1298	C
177	151	0.2649	C
175	174	0.3053	C
UGEP77			
247	1	0.0018	R
227	2	0.0037	R
249	2	0.0037	R
223	8	0.0148	C
253	8	0.0148	C
265	8	0.0148	C
255	14	0.0258	C
251	18	0.0332	C
225	30	0.0554	C
263	36	0.0664	C
261	46	0.0849	C
257	114	0.2103	C
259	255	0.4705	C
UGEP18			
311	2	0.0034	R
315	2	0.0034	R
337	2	0.0034	R
309	4	0.0067	R
313	6	0.0101	C
329	7	0.0118	C
321	13	0.0219	C
325	13	0.0219	C
317	26	0.0438	C
323	134	0.2256	C
319	156	0.2626	C
327	229	0.3855	C
UGEP26			
215	1	0.0018	R
197	2	0.0036	R
227	2	0.0036	R
185	5	0.0089	R
221	10	0.0179	C
206	26	0.0464	C
200	27	0.0482	C
203	29	0.0518	C
191	43	0.0768	C
218	69	0.1232	C
224	346	0.6179	C
UGEP3			
193	2	0.0034	R
195	2	0.0034	R
191	3	0.0051	R
207	10	0.017	C
197	28	0.0476	C
205	34	0.0578	C
199	42	0.0714	C
201	202	0.3435	C
203	265	0.4507	C
UGEP31			
227	2	0.0034	R
229	2	0.0034	R
245	2	0.0034	R
235	12	0.0207	C
231	13	0.0224	C
237	17	0.0293	C
243	20	0.0345	C
233	36	0.0621	C
239	191	0.3293	C
241	285	0.4914	C
UGEP65			
182	2	0.0034	R
188	2	0.0034	R
190	2	0.0034	R
204	2	0.0034	R
194	6	0.0102	C
202	6	0.0102	C
192	15	0.0256	C
196	18	0.0307	C
200	168	0.2867	C
198	365	0.6229	C
UGEP81			
184	1	0.0017	R
200	1	0.0017	R
204	1	0.0017	R
182	2	0.0034	R
190	12	0.0205	C
194	28	0.0478	C
186	42	0.0717	C
188	114	0.1945	C
192	385	0.657	C
UGEP90			
229	2	0.0034	R
245	2	0.0034	R
241	4	0.0068	R
239	24	0.0411	C
231	56	0.0959	C
237	74	0.1267	C
235	166	0.2842	C
233	256	0.4384	C
UGEP56			
155	2	0.0035	R
165	2	0.0035	R
153	3	0.0052	R
159	5	0.0087	R
161	21	0.0365	C
157	98	0.1701	C
163	445	0.7726	C
UGEP8			
302	2	0.0035	R
312	2	0.0035	R
300	3	0.0053	R
290	8	0.0141	C
292	11	0.0194	C
298	11	0.0194	C
296	251	0.4419	C
294	280	0.493	C
UGEP5			
225	1	0.0018	R
187	2	0.0036	R
195	2	0.0036	R
227	2	0.0036	R
233	2	0.0036	R
245	2	0.0036	R
229	3	0.0054	R
203	4	0.0072	R
205	4	0.0072	R
199	8	0.0144	C
217	8	0.0144	C
221	8	0.0144	C
207	11	0.0199	C
219	25	0.0451	C
201	27	0.0487	C
215	51	0.0921	C
213	125	0.2256	C
211	269	0.4856	C



Composite collection

Reference Set

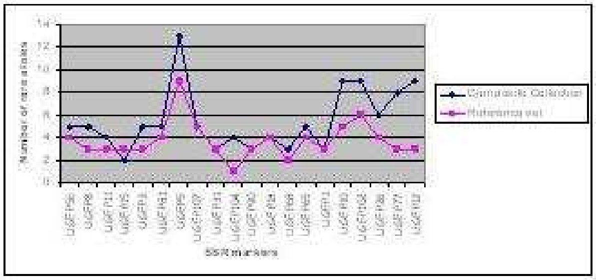
Composite collection

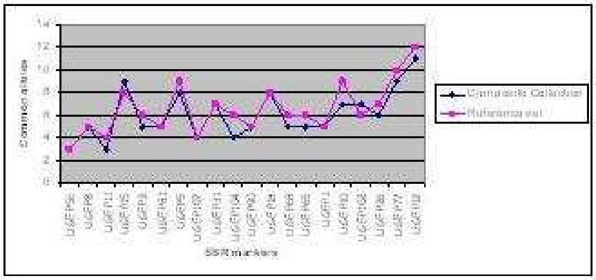
Reference Set

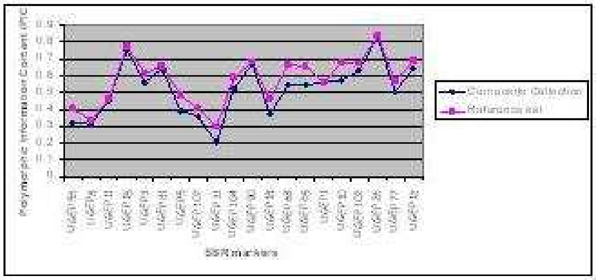
Figure: 4.10. Representation of accessions of composite collection and reference set based on biological race and geographical origin

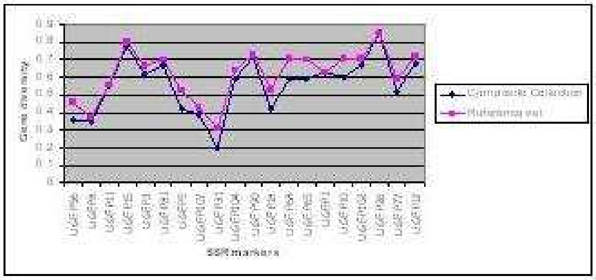
a. Composite collection (biological race) b. Reference set (biological race)

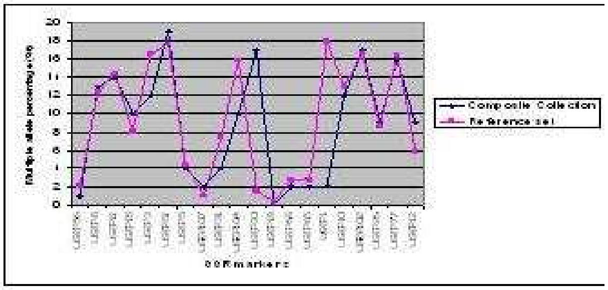
c. Composite collection (geographical origin) d. Reference set (geographical origin)


Number of rare alleles
14
12
10
8
6
4
2
0
SSR markers
Composite Collection
Reference set


Common alleles
14
12
10
8
6
4
2
0
SSR markers
Composite Collection
Reference set


Polymorphic Information Content (PIC
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
SSR markers
Composite Collection
Reference set


Gene diversity
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
SSR markers
Composite Collection
Reference set


Multiple allele percentage (%)
20
18
16
14
12
10
8
6
4
2
0
SSR markers
Composite Collection
Reference set

(0.669), However, low PIC was recorded by the markers UGEP31 and UGEP8. Frequency of rare alleles, common alleles, gene diversity and heterozygosis of global composite and reference set were illustrated in Figure 4. 8.

2.2.4. Description of global finger millet reference set

The reference set represented adequate diversity in both biological race and geographical origin of composite collection. It composed with accessions from the races *Africana* (1 accession), *Elongata* (19 accessions), *Vulgaris* (164 accessions), *Compacta* (42 accessions), *Plana* (70 accessions), and *Spontanea* (4 accessions). Country wise, reference set constituted accessions from Burundi (1 accession), Cameroon (1 accession), Ethiopia (2 accessions), India (64 accessions), Italy (1 accession), Uganda (65 accessions),Kenya (42 accessions), Malawi (24 accessions), Maldives (1 accession), Mexico (1 accession), Mozambique (1 accession), Tanzania (3 accessions), USA (2 accessions),Nepal (29 accessions), Nigeria (3 accessions), Pakistan (1 accession), Senegal (1 accession), Sri Lanka (1 accession), Zambia (11 accessions), Zimbabwe (37 accessions) and Unknown (9 accessions). Representation of accessions of composite collection and reference set based on biological race and geographical origin were illustrated in Figure 4.9

4.2.5 Association of markers with phenotypic traits

All the accessions of composite collection were considered as a single unit and used for association analysis. Significant genotype x environment interaction was observed for most of the traits (Table: 4. 2). Therefore, the association analysis was done by using phenotypic data of composite collection and reference set of each environment separately and overall, using 20 SSR marker data and population structure data (Q matrix). The results of association analysis using simple linear regression markers, and their association with traits, linkage group and position, F-value and probability and percentage of phenotypic variance explained by each QTL (R^2%) are presented in Table 4.35 for composite collection and Table 4.36 for reference set.

Table: 4.35 Single marker allele and phenotype association analysis for quantitative traitsof composite collection evaluated at 2005/2006 post rainy season (E1) at Coimbatore, 2006 rainy season (E2) and 2007 rainy season (E3) at Patancheru by using 20 mapped polymorphic SSR markers.

	2005/2006 post rainy season (E1)						2006 Rainy season (E2)						2007 rainy season (E3)								
Trait	Marker	LG	Position (cM)	F ratio	*P*	R^2(%)	Marker	LG	Position (cM)	F ratio	*P*	R^2(%)	Marker	LG	Position (cM)	F ratio	*P*	R^2(%)	Marker	LG	
DF	UGEP11	5	63.5	1.9	0.034	2.3	UGEP56			1.9	0.028	10.3	UGEP56	9	7.4	1.9	0.025	3.5	UGEP8	3B	
							UGEP8	3B	65.2	2.4	0.001	10.1	UGEP8	3B	65.2	1.7	0.016	2.4	-	-	
PH	UGEP3	3A & 3B	3A(75.8),3B(64)	1.8	0.013	13.5	UGEP68	9B	0	1.8	0.046	3.1	-	-	-	-	-	-	-	-	
	UGEP65	8A	31.6	1.8	0.044	10.6	UGEP104	3B	124.7	1.8	0.042	2.2	-	-	-	-	-	-	-	-	
BTN	-	-	-	-	-	-	UGEP3	3A & 3B	3A(75.8),3B(64)	1.6	0.039	14.2	-	-	-	-	-	-	-	-	
	-	-	-	-	-	-	UGEP8	3B	65.2	2.1	0.003	4.1	-	-	-	-	-	-	-	-	
CB	-	-	-	-	-	-	UGEP8	3B	65.2	1.6	0.047	1.6	-	-	-	-	-	-	-	-	
	-	-	-	-	-	-	UGEP26	5B	121.1	1.8	0.017	11.6	-	-	-	-	-	-	-	-	
FLBL	-	-	-	-	-	-	UGEP90	6B	23.3	2	0.035	5.8	-	-	-	-	-	-	UGEP26	5B	
FLBW	-	-	-	-	-	-	UGEP56	9A	7.4	2	0.019	21.6	-	-	-	-	-	-	UGEP3	3A & 3B	3A(
	-	-	-	-	-	-	UGEP65	8A	31.6	10.6	0.001	11.5	-	-	-	-	-	-	-	-	
FLSH	-	-	-	-	-	-	UGEP26	5B	121.1	1.8	0.016	8.5	-	-	-	-	-	-	-	-	
	-	-	-	-	-	-	UGEP18	1B	70.3	2.1	0.001	8.6	-	-	-	-	-	-	-	-	
PL	UGEP18	1B	70.3	1.6	0.024	32.5	UGEP65	8A	31.6	2	0.028	3.5	-	-	-	-	-		UGEP11	5	
EHL	UGEP56	9A	7.4	2.4	0.001	13.5	UGEP8	3B	65.2	2.8	0.001	8.2	UGEP107	1A	9.5	2.5	0.001	21.9	UGEP26	5B	
LLF	-	-	-	-	-	-	UGEP68	1XB	0	1.7	0.054	6.3	UGEP3	3A & 3B	3A(75.8),3B(64)	2.0	0.001	7.0	-	-	
PY	-	-	-	-	-	-	-	-	-	-	-	-	UGEP104	3B	124.7	1.8	0.030	2.3	-	-	

DF- Days to 50 % flowering, PH - Plant height, BTN- Basal tiller number, CB- Clum branching, FLBL- Flag leaf blade length, FLBW - flag leaf blade width, FLSL - Flag leaf sheath length, PL - Peduncle length, PE – Panicle excertion
longest finger, NF - number of fingers and PY- Plot yield

Table:4.36 Single marker allele and phenotype association analysis for quantitative traits of refernce set evaluated at 2005/2006 post rainy season (E1) at Coimbatore, 2006 Rainy season (E2) and 2007 rainy season (E3) at Patancheru by using 20 mapped polymorphic SSR markers.

	2005/2006 Post rainy (E1)						2006 rainy (E2)						2007 Rainy (E3)							
Trait	Marker	LG	Position (cM)	F ratio	*P*	R^2(%)	Marker	LG	Position (cM)	F ratio	*P*	R^2(%)	Marker	LG	Position (cM)	F ratio	*P*	R^2(%)	Marker	LG
FL	UGEP56	9A	7.4	2.1	0.040	7.6	UGEP8	3B	65.2	3.0	0.001	15.7	UGEP8	3B	65.2	2.9	0.001	58.9	UGEP10	
	-	-	-	-	-	-	UGEP11	5	63.5	2.0	0.050	7.595	-	-	-	-	-	-	UGEP8	3B
PH	UGEP65	8A	31.6	2.1	0.027	12.0	UGEP68	9B	0	3.6	0.001	4.465	UGEP18	1B	70	1.8	0.023	7.1	-	-
	-	-	-	-	-		UGEP104	3B	125	2.0	0.039	3.6							-	-
BT	UGEP1	5Ab	25.9	1.8	0.017	1.4	UGEP8	3B	65.2	5.3	0.001	3.403	UGEP15		6.5	3.0	0.001	3.5	UGEP1	5Ab
	UGEP8	3B	65.2	2.0	0.027	1.5	UGEP65	8A	31.6	2.0	0.036	4.367	UGEP1	5Ab	26	1.9	0.013	1.4	UGEP8	3B
CB	UGEP10	8A	52.2	1.6	0.047	1.5	UGEP10	8A	52.2	2.1	0.003	1.534	-	-	-	-	-	-	UGEP1	5Ab
	-	-	-	-	-	-	UGEP31	3A	75.8	1.9	0.010	1.541	-	-	-	-	-	-	UGEP15	3A
FLBL	UGEP90	6B	23.3	3.2	0.002	11.5	UGEP31	3A	75.8	1.6	0.039	4.3	UGEP31	3A & 3B	3A(75.8),3B(64)	2.1	0.004	95.2	UGEP90	6B
	UGEP8	3B	65.2	2.1	0.016	16.9	-	-	-	-	-	-	UGEP90	6B	23	2.0	0.047	3.9	-	-
FLBW	UGEP18	1B	70.3	2.2	0.002	2.6	UGEP65	8A	31.6	8.4	0.001	207.95	UGEP3	3A & 3B	3A(75.8),3B(64)	1.9	0.017	3.5	-	-
FLSL	-	-	-	-	-	-	UGEP26	5B	121	2.6	0.001	25.913	-	-	-	-	-	-	-	-
	-	-	-	-	-	-	UGEP77	15B	4.8	2.0	0.008	11.739	-	-	-	-	-	-	-	-
							UGEP8	3B	65.2	1.9	0.036	2.968	-	-	-	-	-	-	-	-
PL	UGEP31	3A	75.8	1.8	0.020	21.3	UGEP56	9A	7.4	3.7	0.001	8.75	-	-	-	-	-	-	-	-
	-	-	-	-	-	-	UGEP31	3A	75.8	1.9	0.008	131.49	-	-	-	-	-	-	-	-
	-	-	-	-	-	-	UGEP8	3B	65.2	2.2	0.012	4.248	-	-	-	-	-	-	-	-
PE	-	-	-	-	-	-	UGEP11	5	63.5	3.2	0.003	2.5	-	-	-	-	-	-	UGEP56	9A
	-	-	-	-	-	-	UGEP26	5B	121	2.1	0.009	3.6	UGEP65	8A	32	2.3	0.018	4.3	-	-
EHL	UGEP56	9A	7.4	2.7	0.009	8.8	-	-	-	-	-	-	UGEP1	5Ab	26	2.9	0.001	10.0	-	-
	UGEP18	1B	70.3	1.7	0.027	42.9	-	-	-	-	-	-	UGEP31	3A	76	2.0	0.006	7.2	-	-
EHW	UGEP104	3B	125	2.0	0.042	7.2	UGEP31			4.7	0.001	7.9	-	-	-	-	-	-	UGEP8	3B
	-	-	-	-	-	-	UGEP68	9B	0	4.8	0.001	15.6	-	-	-	-	-	-	-	-
FN	UGEP8	3B	65.2	2.2	0.013	3.7	UGEP8	3B	65.2	2.9	0.001	3.055	UGEP1	5Ab	26	2.4	0.001	3.6	-	-
	-	-	-	-	-	-	UGEP65	8A	31.6	2.1	0.028	3.14	UGEP107	1A	9.5	2.1	0.019	3.8	-	-
PY	UGEP18			1.7	0.024	2.3	-	-	-	-	-	-	UGEP10	8A	52	1.9	0.012	8.5	UGEP3	
	UGEP3	3A & 3B	3A(75.8), 3B(64)	1.7	0.043	3.5	- -	- -	- -	- -	- -	- -	UGEP107	1A	9.5	2.0	0.032	8.5	UGEP11	5

DF- Days to 50 % flowering, PH - Plant height, BTN- Basal tiller number, CB- Clum branching, FLBL- Flag leaf blade length, FLBW - flag leaf blade width, FLSL - Flag leaf sheath length, PL - Peduncle length, PE – Panicle excertio length of longest finger, NF - number of fingers and PY- Plot yield

Composite collection

Based on simple linear regressions models, five QTL were detected in the composite collection with the probability level ≤0.005 in E1: UGEP11 in LG5 for days to 50% flowering, UGEP65 in LG7 for plant height and UGEP3 in LG3 for Plant height and UGEP18 in LG1 for peduncle length and UGEP56 in LG9 for ear head length. In E2, total 16 QTL were detected, of which 6 QTL were located in LG3, UGEP8 for days to 50% flowering, clum branching, basal tiller number and ear head length; UGEP104 for plant height and UGEP3 for basal tiller numbers); 4 QTL in LG9 (UGEP56 for days to 50% flowering and flag leaf blade width and UGEP68 for plant height and Grain yield per hectare); 2 QTL in LG8 (UGEP65 for flag leaf blade length and peduncle length) and 2 QTL in LG5 (UGEP26 for clum branching and flag leaf sheath length) and one each in LG6 (UGEP90 for flag leaf blade length) and LG1 (UGEP18 for flag leaf sheath length). No QTL was found for panicle excertion, width of longest finger, number of fingers and grain yield per hectare in E2.

In E3, five QTL were detected, of which 3 QTL were located in LG3 (UGEP8 for days to 50% flowering; UGEP3 for length of longest finger and UGEP104 LG3 for grain yield per hectare) and each one QTL in LG9 (UGEP56 for days to 50% flowering) and LG1 (UGEP107 for ear head length). In combined analysis, 5 QTL were detected, of which 3 QTL which in LG5 (UGEP2 for flag leaf blade; UGEP1 for peduncle length; UGEP2 for ear head length) and 2 QTL in LG3 (UGEP8 for days to 50% flowering and UGEP3 for flag leaf blade width). The number of QTL identified in both composite and reference set were 2 in E1, 5 in E2, 1 in E3, and one in pooled analysis.

Reference set:

Association analysis using phenotypic data on reference set data (300 accessions) and 20 SSR markers revealed 15 QTL in E1, 22 QTL in E2, 14 QTL in E3, and 11 QTL in combined analysis (Table 4. 36). Most of the QTL were not consistent over environments. However, few QTL such as UGEP1 in LG5 for basal tillers (E1 and combined); UGEP8 in LG3 for days to 50% flowering (E2, E3 and combined), basal tillers (E2 and pooled) and finger number (E1 and E2); UGEP31 in LG3 flag leaf blade length (E2 and E3) had relatively consistent QTL at least in two environments.

4.2.6 Cophenetic correlation

The dendrogram of the GDs calculated by the UPGMA method based on the microsatellite data showed a high cophenetic value ($r = 0.59$, $P < 0.0001$; 10,000 permutations).

Discussion

CHAPTER V

DISCUSSION

Finger millet is the third important millet crop after sorghum and pearl millet in African countries and in India (National Research Council, 1996). It is one of the food grains that contains high amount of dietary fiber and is widely recommended for the diabetics (Malleshi *et al.,* 1996). Among millets, finger millet was reported to contain high amounts of iron and zinc (Ramachandra *et al.*, 1977). It also contains high amount of unsaturated fatty acid that reduces the heart-related problems (Premavalli *et al.,* 2003). Its seeds are rich in minerals such as calcium and phosphorous in addition to antioxidants (Sankara Rao and Deosthale, 1983). Hence, finger millet deserves to be a priority crop for improving yield and quality attributes in terms of food and nutritional security.

Genetic diversity is basic requirement for the crop improvement programme. The genetic variation within and between species is generated by mutation, sexual reproduction and selection. Knowledge of germplasm diversity has significant impact on the crop improvement. Efficient use of conserved bio-diversity requires information about the degree and distribution of genetic diversity. The variation in the genetic makeup and its interaction with environment indicates the observable pattern of diversity. Assessment of diversity using molecular markers would provide an opportunity to select appropriate parents for crop improvement with higher precision. The importance of increased use of genetic resources in enhancing genetic potential of crops alleviating biotic and abiotic stresses and broadening genetic base of crop has been very well recognized (Banks, 1976).

Emphasis on the importance of preserving crop germplasm in recent times has resulted in assembling and maintaining very large germplasm collections. Large collections of finger millet germplasm (5949 accessions) are maintained at ICRISAT genebank. Despite such an impressive number of accessions, there has been only limited use of genebank material for genetic enhancement of finger millet. For example, during the period of 1978 – 2005, only two varieties were released in namely Lima (IE2929 originated from Malawi) and FMV 287 (IE2947 originated from India) in Zambia in 1987. Several popular varieties released in India since the 1970s, including the Indaf, MR and

GPU lines, are products of Indian–African hybrid (Seetharam *et al*., 2006) which involved germplasm accessions of African origin that narrowed down the variability. A very small portion the germplasm has been used in finger millet breeding in India (Ramakrishna *et al.,* 1996).

Means to enhance use of germplasm in crop improvement

There are numerous examples where plant breeders have effectively exploited the exotic germplasm by introgressing gene(s) for disease resistance or single genes controlling other traits (Stalker, 1980). The use of exotic germplasm in improvement of quantitative traits is conspicuously rare, although large proportions of breeding efforts in different breeding programmes are directed towards improving such traits. There are many reasons for the low use of diverse germplasm for improvement of the quantitative traits in the adapted germplasm pool. Foremost among these, is the supposition that these germplasm lines have little to offer the improvement of elite cultivars, or that it would require such an extended effort to exploit that the investment of time and resources are not justified (Goodman, 1985; Hallauer, 1978). Improvement programmes aimed at short-term rapid cultivar development rely mostly on established cultivars and elite breeding lines in developing breeding materials, rather than long-term germplasm development using exotic germplasm (Halward and Wynne, 1991). The large variability in the germplasm in genebanks rather than prompting greater utilization creates the problem of not knowing what germplasm to use to begin the genetic enhancement of the crop breeding pool(s). This situation has arisen because of incomplete knowledge of large number of germplasm accessions, the relationships among them, unavailability of descriptive characters, and uncertainty about the best evaluation methods for tapping germplasm resources. This implies that the main collection needs to be reduced to a manageable level. Recognizing this, Frankel (1984) proposed that the collection should be pruned to a manageable sample or core collection. Core collections are being important tools to overcome this situation and enhance utilization of genetic resources in crop improvement programmes.

Core collection

A core collection is a subset of accessions about 10 per cent of entire collection that capture most of available genetic diversity of the species (Brown, 1989a). A core subset can be extensively evaluated and the information derived be used to plan a more efficient utilization of the entire collection (Tohme *et al*., 1995; Brown, 1989b). Since the original proposal of Frankel (1984), core collections have been established for many cereal species *viz.,* sorghum (2247 accessions; Grenier *et al*, 2001); pearl millet (1600 accessions; Bhattacharjee, 2000, 2094 accessions, Upadhyaya *et al*., 2009); finger millet (622 accessions; Upadhyaya *et al*., 2006a) and foxtail millet (155 accessions; Upadhyaya *et al.,* 2008a).

Global composite collection of finger millet

A global composite collection which included 622 accessions of core collection and other trait specific and important genotypes was established at ICRISAT (Upadhyaya *et al.,* 2006b). The objectives of this study were to evaluate the composite collection for phenotypic diversity by 18 quantitative traits and six qualitative traits, assess genotypic diversity by using 20 SSR markers, develop a genotype-based reference set, and identify genetically diverse trait-specific germplasm lines for use in breeding programme to develop high yielding cultivars with a broad genetic base.

Diversity in finger millet global composite collection

Wide spectrum of diversity in terms of races and regions has been captured in the composite collection from entire collection. It represented adequately biological diversity (579 accessions of *vulgaris*; 207 of *plana*; 132 of *compacta*; 72 of *elongata*; 7 of *spontanea* and 3 accessions of *africana*) and geographical diversity (362 accessions, East Africa; 275, South Asia; 261, Southern Africa; 67, West Africa; 7, Central Africa; 7, Europe; 5, America).

The composite collection consisted of 89.8% of accessions from East Africa, South Asia and Southern Africa representing dry semi-arid tropical ecology. According to Harlan and De Wet (1971), the greatest morphological diversity in finger millet occurs in the dry semi-arid tropical regions. The germplasm from other regions such as Europe and America appears to be under-represented in the composite collection mainly due to less availability of diversity and difficulty in collection/acquisition of germplasm. However, this represented a wide distribution of finger millet growing areas over the world. The unequal representation of landraces from different countries may be due to the result of use of improved varieties instead of landraces according to farmer's needs in the past. The entire landraces collection, however, fits the evolutionary patterns, nearly representing the geographical distribution and ecological zones of the crop.

5.1 Phenotypic diversity of composite collection

5.1.1 Qualitative traits

Qualitative traits are useful in characterization of accessions, as they show high heritability and stable expression. Out of the six qualitative characters studied, distinction could be seen in accessions for inflorescence shape between races such as *compacta* (fist), *vulgaris* (incurved and top curved) and *plana* (top curved). This is not surprising as the classification of finger millet races is based on inflorescence shape (Prasada Rao *et al*, 1997). Purple pigmentation and low glume prominence was rare in the South Asian accessions, whereas more in the East African accessions. This suggests the presence of greater variability in African material, supporting Africa as the place of origin and domestication. Further in South Asian accessions, top curved and light brown colour seed were more common compared to other groups as they are the most preferred types in cultivation indicating the greater role of human selection in this region compared to African regions. Similarly, East African accessions were predominated by the erect plant habit, green pigmented, top curved, low prominence and light brown seed colour. The *vulgaris* race accessions were erect type, green pigmented, incurved, medium prominence and light brown colour seed. The wide variability for these six qualitative traits were reported earlier in finger millet with 185 ICRISAT accessions (Geetharani, 2005), 622 accessions of core collection (Upadhyaya *et al*, 2006a), and in the 909 East African accessions (Upadhyaya *et al.*, 2007a). More lodging was observed in *vulgaris* race and South Asian accessions as they are tall (> 75cm) compared to other races and region.

5.1.2. Quantitative characters

5.1.2.1 Variance components

The statistical procedure REML (Restricted Maximum Likelihood) allows estimating the variance components in a situation of highly unbalanced data (Resende *et al.*, 1996). The three environments differed significantly indicating that choice of the environments was appropriate in expressing the variability of composite collection for various traits. Estimates of variance components due to genotypes were significant for most of the quantitative traits (days to 50 per cent flowering, plant height, basal tiller number, culm branching, flag leaf blade length, flag leaf blade width, flag leaf sheath length, peduncle length, panicle exertion, ear head length, ear head width, length of longest finger, width of longest finger and number of fingers) in all the three environments and in pooled indicating that the composite collection had sufficient genetic variation for these traits. In the pooled analysis of three environments, variance components due to genotypes and G x E were estimated and tested against their respective standard errors and they were significant for all the traits except grain yield per hectare indicating the genotypes had variation and their performance differed in different environments. The genotypic variance was greater than the variance due to G x E interaction for most of the traits except flag leaf blade length, flag leaf sheath length, ear head length, number of fingers and grain yield per hectare (Table 4. 2). This indicated that for these traits the relative importance of G x E was low. Significant genotypic variance in most of the traits in individual and pooled analysis showed that the genotypes in the composite collection were diverse and had ample scope for selection and utilization in crop improvement programme.

Variance due to genotypes has been reported significant for the traits such as plant height, days to 50 per cent flowering, flag leaf blade length, peduncle length, panicle exertion, ear head length, ear head width and grain yield (Ramasamy *et al.*, 1996; Sivagurunathan, 2005 and Yazhini, 2006).

5.1.2.2.1 Mean performance of the global finger millet composite collection accessions for quantitative traits in different environments

The three environments were significantly different indicating adequacy of these environments in differentiating the genotypes.

The increasing trend of mean was observed in most of the vegetative traits (except flag leaf blade width and flag leaf sheath length) in rainy seasons (E2 and E3) than post rainy season (E1). Finger millet is photo and thermo-sensitive crop, and therefore any fluctuation in day length and daily temperature would have direct effect on the growth and development of vegetative growth of the crop (Senthil *et al*., 2005). This was well depicted in the performance of accessions during these two different seasons (post rainy season at Coimbatore with short day length (12.23 hours) and low day temperature (28°C) with 378 mm average rainfall, whereas rainy seasons at Patancheru had longer day length (13.56 hours) and high day temperature (29.97 °C) with 614 mm (E2) and 480 mm (E3) of average rainfall). This could be due to higher radiation and lower temperatures in the rainy season.

The seven accessions IEs 4708, 4442, 3537, 588, 4759, 4755 and 2158 recorded consistently early flowering (<50 days) in all environments indicating that these accessions could be source of genes for early flowering in developing of early maturing cultivars. Early flowering accessions were reported in finger millet (Geetharani, 2005), pearl millet (Bhattacharjee, 2000), sorghum (Kamala, 2004) and chickpea (Upadhyaya *et al.,* 2007b).

The 11 accessions (IEs 2055, 2502, 6491, 2546, 2589, 2957, 3104, 3450, 518, 5343, 4017) were dwarf (< 85 cm) while 8 accessions (IEs 2737, 3973, 3533, 2713, 6435, 6451, 3825, 2772) were tall (> 130 cm) in all the three environments. The taller accessions could be evaluated in multilocation environment to find their suitability for fodder yield. The mean basal tiller number was almost similar in all the three environments (1- 18 in E1 and E3 and 1- 19 in E2) indicating this trait was not influenced by seasons. The 12 accessions (IEs 3070, 2921, 2180, 3070, 96, 2296, 2868, 5281, 6451, 797, 120, and 2034) had consistently high basal tillers (13-19) than the best control VR 708 (7) in all the environments, whereas the eight accessions IEs 2540, 2561, 4296, 3935, 3317, 4677, 3120 and 6033 had no basal tillers in any of the environments.

In general, traits appreciably affected by environmental factors were mostly vegetative, while reproductive components associated with ear head traits were lEast affected. However the vegetative characters such as flag leaf blade width and length of longest finger were not greatly affected by environment, as also observed by Goodman (1985) in maize. Means and range of the composite collection studied in the present study were similar with entire collection and core collection of finger millet (Upadhyaya *et al.*, 2006a).

The similar range for quantitative traits has been reported earlier in finger millet germplasm characterization with varying number of accessions (729 accessions, Hussaini *et al.*, 1977; 130 accessions, Naik *et al.,* 1993; 4953 accessions, Prasada Rao and De Wet, 1997; 185 accessions, Geetharani., 2005; and 909 East African accession, Upadhyaya *et al.*, 2007a).

5.1.2.2.2 Mean performance of the accessions according to biological races

Mean number of days to 50 per cent flowering was higher for the accessions of wild *spontanea* and lower for the accessions of wild *Africana*, whereas the means of four cultivated races were similar for most of the traits in three environments. Similar results were reported in tetraploid and hexaploid wheats (Bekele, 1984) and in tetraploid wheat (Pecetti and Damania, 1996). Mean basal tiller number was higher for wild *africana* (7.67 to 9.98) and *spontanea* (13.69 to 17.06) than cultivated races (3.72 to 4.79) across three environments may be due to adaptive nature of wild accessions. Association between spreading morphological habit and high number of tillers was reported in wild races (Suryakumar *et al.,* 1997; Anandharaju., 2001).

5.1.2.2.3 Mean performances of the accessions according to their geographical origins

The accessions of Central Africa (< 64.33 days) and South Asia (< 66.1 days) flowered early while the accessions from Southern Africa (> 77.4 days) flowered late. Since evaluation of composite collection in the present study was carried out at semi-arid tropics locations (Coimbatore and Patancheru), this could be the reason for delayed flowering of accessions from Southern Africa or other arid tropic region. Seetharam (1983) also noted early flowering of South Asian accessions and late flowering of Southern African accessions that were evaluated in semi-arid tropics (India).

The mean yield was similar for accessions from different regions indicated the wider adaptability of finger millet (Hussaini *et al.*, 1977: Prasada Rao and De Wet, 1997).

Most of the East African accessions had high number of tillers. The mean of vegetative traits such as flag leaf blade length, flag leaf blade width, flag leaf sheath length and peduncle length was similar for accessions from different regions indicated the minimum variation of these traits in accessions from different regions. Similarly, Appo Rao et al, (1996) studied regional and seasonal variation of morphological characteristics of sorghum in India and attributed the considerable regional and seasonal variations for mean plant height and for mean number of days to 50 per cent flowering to difference in growing season, temperature and day length.

5.1.2.3 Phenotypic and Genotypic Coefficients of Variation

The traits such as basal tiller number, flag leaf blade width, flag leaf sheath length, peduncle length, finger number, ear head length, ear head width, days to maturity, and grain yield per hectare showed high estimates of PCV and GCV and narrow difference between them in all the three environments or atleast in two environments (Table 4. 6), indicating that the yield attributes affected to a lesser extent by environment. Ravikumar and Seetharam, 1994; Thakur and Saini, 1995; Chunilal *et al*, 1996; Bandyopadhyay, 1998, and Mahto *et al*, 2000 also reported higher estimates of PCV than GCV for most of these traits.

5.1.2.4 Heritability

The simple measures of variability like mean, variance and coefficient of variation reveals the extent of variability but not the heritable portion of the total variation. To have the knowledge of the heritable portion of variability, it is necessary to estimate the heritability which is the ratio of genetic variance to phenotypic variance (Singh, 1977) and expressed in percentage. The knowledge of heritability helps the plant breeder in predicting the behavior of characters in succeeding generations and to make desirable selections.

The estimates of broad-sense heritability were high for most of the traits such as days to 50 per cent flowering, plant height, ear head length and ear head width, and medium to high for flag leaf blade length, peduncle length, number of fingers in all the environments/atleast in two environments (Table 4. 6) indicated that the environments had relatively low influence on these traits and selection will be appropriate on these traits in the composite collection.

In the literature high to moderate estimates of heritability are reported (Ramaswamy *et al*., 1994; Thakur and Saini, 1995; Suryakumar, 1995; Bandhopadhya, 1998; Ananadharju, 2001; Sivagurunathan, 2005; and Yazhini, 2006. However, medium estimates of heritability was reported for ear head length and ear head width (Thakur and Saini, 1995; Ravishankar *et al.,* 1997.

5.1.2.5 Correlation coefficients

Phenotypic correlation coefficients were estimated to know the association among traits which could be used as guide while making selections to exploit correlated response in the breeding programs and the traits that could be ignored in the initial characterization of germplasm. In the present study correlations were calculated in each environment separately and also based on the mean values obtained from the pooled analysis. Out of total 352, the number of significant correlations was 19 in E1, 68 in E2, 83 in E3 and 33 in combined analysis (Table 4.7 – 4.10).

In the present study, the correlation between number of days to 50 per cent flowering and ear head length, and length of longest finger; and between plant height and ear head length and peduncle length were positive and significant in two rainy seasons (E2 and E3), in post rainy season (E1) these correlation were not significant. This indicated relative influence of photo sensitiveness on the expression of these traits and correlations. The flag leaf sheath length and grain yield per hectare was positively correlated in one rainy season and negatively correlated in another rainy season indicating high sensitivity of the traits towards environmental changes. Therefore, selection of these traits could need attention for further characterization and improvement. Days to 50 % flowering and plant height were highly, significantly and positively correlated in all three environments. However, magnitude of relationship different in differed environment indicating the influence of environments a these association. Sivagurunathan (2005) reported a positive correlation of plant height with ear head length, panicle exertion and grain yield, contrasting negative association has been reported between plant height and grain yield (Anandharaju, 2001). This discrepancy could be due to the fact that in the present study a large number of germplasm representing global diversity have been used compared to very limited number of entries (135, Anandharaju, 2001).

With such as large degrees of freedom (998), any correlation coefficient with an absolute value greater than 0.05 will be significant at $p = 0.001$. However, the proportion of variance in one trait that can be attributed to its linear regression on second trait is indicated by the square of the correlation coefficient (Snedecor and Cochran, 1980). Therefore, the correlation coefficient with an absolute value greater than 0.707 or less than -0.707 have been suggested to be as biologically meaningful (Skinner *et al*, 1999), so that more than 50 % of the variation in one traits is predicted by the other.

In the present study, eight pairs of characters Viz., days to 50% flowering with plant height (E1) and flag leaf blade width (E3); plant height with basal tiller number (E2) and flag leaf blade length (combined); ear head length with length of longest finger (E2 and E3); grain yield per hectare with length of longest finger (E2)and width of longest finger (E3) and panicle weight with grain yield per hectare (E3) were biologically meaningful indicating strong association between these traits. Therefore future characterization of finger millet germplasm based on these traits could be more reliable. The biological meaningful correlation between peduncle length and panicle exsertion (0.839) and length of longest finger and inflorescence length (0.795) has been reported in the core collection of finger millet (Upadhyaya *et al.*, 2006a). Significant genotypic correlations were observed for most of the traits indicate high correlation between the traits. Similar genotypic correlation was reported (Anandharaju, 2001).

5.1.2.6 Path coefficient analysis

Information based on correlation coefficients is only partial, whereas the path coefficient analysis permits the partitioning of correlation coefficients into direct and indirect effects and gives a more realistic relationship of the characters and helps in identifying the effective components. The low residual value indicated the adequacy of the characters chosen for path analysis.

In the present study, number of basal tillers contributed to the maximum direct effect on grain yield followed by flag leaf blade width and ear head length and ear head width. The effect of finger number was further increased to a little extent by its positive indirect effect through finger length. This revealed the true relationship of these traits with grain yield and direct selection for these traits would be rewarding for yield improvement (Dewey and Lu, 1959). Though plant height had high positive and significant association with grain yield, its direct effect was very low. Similar findings of direct and indirect effects of the traits to yield has been reported in finger millet (Prabhakar and Prasad, 1983; Ravikumar, 1988; Chaudhary, 1989; Cauvery, 1993; Marimuthu, 1993; Anantharaju, 2001). Hence from the results, it could be inferred that the traits such as basal tiller number, flag leaf blade length, peduncle length, ear head length and ear head width have to be considered in selection for improvement of yield.

5.1.2.7 Stability analysis

Both linear (b_i) and non-linear (S^2d_i) components of GE interactions are important for judging the stability of genotypes (Eberhart and Russell, 1966). A regression coefficient (b_i) approximately 1.0 coupled with an S^2d_i equal to zero indicates good stability of genotypes. Regression values above 1.0 indicate the higher sensitivity of genotype to environmental change and below 1.0 provides a measurement of greater resistance to environmental change.

Wider range of linear regression was observed and it indicated differential response of genotypes to environmental changes. Only 40 accessions for days to 50 per cent flowering and 7 accessions for grain yield per hectare recorded a regression coefficient equal to unity ($b = 1$) and small deviations from regression ($S^2d = 0$) and these were considered as stable genotypes over environments. In earlier studies also a number of finger millet genotypes with good stability for the days to flowering and grain yield has been reported in multilocational evaluations at 6 locations by Ramasamy *et al*, (1997) and at 2 locations by Sheriff *et al*, (1986).

5.1.2.8 Phenotypic diversity

The Shannon-Weaver diversity index (H`) was calculated for different traits in each environment separately and also pooled environments. The index is used as a measure of allelic richness and evenness; a low H` indicates an extremely unbalanced frequency class for an individual and lack of genetic diversity.

Out of six qualitative traits studied, Inflorescence shape showed high H`, indicated the relative high diversity for this trait. High mean H` was observed for quantitative traits, ear head length, days to 50 per cent flowering, flag leaf blade length and plant height in all environments or atleast in two environments indicated evenness and richness. Flag leaf blade width showed low mean H` in all the environments indicated relatively unevenness distribution of alleles and low in allelic richness. The mean and range of H` for all the traits in the present study, is comparable with the H` of entire and core collection of finger millet (Upadhyaya *et al.*, 2006a) indicating that the composite collection represents the diversity in entire collection.

5.1.2.8.1 Phenotypic diversity according to biological race and geographical origin

The accessions of race *elongata* and *compacta* had high mean H` for most of the traits in all three or atleast two environments, indicating the greater diversity in these races, even though, wild races (*spontanea* and *africana*) has distinct morphological nature.

Considering different regions, accessions from East Africa and South Asia showed high H`, whereas Central Africa accessions showed low H` for most of the quantitative traits and this may be due to the fact that finger millet had originated from Ethiopia (East Africa) with secondary centre of origin in South Asia (Hilu and De Wet, 1976a), and original gene pool being conserved in these two regions.

The traits flag leaf blade length, panicle length, days to 50 per cent flowering, plant height, ear head length had more H` for the accessions from different races and regions indicated relatively more diversity for these traits.

5.1.2.9 Principal component analysis

Principal Component Analysis (PCA) was used to provide a reduced dimension model that would indicate measured differences among groups.

In all the three environments and also in the pooled analysis, a large proportion of the total variation was explained by the first seven Principal Components (PCs). The percentage variation explained by first seven principal components was 59.63 per cent in E1, 62.50 per cent in E2, 68.29 per cent in E3 and 87.88 per cent in combined analysis (Table 4.20 – 4.24). The percent variation explained by 7 PCs in present study is lower than earlier report (Upadhyaya *et al.,* 2002).

In the present study, considering over three environments and combined analysis, the traits such as days to 50 per cent flowering, plant height, peduncle length, ear head length and panicle exertion contributed repeatedly to total divergence atleast in two environments. The traits flag leaf blade width, width of longest finger, 1000 grain weight had low or no contribution in explaining variation in the first seven PCs of the composite collection.

5.1.2.10 Cluster Analysis

Clustering analysis using Ward's (1963) method was performed using score of first four PCs (80.90%) on the pooled data based on biological race and geographical origin.

5.1.2.10.1 Biological race:

According to the biological races, the four cultivated races (*elongata*, *plana*, *vulgaris* and *compacta*) were delineated in to Cluster I, whereas wild races were grouped separately in two clusters *viz.,* Cluster II (wild *spontanea*) and Cluster III (wild *africana*) (Figure 4.3). The linkage distance between the wild races *spontanea* and *africana* was more than 50 per cent, so it was grouped in to two different clusters. The variation of these wild races was reported at Mitochondrial DNA level (Muza *et al.*, 1995). Cytogenetically, *E. coracana and E. africana* are reported to be an allotetraploid with genomic notation of AABB with distinct genetic back ground (Chennaveeraiah and Hiremath, 1974). This could be the reason for difference in clustering pattern of these major sub species. This clustering observed in this study is in agreement with earlier reports based on molecular markers (RFLP, Salimath *et al.*, 1995; RAPD, Fakrudin *et al*., 2004; SSR, Dida *et al.*, 2008).

5.1.2.10.2 Geographical origin:

Regional clustering revealed that America and Europe were grouped together in Cluster I, whereas the major finger millet growing regions such as East Africa, southern Africa, South Asia and accessions from unknown origin grouped together in Cluster II. The accessions West Africa and Central Africa grouped in Cluster III and Cluster IV respectively (Figure 4.4). This clustering is not surprising considering the dispersion of finger millet from Africa (Harlan and De Wet, 1971). The grouping of Africa (East Africa and Southern Africa) and South Asian accessions (mostly from India) was noted in the present study. It implies that these primary and secondary centre of origin of finger millet conserves common gene pool (Hilu and De Wet, 1979). Since time immemorial, there has been trade relationship between the South-Western India and African through South- West Arabia (Moore and Dunbur, 1969) and possibility of exchange of food grains on these regions took place. So most of the accessions from these regions might be sharing common ancestry. Similarity between Indian and African accessions has been reported in a study by using RAPD markers (Hiremath, 1997).

In cluster III and IV, West African and Central African materials occupied respectively and proved themselves to be distinct. Difference in climatic and ecological conditions may have restricted gene flow between these adjoining areas with other African regions.

5.1.3 Identification of accessions for high micronutrient (iron and zinc) content

According to recent estimate more than 3 billion people globally suffer from Zn and Fe deficiency (Shankar *et al.*, 2006). Finger millet is a very good source of micronutrients, which could alleviate the wide spread micronutrient malnutrition in the vulnerable segments in the developing country like India (Shashi *et al.,* 2007). The processing of finger millet (malting, grinding, sprouting, and puffing) reduces anti-nutritional factors, thereby resulting in better availability of micronutrients (Sankara Rao and Deosthale, 1983; Malleshi *et al.*, 1996). So, identification of genotypes with good sources of micronutrient content will be useful for alleviating micronutrient deficiency.

In the present study, 65 diverse accessions (selected from composite collection) and two control cultivars (VL 149 and PR 202) were used to estimate Fe and Zn content by Atomic Spectra Photometric Meter (ASPM). The accessions, for Fe content (IE 5941, 63.4 mg/g; IE 2572, 54.5 mg/g; IE 3475, 39.8 mg/g; IE 4545, 38.1 mg/g and IE 4734, 35.5 mg/g) and Zn content (IE 5870, 31.7 mg/g; IE 2589, 30.7 mg/g; IE 5941, 29.9 mg/g; IE 3045, 29.3 mg/g) had higher mean content than the best control VL 149 (29.5 ± 0.86 and 29.5 ± 0.40 mg/g of Fe and Zn). It indicated the availability of good source of micronutrients in this small sample from composite collection and these accessions could be useful in breeding programmes.

Most of the *vulgaris* and *plana* race accessions showed high Fe and Zn content compared to other races. Samantray *et al*. (1989) also reported high Fe in *vulgaris* accession.

In our study, the white seeded finger millet accessions like IE 2872 (35.9 mg/g and 27.1 mg/g), IE 2296 (29.7 mg/g and 23.1 mg/g) and IE 5367 (33.0 mg/g and 24.7 mg/g) had medium Fe and Zn, which is higher than in brown seeded accessions. Vadivoo *et al.* (2004) also reported higher Fe content in white seeded varieties than brown seeded varieties in finger millet.

5.1.4 Identification of trait specific accessions

By evaluating the global finger millet composite collection over three seasons [2005/2006 post-rainy (E1), 2006 rainy (E2), 2007 rainy (E3)], the number of accessions performed repeatedly better than the best control cultivar for the particular trait(s) for traits, were 34 for early flowering; 28 for high grain yield; 25 for more number of fingers; 25 for high basal tiller number and 28 for ear head length (Table 4. 25). Extensive evaluation of these accessions in different locations may be useful to assess the stability for identifying the stable trait specific accessions.

5.2 Genotypic diversity

Finger millet, like other millets, has a narrow genetic base in spite of the large collection of germplasm and globally active genetic enhancement programme. Past efforts led to believe that low molecular variation exists in cultivated finger millet;

however, this conclusion was based on limited number of germplasm and markers involved in these studies. With the discovery of large numbers of genomic SSR markers (Dida *et al.,* 2008), it is now possible to conduct extensive molecular diversity in finger millet for identifying genetically diverse germplasm with beneficial traits for use in crop improvement programmes.

5.2.1 Simple Sequence Repeat (SSR) marker based diversity

Traditionally, characterization and identification of cultivars has been performed by using morphological, agronomic and physiological traits. However, such traits are not always available for analysis and even if available they exhibit high G x E interaction. The deployment of environment neutral, biochemical markers, the isozymes, protein electrophoresis, and molecular markers such as RFLP, AFLP and RAPD have circumvented these limitations by focusing directly on the variation at the DNA level. The high resolution of molecular markers such as Simple Sequence Repeats (SSR) or microsatellites make them a valuable tool for a variety of purposes, such as fingerprinting, facilitating appropriate choice of parents for breeding programmes, analyzing quantitative traits, location and detection of QTLs, genetic mapping, marker assisted selection, gene transfer, studying evolutionary pathways and for assessing genetic diversity of plant germplasm.

SSRs have been considered useful and advantageous over other molecular markers especially for marker-assisted selection and genetic diversity studies as they are co-dominant and multi-allelic in nature (Gupta and Varshney, 2000). The high diversity obtained with SSRs are consistent with the known characteristics and they are more variable and highly polymorphic than the RAPDs, or AFLPs (Powell *et al*., 1996). Three mechanisms were proposed as responsible for new SSR alleleic creation: replication slippage (Tachida and Iizuka, 1992), unequal crossing over and genetic recombination (Harding *et al*., 1992). The most important factor affecting the number of alleles per locus is the characteristic of material used. The number of alleles is usually higher in the genebank accessions than related cultivated varieties, often of common origin (Varshney *et al*., 2001). The ability to determine genetic variation among the accessions at the molecular level was directly related to the number of polymorphism and their reproducibility.

5.2.2 Genotypic diversity of global finger millet composite collection

5.2.2.1 Allelic richness

Twenty SSR loci data on 959 finger millet accessions detected a total of 231 alleles (121 common and 110 rare alleles) with allelic frequency of 11.55 alleles per SSR loci. The allele number per SSR locus in this study, was higher than the earlier studies finger millet (6.42 alleles per locus, Dida *et al.*, 2008), sorghum (7.3 alleles per locus, Assar *et al.*, 2005) and pearl millet (5 alleles per locus, Budak *et al.*, 2004). However, allele per locus was higher (35 alleles) in case of chickpea composite collection (Upadhyaya *et al.,* 2008b) in which higher number of polymorphic SSR marker (48) and large population (2915 accessions) were used and it could be the reason for higher allele per locus. In addition to the total number of alleles and unique alleles, the number of rare alleles obtained indicated the diversity at a given SSR locus. Considering, the alleles with frequencies of atleast 99 per cent as common and alleles with frequencies of less than 1 per cent as rare. Rare alleles in the composite collection for the marker (UGEP5) were quite higher (9). The presence of many rare alleles could be due to the higher rate of mutation at SSR loci (Henderson and Petes, 1992).

This study revealed some highly significant ($p < 0.01$) positive correlation between different parameters. Thus alleles per locus was correlated with gene diversity; allele size and number of rare alleles; allele size with gene diversity and number of common alleles with number of rare alleles. However, variable and inconsistent relationship between repeat unit length and SSR polymorphism has been reported in several self pollinated crops, Wheat (Prasad *et al*., 2000) and sorghum (Folkerstma *et al.*, 2005). Information available on these alleles present in different germplasm lines will be very useful for developing the mapping populations for genome analysis as well as applied breeding programmes.

5.2.2.2 Polymorphic Information Content (PIC)

The PIC values of the SSR markers in the present study ranged from 0.196 to 0.834 with an average of 0.518. The PIC of an SSR marker provides an estimate of the discriminatory power of that SSR marker by taking into account of not only the number of alleles that are detected but also the shared frequencies of those alleles (Smith *et al*, 2000).

In the present study, the number of SSR markers is considerably less than found necessary for getting high PIC (Fregene *et al.*, 2003), indicated that a minimum of 30 unlinked SSR markers are required to assess genetic diversity of 283 land race accessions of cassava. Gupta *et al.* (2003) reported increased PIC with greater number of markers. They obtained PIC of 0.469 with 65 SSRs markers compared to 0.210 with 20 SSRs on 52 wheat genotypes. Most of the self pollinated crops such as sorghum (Folkertsma *et al.*, 2005), barley (Turuspekoy *et al.*, 2001) and wheat (Stepien *et al.*, 2003) produced the optimum PIC range of 0.600 to 0.700.

Although, the number of SSR marker in this study was limited, high polymorphism was revealed indicating wide diversity among accessions. The high diversity obtained with SSRs is consistent with their known characteristics- that they are more variable, and provide higher resolution and higher expected heterozygosity than the RFLPs, RAPDs or AFLPs (Pejei*.,* 1989; Powell *et al.,* 1996; Taramino and Tingey, 1996). The high levels of polymorphism associated with SSRs are expected because of the unique mechanism responsible for generating SSR allelic diversity by replication slippage (Tautz and Renz, 1984; Tautz *et al.,* 1986) rather than by simple mutations, insertions or deletions.

The Markers, UGEP8 (0.452), UGEP3 (0.568), and UGEP31 (0.522) had high PIC value, whereas the markers UGEP81 (0.380) and UGEP65 (0.369) had low PIC for the similar number of alleles (10). This result indicated that PIC values depend not only on the number of alleles but also the gene diversity (Varshney *et al.*, 2001; Smith *et al.*, 2000). As expected the amount of marker polymorphism (52%) exhibited in this finger millet composite collection is higher than that normally found in self pollinated cereal crop species like rice (Mc Couch *et al.,* 1988) and Wheat (Chao *et al.*, 1989; Devos *et al.,* 1997). In barley, the amount of polymorphism observed was less than 28 per cent (Graner *et al.,* 1991). Normally in inbreeding species, the level of polymorphism is expected to be generally lower than in out crossing species (Miller and Tanksley, 1990).

5.2.2.3 Gene diversity

In the past, random genomic DNA markers (RFLP and RAPD) have been extensively used for the study of genetic diversity in finger millet. Most of these markers may assay polymorphism located in the non-coding regions of the genome that are poorly conserved among species (Varshney *et al.,* 2001). Therefore, the genetic diversity detected by these markers may not represent true or functional diversity. In contrast functional markers such as EST/SSR assay polymorphism that is associated with the coding regions of the genome and should detect "true gene diversity" available inside or adjacent to the genes (Thiel *et al.,* 2003). In the present study, mean gene diversity was 0.58 with wide range of 0.200 (UGEP31) to 0.850 (UGEP12). This value is higher than earlier report based on RAPD markers in finger millet (0.330, Babu *et al.,* 2007).

5.2.2.4 Heterozygozity

Single allele per locus in each genotype was observed in most of the accessions. These observations are as expected as the SSR markers are locus-specific and generally amplify one locus (Gupta and Varshney, 2000). In spite of this, a wide range of heterozygosity (%) was detected in the investigated materials, from 0.00 to 19.00 per cent, with an average of 9.00 per cent. One SSR loci (UGEP18) detected no heterozygosity, while the markers UGEP3 and UGEP10 (12%), UGEP8 (13%), UGEP11 (14%), UGEP77 (16%), UGEP90 and UGEP102 (17%) and UGEP81 (19%) detected more than 10 per cent in 959 accessions. This was in spite of the fact that DNA was extracted from a single plant of the accessions and crop is highly self-pollinated. The reason for such high heterozygosity would be allotetraploid nature of the finger millet having A and B genomes, locus UGEP3 was mapped in both the genomes and this could be the reason for occurring two alleles and resulting high heterozygozity for this locus (Dida *et al*., 2007). Also a large number of landraces are involved in this study and it is possible that these accessions may still possess some residual heterozygosity atleast at some of the SSR loci. The heterozygosity observed at some of the loci could also be due to high mutational rate and mutational bias at SSR loci (Udupa and Baum, 2001). The loci with large number of repeat units (SSR units) tend to show high mutational rate. As a result, any mutations in any one of the alleles may create a heterozygous condition. Many of the loci which displayed heterozygous status have a large number of SSR units. High allelic variability and low heterozygozity observed in this study implies the inbreeding nature of finger millet as reported in sorghum (Dje *et al.*, 2000).

5.2.2.5 Biological racial diversity

The average number of alleles per locus was high in the accessions from race *vulgaris* (10.3) and minimum in race *africana* (2.1). This might be due to the variable number of accessions, high in case of *vulgaris* (579) and low incase of *Africana* (2 accessions). Parallel to allele number, more number of unique alleles also observed high in race *vulgaris* (37 alleles) whereas in other races it ranged from 1 in *elongata*, 2 each in *africana* and *compacta* and 5 in *plana*.

Among the races, the accessions of wild *spontanea* showed high PIC (0.611), whereas all the cultivated races had the similar range of PIC (0.501 to 0.521). It indicated lower polymorphism in among the cultivated accessions than in wild races. Dida *et al., (*2008) also reported low polymorphism in the cultivated races of finger millet. The mean gene diversity was high for accessions of *elongata* (0.542) and low for accessions of *africana* (0.422). Less number of *africana* accessions could be the reason for low PIC and gene diversity in these group.

5.2.2.6 Geographical diversity

The average number of allele per locus was high for accessions from East Africa (9.9) and South Asia (8.8), whereas accessions from Europe had low allele per locus (2.2). A similar situation of less diversity was observed for European accessions by morphological data also. Unique alleles were also found more in East Africa (29 alleles), South Asia (12), and Southern Africa (11) and shared alleles between East Africa and South Asia were high (11 alleles). This shows clearly a high level of gene flow between these regions. The accessions from America and West Africa have no unique alleles. Interestingly, most of the accessions carrying rare alleles were from East Africa, which is believed as centre of origin. It might be the founder alleles which are retained in gene pool even after so many years of crop evolution (De Wet *et al.,* 1984). Such rare alleles are important, because they may be diagnostic for particular regions of the genome specific to a particular trait/type of finger millet.

As expected, East Africa (centre of origin) had high mean PIC (0.523) and Europe had low PIC (0.359). In the present study, gene diversity was high for accessions of *spontanea* (0.566) and low for accessions of *africana* (0.345). Dida *et al*. (2007) also reported that wild Subspecies *africana* germplasm had highest level of gene diversity (0.390).

5.2.2.7 Clustering

5.2.2.7.1 Biological racial clustering

The clustering of biological races resulted in to two major distinct groups (Figure 4. 7). Even though, there is no exact separation of accessions between cultivated biological races, wild *spontanea* accessions were grouped in a separate cluster VI. According to Hilu and De Wet (1976a), the cultivated races *vulgaris*, *elongata*, *plana* and *compacta* probably evolved from cultivation of Subsp. c*oracana* and that could be the reason for lower diversity in this group.

5.2.2.7.2 Geographical origin clustering:

Clear patterns of genetic diversity among the African and Asian accessions were observed based on similarity index of SSR allelic patterns. This distinction between African and Asian accessions is supported by findings of Dida *et al.,* (2008) also regarding divergence between East Africa and South Asian accessions of finger millet based on SSRs. However, the dendrogram does not classify genotypes unequivocally on the basis of country of origin as it was shown in some earlier studies: sorghum (Smith *et al.*, 2000; Agrama and Tuinstra, 2003; Folkertsma *et al.*, 2005), wheat (Holton *et al.*, 2002; Gupta *et al.*, 2003) and barley (Xiao *et al.*, 1996; Hokanson *et al.*,1998; Holton *et al.,* 2002; Thiel *et al.*, 2003). This could be due to two major facts: (i) it can be assumed that the finger millet composite collection (or atleast the accessions analyzed in the present study) not only represented the broad range of genetic variability for morphological or agronomic traits but also at DNA level. The finger millet composite collection (consisting 622 accessions of core collection), therefore, represents a broad picture of genetic diversity as expected of core collection (Frankel, 1984). (ii) The present day finger millet has only one center of origin and a recent worldwide dispersal, thereby leading to the genetically similar backgrounds (De Wet *et al.,* 1984).

5.2.2.4 Factorial analysis

In order to link the genetic diversity with the phenotypic diversity, efforts were made by analyzing the phenotypic data for four agronomic traits i.e. days to 50 per cent flowering, plant height, ear head length and grain yield together with genotyping data by using Principle Coordinate Analysis (PCoA). The grouping of genotypes was not congruent with the genetic diversity data except for plant height. According to phenotypic data for plant height, dwarf accessions were grouped in the 3rd and 4 th quadrant and the accessions from East Africa and Southern Africa grouped in the same quadrant for genotypic data. Medium and tall accessions were scattered in the first and second quadrant in which the accessions were present on the basis of genotypic data from South Asia. Priti (2006) also reported the similar grouping of early flowering accessions in a USDA collection of chickpea germplasm by SSR marker data. For other traits, phenotypic classes were not associated with racial or regional classification based on SSR markers. It mainly due to limited number and non trait markers used in the present study.

5.2.2.8 Population Structure

In the present study of 959 accessions, majority of the accessions were *coracana* accessions (99%) and very few of *africana* accessions (1%). So dissection of population structure according to biological race may not be appropriate and lead to inconsist interpretation about the original structure of the population. So it was decided to consider the population based on geographical origin, and there are three major regions with large number and equal proportion of accessions (East Asia, South Asia and Southern Africa). Further k value was 5, therefore, grouping was considered in to four subpopulation. Dida *et al.* (2008) reported the population structure of 78 accessions of finger millet in to three subpopulations (Asian *coracana*, African *coracana*, and African *africana* population).

Using the software programme STRUCTURE, the population was grouped into four subpopulations: subpopulation1 and subpopulation 2 with mixture of East Africa and South Asian accessions, subpopulation 3 with maximum number of South Asia accessions, and subpopulation 4 with mixture of all other geographical origins. There was good correspondence between the geographic patterning observed in the population structure.

Although the population subgroups corresponded largely to geographic regions, there were some notable exceptions. Excluding any accession that showed evidence of admixture (<90% of alleles in one subpopulation), 95 per cent of the cultivated African accessions belonged to the African subpopulation. In a few African accessions that grouped with the Asian subpopulation are IE4585, accession originated from Zimbabwe, and IE3855, an accession originating from Uganda showed more admixtures (>60%) and grouped with Asian population. Most of the accessions in subpopulation 3 were having 10 to 60 per cent admixture, which might be due to the result of hybridization between adapted African and Asian (especially Indian) accessions and these are called as Indaf varieties. Evidence of admixture between Indian and African germplasm was found in the Indian accessions, probably as a result of intercrossing between Indian and African germplasm, a breeding strategy that was adapted in India in the 1970s. This was confirmed by removing Indaf varieties which gave clear population structure.

The two subpopulations 1 and 2 were closer together, but distinctly isolated from the other subpopulations. It is possible that these two groups should not be separated, but considered as two subpopulations. Chandola (1959) proposed that finger millet developed simultaneously both in Africa and in India and the genus *Eleusine* has several common features like dominant genes and similar diversity of species and their cytological behavior. Interestingly in subpopulation3, 105 Southern African accessions were clustered which were mostly from Zimbabwe. It supports the facts that these accessions were quite diverse from South Asia and East Asian accessions. The major reason, for this could be that Zimbabwe is away from Equator towards South and has different climate, whereas, East Africa and South Asia were nearer to the equator or towards north of equator. The subpopulation 4, is a small group, consisting of only 141 accessions, mixture of all accessions, and a greater proportion of accessions are from South Asia and East Africa.

No information is available about origin of 27 accessions in the composite collection. Among these 8 accessions were represented in subpopulation 1, 7 in subpopulation 2, 10 in subpopulation 3 and 2 were in subpopulation 4. So it can be predicted that most possibility of these accessions with unknown origin would have originated either in South Asia or East Africa. The clustering based on morphological data also revealed the same pattern of relationship of accessions with unknown origin to South Asia and East African origin.

5.2.2.9 Reference set

A reference set consisting of 300 genetically most diverse accessions have been formed, capturing 206 (89.2%) of the 231 alleles detected in the composite collection. The reference set captured both biological and geographical diversity from the entire spectrum of composite collection. Similarly, reference set was developed in chickpea by using 48 SSR markers (Upadhyaya *et al.,* 2008b). This reference set with most diverse accessions can be used for identifying the trait specific accessions, future functional genomics and finger millet crop improvement.

5.2.2.10 Association of markers with phenotypic traits

Association mapping often involves a relatively large number of diverse accessions; phenotypic data collection with adequate replications across multiple years and multiple locations (Zhu *et al.*, 2008). Efficient field design, appropriate statistical methods and consideration of QTL × environmental interaction should be explored to increase the mapping power, particularly if the field conditions are not homogenous (Eskridge, 2003). The co-dominant SSRs and SNPs are more powerful in estimating population structure and the relative kinship matrix (Zhu *et al.,* 2008).

In the present study, association analysis resulted in inconsistent association between the traits and markers for most of the traits mainly due to limited number of random and non trait specific markers. Also the association varied in different samples, composite collection with 1000 accessions and reference set with 300 accessions. Jensen *et al.* (2003) suggested that large numbers of molecular markers are needed to better cover the entire nuclear genome for such association studies. However, in the present study, QTL for days to 50 per cent flowering had consistent association with UGEP8 in LG3 (E2, E3 and combined for both composite collection and reference set) and UGEP56 in LG9 (E2 and E3 in composite collection and E1 in reference set). It indicated relatively tight linkage between the trait and marker. QTL mapping of these markers using mapping population would give better idea of consistency of marker's association.

The loci UGEP56 (days to 50 per cent flowering and flag leaf blade length), UGEP8 (days to 50 per cent flowering, basal tiller number and flag leaf blade length), UGEP65 (flag leaf blade width and peduncle length) had multi trait association in E2 in the composite collection and UGEP8 (basal tiller number, flag leaf sheath length, peduncle length and finger number) and UGEP31 (clum branching, flag leaf blade length, peduncle length and ear head length) in E2 in the reference set. Extensive study of these associated QTL would be useful for confirmation of these multi-trait QTL. Similar results of multi trait association were reported for grain and stover yield in pearl millet (Bhaskaran, 2007).

Over all, more number of QTL were observed in LG3 (20 in composite; 12 in reference) and LG5 (7 in composite; 11 in reference) in three environments and pooled, indicated relative importance of these linkage groups for most of the quantitative traits. Finding more number of markers/loci in these linkage groups will be helpful to identify some important QTL.

5.2.2.11 Cophenetic correlation

By the Mantel critical r ($P \leq 0.05$), the positive limit was 0.59, inferring that the correlation index was very close to significance clustering is realiable. According to Vaz patto *et al.* (2004) an ideal index for this type of correlation would be greater than 0.56.

Summary

CHAPTER VI

SUMMARY

The importance of crop genetic resources was realized with the expansion of breeding programmes, as the success of these programmes largely dependent on availability of wide genetic diversity. The extensive cultivation of high yielding varieties, crop substitution, recurrent droughts and urbanization created potential threat of erosion of traditional landraces for the farmer's field. This prompted global community to collect and conserve the genetic diversity in *ex-situ* collection before it disappears. The systematic collection missions were launched for major crops. This resulted in large collections which contribute to grow even now. However, a very small portion of the germplasm collection has been used in the crop improvement programmes of most crops including finger millet. This was mainly due to lack of information on traits of breeders interest which show high genotype x environment interaction and require multilocation evaluation to identify parents for use in breeding programme. Recognising this, Frankel (1984) suggested use of core collection (10% of entire collection) with minimum repetitiveness.

At ICRISAT finger millet core collection (622 accessions) was developed from the 5949 accessions. Molecular markers particularly SSR (microsatellites) are good instrument to dissect genetic diversity at DNA level. ICRISAT in collaboration with the Generation Challenge Programmeme (GCP) developed a composite collection of 1000 accessions that included 622 accessions, to study diversity and population structure and develop a reference set of 300 genetically most diverse accessions using SSRs. This reference set would be used a base material for extensive evaluation for various traits to identify trait specific accessions and for allele mining.

The global composite collection of finger millet (1000 accessions) was evaluated in three environments *Viz.,* 2005/2006 post rainy season at Tamil Nadu Agricultural University (TNAU), Coimbatore (E1), in 2006 (E2) and 2007 rainy season (E3) at ICRISAT, Patancheru centre, Hyderabad for various morpho-agronomic traits under field conditions. Data was recorded on six morphological (growth habit, plant pigmentation, inflorescence shape, glume prominence, seed colour and lodging in all three environments) and 18 agronomic traits (days to 50% flowering, plant height, basal number of tillers, flag leaf blade length, flag leaf blade width, flag leaf sheath length, peduncle length, ear head length, ear head width, number of fingers and plot yield in all environments, culm branching only in E1 and E2, panicle exertion, length of longest finger, width of longest finger only in E2 and E3, days to maturity only in E1, 1000-grain weight only in E2, panicle weight only in E3).

DNA was extracted from a single representative plant in each accessions was used for molecular profiling by using 20 polymorphic SSR markers. Seeds were harvested separetly from single plant from which DNA was extracted. Molecular diversity and population structure of the composite collection was determined.

The results of the present study are summarized below:

Phenotypic diversity

- For qualitative traits, the accessions of composite collection showed higher frequency for erect plant habit, green pigmentation, non lodging plant types, medium glume prominence, semi-compact inflorescence and light brown seed colour.
- Estimates of variance components due to genotypes were significant for most of the traits indicated that the composite collection had sufficient genetic variation for these traits. Variance components due to G x E were significant for all the traits except plot yield indicated the accessions had variation and their performance differed in different environments.
- Mean and range of all the traits were similar with entire and core collection of finger millet indicated the composite collection captured the entire diversity.
- High estimates of PCV and GCV and a narrow difference between them for most of the traits indicated that the yield attributes were stable with minimal environmental influence and variability could be exploited for selection of these traits.
- High estimates of broad sense heritability for most of the traits were observed in all environments or at least two environments suggested relatively low influence of environment in the expression of these traits.
- The traits such as number of basal tillers, ear head length, finger number, length of longest finger and flag leaf blade length exhibited a positive and significant phenotypic correlation with grain yield in all the environments or at least two environments indicating selection on these traits will simultaneously improve the yield.

- Path coefficient analysis of pooled data revealed that the traits number of basal tillers, finger length, flag leaf blade length, peduncle length, ear head length, and ear head width have to be account for direct selection for yield improvement.
- Stability analysis revealed wide range for linear regression indicated different response of genotypes to environmental changes. Only 40 accessions (days to 50 % flowering) and 7 accessions (plot yield) had b = 1 and $S^2d = 0$ are considered as stable genotypes over environments.
- The mean and range of Shannon- Weaver diversity index (H`) for all the traits in the present study, is comparable with entire and core collection of finger millet indicated that the composite collection represents the diversity of entire collection.
- Accessions of races Elongata and Compacta and from the regions east Africa, southern Africa and south Asia region showed higher mean H` for most of the traits in all three environments.
- Principal Component Analysis (PCA) based on first seven PCs, the traits (days to 50% flowering, plant height, peduncle length, ear head length and panicle exertion) contributed repeatedly to total divergence at least in two environments indicating the relatively greater contribution towards divergence. The traits such as flag leaf blade width, width of longest finger, 1000 grain weight showed relatively low contribution towards divergence.
- Clustering analysis using Ward's methods (1963) grouped biological races in to three clusters: cultivated races v*ulgaris, plana, elongata, and compacta* clustered in Cluster I and wild race *spontanea* in Cluster II and *africana* in Cluster III). Geographical region wise there were four clusters: America and Europe grouped in Cluster I, south Asia, east Africa and southern Africa grouped together in Cluster II., centre Africa in Cluster III and west African Cluster IV. The clustering pattern revealed high diversity nature of composite collection based on racial and regional diversity.

Identification of trait specific accessions

- Accessions for different traits were selected for use in improvement programmeme: early flowering (24); high grain yield (36), fodder yield (17); more fingers (21); basal tiller number (19) and ear head length (20). Extensive evaluation of these accessions in different locations will be useful for identifying their agronomic potential and stability.
- The accessions with high Fe content (IEs 5941, 2572, 3475, 4545, 4734) and Zn (IEs 5870, 2589, 5941, and 3045) were identified as a good source material for micronutrients from composite collection.

Genotypic diversity

Using ABI 3700 automated sequencing platform at ICRISAT, 20,000 (1000 accessions x 20 SSR loci data) data points were generated. After quality assessment using the binning procedure (Idury and Cardon. 1997*)*, 19180 data points (959 accessions x 20 SSR loci data) were used for analysis.

- The global composite collection showed rich allelic diversity, 231 alleles, 11.6 alleles per locus, 121 common alleles and 110 rare alleles at 1%.
- Markers UGEP81, UGEP10, UGEP102, UGEP26, and UGEP77 had high number of alleles (10 - 21). The large number of multiple alleles detected in few markers (UGEP3, UGEP5, UGEP31 and UGEP104). Markers with high PIC values (> 0.636) were UGEP15, UGEP5, UGEP18, UGEP102, UGEP12, and UGEP77.
- Unique alleles are those detected in a group of accessions but absent in other groups. Race-specific unique alleles were 37 *(vulgaris*), 5 (*plana*), 4 (*africana*), and 2 (*compacta*) and region-specific alleles were 29 (east Africa), 12 (south Asia), 11 (southern Africa), and one each in central Africa and Europe. The common alleles shared by two groups were 15 (east Africa and south Asia), 5 (east Africa and southern Africa), and 3 (south Asia and southern Africa).
- The composite collection showed wide range of PIC from 0.196 to 0.834 with mean of 0.518 and gene diversity from 0.200 to 0.850 with mean of 0.560.

- The mean of PIC, gene diversity and heterozygosity was similar between the cultivated race accessions. High gene diversity (0.611) and heterozygosity (13.6%) was observed for accessions of wild spontanea. Accessions from east Africa had high PIC (0.523) and gene diversity (0.564).
- Unweighted neighbour-joining tree was constructed using simple matching pair wise dissimilarity matrix in DARwin-5.0 (Perrier *et al.,* 2003). It grouped into two major groups Viz., Group I, (Cluster I, 148 accessions; Cluster II, 162 accessions; Cluster III, 103 accessions) and Group II (Cluster IV, 125 accessions; Cluster V, 330 accessions; cluster VI, 89 accessions). There is no exact separation between cultivated races indicated minimum diversity between these races. Wild races *spontanea* and *africana* were grouped in a separate cluster VI revealed distinct genetic background at genome level also, as already discussed based on phenotypic data. Grouping based on geographical regions was not clear. However, Asian accessions were grouped in Group I and African accessions in group II.
- No significant correlation was observed between genotypic diversity and phenotypic diversity for the agronomic traits examined expect for plant height. This study suggested that using a larger number of molecular markers covering the whole genome (based on LD-decay in the germplasm collection) or traits-associated molecular markers for classification of genotypes according to the agronomic traits.
- Population structure of the composite collection was dissected in to four Subpopulations based on geographical origin using STRUCTURE. The Subpopulations 1 and 2 are closer together with south Asian and east African accessions; Subpopulation 3 (southern African accessions), and Subpopulation 4 (mixture of all accessions).
- A reference set consisting of 300 genetically most diverse accessions (from 23 countries) have been formed, capturing 206 (89.2%) of the 231 alleles detected in the composite collection. It will be useful to select diverse parental lines for generating intra-specific mapping population(s) with larger genetic diversity to prepare dense genetic maps and QTL analysis for complex traits for assisting the finger millet breeding programmes.

- Association analysis of markers with traits showed inconsistent QTL for many traits. However, QTL UGEP8 in LG3 and UGEP56 in LG6 for days to 50% flowering were consistent at least in two environments indicating relative strong association between marker and traits. Extensive study of these markers in mapping population would be helpful for confirmation of QTL.
- The positive limit of cophenetic correlation was obtained, indicating reliability of clustering

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Appendix

Appendix: I Passport data of global finger millet composite collection

S. No	IE Number	Source country	Race	Sub Race	Source
1	IE2517	Kenya	Plana	Confundere	Replaced in ICRISAT core with FAO designated
2	IE895	Uganda	Vulgaris	Digitata	ICRISAT core
3	IE5201	India	Vulgaris	Digitata	ICRISAT core
4	IE4295	Zimbabwe	Plana	Confundere	ICRISAT core
5	IE3804	Uganda	Vulgaris	Incurved	Replaced in ICRISAT core with FAO designated
6	IE5653	Nepal	Elongata	Sparsa	ICRISAT core
7	IE2621	Malawi	Elongata	Laxa	Replaced in ICRISAT core with FAO designated-AICSMIP ICRISAT core- Grain yield+FL
8	IE5142	India	Vulgaris	Incurved	ICRISAT core
9	IE2718	Malawi	Plana	Confundere	AICSMIP ICRISAT core-
10	IE6175	Nepal	Vulgaris	Incurved	ICRISAT core
11	IE3449	UK	Vulgaris	Incurved	ICRISAT core
12	IE3135	India	Vulgaris	Digitata	ICRISAT core
13	IE4024	Uganda	Vulgaris	Incurved	HRD ICRISAT core & VGPA ICRISAT core
14	IE4984	Uganda	Vulgaris	Incurved	ICRISAT core
15	IE5123	India	Vulgaris	Digitata	ICRISAT core
16	IE3340	Zimbabwe	Vulgaris	Digitata	AICSMIP ICRISAT core- PLHT
17	IE3827	Uganda	Plana	Confundere	ICRISAT core
18	IE3628	Uganda	Plana	Confundere	AICSMIP ICRISAT core- Grain yield+BM+calcium+PT
19	IE2760	Malawi	Plana	Confundere	ICRISAT core
20	IE3291	Zimbabwe	Vulgaris	Digitata	ICRISAT core
21	IE6280	Zimbabwe	Vulgaris	Incurvata	ICRISAT core
22	IE4425	India	Vulgaris	Incurvata	ICRISAT core
23	IE5862	Nepal	Compact	NA	VG Plant aspect sICRISAT core and ICN
24	IE6421	Uganda	Vulgaris	Digitata	ICRISAT core
25	IE2452	Kenya	Vulgaris	Digitata	ICRISAT core
26	IE4801	India	Vulgaris	Incurved	ICRISAT core
27	IE3000	India	Vulgaris	Incurvata	ICRISAT core
28	IE4108	Uganda	Plana	Confundere	HRD ICRISAT core & VGPA ICRISAT core
29	IE2657	Malawi	Vulgaris	Digitata	AICSMIP ICRISAT core-
30	IE49	India	Vulgaris	Incurved	AICSMIP ICRISAT core- Yield+HI
31	IE3993	Uganda	Compact	NA	Replaced in ICRISAT core with FAO designated
32	IE4711	Burundi	Africa	NA	ICRISAT core-AICSMIP ICRISAT core- 1000-GW
33	IE971	Unknown	Vulgaris	Digitata	AICSMIP ICRISAT core-
34	IE2187	India	Vulgaris	Incurved	ICRISAT core
35	IE4653	Zimbabwe	Compact	NA	Range
36	IE6488	Uganda	Plana	Confundere	Replaced in ICRISAT core with FAO designated
37	IE5112	India	Compacta	NA	ICRISAT core
38	IE3913	Uganda	Plana	Confundere	VG Plant aspect sICRISAT core and ICN
39	IE4957	Uganda	Compacta	NA	VG Plant aspect sICRISAT core and ICN
40	IE3475	India	Vulgaris	Incurved	ICRISAT core
41	IE2954	Malawi	Elongata	Laxa	AICSMIP ICRISAT core- 1000-GW+calcium+FL
42	IE858	India	Vulgaris	Incurved	AICSMIP ICRISAT core-

43	IE3821	Uganda	Compacta	NA	ICRISAT core
44	IE3128	India	Vulgaris	Digitata	VG Plant aspect sICRISAT core and ICN
45	IE5525	Nepal	Elongata	Sparse	ICRISAT core
46	IE6221	Nepal	Vulgaris	Stelleta	ICRISAT core
47	IE4586	Zimbabwe	Compacta	NA	VG Plant aspect sICRISAT core and ICN
48	IE4646	Zimbabwe	Plana	Confundere	ICRISAT core
49	IE3111	India	Vulgaris	Incurved	ICRISAT core
50	IE5390	Kenya	Vulgaris	Stelleta	ICRISAT core
51	IE6294	Zimbabwe	Vulgaris	Incurved	ICRISAT core
52	IE4084	Uganda	Plana	Confundere	HRD ICRISAT core & VGPA ICRISAT core
53	IE3780	Uganda	Vulgaris	Digitata	ICRISAT core
54	IE5421	Kenya	Plana	Confundere	ICRISAT core
55	IE454	India	Plana	Grandig	AICSMIP ICRISAT core- Grain yield
56	IE633	India	Vulgaris	Incurved	ICRISAT core
57	IE2088	India	Vulgaris	Digitata	ICRISAT core
58	IE2275	India	Vulgaris	Stelleta	AICSMIP ICRISAT core- Grain yield+plht
59	IE3706	Uganda	Plana	Confundere	AICSMIP ICRISAT core- 1000-GW+SW+BM
60	IE2350	Kenya	Plana	Confundere	ICRISAT core
61	IE5320	India	Compacta	NA	ICRISAT core
62	IE6332	Zimbabwe	Vulgaris	Digitata	ICRISAT core
63	IE3483	Kenya	Vulgaris	Digitata	AICSMIP ICRISAT core- 1000-GW+HI+calcium
64	IE927	Uganda	Plana	Confundere	AICSMIP ICRISAT core- 1000-GW+HI
65	IE2881	Zambia	Compacta	NA	HRD ICRISAT core & VGPA ICRISAT core
66	IE4062	Uganda	Vulgaris	Incurved	HRD ICRISAT core & VGPA ICRISAT core
67	IE5845	Nepal	Vulgaris	Incurved	ICRISAT core
68	IE4186	Uganda	Plana	Confundere	HRD ICRISAT core & VGPA ICRISAT core
69	IE6025	Nepal	Elongata	Sparse	ICRISAT core
70	IE3038	India	Vulgaris	Liliaceae	ICRISAT core
71	IE4808	India	Vulgaris	Liliaceae	More finger width
72	IE3653	Uganda	Compacta	NA	VG Plant aspect sICRISAT core and ICN
73	IE2091	India	Vulgaris	Digitata	ICRISAT core
74	IE6167	Nepal	Vulgaris	Stelleta	ICRISAT core
75	IE4121	Uganda	Plana	Confundere	ICRISAT core
76	IE196	India	Vulgaris	Stelleta	ICRISAT core
77	IE2380	Kenya	Plana	Confundere	HRD ICRISAT core & VGPA ICRISAT core
78	IE9	India	Vulgaris	Incurved	ICRISAT core
79	IE798	India	Elongata	Laxa	AICSMIP ICRISAT core-
80	IE2534	Kenya	Plana	Confundere	HRD ICRISAT core & VGPA ICRISAT core
81	IE5584	Nepal	Vulgaris	Digitata	ICRISAT core
82	IE2636	Malawi	Vulgaris	Digitata	AICSMIP ICRISAT core- G Ca
83	IE5877	Nepal	Compacta	NA	VG Plant aspect sICRISAT core and ICN
84	IE2534	Kenya	Plana	Confundere	HRD ICRISAT core & VGPA ICRISAT core
85	IE680	India	Vulgaris	Incurved	ICRISAT core
86	IE3482	Kenya	Vulgaris	Digitata	Replaced in ICRISAT core with FAO designated
87	IE2574	Kenya	Plana	Confundere	ICRISAT core
88	IE2729	Malawi	Vulgaris	Digitata	Replaced in ICRISAT core with FAO designated

89	IE4578	Zimbabwe	Vulgaris	Incurved	Replaced in ICRISAT core with FAO designated
90	IE5239	India	Vulgaris	Digitata	ICRISAT core
91	IE2354	Kenya	Compacta	NA	ICRISAT core
92	IE1009	Unknown	Vulgaris	Digitata	Replaced in ICRISAT core with FAO designated
93	IE4972	Uganda	Plana	Confundere	ICRISAT core
94	IE4092	Uganda	Vulgaris	Stelleta	HRD ICRISAT core & VGPA ICRISAT core
95	IE2288	India	Vulgaris	Incurved	ICRISAT core
96	IE4022	Uganda	Vulgaris	Incurved	HRD ICRISAT core & VGPA ICRISAT core
97	IE6484	Uganda	Vulgaris	Digitata	Replaced in ICRISAT core with FAO designated
98	IE4594	Zimbabwe	Compacta	NA	VG Plant aspect sICRISAT core and ICN
99	IE924	Uganda	Vulgaris	Incurved	AICSMIP ICRISAT core- 1000-GW
100	IE4060	Uganda	Vulgaris	Digitata	HRD ICRISAT core & VGPA ICRISAT core
101	IE563	India	Vulgaris	Liliaceae	ICRISAT core
102	IE4734	India	Vulgaris	Digitata	ICRISAT core
103	IE3446	Zimbabwe	Plana	Confundere	ICRISAT core
104	IE2754	Malawi	Vulgaris	Incurved	AICSMIP ICRISAT core- PlLHT
105	IE2838	India	Vulgaris	Stelleta	ICRISAT core
106	IE2789	Malawi	Elongata	Laxa	Long FL
107	IE6313	Zimbabwe	Vulgaris	Incurved	ICRISAT core
108	IE2528	Kenya	Vulgaris	Digitata	AICSMIP ICRISAT core- SW
109	IE2909	Zambia	Plana	Confundere	ICRISAT core
110	IE2591	America	Plana	Confundere	ICRISAT core
111	IE2710	Malawi	Plana	Confundere	ICRISAT core
112	IE2957	Germany	Vulgaris	Liliaceae	ICRISAT core
113	IE2765	Malawi	Plana	Confundere	AICSMIP ICRISAT core- Straw weigtht+BM
114	IE5350	Kenya	Vulgaris	Stellate	Replaced in ICRISAT core with FAO designated
115	IE4070	Uganda	Vulgaris	Incurved	ICRISAT core
116	IE5494	Unknown	Plana	Confundere	Replaced in ICRISAT core with FAO designated
117	IE2689	Malawi	Vulgaris	Digitata	ICRISAT core
118	IE2299	India	Vulgaris	Digitata	ICRISAT core
119	IE3766	Uganda	Plana	Confundere	VG Plant aspect sICRISAT core and ICN
120	IE5066	Senegal	Vulgaris	Incurved	ICRISAT core
121	IE3974	Uganda	Plana	Confundere	Replaced in ICRISAT core with FAO designated
122	IE2903	Zambia	Compacta	NA	VG Plant aspect sICRISAT core and ICN
123	IE4274	Zimbabwe	Vulgaris	Digitata	ICRISAT core
124	IE6082	Nepal	Plana	Confundere	ICRISAT core
125	IE2212	India	Elongata	Rectusa	ICRISAT core
126	IE3652	Uganda	Plana	Confundere	VG Plant aspect sICRISAT core and ICN
127	IE431	India	Vulgaris	Digitata	Early flowering
128	IE5147	India	Compacta	NA	VG Plant aspect sICRISAT core and ICN
129	IE2047	India	Vulgaris	Digitata	ICRISAT core
130	IE5417	Kenya	Plana	Confundere	VG Plant aspect sICRISAT core and ICN
131	IE4230	Zimbabwe	Vulgaris	Incurved	HRD ICRISAT core & VGPA ICRISAT core
132	IE4147	Uganda	Vulgaris	Incurved	ICRISAT core
133	IE3176	Zambia	Vulgaris	Digitata	AICSMIP ICRISAT core- Calcium
134	IE4680	India	Vulgaris	Stelleta	VG Plant aspect sICRISAT core and ICN

135	IE546	India	Vulgaris	Liliaceae	ICRISAT core
136	IE2748	Malawi	Plana	Confundere	AICSMIP ICRISAT core-
137	IE2014	India	Seriata	Seriata	ICRISAT core
138	IE2703	Malawi	Incurved	Incurved	Replaced in ICRISAT core with FAO designated
139	IE106	India	Lilaca	Liliaceae	Early flowering
140	IE4110	Uganda	Confundere	Confundere	ICRISAT core
141	IE24	India	reclusa	Recluse	AICSMIP ICRISAT core- FL
142	IE4700	India	Incurved	Incurved	AICSMIP ICRISAT core- 1000-GW+Grain yield+SW+bioma
143	IE6514	Zimbabwe	Incurved	Incurved	ICRISAT core
144	IE3753	Uganda	Incurved	Incurved	ICRISAT core
145	IE2254	India	Vulgaris	Incurved	AICSMIP ICRISAT core- 1000-Grain weigth
146	IE2393	Kenya	Compacta	NA	ICRISAT core
147	IE5186	India	Plana	Confundere	ICRISAT core
148	IE2183	India	Vulgaris	Digitata	ICRISAT core
149	IE6472	Uganda	Vulgaris	Incurved	ICRISAT core
150	IE3543	India	Vulgaris	Incurved	ICRISAT core
151	IE6533	Nigeria	Elongata	Sparsa	ICRISAT core
152	IE2332	Kenya	Plana	Confundere	VG Plant aspect sICRISAT core and ICN
153	IE2818	Nepal	Elongata	Liliaceae	ICRISAT core
154	IE4401	Zimbabwe	Vulgaris	Digitata	ICRISAT core
155	IE5065	Malawi	Vulgaris	Incurved	ICRISAT core
156	IE2746	Malawi	Vulgaris	Digitata	AICSMIP ICRISAT core- Finger number
157	IE3278	Zimbabwe	Vulgaris	Digitata	ICRISAT core
158	IE3930	Uganda	Compacta	NA	VG Plant aspect sICRISAT core and ICN
159	IE4011	Uganda	Plana	Confundere	HRD ICRISAT core & VGPA ICRISAT core
160	IE5023	Uganda	Compacta	NA	Replaced in ICRISAT core with FAO designated
161	IE2860	Zambia	Compacta	NA	HRD ICRISAT core & VGPA ICRISAT core
162	IE4126	Uganda	Vulgaris	Stelleta	HRD ICRISAT core & VGPA ICRISAT core
163	IE6447	Uganda	Compacta	NA	ICRISAT core
164	IE2686	Malawi	Vulgaris	Digitata	AICSMIP ICRISAT core- FL
165	IE5378	Kenya	Vulgaris	Digitata	Replaced in ICRISAT core with FAO designated
166	IE5179	India	Vulgaris	Stelleta	ICRISAT core
167	IE5812	Nepal	Vulgaris	Incurved	ICRISAT core
168	IE3667	Uganda	Plana	Confundere	VG Plant aspect sICRISAT core and ICN
169	IE821	India	Vulgaris	Liliaceae	ICRISAT core
170	IE2407	Kenya	Vulgaris	Digitata	Replaced in ICRISAT core with FAO designated
171	IE5424	Kenya	Plana	Confundere	VG Plant aspect sICRISAT core and ICN
172	IE3855	Uganda	Vulgaris	Digitata	VG Plant aspect sICRISAT core and ICN
173	IE2368	Kenya	Plana	Confundere	Replaced in ICRISAT core with FAO designated
174	IE2604	Malawi	Elongata	Laxa	Long FL
175	IE777	India	Plana	Grandigluma	AICSMIP ICRISAT core-
176	IE5377	Kenya	Vulgaris	Incurved	Replaced in ICRISAT core with FAO designated
177	IE797	India	Elongata	Laxa	AICSMIP ICRISAT core-
178	IE3238	Zimbabwe	Vulgaris	Digitata	ICRISAT core
179	IE2598	Malawi	Elongata	Laxa	AICSMIP ICRISAT core- FL
180	IE3636	Uganda	Plana	Confundere	Replaced in ICRISAT core with FAO designated

181	IE2868	Zambia	Compacta	NA	ICRISAT core
182	IE4329	Zimbabwe	Vulgaris	Incurved	ICRISAT core
183	IE2888	Zambia	Compacta	NA	AICSMIP ICRISAT core-
184	IE501	India	Vulgaris	Stelleta	ICRISAT core
185	IE6229	Nepal	Vulgaris	Incurved	ICRISAT core
186	IE2606	Malawi	Vulgaris	Incurved	ICRISAT core
187	IE5281	India	Vulgaris	Digitata	VG Plant aspect sICRISAT core and ICN
188	IE4112	Uganda	Vulgaris	Incurved	HRD ICRISAT core & VGPA ICRISAT core
189	IE2489	Kenya	Plana	Confundere	Replaced in ICRISAT core with FAO designated
190	IE991	Unknown	Plana	Confundere	ICRISAT core
191	IE2704	Malawi	Plana	Seriata	ICRISAT core
192	IE2694	Malawi	Plana	Grandigluma	AICSMIP ICRISAT core- Grain yield
193	IE4057	Uganda	Plana	Seriata	ICRISAT core
194	IE3248	Zimbabwe	Vulgaris	Digitata	ICRISAT core
195	IE2777	Malawi	Vulgaris	Digitata	VG Plant aspect sICRISAT core and ICN
196	IE2523	Kenya	Compacta	NA	ICRISAT core
197	IE5345	Kenya	Compacta	NA	VG Plant aspect sICRISAT core and ICN
198	IE847	India	Vulgaris	Stelleta	ICRISAT core+AICSMIP ICRISAT core- Finger blast
199	IE3533	Kenya	Vulgaris	Digitata	ICRISAT core
200	IE2781	Malawi	Elongata	Laxa	AICSMIP ICRISAT core- G Ca+FL
201	IE2821	Nepal	Compacta	NA	ICRISAT core
202	IE2437	Kenya	Plana	Confundere	ICRISAT core
203	IE4339	Zimbabwe	Plana	Digitata	ICRISAT core
204	IE2337	Kenya	Plana	Confundere	AICSMIP ICRISAT core- Neck blast
205	IE3287	Zimbabwe	Vulgaris	Incurved	ICRISAT core
206	IE5208	India	Compacta	NA	ICRISAT core
207	IE189	India	Vulgaris	Stelleta	AICSMIP ICRISAT core- FL
208	IE6020	Nepal	Vulgaris	Stelleta	ICRISAT core
209	IE5429	Kenya	Compacta	NA	VG Plant aspect sICRISAT core and ICN
210	IE4565	Zimbabwe	Elongata	Recluse	ICRISAT core
211	IE3028	India	Vulgaris	Stelleta	ICRISAT core
212	IE3612	Unknown	Vulgaris	Incurved	ICRISAT core
213	IE3537	Kenya	Plana	Seriata	Replaced in ICRISAT core with FAO designated
214	IE5475	India	Plana	Confundere	ICRISAT core
215	IE3744	Uganda	Plana	Confundere	VG Plant aspect sICRISAT core and ICN
216	IE3196	Tanzania	Vulgaris	Digitata	ICRISAT core
217	IE5689	Nepal	Vulgaris	Incurved	ICRISAT core
218	IE5037	Zimbabwe	Vulgaris	Incurved	Replaced in ICRISAT core with FAO designated
219	IE4136	Uganda	Vulgaris	Digitata	HRD ICRISAT core & VGPA ICRISAT core
220	IE6396	Zimbabwe	Vulgaris	Digitata	ICRISAT core
221	IE3723	Uganda	Plana	Confundere	ICRISAT core
222	IE2997	India	Vulgaris	Incurved	Replaced in ICRISAT core with FAO designated
223	IE4709	Burundi	*	*	ICRISAT core
224	IE4113	Uganda	Vulgaris	Incurved	HRD ICRISAT core & VGPA ICRISAT core
225	IE3654	Uganda	Vulgaris	Incurved	ICRISAT core
226	IE5161	India	Plana	Confundere	VG Plant aspect sICRISAT core and ICN

227	IE4296	Zimbabwe	Vulgaris	Digitata	ICRISAT core
228	IE6300	Zimbabwe	Vulgaris	Digitata	ICRISAT core
229	IE1034	Unknown	Vulgaris	Liliaceae	Replaced in ICRISAT core with FAO designated
230	IE2425	Kenya	Plana	Confundere	ICRISAT core
231	IE2568	Kenya	Vulgaris	Incurved	ICRISAT core
232	IE2367	Kenya	Vulgaris	Digitata	HRD ICRISAT core & VGPA ICRISAT core
233	IE3745	Uganda	Vulgaris	Incurved	Replaced in ICRISAT core with FAO designated
234	IE6510	Zimbabwe	Vulgaris	Incurved	Replaced in ICRISAT core with FAO designated
235	IE3635	Uganda	Plana	Confundere	Replaced in ICRISAT core with FAO designated
236	IE4630	Zimbabwe	Compacta	NA	VG Plant aspect sICRISAT core and ICN
237	IE2532	Kenya	Plana	Confundere	HRD ICRISAT core & VGPA ICRISAT core
238	IE6154	Nepal	Vulgaris	Incurved	ICRISAT core
239	IE2486	Kenya	Plana	Confundere	ICRISAT core
240	IE4287	Zimbabwe	Plana	Confundere	ICRISAT core
241	IE2910	Zambia	Vulgaris	Digitata	AICSMIP ICRISAT core- BM+HI
242	IE6451	Uganda	Africa	NA	Long FL
243	IE5043	Zimbabwe	Vulgaris	Incurved	Replaced in ICRISAT core with FAO designated
244	IE4679	India	Vulgaris	Digitata	VG Plant aspect sICRISAT core and ICN
245	IE4143	Uganda	Plana	Confundere	HRD ICRISAT core & VGPA ICRISAT core
246	IE5193	India	Vulgaris	Incurved	ICRISAT core
247	IE3101	India	Vulgaris	Incurved	ICRISAT core
248	IE143	India	Vulgaris	Incurved	VG Plant aspect sICRISAT core and ICN
249	IE2677	Malawi	Compacta	NA	AICSMIP ICRISAT core- Finger number
250	IE6495	Uganda	Vulgaris	Incurved	ICRISAT core
251	IE3187	Zambia	Vulgaris	Digitata	VG Plant aspect sICRISAT core and ICN
252	IE4476	Zimbabwe	Sparsa	NA	ICRISAT core
253	IE3559	India	Vulgaris	Incurved	ICRISAT core
254	IE2691	Malawi	Vulgaris	Digitata	AICSMIP ICRISAT core-
255	IE4120	Uganda	Vulgaris	Digitata	HRD ICRISAT core & VGPA ICRISAT core
256	IE336	India	Vulgaris	Stelleta	Early flowering
257	IE4443	Cameroon	*	*	ICRISAT core
258	IE2379	Kenya	Plana	Confundere	ICRISAT core
259	IE629	India	Vulgaris	Incurved	AICSMIP ICRISAT core- Yield+PT
260	IE5813	Nepal	Elongata	Sparse	ICRISAT core
261	IE2561	Kenya	Compacta	NA	Replaced in ICRISAT core with FAO designated
262	IE6440	Uganda	Vulgaris	Incurved	ICRISAT core
263	IE2872	Zambia	Vulgaris	Digitata	ICRISAT core
264	IE2410	Kenya	Compacta	NA	HRD ICRISAT core & VGPA ICRISAT core
265	IE2713	Malawi	Elongata	Reclusa	ICRISAT core
266	IE5591	Nepal	Elongata	Sparse	ICRISAT core
267	IE5107	Zimbabwe	Elongata	Reclusa	ICRISAT core
268	IE5339	Kenya	Vulgaris	Stelleta	Replaced in ICRISAT core with FAO designated
269	IE3317	Zimbabwe	Vulgaris	Digitata	ICRISAT core
270	IE2581	Italy	Plana	Confundere	ICRISAT core
271	IE678	India	Vulgaris	Incurved	ICRISAT core
272	IE613	India	Vulgaris	Digitata	AICSMIP ICRISAT core- PlHT

273	IE2873	Zambia	Vulgaris	Incurved	Replaced in ICRISAT core with FAO designated
274	IE726	India	Vulgaris	Incurved	AICSMIP ICRISAT core-
275	IE2702	Malawi	Plana	Confundere	AICSMIP ICRISAT core-
276	IE2502	Kenya	Plana	Confundere	ICRISAT core
277	IE2030	India	Vulgaris	Incurved	ICRISAT core
278	IE4257	Zimbabwe	Vulgaris	Digitata	ICRISAT core
279	IE3334	Zimbabwe	Vulgaris	Digitata	ICRISAT core
280	IE2378	Kenya	Compacta	NA	AICSMIP ICRISAT core-
281	IE2744	Malawi	Vulgaris	Digitata	AICSMIP ICRISAT core- Straw weigth+BM
282	IE4963	Uganda	Compacta	NA	ICRISAT core
283	IE3104	India	Vulgaris	Incurved	ICRISAT core
284	IE234	India	Vulgaris	Digitata	AICSMIP ICRISAT core- Grain yield
285	IE804	India	Vulgaris	Digitata	AICSMIP ICRISAT core-
286	IE4658	India	Plana	Grandigluma	ICRISAT core
287	IE6055	Nepal	Vulgaris	Incurved	ICRISAT core
288	IE6512	Zimbabwe	Vulgaris	Digitata	Replaced in ICRISAT core with FAO designated
289	IE2573	Kenya	Plana	Grandigluma	ICRISAT core
290	IE5022	Uganda	Plana	Confundere	VG Plant aspect sICRISAT core and ICN
291	IE4131	Uganda	Vulgaris	Incurved	HRD ICRISAT core & VGPA ICRISAT core
292	IE6252	Zimbabwe	Vulgaris	Incurved	ICRISAT core
293	IE2968	Zambia	Compacta	NA	AICSMIP ICRISAT core-
294	IE3073	India	Digitata	Rectuse	ICRISAT core
295	IE4568	Zimbabwe	Compacta	NA	VG Plant aspect sICRISAT core and ICN
296	IE2108	India	Elongata	Rectuse	ICRISAT core
297	IE2932	Malawi	Vulgaris	Digitata	AICSMIP ICRISAT core- 1000-GW
298	IE4376	Zimbabwe	Compacta	NA	VG Plant aspect sICRISAT core and ICN
299	IE2827	India	Vulgaris	Digitata	VG Plant aspect sICRISAT core and ICN
300	IE2413	Kenya	Vulgaris	Digitata	Replaced in ICRISAT core with FAO designated
301	IE3119	India	Vulgaris	Incurved	Range
302	IE2169	India	Vulgaris	Liliaceae	ICRISAT core
303	IE2645	Malawi	Elongata	Laxa	ICRISAT core
304	IE3077	India	Vulgaris	Incurved	ICRISAT core
305	IE5492	Unknown	Plana	Confundere	Replaced in ICRISAT core with FAO designated
306	IE2938	Malawi	Plana	Confundere	ICRISAT core
307	IE4118	Uganda	Plana	Confundere	ICRISAT core
308	IE2065	India	Vulgaris	Incurved	ICRISAT core
309	IE4023	Uganda	Vulgaris	Incurved	HRD ICRISAT core & VGPA ICRISAT core
310	IE3738	Uganda	Vulgaris	Shortopen	ICRISAT core
311	IE2217	India	Vulgaris	Stelleta	ICRISAT core
312	IE3045	India	Vulgaris	Liliaceae	ICRISAT core
313	IE739	India	Vulgaris	Liliaceae	Replaced in ICRISAT core with FAO designated
314	IE3510	Kenya	Plana	Confundere	ICRISAT core
315	IE6165	Nepal	Vulgaris	Incurved	ICRISAT core
316	IE6420	Uganda	Plana	Confundere	More finger width
317	IE4462	Tanzania	Plana	Confundere	Replaced in ICRISAT core with FAO designated
318	IE4083	Uganda	Plana	Confundere	HRD ICRISAT core & VGPA ICRISAT core

319	IE2732	Malawi	Elongata	Reclusa	ICRISAT core
320	IE3070	India	Vulgaris	Liliaceae	ICRISAT core
321	IE2293	India	Vulgaris	Liliaceae	ICRISAT core
322	IE4821	India	Vulgaris	Digitata	VG Plant aspect sICRISAT core and ICN
323	IE4383	Zimbabwe	Plana	Confundere	ICRISAT core
324	IE2312	India	Elongata	Sparsa	ICRISAT core
325	IE2525	Kenya	Compacta	NA	HRD ICRISAT core & VGPA ICRISAT core
326	IE872	Mexico	Vulgaris	Digitata	ICRISAT core
327	IE3062	India	Plana	Confundere	ICRISAT core
328	IE2676	Malawi	Elongata	Reclusa	AICSMIP ICRISAT core- Finger number
329	IE5495	Unknown	Plana	Confundere	ICRISAT core
330	IE6464	Uganda	Plana	Confundere	Replaced in ICRISAT core with FAO designated
331	IE6436	Uganda	Plana	Confundere	Replaced in ICRISAT core with FAO designated
332	IE4716	India	Vulgaris	Digitata	VG Plant aspect sICRISAT core and ICN
333	IE4181	Uganda	Compacta	NA	ICRISAT core
334	IE2235	India	Vulgaris	Incurved	ICRISAT core
335	IE5005	Uganda	Plana	C	More finger width
336	IE4649	Zimbabwe	Vulgaris	Digitata	Replaced in ICRISAT core with FAO designated
337	IE2684	Malawi	Vulgaris	Digitata	AICSMIP ICRISAT core- 1000-GW+grain yield+FL
338	IE3134	India	Vulgaris	Incurved	ICRISAT core
339	IE3790	Uganda	Compacta	NA	VG Plant aspect sICRISAT core and ICN
340	IE5406	Kenya	Plana	Confundere	VG Plant aspect sICRISAT core and ICN
341	IE2322	India	Elongata	Laxa	ICRISAT core
342	IE4688	India	Vulgaris	Liliaceae	ICRISAT core
343	IE3203	Tanzania	Vulgaris	Digitata	AICSMIP ICRISAT core- PT
344	IE2779	Malawi	Elongata	Laxa	AICSMIP ICRISAT core- FL
345	IE808	India	Vulgaris	Incurved	ICRISAT core
346	IE2440	Kenya	Compacta	NA	ICRISAT core
347	IE174	India	Vulgaris	Liliaceae	Early flowering
348	IE3825	Uganda	Vulgaris	Digitata	VG Plant aspect sICRISAT core and ICN
349	IE4145	Uganda	Plana	Confundere	HRD ICRISAT core & VGPA ICRISAT core
350	IE2921	Malawi	Shortopen	NA	ICRISAT core
351	IE2495	Kenya	Plana	Confundere	Replaced in ICRISAT core with FAO designated
352	IE3066	India	Vulgaris	Stelleta	ICRISAT core
353	IE593	India	Vulgaris	Stelleta	ICRISAT core
354	IE4797	Maldives	Vulgaris	Liliaceae	ICRISAT core
355	IE2365	Kenya	Plana	Confundere	HRD ICRISAT core & VGPA ICRISAT core
356	IE5198	India	Plana	Confundere	VG Plant aspect sICRISAT core and ICN
357	IE2594	Unknown	Vulgaris	Incurved	Replaced in ICRISAT core with FAO designated
358	IE3769	Uganda	Compacta	NA	ICRISAT core
359	IE5672	Nepal	Vulgaris	Digitata	ICRISAT core
360	IE4218	Burundi	Vulgaris	Incurved	ICRISAT core
361	IE3643	Uganda	Compacta	NA	VG Plant aspect sICRISAT core and ICN
362	IE3254	Zimbabwe	Vulgaris	Digitata	ICRISAT core
363	IE509	India	Vulgaris	Incurved	AICSMIP ICRISAT core-Early flowering
364	IE6358	Zimbabwe	Vulgaris	Digitata	ICRISAT core

365	IE2825	Tanzania	Vulgaris	Digitata	ICRISAT core
366	IE3901	Uganda	Vulgaris	Incurved	ICRISAT core
367	IE972	Unknown	Plana	Confundere	Replaced in ICRISAT core with FAO designated
368	IE5295	Zimbabwe	Vulgaris	Incurved	ICRISAT core
369	IE5416	Kenya	Plana	Confundere	VG Plant aspect sICRISAT core and ICN
370	IE3257	Zimbabwe	Compacta	NA	ICRISAT core
371	IE2551	Kenya	Vulgaris	Incurved	ICRISAT core
372	IE2504	Kenya	Plana	Confundere	Replaced in ICRISAT core with FAO designated
373	IE4491	Zimbabwe	Elongata	Reclusa	ICRISAT core
374	IE5597	Nepal	Vulgaris	Digitata	VG Plant aspect sICRISAT core and ICN
375	IE4911	Uganda	Plana	Confundere	ICRISAT core
376	IE3711	Uganda	Vulgaris	Digitata	AICSMIP ICRISAT core- Grain yield+SW+BM+productive till
377	IE3194	Tanzania	Compacta	NA	VG Plant aspect sICRISAT core and ICN
378	IE4975	Uganda	Plana	Confundere	VG Plant aspect sICRISAT core and ICN
379	IE3308	Zimbabwe	Vulgaris	Digitata	AICSMIP ICRISAT core- 1000-GW+finger number
380	IE2439	Kenya	Plana	Confundere	HRD ICRISAT core & VGPA ICRISAT core
381	IE4151	Uganda	Plana	Confundere	HRD ICRISAT core & VGPA ICRISAT core
382	IE4817	India	Vulgaris	Stelleta	ICRISAT core
383	IE2233	India	Vulgaris	Incurved	AICSMIP ICRISAT core-
384	IE6117	Nepal	Vulgaris	Digitata	ICRISAT core
385	IE406	India	Vulgaris	Incurved	AICSMIP ICRISAT core- Neck & finger blast disease
386	IE2179	India	Vulgaris	Digitata	Range
387	IE2399	Kenya	Vulgaris	Digitata	ICRISAT core
388	IE1023	Unknown	Vulgaris	Digitata	ICRISAT core
389	IE3489	Kenya	Vulgaris	Incurved	ICRISAT core
390	IE2669	Malawi	Vulgaris	Digitata	AICSMIP ICRISAT core- FL
391	IE2063	India	Vulgaris	Incurved	Range
392	IE588	India	Plana	Stelleta	ICRISAT core
393	IE6416	Uganda	Plana	Confundere	Replaced in ICRISAT core with FAO designated
394	IE2327	Kenya	Plana	Confundere	AICSMIP ICRISAT core-
395	IE3391	Zimbabwe	Vulgaris	Digitata	ICRISAT core
396	IE615	India	Vulgaris	Incurved	ICRISAT core
397	IE3129	India	Vulgaris	Digitata	AICSMIP ICRISAT core- Neck & finger blast disease
398	IE5169	India	Plana	Confundere	VG Plant aspect sICRISAT core and ICN
399	IE3339	Zimbabwe	Vulgaris	Digitata	Replaced in ICRISAT core with FAO designated
400	IE5362	Kenya	Plana	Confundere	Replaced in ICRISAT core with FAO designated
401	IE667	India	Vulgaris	Incurved	ICRISAT core
402	IE5009	Uganda	Vulgaris	Incurved	Replaced in ICRISAT core with FAO designated
403	IE2983	Sri Lanka	Compacta	NA	ICRISAT core
404	IE4125	Uganda	Vulgaris	Incurved	HRD ICRISAT core & VGPA ICRISAT core
405	IE2408	Kenya	Plana	Confundere	AICSMIP ICRISAT core-
406	IE2539	Kenya	Plana	Confundere	Replaced in ICRISAT core with FAO designated
407	IE2093	India	Vulgaris	Incurved	ICRISAT core
408	IE4759	India	Vulgaris	Stelleta	ICRISAT core
409	IE5336	Kenya	Plana	Confundere	VG Plant aspect sICRISAT core and ICN
410	IE2688	Malawi	Plana	Confundere	AICSMIP ICRISAT core- Grain yield+FL+PT

411	IE4403	Zimbabwe	Vulgaris	Digitata	ICRISAT core
412	IE4350	Zimbabwe	Vulgaris	Digitata	ICRISAT core
413	IE5491	Unknown	Vulgaris	Incurved	ICRISAT core
414	IE914	Uganda	Compacta	NA	Replaced in ICRISAT core with FAO designated-AICSMIP ICRISAT core-
415	IE3778	Uganda	Compacta	NA	VG Plant aspect sICRISAT core and ICN
416	IE4800	Maldives	Vulgaris	Incurved	More finger width
417	IE5206	India	Compacta	NA	VG Plant aspect sICRISAT core and ICN
418	IE2911	Zambia	Vulgaris	Incurved	ICRISAT core
419	IE5306	Zimbabwe	Vulgaris	Digitata	ICRISAT core
420	IE4919	Uganda	Compacta	NA	Range
421	IE3413	Zimbabwe	Vulgaris	Digitata	ICRISAT core
422	IE2345	Kenya	Plana	Confundere	Replaced in ICRISAT core with FAO designated
423	IE907	Uganda	Vulgaris	Digitata	AICSMIP ICRISAT core- Neck & finger blast disease
424	IE905	Uganda	Vulgaris	Digitata	Replaced in ICRISAT core with FAO designated
425	IE2564	Kenya	Compacta	NA	ICRISAT core
426	IE4755	India	Vulgaris	Stelleta	ICRISAT core
427	IE3699	Uganda	Vulgaris	Digitata	AICSMIP ICRISAT core- 1000-GW+grain yield
428	IE2743	Malawi	Vulgaris	Incurved	Replaced in ICRISAT core with FAO designated
429	IE3604	India	Vulgaris	Stelleta	ICRISAT core
430	IE4081	Uganda	Elongata	Reclusa	HRD ICRISAT core & VGPA ICRISAT core
431	IE815	India	Vulgaris	Stelleta	AICSMIP ICRISAT core- Grain yield
432	IE5314	Zambia	Vulgaris	Digitata	ICRISAT core
433	IE3657	Uganda	Vulgaris	Incurved	ICRISAT core
434	IE6127	Nepal	Vulgaris	Incurved	ICRISAT core
435	IE5383	Kenya	Vulgaris	Incurved	ICRISAT core
436	IE3470	India	Vulgaris	Stelleta	ICRISAT core
437	IE795	India	Vulgaris	Stelleta	AICSMIP ICRISAT core- Grain yield
438	IE5647	Nepal	Vulgaris	Stelleta	ICRISAT core
439	IE5782	Nepal	Compacta	NA	ICRISAT core
440	IE6326	Zimbabwe	Vulgaris	Digitata	ICRISAT core
441	IE5090	Zimbabwe	Vulgaris	Incurved	ICRISAT core
442	IE5008	Uganda	Compacta	NA	Replaced in ICRISAT core with FAO designated
443	IE4725	India	Vulgaris	Digitata	VG Plant aspect sICRISAT core and ICN
444	IE413	India	Vulgaris	Incurved	AICSMIP ICRISAT core- 1000-GW
445	IE5733	Nepal	Vulgaris	Digitata	ICRISAT core
446	IE2503	Kenya	Plana	Confundere	ICRISAT core
447	IE2500	Kenya	Compacta	NA	ICRISAT core
448	IE5794	Nepal	Vulgaris	Digitata	ICRISAT core
449	IE5748	Nepal	Elongata	Sparsa	ICRISAT core
450	IE1008	Unknown	Vulgaris	Digitata	Replaced in ICRISAT core with FAO designated
451	IE6013	Nepal	Vulgaris	Liliaceae	ICRISAT core
452	IE2586	Italy	Vulgaris	Digitata	ICRISAT core
453	IE4930	Uganda	Vulgaris	Incurved	Replaced in ICRISAT core with FAO designated
454	IE6122	Nepal	Vulgaris	Incurved	ICRISAT core
455	IE4887	India	Vulgaris	Incurved	ICRISAT core

456	IE3614	Unknown	Plana	Confundere	ICRISAT core
457	IE2396	Kenya	Plana	Confundere	AICSMIP ICRISAT core- SW+BM+PT
458	IE2370	Kenya	Vulgaris	Digitata	AICSMIP ICRISAT core- 1000-GW+neck blast+FL
459	IE2223	India	Elongata	Reclusa	ICRISAT core
460	IE2340	Kenya	Compacta	NA	Replaced in ICRISAT core with FAO designated
461	IE6033	Nepal	Vulgaris	Incurved	ICRISAT core
462	IE2698	Malawi	Compacta	NA	AICSMIP ICRISAT core-
463	IE5033	Zimbabwe	Vulgaris	Digitata	VG Plant aspect sICRISAT core and ICN
464	IE3952	Uganda	Plana	Confundere	ICRISAT core
465	IE5876	Nepal	Compacta	NA	VG Plant aspect sICRISAT core and ICN
466	IE3940	Uganda	Compacta	NA	VG Plant aspect sICRISAT core and ICN
467	IE3663	Uganda	Compacta	NA	ICRISAT core
468	IE5364	Kenya	Vulgaris	Stelleta	ICRISAT core
469	IE3255	Zimbabwe	Vulgaris	Digitata	Replaced in ICRISAT core with FAO designated
470	IE2992	Zambia	Compacta	NA	VG Plant aspect sICRISAT core and ICN
471	IE4035	Uganda	Vulgaris	Incurved	ICRISAT core
472	IE3600	India	Vulgaris	Digitata	VG Plant aspect sICRISAT core and ICN
473	IE6352	Zimbabwe	Vulgaris	Incurved	Replaced in ICRISAT core with FAO designated
474	IE2790	Malawi	Elongata	Laxa	ICRISAT core
475	IE5457	Kenya	Vulgaris	Incurved	ICRISAT core
476	IE4563	Zimbabwe	Vulgaris	Incurved	ICRISAT core
477	IE2331	Kenya	Plana	Confundere	AICSMIP ICRISAT core- Neck & finger blast disease+calcium+finger lengt
478	IE2540	Kenya	Vulgaris	Digitata	HRD ICRISAT core & VGPA ICRISAT core
479	IE3120	India	Vulgaris	Incurved	ICRISAT core
480	IE3861	Uganda	Vulgaris	Incurved	Replaced in ICRISAT core with FAO designated
481	IE929	Uganda	Vulgaris	Digitata	AICSMIP ICRISAT core- G Ca
482	IE4414	India	Vulgaris	Digitata	ICRISAT core
483	IE5349	Kenya	Vulgaris	Stelleta	ICRISAT core
484	IE3885	Uganda	Longopen	NA	VG Plant aspect sICRISAT core and ICN
485	IE2875	Zambia	Plana	Confundere	HRD ICRISAT core & VGPA ICRISAT core
486	IE6255	Zimbabwe	Vulgaris	Incurved	ICRISAT core
487	IE5106	Zimbabwe	Vulgaris	Incurved	ICRISAT core
488	IE641	India	Vulgaris	Incurved	AICSMIP ICRISAT core-
489	IE5537	Nepal	Vulgaris	Incurved	ICRISAT core
490	IE4128	Uganda	Vulgaris	Stelleta	HRD ICRISAT core & VGPA ICRISAT core
491	IE6240	Zimbabwe	Vulgaris	Incurved	ICRISAT core
492	IE4950	Uganda	Vulgaris	Incurved	Replaced in ICRISAT core with FAO designated
493	IE2741	Malawi	Plana	Confundere	AICSMIP ICRISAT core- Grain yield+SW+BM+calcium+product
494	IE3947	Uganda	Vulgaris	Digitata	ICRISAT core
495	IE5140	India	Plana	Confundere	VG Plant aspect sICRISAT core and ICN
496	IE2855	Zambia	Plana	Confundere	AICSMIP ICRISAT core-
497	IE4340	Zimbabwe	Plana	Confundere	ICRISAT core
498	IE4585	Zimbabwe	Compacta	NA	ICRISAT core
499	IE2587	Italy	Vulgaris	Digitata	ICRISAT core
500	IE990	Unknown	Vulgaris	Digitata	AICSMIP ICRISAT core- Grain yield

501	IE4135	Uganda	Vulgaris	Digitata	HRD ICRISAT core & VGPA ICRISAT core
502	IE2652	Malawi	Vulgaris	Incurved	ICRISAT core
503	IE2139	India	Plana	Confundere	ICRISAT core
504	IE4909	Uganda	Plana	Confundere	ICRISAT core
505	IE51	India	Plana	Seriata	AICSMIP ICRISAT core- Yield+PT
506	IE4795	Zimbabwe	Vulgaris	Digitata	ICRISAT core
507	IE5182	India	Elongata	Reclusa	ICRISAT core
508	IE2836	India	Vulgaris	Digitata	VG Plant aspect sICRISAT core and ICN
509	IE5419	Kenya	Compacta	NA	ICRISAT core
510	IE4889	India	Compacta	NA	VG Plant aspect sICRISAT core and ICN
511	IE4059	Uganda	Vulgaris	Incurved	HRD ICRISAT core & VGPA ICRISAT core
512	IE2430	Kenya	Vulgaris	Digitata	ICRISAT core
513	IE4570	Zimbabwe	Plana	Confundere	ICRISAT core
514	IE2683	Malawi	Compacta	NA	HRD ICRISAT core & VGPA ICRISAT core
515	IE3357	Zimbabwe	Vulgaris	Digitata	Replaced in ICRISAT core with FAO designated
516	IE2884	Zambia	Compacta	NA	ICRISAT core
517	IE5379	Kenya	Plana	Confundere	VG Plant aspect sICRISAT core and ICN
518	IE4986	Uganda	Compacta	NA	VG Plant aspect sICRISAT core and ICN
519	IE2971	Sri Lanka	Vulgaris	Incurved	ICRISAT core
520	IE2999	India	Vulgaris	Incurved	ICRISAT core
521	IE3727	Uganda	Vulgaris	Incurved	AICSMIP ICRISAT core- 1000-GW
522	IE4584	Zimbabwe	Vulgaris	Digitata	ICRISAT core
523	IE2533	Kenya	Vulgaris	Digitata	HRD ICRISAT core & VGPA ICRISAT core
524	IE3412	Zimbabwe	Vulgaris	Digitata	ICRISAT core
525	IE1026	Unknown	Vulgaris	Incurved	ICRISAT core
526	IE2361	Kenya	Plana	Confundere	AICSMIP ICRISAT core- 1000-GW+grain yield
527	IE2008	India	Vulgaris	Incurved	ICRISAT core
528	IE5388	Kenya	Vulgaris	Stelleta	ICRISAT core
529	IE510	India	Vulgaris	Incurved	ICRISAT core
530	IE3094	India	Vulgaris	Liliaceae	ICRISAT core
531	IE2858	Zambia	Vulgaris	Digitata	Replaced in ICRISAT core with FAO designated
532	IE3758	Uganda	Compacta	NA	ICRISAT core
533	IE4245	Zimbabwe	Vulgaris	Incurved	ICRISAT core
534	IE5215	India	Plana	Confundere	VG Plant aspect sICRISAT core and ICN
535	IE3478	Kenya	Vulgaris	Digitata	ICRISAT core
536	IE5831	Nepal	Vulgaris	Liliaceae	ICRISAT core
537	IE6479	Uganda	Vulgaris	Incurved	Replaced in ICRISAT core with FAO designated
538	IE4028	Uganda	Vulgaris	Incurved	ICRISAT core
539	IE6432	Uganda	Compacta	NA	Replaced in ICRISAT core with FAO designated
540	IE888	Uganda	vulgaris	stellata	AICSMIP ICRISAT core-
541	IE2742	Malawi	Vulgaris	Incurved	AICSMIP ICRISAT core- FL
542	IE3808	Uganda	Vulgaris	Incurved	ICRISAT core
543	IE5791	Nepal	Vulgaris	Stelleta	ICRISAT core
544	IE4916	Uganda	Compacta	NA	ICRISAT core
545	IE1055	Unknown	Vulgaris	Digitata	ICRISAT core
546	IE4044	Uganda	Vulgaris	Incurved	HRD ICRISAT core & VGPA ICRISAT core

547	IE6553	India	Vulgaris	Incurved	ICRISAT core-AICSMIP ICRISAT core- 1000-GW
548	IE2386	Kenya	Plana	Confundere	ICRISAT core
549	IE4073	Uganda	Elongata	Reclusa	ICRISAT core
550	IE5999	Nepal	Elongata	Sparsa	ICRISAT core
551	IE3705	Uganda	Vulgaris	Incurved	ICRISAT core
552	IE2356	Kenya	Compacta	NA	AICSMIP ICRISAT core- PLHT
553	IE3694	Uganda	Vulgaris	Incurved	ICRISAT core
554	IE3509	Kenya	Vulgaris	Digitata	Replaced in ICRISAT core with FAO designated
555	IE3174	Zambia	Vulgaris	Digitata	ICRISAT core
556	IE5297	Zimbabwe	Plana	Confundere	VG Plant aspect sICRISAT core and ICN
557	IE6417	Uganda	Compacta	NA	ICRISAT core
558	IE5442	Kenya	Vulgaris	Digitata	VG Plant aspect sICRISAT core and ICN
559	IE4905	Uganda	Plana	Confundere	ICRISAT core
560	IE4816	India	Elongata	Reclusa	ICRISAT core
561	IE2042	India	Vulgaris	Incurved	ICRISAT core
562	IE4708	Burundi	Shortopen	NA	ICRISAT core
563	IE4220	Zimbabwe	Vulgaris	Incurved	ICRISAT core
564	IE4677	India	Vulgaris	Digitata	ICRISAT core
565	IE2724	Malawi	Compacta	NA	AICSMIP ICRISAT core-
566	IE2224	India	Elongata	Reclusa	AICSMIP ICRISAT core- Grain yield
567	IE3722	Uganda	Plana	Confundere	AICSMIP ICRISAT core- SW
568	IE4789	Zimbabwe	Vulgaris	Digitata	ICRISAT core
569	IE4917	Uganda	Plana	Confundere	More finger width
570	IE3935	Uganda	Vulgaris	Digitata	ICRISAT core
571	IE2822	Tanzania	Plana	Confundere	HRD ICRISAT core & VGPA ICRISAT core
572	IE6466	Uganda	Plana	Confundere	Replaced in ICRISAT core with FAO designated
573	IE3504	Kenya	Vulgaris	Digitata	AICSMIP ICRISAT core- 1000-GW
574	IE4005	Uganda	Elongata	Reclusa	HRD ICRISAT core & VGPA ICRISAT core
575	IE4221	Zimbabwe	Vulgaris	Digitata	HRD ICRISAT core & VGPA ICRISAT core
576	IE5337	Kenya	Compacta	NA	VG Plant aspect sICRISAT core and ICN
577	IE5317	Zambia	Plana	Confundere	ICRISAT core
578	IE3434	Zimbabwe	Plana	Seriata	AICSMIP ICRISAT core-
579	IE2336	Kenya	Plana	Confundere	Replaced in ICRISAT core with FAO designated
580	IE2134	India	Vulgaris	Incurved	AICSMIP ICRISAT core-
581	IE3566	India	Vulgaris	Incurved	ICRISAT core
582	IE2820	Nepal	Compacta	NA	ICRISAT core
583	IE3392	Zimbabwe	Compacta	NA	ICRISAT core
584	IE5292	Zimbabwe	Compacta	NA	VG Plant aspect sICRISAT core and ICN
585	IE2953	Malawi	Elongata	Laxa	AICSMIP ICRISAT core- 1000-GW+calcium+FL
586	IE2614	Malawi	Elongata	Laxa	AICSMIP ICRISAT core- FL
587	IE2572	Kenya	Plana	Grandigluma	ICRISAT core
588	IE3130	India	Vulgaris	Digitata	AICSMIP ICRISAT core-
589	IE3687	Uganda	Vulgaris	Digitata	VG Plant aspect sICRISAT core and ICN
590	IE4297	Zimbabwe	Compacta	NA	VG Plant aspect sICRISAT core and ICN
591	IE4450	Tanzania	Vulgaris	Digitata	VG Plant aspect sICRISAT core and ICN
592	IE2644	Malawi	Plana	Grandigluma	ICRISAT core

593	IE2106	India	Elongata	Reclusa	ICRISAT core
594	IE2229	India	Vulgaris	Incurved	AICSMIP ICRISAT core- Finger number
595	IE3655	Uganda	Vulgaris	Stelleta	AICSMIP ICRISAT core-
596	IE4053	Uganda	Vulgaris	Incurved	HRD ICRISAT core & VGPA ICRISAT core
597	IE3515	Kenya	Vulgaris	Digitata	ICRISAT core
598	IE2871	Zambia	Compacta	NA	ICRISAT core
599	IE900	Uganda	Vulgaris	Digitata	Replaced in ICRISAT core with FAO designated
600	IE5875	Nepal	Compacta	NA	VG Plant aspect sICRISAT core and ICN
601	IE2890	Zambia	Vulgaris	Incurved	ICRISAT core
602	IE6482	Uganda	Compacta	NA	Replaced in ICRISAT core with FAO designated
603	IE4992	Uganda	Plana	Confundere	VG Plant aspect sICRISAT core and ICN
604	IE4483	Zimbabwe	Vulgaris	Incurved	ICRISAT core
605	IE5620	Nepal	Vulgaris	Liliaceae	ICRISAT core
606	IE5488	India	Vulgaris	Digitata	VG Plant aspect sICRISAT core and ICN
607	IE4229	Zimbabwe	Vulgaris	Incurved	ICRISAT core
608	IE4223	Zimbabwe	Vulgaris	Incurved	HRD ICRISAT core & VGPA ICRISAT core
609	IE3817	Uganda	Vulgaris	Incurved	ICRISAT core
610	IE4997	Uganda	Plana	Confundere	ICRISAT core
611	IE2787	Malawi	Elongata	Laxa	Long FL
612	IE4152	Uganda	Vulgaris	Incurved	ICRISAT core
613	IE3613	Unknown	Plana	Confundere	Replaced in ICRISAT core with FAO designated
614	IE1013	Unknown	Vulgaris	Incurved	AICSMIP ICRISAT core-
615	IE5177	India	Vulgaris	Incurved	ICRISAT core
616	IE4671	India	Vulgaris	Digitata	ICRISAT core
617	IE2609	Malawi	Vulgaris	Digitata	AICSMIP ICRISAT core- PT
618	IE4107	Uganda	Plana	Confundere	ICRISAT core
619	IE4377	Zimbabwe	Compacta	NA	VG Plant aspect sICRISAT core and ICN
620	IE2339	Kenya	Compacta	NA	AICSMIP ICRISAT core-
621	IE3704	Uganda	Vulgaris	Digitata	ICRISAT core
622	IE942	India	Vulgaris	Liliaceae	ICRISAT core
623	IE5180	India	Compacta	NA	VG Plant aspect sICRISAT core and ICN
624	IE3106	India	Vulgaris	Incurved	ICRISAT core
625	IE3697	Uganda	Vulgaris	Incurved	ICRISAT core
626	IE5992	Nepal	Vulgaris	Stelleta	ICRISAT core
627	IE6550	Nigeria	Vulgaris	Liliaceae	Replaced in ICRISAT core with FAO designated
628	IE954	India	Vulgaris	Incurved	ICRISAT core
629	IE6528	Zimbabwe	Compacta	NA	ICRISAT core
630	IE4172	Uganda	Plana	Confundere	HRD ICRISAT core & VGPA ICRISAT core
631	IE5496	Unknown	Vulgaris	Stelleta	Replaced in ICRISAT core with FAO designated
632	IE2839	India	Vulgaris	Incurved	HRD ICRISAT core & VGPA ICRISAT core
633	IE2045	India	Vulgaris	Digitata	HRD ICRISAT core & VGPA ICRISAT core
634	IE4156	Uganda	Vulgaris	Incurved	HRD ICRISAT core & VGPA ICRISAT core
635	IE5359	Kenya	Vulgaris	Incurved	ICRISAT core
636	IE6251	Zimbabwe	Vulgaris	Incurved	Replaced in ICRISAT core with FAO designated
637	IE4757	India	Vulgaris	Stelleta	ICRISAT core
638	IE2613	Malawi	Elongata	Reclusa	AICSMIP ICRISAT core- Grain yiel+calcium

639	IE3114	India	Vulgaris	Liliaceae	ICRISAT core
640	IE3443	Zimbabwe	Vulgaris	Digitata	ICRISAT core
641	IE5485	India	Vulgaris	Stelleta	ICRISAT core
642	IE5091	Zimbabwe	Vulgaris	Digitata	ICRISAT core
643	IE2593	America	Plana	Confundere	ICRISAT core
644	IE5214	India	Plana	Confundere	VG Plant aspect sICRISAT core and ICN
645	IE6546	Nigeria	Plana	Confundere	ICRISAT core
646	IE2596	Malawi	Vulgaris	Incurved	AICSMIP ICRISAT core- G Ca
647	IE3455	United Kingdom	Vulgaris	Digitata	ICRISAT core
648	IE2303	India	Vulgaris	Stelleta	VG Plant aspect sICRISAT core and ICN
649	IE4347	Zimbabwe	Vulgaris	Digitata	ICRISAT core
650	IE4216	Burundi	Plana	Confundere	Replaced in ICRISAT core with FAO designated
651	IE2146	India	Plana	Seriata	ICRISAT core
652	IE5788	Nepal	Compacta	NA	ICRISAT core
653	IE4647	Zimbabwe	Vulgaris	Incurved	ICRISAT core
654	IE4478	Zimbabwe	Vulgaris	Liliaece	Range
655	IE2589	America	Plana	Confundere	ICRISAT core
656	IE6387	Zimbabwe	Plana	Confundere	ICRISAT core
657	IE955	India	Vulgaris	Digitata	AICSMIP ICRISAT core- HI
658	IE848	India	Vulgaris	Digitata	ICRISAT core
659	IE2869	Zambia	Vulgaris	Incurved	ICRISAT core
660	IE4209	Uganda	Vulgaris	Incurved	HRD ICRISAT core & VGPA ICRISAT core
661	IE4497	Zimbabwe	Vulgaris	Digitata	ICRISAT core
662	IE2772	Malawi	Vulgaris	Digitata	AICSMIP ICRISAT core-
663	IE4020	Uganda	Plana	Seriata	HRD ICRISAT core & VGPA ICRISAT core
664	IE2633	Malawi	Vulgaris	Digitata	ICRISAT core
665	IE2649	Malawi	Compacta	NA	AICSMIP ICRISAT core- PT
666	IE5870	Nepal	Compacta	NA	ICRISAT core
667	IE4866	India	Vulgaris	Incurved	ICRISAT core
668	IE3400	Zimbabwe	Compacta	NA	AICSMIP ICRISAT core- 1000-GW
669	IE5393	Kenya	Compacta	NA	VG Plant aspect sICRISAT core and ICN
670	IE2907	Zambia	Vulgaris	Incurved	VG Plant aspect sICRISAT core and ICN
671	IE5030	Zimbabwe	Plana	Grandigluma	ICRISAT core
672	IE2962	Zambia	Vulgaris	Incurved	Replaced in ICRISAT core with FAO designated
673	IE3721	Uganda	Vulgaris	Digitata	ICRISAT core
674	IE44	India	Vulgaris	Digitata	ICRISAT core-AICSMIP ICRISAT core- SW+BM+PT
675	IE2638	Malawi	Vulgaris	Digitata	AICSMIP ICRISAT core- Finger blast
676	IE5578	Nepal	Plana	Confundere	ICRISAT core
677	IE3364	Zimbabwe	Vulgaris	Incurved	AICSMIP ICRISAT core- PLHT
678	IE2728	Malawi	Vulgaris	Stelleta	VG Plant aspect sICRISAT core and ICN
679	IE6149	Nepal	Vulgaris	Incurved	VG Plant aspect sICRISAT core and ICN
680	IE4141	Uganda	Elongata	Sparsa	HRD ICRISAT core & VGPA ICRISAT core
681	IE2627	Malawi	Vulgaris	Incurvata	AICSMIP ICRISAT core- Finger blast
682	IE5968	Nepal	Elongata	Reclusa	ICRISAT core
683	IE5124	India	Vulgaris	Incurvata	ICRISAT core

684	IE5384	Kenya	Compacta	NA	VG Plant aspect sICRISAT core and ICN
685	IE2996	India	Compacta	NA	ICRISAT core
686	IE3127	India	Vulgaris	Incurved	ICRISAT core
687	IE2329	Kenya	Compacta	NA	VG Plant aspect sICRISAT core and ICN
688	IE5896	Nepal	Elongata	Sparsa	ICRISAT core
689	IE5087	Zimbabwe	Plana	Confundere	VG Plant aspect sICRISAT core and ICN
690	IE1022	Unknown	Plana	Confundere	AICSMIP ICRISAT core-
691	IE2055	India	Vulgaris	Incurved	AICSMIP ICRISAT core- Productive tiller
692	IE4163	Uganda	Vulgaris	Digitata	ICRISAT core
693	IE2062	India	Vulgaris	Incurved	ICRISAT core
694	IE4130	Uganda	Plana	Confundere	HRD ICRISAT core & VGPA ICRISAT core
695	IE2945	Malawi	Vulgaris	Digitata	ICRISAT core
696	IE2131	India	Vulgaris	Stelleta	ICRISAT core
697	IE5545	Nepal	Vulgaris	Incurved	Replaced in ICRISAT core with FAO designated
698	IE6074	Nepal	Elongata	Sparsa	ICRISAT core
699	IE3676	Uganda	Vulgaris	Digitata	AICSMIP ICRISAT core- 1000-GW
700	IE5945	Nepal	Vulgaris	Stelleta	ICRISAT core
701	IE3329	Zimbabwe	Vulgaris	Digitata	ICRISAT core
702	IE3136	India	Vulgaris	Digitata	Replaced in ICRISAT core with FAO designated
703	IE5961	Nepal	Elongata	Sparsa	ICRISAT core
704	IE4114	Uganda	Vulgaris	Incurved	HRD ICRISAT core & VGPA ICRISAT core
705	IE6350	Zimbabwe	Vulgaris	Incurved	ICRISAT core
706	IE3734	Uganda	Compacta	NA	VG Plant aspect sICRISAT core and ICN
707	IE4554	Zimbabwe	Vulgaris	Digitata	ICRISAT core
708	IE886	Pakistan	Vulgaris	Incurved	ICRISAT core
709	IE1015	Unknown	Plana	Confundere	Replaced in ICRISAT core with FAO designated
710	IE4431	India	Vulgaris	Digitata	ICRISAT core-Early flowering
711	IE5435	Kenya	Elongata	Topcurved	ICRISAT core
712	IE2941	Malawi	Vulgaris	Digitata	AICSMIP ICRISAT core- 1000-GW+SW+FL+pro
713	IE6362	Zimbabwe	Plana	Confundere	ICRISAT core
714	IE3280	Zimbabwe	Plana	Seriata	ICRISAT core
715	IE897	Uganda	Plana	Confundere	Replaced in ICRISAT core with FAO designated- 1000-GW+finger number
716	IE2675	Malawi	Plana	Confundere	AICSMIP ICRISAT core- Grain clacium+PT
717	IE6491	Uganda	Vulgaris	Incurved	Range
718	IE61	India	Elongata	Reclusa	ICRISAT core
719	IE6029	Nepal	Elongata	Sparsa	ICRISAT core
720	IE864	India	Vulgaris	Digitata	AICSMIP ICRISAT core- PT
721	IE2769	Malawi	Plana	Confundere	AICSMIP ICRISAT core- Finger number
722	IE3358	Zimbabwe	Vulgaris	Incurved	Replaced in ICRISAT core with FAO designated
723	IE5711	Nepal	Vulgaris	Incurved	ICRISAT core
724	IE2861	Zambia	Vulgaris	Incurved	ICRISAT core
725	IE5231	India	Vulgaris	Incurved	ICRISAT core
726	IE906	Uganda	Plana	Confundere	AICSMIP ICRISAT core- 1000-GW+yield+finger number
727	IE3656	Uganda	Comacta	NA	VG Plant aspect sICRISAT core and ICN
728	IE3984	Uganda	Vulgaris	Digitata	AICSMIP ICRISAT core-

729	IE3581	India	Vulgaris	Liliaceae	ICRISAT core
730	IE2227	India	Vulgaris	Incurved	AICSMIP ICRISAT core- 1000-grain weigtht
731	IE3431	Zimbabwe	Vulgaris	Digitata	ICRISAT core
732	IE4699	India	Plana	Confundere	AICSMIP ICRISAT core- 1000-grain weigth+grain yield
733	IE6443	Uganda	Plana	Confundere	ICRISAT core
734	IE2549	Kenya	Vulgaris	Digitata	Replaced in ICRISAT core with FAO designated
735	IE5245	India	Vulgaris	Incurved	ICRISAT core
736	IE4222	Zimbabwe	Vulgaris	Incurved	HRD ICRISAT core & VGPA ICRISAT core
737	IE5960	Nepal	Vulgaris	Stelleta	ICRISAT core
738	IE5105	Zimbabwe	Plana	Confundere	ICRISAT core
739	IE4492	Zimbabwe	Vulgaris	Digitata	VG Plant aspect sICRISAT core and ICN
740	IE2353	Kenya	Plana	Confundere	AICSMIP ICRISAT core- Neck blast
741	IE2238	India	Vulgaris	Incurved	ICRISAT core
742	IE5563	Nepal	Vulgaris	Liliaceae	ICRISAT core
743	IE3942	Uganda	Vulgaris	Incurved	Replaced in ICRISAT core with FAO designated
744	IE5736	Nepal	Vulgaris	Stelleta	ICRISAT core
745	IE5321	India	Vulgaris	Liliaceae	ICRISAT core
746	IE4091	Uganda	Vulgaris	Digitata	HRD ICRISAT core & VGPA ICRISAT core
747	IE4119	Uganda	Plana	Confundere	HRD ICRISAT core & VGPA ICRISAT core
748	IE2384	Kenya	Plana	Congundere	ICRISAT core
749	IE3484	Kenya	Vulgaris	Digitata	AICSMIP ICRISAT core-
750	IE5229	India	Vulgaris	Stelleta	ICRISAT core
751	IE3225	Mozambique	Plana	Seriata	ICRISAT core
752	IE2362	Kenya	Plana	Confundere	VG Plant aspect sICRISAT core and ICN
753	IE6426	Uganda	Plana	Confundere	Replaced in ICRISAT core with FAO designated
754	IE3826	Uganda	Vulgaris	Stelleta	ICRISAT core
755	IE712	India	Vulgaris	Incurved	ICRISAT core
756	IE4545	Zimbabwe	Compacta	NA	ICRISAT core
757	IE3547	India	Vulgaris	Stelleta	ICRISAT core
758	IE4368	Zimbabwe	Vulgaris	Digitata	Replaced in ICRISAT core with FAO designated
759	IE2476	Kenya	Vulgaris	Incurved	ICRISAT core
760	IE5164	India	Plana	Confundere	VG Plant aspect sICRISAT core and ICN
761	IE2851	India	Vulgaris	Incurved	HRD ICRISAT core & VGPA ICRISAT core
762	IE3270	Zimbabwe	Vulgaris	Digitata	ICRISAT core
763	IE4991	Uganda	Vulgaris	Digitata	VG Plant aspect sICRISAT core and ICN
764	IE2678	Malawi	Vulgaris	Digitata	AICSMIP ICRISAT core- PT
765	IE2366	Kenya	Plana	Confundere	HRD ICRISAT core & VGPA ICRISAT core
766	IE4192	Uganda	Vulgaris	Digitata	ICRISAT core
767	IE2773	Malawi	Compacta	NA	VG Plant aspect sICRISAT core and ICN
768	IE610	India	Vulgaris	Incurved	AICSMIP ICRISAT core- Finger number
769	IE4842	India	Vulgaris	Incurved	ICRISAT core
770	IE6227	Nepal	Vulgaris	Digitata	ICRISAT core
771	IE3945	Uganda	Plana	Confundere	ICRISAT core
772	IE5248	India	Vulgaris	Digitata	VG Plant aspect sICRISAT core and ICN
773	IE6012	Nepal	Vulgaris	Stelleta	ICRISAT core
774	IE2695	Malawi	Plana	Seriata	AICSMIP ICRISAT core-

775	IE3693	Uganda	Plana	Confundere	ICRISAT core
776	IE2335	Kenya	Plana	Confundere	VG Plant aspect sICRISAT core and ICN
777	IE2608	Malawi	Elongata	Reclusa	ICRISAT core
778	IE5956	Nepal	Vulgaris	Incurved	ICRISAT core
779	IE5133	India	Plana	Confundere	VG Plant aspect sICRISAT core and ICN
780	IE2296	India	Vulgaris	Digitata	ICRISAT core
781	IE6241	Zimbabwe	Elongata	Sparsa	ICRISAT core
782	IE3223	Ethiopia	Elongata	Laxa	Range
783	IE4122	Uganda	Plana	Confundere	ICRISAT core
784	IE5806	Nepal	Vulgaris	Incurved	ICRISAT core
785	IE947	Ethiopia	Vulgaris	Incurved	Replaced in ICRISAT core with FAO designated
786	IE3492	Kenya	Vulgaris	Digitata	ICRISAT core
787	IE2576	Kenya	Compacta	NA	AICSMIP ICRISAT core- PLHT
788	IE5187	India	Compacta	NA	VG Plant aspect sICRISAT core and ICN
789	IE6059	Nepal	Vulgaris	Digitata	ICRISAT core
790	IE5418	Kenya	Plana	Confundere	VG Plant aspect sICRISAT core and ICN
791	IE5315	Zambia	Vulgaris	Digitata	ICRISAT core
792	IE3046	India	Elongata	Reclusa	ICRISAT core
793	IE2037	India	Vulgaris	Incurved	HRD ICRISAT core & VGPA ICRISAT core
794	IE3096	India	Vulgaris	Liliaceae	ICRISAT core
795	IE5502	Nepal	Vulgaris	Incurved	ICRISAT core
796	IE2739	Malawi	Vulgaris	Digitata	AICSMIP ICRISAT core- Finger number
797	IE2118	India	Elongata	Reclusa	ICRISAT core
798	IE6112	Nepal	Compacta	NA	ICRISAT core
799	IE4956	Uganda	Compacta	NA	VG Plant aspect sICRISAT core and ICN
800	IE4320	Zimbabwe	Vulgaris	Incurved	Replaced in ICRISAT core with FAO designated
801	IE4137	Uganda	Vulgaris	Incurved	HRD ICRISAT core & VGPA ICRISAT core
802	IE4442	Cameroon	Shortopen	NA	Long FL
803	IE2333	Kenya	Compacta	NA	HRD ICRISAT core & VGPA ICRISAT core
804	IE2780	Malawi	Elongata	Reclusa	ICRISAT core
805	IE4127	Uganda	Vulgaris	Incurved	HRD ICRISAT core & VGPA ICRISAT core
806	IE2498	Kenya	Compacta	NA	Replaced in ICRISAT core with FAO designated
807	IE2535	Kenya	Plana	Confundere	ICRISAT core
808	IE5386	Kenya	Compacta	NA	VG Plant aspect sICRISAT core and ICN
809	IE2913	Zambia	Compacta	NA	AICSMIP ICRISAT core- FL
810	IE4159	Uganda	Compacta	NA	HRD ICRISAT core & VGPA ICRISAT core
811	IE1011	Unknown	Vulgaris	Digitata	AICSMIP ICRISAT core-
812	IE2712	Malawi	Compacta	NA	HRD ICRISAT core & VGPA ICRISAT core
813	IE2341	Kenya	Vulgaris	Incurved	ICRISAT core
814	IE3450	United Kingdom	Vulgaris	Stelleta	ICRISAT core
815	IE5331	India	Vulgaris	Stelleta	ICRISAT core
816	IE5170	India	Plana	Confundere	VG Plant aspect sICRISAT core and ICN
817	IE2355	Kenya	Plana	Confundere	ICRISAT core
818	IE4185	Uganda	Plana	Seriata	HRD ICRISAT core & VGPA ICRISAT core
819	IE6088	Nepal	Elongata	Sparsa	ICRISAT core

820	IE4525	Zimbabwe	Vulgaris	Digitata	ICRISAT core
821	IE4600	Zimbabwe	Compacta	NA	VG Plant aspect sICRISAT core and ICN
822	IE3025	Ethiopia	Elongata	Reclusa	ICRISAT core
823	IE3746	Uganda	Plana	Confundere	VG Plant aspect sICRISAT core and ICN
824	IE5343	Kenya	Plana	Seriata	ICRISAT core
825	IE3538	Unknown	Vulgaris	Incurved	Replaced in ICRISAT core with FAO designated
826	IE1010	Unknown	Compacta	NA	ICRISAT core
827	IE4231	Zimbabwe	Vulgaris	Incurved	HRD ICRISAT core & VGPA ICRISAT core
828	IE5480	India	Vulgaris	Incurved	ICRISAT core
829	IE581	India	Vulgaris	Incurved	AICSMIP ICRISAT core- 1000-GW
830	IE2656	Malawi	Plana	Grandigluma	AICSMIP ICRISAT core-
831	IE4432	India	Vulgaris	Digitata	ICRISAT core-AICSMIP ICRISAT core- 1000-GW
832	IE2441	Kenya	Compacta	NA	VG Plant aspect sICRISAT core and ICN
833	IE2006	India	Vulgaris	Digitata	ICRISAT core
834	IE5156	India	Vulgaris	Stelleta	ICRISAT core
835	IE6455	Uganda	Plana	Confundere	Replaced in ICRISAT core with FAO designated
836	IE2857	Zambia	Vulgaris	Incurved	ICRISAT core
837	IE912	Uganda	Vulgaris	Stelleta	AICSMIP ICRISAT core- 1000-GW
838	IE2737	Malawi	Compacta	NA	AICSMIP ICRISAT core- Finger number
839	IE2323	India	Vulgaris	Stelleta	ICRISAT core
840	IE5542	Nepal	Vulgaris	Stelleta	ICRISAT core
841	IE5260	India	Vulgaris	Stelleta	ICRISAT core
842	IE3366	Zimbabwe	Vulgaris	Digitata	Replaced in ICRISAT core with FAO designated
843	IE2939	Malawi	Plana	Confundere	ICRISAT core
844	IE5149	India	Vulgaris	Incurved	ICRISAT core
845	IE3575	India	Vulgaris	Stelleta	ICRISAT core
846	IE8	India	Plana	Seriata	AICSMIP ICRISAT core- 1000-grain weigth+Grain yield
847	IE2758	Malawi	Vulgaris	Incurved	Replaced in ICRISAT core with FAO designated
848	IE2546	Kenya	Vulgaris	Incurved	Replaced in ICRISAT core with FAO designated
849	IE5342	Kenya	Vulgaris	Digitata	Replaced in ICRISAT core with FAO designated
850	IE2590	America	Vulgaris	Digitata	ICRISAT core
851	IE817	India	Vulgaris	Liliacea	ICRISAT core
852	IE5328	India	Vulgaris	Stellata	Replaced in ICRISAT core with FAO designated
853	IE6435	Uganda	Plana	Confundere	Replaced in ICRISAT core with FAO designated
854	IE2619	Malawi	Vulgaris	Incurvata	ICRISAT core
855	IE4097	Uganda	Compacta	NA	ICRISAT core
856	IE6235	Zimbabwe	Compacta	NA	VG Plant aspect sICRISAT core and ICN
857	IE2402	Kenya	Plana	Confundere	ICRISAT core
858	IE6541	Nigeria	Vulgaris	Incurvata	ICRISAT core
859	IE6537	Nigeria	Vulgaris	Incurvata	ICRISAT core
860	IE6549	Nigeria	Vulgaris	Incurvata	ICRISAT core
861	IE3502	Kenya	Vulgaris	Digitata	ICRISAT core
862	IE3637	Uganda	Plana	Confundere	AICSMIP ICRISAT core-
863	IE2158	India	Vulgaris	Incurvata	ICRISAT core+AICSMIP ICRISAT core- Grain yield+protein+PT+FL
864	IE3531	Kenya	Vulgaris	Digitata	ICRISAT core

865	IE2358	Kenya	Plana	Confundere	ICRISAT core
866	IE4999	Uganda	Compacta	NA	VG Plant aspect sICRISAT core and ICN
867	IE3803	Uganda	Compacta	NA	ICRISAT core
868	IE2794	Malawi	Spontanea	NA	ICRISAT core
869	IE4149	Uganda	Vulgaris	Incurvata	HRD ICRISAT core & VGPA ICRISAT core
870	IE4622	Zimbabwe	Compacta	NA	ICRISAT core
871	IE4166	Uganda	Plana	Confundere	HRD ICRISAT core & VGPA ICRISAT core
872	IE3670	Uganda	Compacta	NA	VG Plant aspect sICRISAT core and ICN
873	IE5519	Nepal	Plana	Confundere	ICRISAT core
874	IE2850	India	Vulgaris	incurvata	ICRISAT core
875	IE2536	Kenya	Vulgaris	digitata	AICSMIP ICRISAT core- Grain yield+1000-GW+SW+bioma
876	IE3124	India	Vulgaris	digitata	ICRISAT core
877	IE5120	India	Vulgaris	incurvata	ICRISAT core
878	IE3661	Uganda	plana	confundere	AICSMIP ICRISAT core- Calcium
879	IE3015	India	elongata	sparsa	ICRISAT core
880	IE928	Uganda	Vulgaris	incurvata	AICSMIP ICRISAT core- Grain yield+1000-GW
881	IE518	India	Vulgaris	incurvata	ICRISAT core
882	IE4017	Uganda	elongata	reclusa	HRD ICRISAT core & VGPA ICRISAT core
883	IE3165	Zambia	Vulgaris	digitata	ICRISAT core
884	IE2457	Kenya	compacta	na	ICRISAT core
885	IE6	India	Vulgaris	liliacea	ICRISAT core
886	IE4165	Uganda	plana	confundere	ICRISAT core
887	IE5472	India	compacta	na	VG Plant aspect sICRISAT core and ICN
888	IE2427	Kenya	Vulgaris	digitata	AICSMIP ICRISAT core- Grain yield+HI+PT
889	IE2896	Zambia	compacta	na	ICRISAT core
890	IE3779	Uganda	Vulgaris	incurvata	ICRISAT core
891	IE2756	Malawi	plana	confundere	AICSMIP ICRISAT core- PLHT
892	IE4386	Zimbabwe	Vulgaris	digitata	ICRISAT core
893	IE4115	Uganda	Vulgaris	incurvata	ICRISAT core
894	IE3802	Uganda	compacta	na	VG Plant aspect sICRISAT core and ICN
895	IE5635	Nepal	Vulgaris	incurvata	ICRISAT core
896	IE984	Unknown	Vulgaris	digitata	Replaced in ICRISAT core with FAO designated
897	IE5354	Kenya	plana	confundere	VG Plant aspect sICRISAT core and ICN
898	IE2611	Malawi	elongata	laxa	Long FL
899	IE4162	Uganda	Vulgaris	incurvata	HRD ICRISAT core & VGPA ICRISAT core
900	IE2487	Kenya	compacta	na	ICRISAT core
901	IE829	India	Vulgaris	digitata	AICSMIP ICRISAT core-
902	IE4036	Uganda	Vulgaris	digitata	ICRISAT core
903	IE3175	Zambia	Vulgaris	digitata	ICRISAT core
904	IE3199	Tanzania	Vulgaris	digitata	AICSMIP ICRISAT core- PT
905	IE4529	Zimbabwe	Vulgaris	digitata	ICRISAT core
906	IE3363	Zimbabwe	Vulgaris	digitata	ICRISAT core
907	IE3485	Kenya	Vulgaris	digitata	AICSMIP ICRISAT core- 1000-GW+Calcium
908	IE2064	India	Vulgaris	stellata	ICRISAT core
909	IE3207	Tanzania	Vulgaris	digitata	AICSMIP ICRISAT core- FL
910	IE3330	Zimbabwe	Vulgaris	digitata	ICRISAT core

911	IE2914	Zambia	Vulgaris	digitata	Replaced in ICRISAT core with FAO designated
912	IE3587	India	Vulgaris	digitata	VG Plant aspect sICRISAT core and ICN
913	IE3477	Kenya	plana	confundere	ICRISAT core
914	IE5817	Nepal	Vulgaris	incurvata	ICRISAT core
915	IE3910	Uganda	plana	confundere	ICRISAT core
916	IE603	India	Vulgaris	liliacea	AICSMIP ICRISAT core- Finger number
917	IE3169	Zambia	Vulgaris	digitata	ICRISAT core
918	IE2653	Malawi	Vulgaris	digitata	ICRISAT core
919	IE3987	Uganda	Vulgaris	incurvata	ICRISAT core
920	IE600	India	Vulgaris	incurvata	ICRISAT core+G Ca&protein
921	IE3208	Tanzania	elongata	laxa	AICSMIP ICRISAT core- SW+BM+clacium+FL
922	IE3733	Uganda	plana	confundere	Replaced in ICRISAT core with FAO designated
923	IE6473	Uganda	plana	confundere	ICRISAT core
924	IE4651	Zimbabwe	compacta	na	Replaced in ICRISAT core with FAO designated
925	IE2372	Kenya	plana	confundere	AICSMIP ICRISAT core- 1000-GW+SW
926	IE4312	Zimbabwe	compacta	na	ICRISAT core
927	IE4519	Zimbabwe	Vulgaris	digitata	ICRISAT core
928	IE3313	Zimbabwe	compacta	na	ICRISAT core
929	IE2116	India	Vulgaris	incurvata	ICRISAT core
930	IE6239	Zimbabwe	plana	seriata	ICRISAT core
931	IE4826	India	elongata	Reclusa	ICRISAT core
932	IE3973	Uganda	Vulgaris	stellata	ICRISAT core
933	IE4116	Uganda	plana	confundere	ICRISAT core
934	IE5232	India	compacta	na	VG Plant aspect sICRISAT core and ICN
935	IE3338	Zimbabwe	Vulgaris	digitata	Replaced in ICRISAT core with FAO designated
936	IE2416	Kenya	Vulgaris	digitata	ICRISAT core
937	IE930	Uganda	Vulgaris	stellata	ICRISAT core
938	IE4134	Uganda	Vulgaris	digitata	ICRISAT core
939	IE5165	India	plana	confundere	ICRISAT core
940	IE2461	Kenya	plana	confundere	HRD ICRISAT core & VGPA ICRISAT core
941	IE3022	Malawi	compacta	na	Replaced in ICRISAT core with FAO designated
942	IE2363	Kenya	Vulgaris	incurvata	ICRISAT core
943	IE6258	Zimbabwe	elongata	Reclusa	Replaced in ICRISAT core with FAO designated
944	IE642	India	Vulgaris	incurvata	AICSMIP ICRISAT core- Grain yield
945	IE968	Unknown	Vulgaris	incurvata	Replaced in ICRISAT core with FAO designated
946	IE4310	Zimbabwe	Vulgaris	digitata	ICRISAT core
947	IE2364	Kenya	compacta	na	AICSMIP ICRISAT core-
948	IE4726	India	compacta	na	VG Plant aspect sICRISAT core and ICN
949	IE6486	Uganda	Vulgaris	incurvata	Replaced in ICRISAT core with FAO designated
950	IE2034	India	Vulgaris	incurvata	ICRISAT core
951	IE595	India	Vulgaris	liliacea	ICRISAT core
952	IE3075	India	elongata	laxa	ICRISAT core
953	IE4890	India	Vulgaris	digitata	VG Plant aspect sICRISAT core and ICN
954	IE224	India	Vulgaris	stellata	ICRISAT core
955	IE5250	Tanzania	Vulgaris	stellata	Replaced in ICRISAT core with FAO designated
956	IE5145	India	Vulgaris	liliacea	ICRISAT core

957	IE5367	Kenya	Vulgaris	liliacea	ICRISAT core
958	IE4047	Uganda	Vulgaris	digitata	ICRISAT core
959	IE2771	Malawi	Vulgaris	digitata	AICSMIP ICRISAT core- G Ca+PT
960	IE913	Uganda	Vulgaris	digitata	AICSMIP ICRISAT core-
961	IE2882	Zambia	Vulgaris	incurvata	HRD ICRISAT core & VGPA ICRISAT core
962	IE120	India	Vulgaris	incurvata	Early flowering
963	IE2891	Zambia	Vulgaris	digitata	AICSMIP ICRISAT core- Grain yield+SW+BM
964	IE6321	Zimbabwe	Vulgaris	digitata	ICRISAT core
965	IE5873	Nepal	elongata	sparsa	ICRISAT core
966	IE2956	Malawi	Vulgaris	digitata	VG Plant aspect sICRISAT core and ICN
967	IE5517	Nepal	Vulgaris	digitata	ICRISAT core
968	IE2150	India	Vulgaris	incurvata	ICRISAT core
969	IE2799	Ethiopia	elongata	Reclusa	ICRISAT core
970	IE2531	Kenya	plana	confundere	Replaced in ICRISAT core with FAO designated
971	IE3698	Uganda	compacta	na	Replaced in ICRISAT core with FAO designated
972	IE2039	India	Vulgaris	incurvata	ICRISAT core
973	IE5173	India	Vulgaris	stellata	ICRISAT core
974	IE5374	Kenya	Vulgaris	incurvata	Replaced in ICRISAT core with FAO designated
975	IE899	Uganda	Vulgaris	digitata	AICSMIP ICRISAT core- FL
976	IE2666	Malawi	Vulgaris	incurvata	AICSMIP ICRISAT core- 1000-grain weigth+yield+calcium+protein
977	IE252	India	Vulgaris	incurvata	Early flowering
978	IE6236	Zimbabwe	Vulgaris	digitata	VG Plant aspect sICRISAT core and ICN
979	IE4446	Cameroon	*	*	Range
980	IE2180	India	vulgaris	stellata	ICRISAT core
981	IE525	India	vulgaris	incurvata	Early flowering
982	IE3529	Kenya	vulgaris	digitata	AICSMIP ICRISAT core-
983	IE4990	Uganda	compacta	na	VG Plant aspect sICRISAT core and ICN
984	IE5058	Zimbabwe	vulgaris	incurvata	Replaced in ICRISAT core with FAO designated
985	IE2622	Malawi	vulgaris	incurvata	ICRISAT core
986	IE2674	Malawi	elongata	reclusa	ICRISAT core
987	IE4232	Zimbabwe	vulgaris	incurvata	HRD ICRISAT core & VGPA ICRISAT core
988	IE3157	Zambia	compacta	na	AICSMIP ICRISAT core-
989	IE5129	India	plana	confundere	ICRISAT core
990	IE96	India	vulgaris	incurvata	Early flowering
991	IE2685	Malawi	plana	grandigluma	AICSMIP ICRISAT core- Grain yield
992	IE694	India	vulgaris	liliaceae	ICRISAT core+AICSMIP ICRISAT core- Calcium
993	IE6428	Uganda	plana	confundere	Replaced in ICRISAT core with FAO designated
994	IE6337	Zimbabwe	vulgaris	incurvata	ICRISAT core
995	IE5113	India	plana	confundere	VG Plant aspect sICRISAT core and ICN
996	IE2264	India	vulgaris	digitata	ICRISAT core
997	IE2395	Kenya	vulgaris	digitata	Replaced in ICRISAT core with FAO designated
998	IE4998	Uganda	compacta	na	ICRISAT core
999	IE6072	Nepal	elongata	sparsa	ICRISAT core
1000	IE2816	Nepal	vulgaris	incurvata	Replaced in ICRISAT core with FAO designated

Annexure: II Stability parameters for two important quantitative traits (days to 50% flowering and plot yield) observed in three environments (E_1, E_2, and E_3) in the global finger millet composite collection

S.no	Accession	Days t0 50% Flowering (days)			Plot yield (tn ha^{-1})			S.no	Accession	Days t0 50% Flowering (days)			Plot yield (tn ha^{-1})		
		Mean	b	S^2d	Mean	b	S^2d			Mean	b	S^2d	Mean	b	S^2d
1	IE1008	71.9	102.06	-0.77	1.10	0.07	31.59	501	IE406	69.8	57.00	2.75	0.67	0.10	51.70
2	IE1009	74.9	320.62	-1.44	1.23	0.00	-9.54	502	IE4060	75.6	74.97	3.01	1.33	0.17	25.03
3	IE1010	79.7	219.45	-1.90	1.23	0.04	-6.56	503	IE4062	72.0	7.84	0.14	1.03	0.25	79.27
4	IE1011	78.1	245.64	-0.35	1.17	0.02	-2.53	504	IE4070	72.9	43.82	2.46	1.00	0.16	-60.19
5	IE1013	73.6	355.57	-2.51	0.90	0.31	88.80	505	IE4073	71.3	9.05	-0.36	0.93	0.04	34.12
6	IE1015	81.6	170.10	-1.87	1.07	0.00	-5.51	506	IE4081	73.0	23.80	1.79	1.13	0.10	-51.70
7	IE1022	76.6	300.82	-2.29	1.33	0.24	40.08	507	IE4083	74.2	31.29	1.91	0.67	0.08	20.12
8	IE1023	77.7	206.34	-0.77	0.97	0.12	-50.66	508	IE4084	72.8	20.06	0.90	1.17	0.08	27.56
9	IE1026	73.7	327.81	-2.04	0.57	0.14	18.63	509	IE4091	72.3	27.21	1.80	1.30	0.07	18.03
10	IE1034	77.5	217.72	-0.02	0.83	0.02	2.53	510	IE4092	74.8	32.44	1.73	0.87	0.17	68.24
11	IE1055	75.1	295.22	-1.95	0.87	0.17	68.24	511	IE4097	72.4	20.25	1.21	1.03	0.37	82.25
12	IE106	83.6	77.56	0.94	0.67	0.06	36.66	512	IE4107	74.6	35.23	2.02	1.37	0.12	0.44
13	IE120	67.1	541.17	-1.47	0.97	0.00	-4.02	513	IE4108	73.4	12.20	0.79	0.77	0.10	-37.10
14	IE143	75.0	181.81	-0.12	1.03	0.01	-11.03	514	IE4110	68.6	7.03	0.96	1.00	0.25	75.24
15	IE174	72.8	206.71	-1.42	1.30	0.13	19.52	515	IE4112	67.0	3.25	-0.68	0.83	0.09	49.17
16	IE189	63.4	455.72	-1.25	0.80	0.07	42.17	516	IE4113	65.7	4.30	0.07	0.87	0.04	6.56
17	IE196	63.3	465.02	-1.07	0.93	0.12	50.66	517	IE4114	66.7	1.77	0.01	0.87	0.34	96.85
18	IE2006	88.0	3.16	-0.27	1.10	0.01	1.49	518	IE4115	71.7	38.92	2.33	1.40	0.63	-130.97
19	IE2008	75.8	129.99	-0.51	0.87	0.17	68.24	519	IE4116	71.2	1.56	-0.13	0.80	0.03	12.07
20	IE2014	83.0	28.37	1.29	1.17	0.14	29.05	520	IE4118	73.6	28.84	1.96	1.17	0.02	-17.58
21	IE2030	65.7	356.52	-1.09	1.03	0.01	19.07	521	IE4119	71.4	31.81	2.04	0.93	0.04	-26.07
22	IE2034	84.0	53.22	1.34	1.23	0.10	23.54	522	IE4120	73.1	10.00	0.61	1.17	0.14	-62.73
23	IE2037	86.0	16.12	1.10	1.13	0.02	-24.59	523	IE4121	71.7	32.40	2.07	0.93	0.09	49.17
24	IE2039	86.2	14.06	0.34	1.00	0.21	73.75	524	IE4122	73.6	85.49	3.36	1.00	0.07	31.59
25	IE2042	70.3	246.96	-2.49	1.03	0.02	-23.10	525	IE4125	74.9	31.84	1.71	0.70	0.13	55.73
26	IE2045	81.2	48.26	0.34	0.93	0.02	17.58	526	IE4126	76.0	90.04	3.29	0.93	0.02	-24.59
27	IE2047	75.5	90.62	-0.75	0.97	0.00	-5.51	527	IE4127	74.4	41.67	1.82	0.63	0.06	1.05
28	IE2055	72.6	226.29	-1.06	1.17	0.14	42.61	528	IE4128	74.7	34.52	1.74	0.73	0.04	32.63
29	IE2062	77.5	129.52	0.29	1.27	0.30	-91.34	529	IE413	74.8	36.16	1.74	0.80	0.01	13.56
30	IE2063	75.3	113.61	-0.32	1.13	0.06	-36.66	530	IE4130	71.5	6.07	-0.32	0.87	0.17	68.24
31	IE2064	78.7	111.44	0.84	0.77	0.17	68.24	531	IE4131	72.0	1.03	0.23	1.13	0.10	-51.70
32	IE2065	76.7	76.25	-1.09	1.00	0.00	0.00	532	IE4134	77.5	107.29	3.09	1.37	0.22	-74.80
33	IE2088	78.8	57.29	-0.68	0.63	0.17	13.12	533	IE4135	74.6	28.94	1.90	1.07	0.04	26.07
34	IE2091	70.7	197.12	-1.84	0.87	0.02	24.59	534	IE4136	77.5	111.52	3.53	0.90	0.00	0.00
35	IE2093	67.6	404.34	1.64	0.60	0.27	-49.61	535	IE4137	76.7	101.11	3.26	0.67	0.04	21.61
36	IE2106	79.5	56.36	-0.35	1.03	0.56	110.85	536	IE4141	73.6	17.41	1.01	0.80	0.07	42.17
37	IE2108	76.0	97.32	0.14	1.03	0.42	95.80	537	IE4143	74.1	32.41	1.92	0.70	0.04	27.12
38	IE2116	72.8	210.49	-1.25	1.13	0.10	37.10	538	IE4145	71.8	11.36	0.81	1.13	0.10	37.10
39	IE2118	77.6	87.94	-0.20	1.00	0.00	0.00	539	IE4147	70.0	6.62	0.93	0.77	0.17	-52.15
40	IE2131	75.5	162.36	-0.29	1.40	0.39	37.54	540	IE4149	72.2	34.63	1.97	0.83	0.01	-11.03
41	IE2134	73.0	170.74	-1.61	0.90	0.07	-31.59	541	IE4151	77.3	115.29	3.82	0.60	0.07	25.63
42	IE2139	71.7	158.25	-1.03	1.03	0.00	5.51	542	IE4152	74.6	40.36	1.78	0.73	0.06	1.05
43	IE2146	85.1	15.21	1.16	0.77	0.06	36.66	543	IE4156	75.7	81.61	3.12	1.00	0.07	-43.66
44	IE2150	72.8	176.58	-1.56	1.10	0.07	31.59	544	IE4159	76.7	74.66	2.86	0.80	0.12	24.14
45	IE2158	60.6	533.20	-1.36	1.23	0.12	9.98	545	IE4162	71.5	6.10	-0.34	1.00	0.13	-58.71
46	IE2169	71.1	143.96	-1.73	0.70	0.07	42.17	546	IE4163	75.6	27.86	1.28	0.70	0.04	-2.98
47	IE2179	67.7	238.63	-1.24	0.77	0.10	-23.54	547	IE4165	75.0	19.63	1.33	0.73	0.21	-44.10
48	IE2180	76.6	120.32	0.02	1.07	0.02	-17.58	548	IE4166	75.1	31.50	1.73	0.83	0.14	-42.61
49	IE2183	70.6	163.05	-1.51	0.87	0.02	-20.56	549	IE4172	72.8	10.22	1.00	0.87	0.00	-5.51
50	IE2187	67.3	290.10	-3.74	0.73	0.30	-45.59	550	IE4181	73.3	16.84	1.28	0.63	0.06	1.05
51	IE2212	72.3	114.54	-1.58	0.77	0.17	-25.03	551	IE4185	73.2	19.92	1.00	0.70	0.09	40.68
52	IE2217	71.3	138.76	-0.91	0.97	0.02	-20.56	552	IE4186	74.4	29.24	1.55	0.90	0.03	-16.54
53	IE2223	79.0	41.29	-0.18	1.07	0.01	11.03	553	IE4192	70.6	12.22	1.27	0.70	0.03	12.07
54	IE2224	67.9	253.96	-1.58	0.90	0.09	-45.15	554	IE4209	70.8	1.66	-0.23	0.97	0.25	71.22
55	IE2227	72.0	167.89	-0.64	0.90	0.03	-16.54	555	IE4216	69.3	4.89	0.78	0.90	0.03	12.07
56	IE2229	71.0	171.94	-0.88	1.30	0.07	-25.63	556	IE4218	65.7	124.83	-4.23	1.40	0.61	-129.48
57	IE2233	71.0	158.77	-1.52	0.87	0.01	8.05	557	IE4220	71.8	17.08	1.36	1.17	0.16	56.17
58	IE2235	78.6	36.57	-0.22	0.97	0.04	26.07	558	IE4221	70.4	30.84	2.10	0.80	0.12	-33.08
59	IE2238	70.4	203.97	-2.02	0.63	0.06	31.14	559	IE4222	72.1	6.70	0.08	1.03	0.02	-24.59
60	IE224	75.3	124.34	-0.62	1.17	0.04	12.51	560	IE4223	76.1	60.10	2.52	1.23	0.06	-36.66
61	IE2254	75.2	77.82	-0.58	1.03	0.00	5.51	561	IE4229	74.2	20.64	0.69	0.90	0.01	15.05
62	IE2264	78.1	168.14	2.36	1.40	0.13	-9.09	562	IE4230	73.9	22.60	1.24	0.93	0.09	49.17
63	IE2275	65.2	328.74	-0.40	1.43	0.25	-2.09	563	IE4231	72.8	31.04	1.64	0.43	0.24	26.68
64	IE2288	77.1	48.01	-0.39	0.57	0.17	65.26	564	IE4232	71.5	21.72	1.74	1.00	0.01	-1.49

S.no	Accession	Days t0 50% Flowering (days)			Plot yield (tn ha^{-1})			S.no	Accession	Days t0 50% Flowering (days)			Plot yield (tn ha^{-1})		
		Mean	b	S^2d	Mean	b	S^2d			Mean	b	S^2d	Mean	b	S^2d
65	IE2293	62.1	397.44	-0.97	1.07	0.01	-19.07	565	IE4245	71.9	11.26	1.24	0.90	0.03	28.61
66	IE2296	69.6	204.33	-2.28	1.10	0.13	46.64	566	IE4257	70.7	35.77	2.27	0.93	0.09	49.17
67	IE2299	70.6	131.92	-1.76	1.10	0.36	90.29	567	IE4274	72.6	50.90	2.60	0.67	0.16	-38.59
68	IE2303	76.1	76.81	0.00	1.20	0.19	48.12	568	IE4287	72.4	18.61	0.66	0.87	0.17	-52.15
69	IE2312	75.9	68.16	0.88	1.10	0.36	-90.29	569	IE4295	73.1	19.20	0.87	1.10	0.01	1.49
70	IE2322	67.8	394.44	3.43	0.73	0.09	46.19	570	IE4296	70.0	1.20	0.11	0.73	0.21	76.29
71	IE2323	62.3	436.82	-1.02	1.00	0.21	61.68	571	IE4297	68.7	35.02	2.20	0.83	0.09	46.19
72	IE2327	78.3	36.67	0.46	0.83	0.02	17.58	572	IE431	70.9	3.80	0.54	1.47	0.16	-59.75
73	IE2329	79.4	53.08	0.40	1.17	0.02	-17.58	573	IE4310	69.3	6.04	0.31	1.10	0.43	91.78
74	IE2331	78.9	37.92	0.45	0.77	0.06	-8.49	574	IE4312	70.1	18.07	1.56	1.00	0.07	42.17
75	IE2332	76.2	51.57	-0.22	1.10	0.01	1.49	575	IE4320	70.1	11.46	1.27	1.57	0.26	-56.77
76	IE2333	76.3	68.41	0.13	1.10	0.07	31.59	576	IE4329	71.6	29.20	1.96	1.00	0.04	-30.10
77	IE2335	80.4	32.61	0.65	0.83	0.25	79.27	577	IE4339	72.9	38.60	1.79	0.93	0.16	64.22
78	IE2336	79.1	33.36	0.33	1.30	0.16	-54.24	578	IE4340	68.6	14.33	1.42	1.20	0.04	-27.12
79	IE2337	76.6	55.52	0.63	1.00	0.01	15.05	579	IE4347	69.2	15.29	1.48	1.13	0.37	82.25
80	IE2339	73.7	123.37	0.22	1.97	0.57	-67.35	580	IE4350	71.3	20.80	1.68	1.07	0.06	-35.61
81	IE234	67.3	373.92	2.98	1.10	0.21	-73.75	581	IE4368	73.4	28.12	1.40	1.23	0.10	-53.19
82	IE2340	71.6	261.64	-5.21	1.40	0.21	-7.60	582	IE4376	72.4	17.37	1.31	0.83	0.04	32.63
83	IE2341	81.4	19.22	-1.33	0.93	0.16	64.22	583	IE4377	68.4	20.92	1.73	1.07	0.01	11.03
84	IE2345	82.3	33.49	1.63	0.67	0.10	51.70	584	IE4383	70.3	29.73	2.07	0.90	0.21	-61.68
85	IE2350	78.3	41.64	0.67	0.97	0.12	54.68	585	IE4386	63.8	19.20	-1.56	1.00	0.07	-43.66
86	IE2353	80.8	48.20	1.54	1.30	0.19	48.12	586	IE44	66.4	107.61	3.43	0.80	0.21	73.75
87	IE2354	78.0	29.85	0.00	0.93	0.00	4.02	587	IE4401	72.0	32.01	2.08	0.77	0.06	36.66
88	IE2355	75.8	78.90	0.25	0.77	0.06	36.66	588	IE4403	73.9	47.02	-0.75	1.20	0.13	46.64
89	IE2356	78.7	39.76	0.27	0.73	0.08	47.68	589	IE4414	67.4	2.83	-0.64	1.23	0.06	8.49
90	IE2358	79.2	41.46	0.19	1.13	0.05	22.05	590	IE4425	57.6	85.17	-0.44	0.90	0.16	60.19
91	IE2361	76.7	116.08	2.17	0.97	0.01	-19.07	591	IE4431	55.3	135.74	0.50	1.00	0.43	91.78
92	IE2362	77.4	54.61	-1.23	1.07	0.04	26.07	592	IE4432	55.3	159.20	-1.40	0.97	0.06	-35.61
93	IE2363	80.1	46.32	0.52	2.37	5.20	210.97	593	IE4442	64.5	181.37	4.30	0.73	0.21	76.29
94	IE2364	79.7	54.04	0.63	0.83	0.08	-27.56	594	IE4443	67.3	71.21	2.98	1.00	0.09	-45.15
95	IE2365	78.1	63.37	1.45	0.60	0.21	69.29	595	IE4446	66.1	35.24	2.03	1.10	0.01	1.49
96	IE2366	77.8	56.37	0.22	0.87	0.04	6.56	596	IE4450	78.8	72.65	2.48	0.83	0.25	79.27
97	IE2367	77.9	44.32	0.73	0.73	0.06	1.05	597	IE4462	73.2	38.61	-1.15	1.23	0.76	113.83
98	IE2368	78.5	28.84	0.17	0.93	0.16	64.22	598	IE4476	69.8	90.32	3.60	1.23	0.17	25.03
99	IE2370	79.3	30.17	-0.04	1.30	0.12	33.08	599	IE4478	71.9	16.12	0.60	1.07	0.00	-4.02
100	IE2372	80.2	142.34	3.26	0.90	0.13	58.71	600	IE4483	69.5	16.48	1.53	1.07	0.01	-19.07
101	IE2378	76.7	44.33	-0.51	1.00	0.03	16.54	601	IE4491	69.5	40.60	2.41	1.00	0.00	0.00
102	IE2379	78.6	30.07	0.28	1.50	1.09	112.79	602	IE4492	72.8	37.87	1.94	1.00	0.04	30.10
103	IE2380	80.5	43.36	1.79	0.80	0.07	42.17	603	IE4497	74.0	38.44	2.00	1.10	0.03	16.54
104	IE2384	78.9	39.66	0.07	1.00	0.49	105.34	604	IE4519	73.8	24.17	1.23	0.93	0.32	-72.71
105	IE2386	82.9	70.42	2.72	0.97	0.04	-34.12	605	IE4525	71.8	4.10	0.39	1.10	0.43	-103.85
106	IE2393	81.2	25.00	1.25	1.03	0.01	-8.05	606	IE4529	70.9	73.53	3.25	0.93	0.01	-11.03
107	IE2395	81.5	38.06	0.39	1.10	0.07	31.59	607	IE454	72.3	7.06	0.67	1.27	0.66	-134.99
108	IE2396	79.5	39.43	0.80	1.00	0.21	61.68	608	IE4545	70.3	6.44	0.02	0.60	0.13	39.19
109	IE2399	78.8	30.37	0.38	0.97	0.09	41.12	609	IE4554	67.9	12.73	1.20	0.77	0.24	81.80
110	IE24	77.6	39.81	0.71	1.07	0.08	-47.68	610	IE4563	70.6	0.42	0.17	0.87	0.01	8.05
111	IE2402	78.7	35.49	0.13	1.50	0.25	7.45	611	IE4565	70.7	15.96	1.44	1.30	0.07	-25.63
112	IE2407	80.0	15.86	0.66	1.03	0.10	-53.19	612	IE4568	68.6	4.97	0.77	0.93	0.00	4.02
113	IE2408	77.8	35.56	0.23	0.90	0.43	103.85	613	IE4570	68.1	9.04	1.13	1.00	0.09	-45.15
114	IE2410	78.9	35.90	1.20	1.50	0.28	-21.16	614	IE4578	68.7	4.64	0.82	1.57	0.36	-86.87
115	IE2413	76.0	38.19	-1.07	1.00	0.43	91.78	615	IE4584	70.8	27.81	1.83	0.97	0.01	-19.07
116	IE2416	78.0	63.44	0.91	0.93	0.02	-24.59	616	IE4585	71.6	18.97	0.99	1.00	0.01	15.05
117	IE2425	76.2	40.69	-0.35	0.93	0.25	79.27	617	IE4586	69.6	28.57	2.01	1.00	0.00	0.00
118	IE2427	74.9	94.96	0.39	0.97	0.00	-4.02	618	IE4594	72.5	31.92	1.33	1.20	0.03	-28.61
119	IE2430	74.4	83.30	0.40	1.10	0.13	-58.71	619	IE4600	67.9	60.37	2.94	0.93	0.58	-102.81
120	IE2437	76.7	30.72	-0.58	0.80	0.19	72.27	620	IE4622	71.8	27.09	1.66	0.70	0.07	25.63
121	IE2439	81.0	37.12	1.82	1.00	0.09	45.15	621	IE4630	75.9	87.62	3.05	0.90	0.57	-106.83
122	IE2440	75.7	61.64	0.67	0.77	0.10	-37.10	622	IE4646	73.8	50.31	1.71	1.00	0.01	15.05
123	IE2441	77.3	54.82	-1.76	0.87	0.37	98.34	623	IE4647	71.7	22.36	-0.02	1.07	0.25	71.22
124	IE2452	78.3	37.96	0.88	0.83	0.08	-27.56	624	IE4649	68.5	4.32	0.79	1.07	0.01	-19.07
125	IE2457	79.4	48.85	1.22	1.67	0.34	-25.19	625	IE4651	67.3	5.06	-0.71	0.73	0.21	-44.10
126	IE2461	79.0	49.74	0.58	1.30	0.07	-10.58	626	IE4653	68.4	9.01	1.08	0.77	0.05	38.14
127	IE2476	77.1	110.82	2.23	0.80	0.04	27.12	627	IE4658	65.3	4.75	-0.77	0.63	0.10	14.61
128	IE2486	74.0	74.41	-1.77	1.17	0.04	-32.63	628	IE4671	65.5	30.14	1.92	1.07	0.06	-35.61

S.no	Accession	Days t0 50% Flowering (days)			Plot yield (tn ha^{-1})			S.no	Accession	Days t0 50% Flowering (days)			Plot yield (tn ha^{-1})		
		Mean	b	S^2d	Mean	b	S^2d			Mean	b	S^2d	Mean	b	S^2d
129	IE2487	78.8	36.01	0.14	0.93	0.09	-41.12	629	IE4677	69.7	21.82	1.76	0.83	0.04	-26.07
130	IE2489	75.7	86.26	1.80	1.43	0.20	11.47	630	IE4679	66.1	28.70	1.80	0.93	0.00	-9.54
131	IE2495	71.4	111.02	-1.08	0.97	0.09	41.12	631	IE4680	68.8	4.89	0.39	0.97	0.26	83.29
132	IE2498	76.2	52.99	-1.32	0.83	0.01	19.07	632	IE4688	71.9	107.52	3.77	1.10	0.25	-75.24
133	IE2500	77.9	40.36	0.51	1.17	0.04	12.51	633	IE4699	74.0	50.89	1.75	1.07	0.09	-49.17
134	IE2502	75.0	111.52	2.01	1.83	2.08	137.81	634	IE4700	63.9	226.92	-5.70	0.87	0.12	-50.66
135	IE2503	71.6	122.26	-1.09	1.23	0.08	-20.12	635	IE4708	67.1	55.05	2.80	1.43	0.16	-48.73
136	IE2504	74.6	105.42	1.61	1.00	0.04	-30.10	636	IE4709	62.1	32.53	0.81	0.77	0.02	-20.56
137	IE2517	72.9	106.75	0.47	1.37	0.30	45.59	637	IE4711	63.1	181.92	4.52	0.83	0.44	107.87
138	IE252	70.9	209.26	0.11	1.10	0.07	31.59	638	IE4716	72.9	33.85	1.46	1.07	0.01	11.03
139	IE2523	69.8	207.29	-4.33	1.13	0.02	-23.10	639	IE4725	73.4	48.30	1.90	1.00	0.09	-45.15
140	IE2525	74.8	82.09	0.99	1.13	0.24	53.64	640	IE4726	67.0	88.44	-3.45	0.97	0.09	41.12
141	IE2528	78.5	112.44	3.24	0.87	0.12	54.68	641	IE4734	56.9	110.66	-1.27	1.10	0.04	2.98
142	IE2531	76.8	141.56	2.30	1.03	0.00	5.51	642	IE4755	60.5	63.96	2.15	0.80	0.01	-1.49
143	IE2532	69.1	154.82	-1.24	1.13	0.24	-81.80	643	IE4757	59.6	68.57	-2.80	0.60	0.21	-21.01
144	IE2533	75.3	92.89	-2.94	0.97	0.12	-50.66	644	IE4759	63.6	167.23	4.33	1.00	0.00	0.00
145	IE2534	78.0	21.61	0.07	1.10	0.01	1.49	645	IE4789	65.9	0.28	-0.20	1.13	0.01	-8.05
146	IE2535	75.9	54.62	-0.80	1.03	0.17	-68.24	646	IE4795	69.0	40.87	2.41	0.93	0.00	4.02
147	IE2536	79.2	41.17	0.76	0.60	0.12	24.14	647	IE4797	67.8	7.86	1.02	0.80	0.19	-34.57
148	IE2539	75.4	90.70	1.31	0.63	0.06	31.14	648	IE4800	65.9	13.45	-1.16	1.60	0.25	7.45
149	IE2540	77.0	65.61	1.21	0.80	0.04	-2.98	649	IE4801	66.7	10.99	1.25	0.87	0.10	53.19
150	IE2546	84.6	16.64	1.42	0.57	0.12	50.21	650	IE4808	72.4	203.10	5.30	1.13	0.04	-21.61
151	IE2549	73.8	115.93	0.77	0.93	0.01	-11.03	651	IE4816	69.7	102.06	-2.86	1.10	0.04	-27.12
152	IE2551	72.8	92.77	-0.13	0.87	0.26	-67.20	652	IE4817	66.4	19.62	1.67	0.93	0.04	34.12
153	IE2561	71.4	109.81	-1.07	0.93	0.20	-69.73	653	IE4821	66.8	12.85	1.30	1.10	0.01	-13.56
154	IE2564	78.2	30.02	0.06	1.10	0.03	16.54	654	IE4826	75.3	367.45	7.02	1.30	0.52	93.27
155	IE2568	87.5	25.69	-0.99	0.97	0.06	39.63	655	IE4842	84.9	250.41	1.50	1.17	0.02	-17.58
156	IE2572	89.8	24.96	0.94	0.90	0.01	13.56	656	IE4866	74.1	60.04	-0.39	1.07	0.00	-5.51
157	IE2573	87.4	17.72	-0.28	1.13	0.05	22.05	657	IE4887	70.0	22.74	1.49	1.30	0.21	-69.29
158	IE2574	83.5	13.08	1.35	1.33	0.14	-33.68	658	IE4889	74.8	83.86	2.39	0.93	0.01	-11.03
159	IE2576	74.0	93.40	-0.18	1.03	0.00	-9.54	659	IE4890	64.7	113.49	-3.91	0.90	0.01	-15.05
160	IE2581	80.5	37.00	1.73	1.10	0.01	13.56	660	IE49	65.4	256.57	5.66	0.97	0.20	69.73
161	IE2586	81.0	41.90	1.79	0.90	0.13	-46.64	661	IE4905	68.8	26.81	-1.07	0.93	0.01	19.07
162	IE2587	77.8	41.62	0.54	0.80	0.03	12.07	662	IE4909	69.6	43.14	2.37	0.93	0.04	-26.07
163	IE2589	82.0	58.87	2.38	0.73	0.14	-42.61	663	IE4911	70.3	22.93	1.13	0.77	0.24	-53.64
164	IE2590	75.9	65.37	-0.91	0.87	0.01	8.05	664	IE4916	69.5	19.75	0.81	0.97	0.01	11.03
165	IE2591	72.8	82.41	0.16	1.10	0.07	-43.66	665	IE4917	72.5	43.92	1.52	0.93	0.01	19.07
166	IE2593	75.4	75.44	0.23	0.77	0.26	83.29	666	IE4919	72.5	43.33	1.49	0.97	0.01	-19.07
167	IE2594	80.1	30.52	1.36	0.77	0.10	-23.54	667	IE4930	72.0	66.04	2.65	0.77	0.06	-8.49
168	IE2596	72.6	111.88	-0.91	1.00	0.07	31.59	668	IE4950	71.8	57.76	2.47	0.90	0.01	13.56
169	IE2598	78.2	40.53	1.17	1.07	0.20	-65.71	669	IE4956	75.3	103.03	2.78	0.87	0.17	-52.15
170	IE2604	75.7	55.74	0.51	1.60	0.76	-141.55	670	IE4957	72.0	32.68	0.63	1.10	0.04	2.98
171	IE2606	80.9	25.14	1.50	0.77	0.16	66.75	671	IE4963	68.4	12.27	0.78	1.00	0.03	-28.61
172	IE2608	80.3	23.71	0.61	0.90	0.07	-31.59	672	IE4972	72.0	52.32	1.78	1.07	0.01	-19.07
173	IE2609	83.8	4.36	0.60	0.97	0.02	-20.56	673	IE4975	70.3	42.58	1.92	0.93	0.02	17.58
174	IE2611	81.1	36.96	1.39	0.90	0.07	43.66	674	IE4984	70.3	25.06	0.65	1.03	0.02	-24.59
175	IE2613	78.6	37.82	0.56	1.07	0.00	-4.02	675	IE4986	70.0	78.03	3.24	0.83	0.14	-42.61
176	IE2614	82.3	46.17	2.24	0.83	0.10	14.61	676	IE4990	71.7	35.89	1.18	0.80	0.07	-31.59
177	IE2619	83.3	21.63	1.41	1.07	0.09	41.12	677	IE4991	70.7	12.52	1.18	0.93	0.36	94.32
178	IE2621	73.7	84.54	0.05	1.13	0.12	-54.68	678	IE4992	70.2	45.44	2.43	1.43	0.34	-93.87
179	IE2622	71.7	173.84	-0.94	1.13	0.02	20.56	679	IE4997	72.2	45.16	1.69	0.87	0.02	-7.00
180	IE2627	70.0	171.25	-2.07	0.77	0.10	51.70	680	IE4998	71.0	49.04	2.29	1.17	0.06	-1.05
181	IE2633	78.8	28.46	-0.37	1.27	0.44	87.76	681	IE4999	73.1	25.57	1.31	0.93	0.02	-24.59
182	IE2636	85.9	8.74	0.86	0.77	0.05	38.14	682	IE5005	68.1	6.13	0.84	1.03	0.06	35.61
183	IE2638	84.6	25.05	1.80	1.30	0.07	-10.58	683	IE5008	68.4	21.20	1.52	0.97	0.12	-50.66
184	IE2644	80.4	38.20	1.57	1.13	0.01	-11.03	684	IE5009	61.4	43.72	-2.41	1.10	0.01	1.49
185	IE2645	82.7	7.34	0.96	0.57	0.17	65.26	685	IE501	62.8	193.50	4.79	0.87	0.01	8.05
186	IE2649	84.7	10.27	1.15	1.27	0.02	-2.53	686	IE5022	71.0	59.23	2.39	1.00	0.04	-30.10
187	IE2652	79.2	29.49	-1.62	1.13	0.00	5.51	687	IE5023	70.0	33.20	-0.39	0.87	0.20	-65.71
188	IE2653	83.1	48.10	2.15	1.10	0.01	15.05	688	IE5030	71.1	34.76	0.85	0.70	0.16	-5.96
189	IE2656	74.0	100.02	-0.08	1.03	0.06	35.61	689	IE5033	70.7	30.61	1.73	1.37	0.17	-43.21
190	IE2657	84.0	9.61	1.14	1.23	0.10	23.54	690	IE5037	72.2	38.14	1.32	0.90	0.16	-60.19
191	IE2666	72.2	161.49	-1.17	1.13	0.10	37.10	691	IE5043	71.8	44.12	-0.01	1.30	0.07	-25.63
192	IE2669	83.2	2.68	0.55	1.00	0.21	61.68	692	IE5058	68.3	21.97	1.53	1.00	0.01	-15.05

S.no	Accession	Days t0 50% Flowering (days)			Plot yield (tn ha^{-1})			S.no	Accession	Days t0 50% Flowering (days)			Plot yield (tn ha^{-1})		
		Mean	b	S^2d	Mean	b	S^2d			Mean	b	S^2d	Mean	b	S^2d
193	IE2674	81.9	33.97	1.30	1.40	0.61	67.64	693	IE5065	68.3	4.96	0.84	0.93	0.04	-26.07
194	IE2675	89.5	14.01	0.17	1.40	0.13	-55.73	694	IE5066	68.2	12.21	0.71	0.97	0.00	9.54
195	IE2676	85.8	8.57	-0.12	1.50	0.31	22.49	695	IE5087	64.3	112.63	-3.81	1.03	0.12	50.66
196	IE2677	83.6	11.20	1.27	1.30	0.12	33.08	696	IE509	64.1	258.12	5.50	1.30	0.03	-12.07
197	IE2678	85.7	13.14	1.36	1.60	0.31	22.49	697	IE5090	70.3	29.56	1.30	1.67	0.33	-40.24
198	IE2683	86.1	12.90	1.17	0.83	0.00	4.02	698	IE5091	64.6	23.96	-1.84	1.17	0.14	29.05
199	IE2684	84.4	5.69	0.84	1.50	0.12	-24.14	699	IE51	63.3	14.80	0.94	0.93	0.12	50.66
200	IE2685	85.7	21.21	1.65	1.20	0.07	-43.66	700	IE510	67.1	9.45	1.10	1.30	0.07	18.03
201	IE2686	86.5	18.16	1.24	0.80	0.12	-33.08	701	IE5105	71.5	45.70	1.94	1.10	0.09	-45.15
202	IE2688	83.3	18.06	1.55	1.13	0.05	22.05	702	IE5106	70.6	20.58	-0.20	1.20	0.07	-42.17
203	IE2689	81.7	31.36	2.03	1.33	0.24	40.08	703	IE5107	69.6	43.68	2.36	1.03	0.10	-53.19
204	IE2691	81.9	20.94	1.61	1.10	0.01	1.49	704	IE5112	72.5	62.53	2.06	0.83	0.02	2.53
205	IE2694	81.2	0.92	-0.22	1.13	0.05	-38.14	705	IE5113	72.3	51.37	1.67	0.97	0.00	-5.51
206	IE2695	84.4	13.42	1.36	0.90	0.25	75.24	706	IE5120	71.3	11.90	-0.33	0.93	0.36	-86.27
207	IE2698	83.4	6.01	0.88	0.97	0.06	-35.61	707	IE5123	67.0	9.22	1.15	1.00	0.13	-46.64
208	IE2702	83.5	10.00	1.20	1.17	0.01	11.03	708	IE5124	71.4	62.26	2.59	0.83	0.04	32.63
209	IE2703	81.4	20.84	1.62	0.93	0.00	4.02	709	IE5129	68.5	14.94	-0.89	1.23	0.05	22.05
210	IE2704	87.1	29.91	-0.82	1.13	0.05	22.05	710	IE5133	68.6	4.74	0.83	1.17	0.06	-1.05
211	IE2710	82.7	16.30	1.52	1.00	0.01	1.49	711	IE5140	69.3	45.88	2.53	0.63	0.05	16.09
212	IE2712	84.5	12.20	1.29	1.30	0.19	-72.27	712	IE5142	71.7	45.80	1.97	0.87	0.17	68.24
213	IE2713	79.8	33.79	1.88	0.97	0.00	-5.51	713	IE5145	68.9	12.04	0.29	0.77	0.24	-53.64
214	IE2718	76.5	33.30	0.71	0.67	0.04	21.61	714	IE5147	69.2	3.90	0.45	0.90	0.04	-30.10
215	IE2724	82.4	2.11	0.52	0.87	0.02	-7.00	715	IE5149	69.8	69.51	2.90	1.00	0.16	-60.19
216	IE2728	74.9	53.41	0.02	0.83	0.08	-27.56	716	IE5156	71.3	27.66	-0.60	1.03	0.00	5.51
217	IE2729	82.3	20.71	1.72	0.93	0.00	-9.54	717	IE5161	70.3	19.69	1.35	0.87	0.10	53.19
218	IE2732	83.5	26.76	1.94	0.73	0.08	47.68	718	IE5164	67.2	9.12	0.91	1.07	0.00	-5.51
219	IE2737	86.1	8.80	0.89	1.20	0.07	18.03	719	IE5165	69.4	52.57	2.72	0.67	0.08	20.12
220	IE2739	78.7	16.54	-1.20	0.67	0.04	21.61	720	IE5169	74.7	68.44	2.52	1.17	0.14	-61.24
221	IE2741	84.5	24.01	1.85	0.83	0.02	2.53	721	IE5170	74.6	66.22	0.61	0.77	0.08	20.12
222	IE2742	85.9	47.11	2.56	1.00	0.01	13.56	722	IE5173	70.6	24.69	1.23	1.03	0.04	-26.07
223	IE2743	83.4	14.23	1.43	0.97	0.06	39.63	723	IE5177	70.7	14.72	1.33	0.90	0.21	-61.68
224	IE2744	82.1	8.62	1.10	1.30	0.07	-10.58	724	IE5179	66.6	5.50	-0.75	0.67	0.16	-38.59
225	IE2746	82.8	7.27	1.01	1.10	0.03	16.54	725	IE518	68.9	71.14	3.12	1.00	0.03	-16.54
226	IE2748	81.7	26.66	1.94	0.57	0.17	-25.03	726	IE5180	72.2	27.00	0.54	1.17	0.44	-107.87
227	IE2754	78.8	174.74	4.53	1.00	0.03	-16.54	727	IE5182	68.7	6.97	0.59	0.87	0.42	-95.80
228	IE2756	82.2	5.64	0.68	1.03	0.00	5.51	728	IE5186	71.6	103.74	3.67	1.13	0.02	7.00
229	IE2758	82.9	5.88	0.84	1.00	0.25	-75.24	729	IE5187	68.7	31.33	1.89	0.93	0.02	20.56
230	IE2760	83.0	13.71	1.40	1.10	0.07	31.59	730	IE5193	71.7	36.84	1.78	0.83	0.14	-42.61
231	IE2765	82.5	17.46	1.58	0.73	0.22	77.78	731	IE5198	74.3	77.42	1.65	1.00	0.04	-30.10
232	IE2769	82.2	40.84	2.24	1.10	0.03	16.54	732	IE5201	69.4	41.29	-1.35	0.97	0.02	-20.56
233	IE2771	75.0	55.87	0.00	0.73	0.41	-74.20	733	IE5206	66.4	18.09	1.61	1.07	0.02	-2.53
234	IE2772	83.6	13.74	1.40	1.10	0.21	61.68	734	IE5208	69.0	30.44	1.96	1.23	0.04	-21.61
235	IE2773	84.9	18.70	1.54	1.03	0.00	5.51	735	IE5214	69.1	22.30	1.16	1.07	0.04	26.07
236	IE2777	82.5	10.02	1.12	1.13	0.16	-66.75	736	IE5215	67.1	9.39	1.16	0.43	0.16	28.16
237	IE2779	77.0	86.52	2.83	1.20	0.03	-12.07	737	IE5229	68.7	28.09	1.87	0.57	0.22	47.24
238	IE2780	78.4	19.74	0.97	1.00	0.43	-91.78	738	IE5231	69.2	15.00	1.23	1.17	0.32	-92.83
239	IE2781	77.5	8.77	0.37	0.97	0.09	41.12	739	IE5232	66.1	0.37	-0.17	0.90	0.39	102.36
240	IE2787	75.7	144.27	3.48	0.57	0.08	20.12	740	IE5239	68.8	4.12	0.45	1.07	0.06	-35.61
241	IE2789	79.1	9.72	0.97	1.47	0.66	-132.02	741	IE5245	67.9	22.92	1.60	1.23	0.06	-36.66
242	IE2790	78.6	20.84	1.15	0.87	0.17	-52.15	742	IE5248	67.5	3.77	-0.32	0.80	0.27	-49.61
243	IE2794	73.4	76.70	0.67	1.07	0.04	12.51	743	IE525	70.3	53.36	2.67	1.13	0.02	-23.10
244	IE2799	91.9	65.71	1.94	0.97	0.16	-64.22	744	IE5250	72.0	31.30	1.94	1.47	0.52	-119.95
245	IE2816	77.9	58.46	-2.55	1.00	0.02	-20.28	745	IE5260	69.8	5.47	0.26	0.67	0.24	-40.08
246	IE2818	66.6	128.50	-1.55	0.63	0.05	16.09	746	IE5281	71.2	65.42	2.94	1.20	0.07	-42.17
247	IE2820	66.3	152.91	-0.56	0.73	0.14	-42.61	747	IE5292	72.1	55.29	1.70	0.83	0.32	-72.71
248	IE2821	70.3	82.86	0.92	0.90	0.04	-2.98	748	IE5295	69.6	15.62	-0.03	1.23	0.17	-68.24
249	IE2822	83.7	14.89	1.30	1.13	0.12	-54.68	749	IE5297	69.4	42.76	2.26	1.10	0.07	-43.66
250	IE2825	76.3	20.57	-1.55	1.00	0.01	15.05	750	IE5306	70.6	20.37	0.58	1.07	0.00	-4.02
251	IE2827	78.8	97.12	3.55	1.00	0.00	0.00	751	IE5314	70.2	84.92	3.41	0.80	0.03	-16.54
252	IE2836	74.1	53.92	-2.58	0.83	0.06	31.14	752	IE5315	71.3	65.42	2.77	0.50	0.19	22.65
253	IE2838	74.6	146.36	3.91	0.87	0.37	-82.25	753	IE5317	69.8	12.65	-0.09	1.10	0.04	-30.10
254	IE2839	71.0	119.11	-3.57	0.90	0.03	-16.54	754	IE5320	69.4	38.52	2.21	1.10	0.16	-60.19
255	IE2850	69.8	165.61	2.28	0.90	0.03	-16.54	755	IE5321	68.3	10.89	0.66	1.43	0.17	-65.26
256	IE2851	73.7	43.64	-1.87	1.07	0.14	42.61	756	IE5328	70.2	42.92	2.34	0.87	0.46	111.90

S.no	Accession	Days t0 50% Flowering (days)			Plot yield (tn ha^{-1})			S.no	Accession	Days t0 50% Flowering (days)			Plot yield (tn ha^{-1})		
		Mean	b	S^2d	Mean	b	S^2d			Mean	b	S^2d	Mean	b	S^2d
257	IE2855	83.9	15.04	0.60	1.03	0.06	35.61	757	IE5331	71.3	41.13	2.15	1.10	0.19	-72.27
258	IE2857	81.9	57.04	2.84	0.70	0.19	70.78	758	IE5336	66.5	60.14	2.90	0.80	0.07	43.66
259	IE2858	85.1	33.64	1.59	1.00	0.07	31.59	759	IE5337	68.4	13.74	0.68	0.80	0.03	12.07
260	IE2860	81.8	16.54	1.37	0.87	0.04	6.56	760	IE5339	65.5	1.77	-0.23	1.27	0.32	-92.83
261	IE2861	82.6	20.29	1.66	1.10	0.09	-45.15	761	IE5342	69.8	124.17	4.10	1.13	0.10	-53.19
262	IE2868	81.8	21.10	1.60	0.83	0.04	32.63	762	IE5343	71.0	33.08	-0.48	1.10	0.04	2.98
263	IE2869	82.6	38.20	2.33	1.10	0.03	16.54	763	IE5345	69.2	20.84	1.14	1.33	0.06	-36.66
264	IE2871	82.4	21.91	1.70	1.13	0.50	-113.39	764	IE5349	68.3	20.32	0.39	1.13	0.04	-26.07
265	IE2872	76.5	87.46	3.13	0.90	0.01	13.56	765	IE5350	70.3	67.62	2.86	1.17	0.58	-122.92
266	IE2873	81.8	52.77	2.74	1.03	0.02	20.56	766	IE5354	73.0	88.49	1.99	1.07	0.01	11.03
267	IE2875	86.3	89.04	3.29	0.63	0.12	-0.44	767	IE5359	71.9	35.06	1.19	0.67	0.26	-26.52
268	IE2881	79.1	49.72	2.58	1.00	0.25	75.24	768	IE5362	69.8	58.30	2.60	0.53	0.10	14.61
269	IE2882	83.8	11.08	1.16	0.80	0.04	-2.98	769	IE5364	71.8	61.37	1.71	1.10	0.28	63.17
270	IE2884	83.2	12.09	0.10	0.73	0.04	32.63	770	IE5367	70.6	57.52	2.24	0.90	0.09	-45.15
271	IE2888	82.2	20.56	1.49	0.77	0.06	-8.49	771	IE5374	67.7	8.81	0.96	0.77	0.14	33.68
272	IE2890	82.5	28.52	1.97	0.83	0.09	49.17	772	IE5377	68.7	30.60	2.07	0.87	0.10	51.70
273	IE2891	82.9	8.71	1.10	1.30	0.27	49.61	773	IE5378	65.6	22.89	1.71	1.23	0.06	8.49
274	IE2896	82.8	10.61	1.15	1.17	0.16	66.75	774	IE5379	68.1	41.59	2.02	1.03	0.12	-54.68
275	IE2903	81.9	34.64	2.10	1.00	0.01	13.56	775	IE5383	69.0	28.51	-0.03	0.80	0.37	100.87
276	IE2907	80.4	5.59	-0.83	0.80	0.03	12.07	776	IE5384	71.1	71.41	2.61	1.03	0.00	5.51
277	IE2909	78.8	68.50	3.07	1.17	0.04	12.51	777	IE5386	70.3	30.40	0.59	1.20	0.39	78.22
278	IE2910	82.0	13.23	1.12	1.33	0.44	70.17	778	IE5388	74.0	430.51	-5.85	0.97	0.09	-49.17
279	IE2911	84.6	21.97	0.94	0.87	0.02	23.10	779	IE5390	67.6	125.66	4.23	1.17	0.44	87.76
280	IE2913	80.3	35.21	2.22	1.03	0.04	34.12	780	IE5393	69.7	36.79	0.56	1.13	0.02	-24.59
281	IE2914	77.9	41.12	-2.40	1.17	0.04	12.51	781	IE5406	62.8	54.14	-2.76	1.63	0.20	-69.73
282	IE2921	81.3	39.20	-2.24	0.83	0.09	-41.12	782	IE5407	69.5	69.74	2.78	0.83	0.16	64.22
283	IE2932	79.0	73.97	3.14	1.35	0.13	-50.71	783	IE5416	71.2	67.57	1.07	1.00	0.16	60.19
284	IE2938	84.7	35.89	1.33	1.33	0.04	-6.56	784	IE5417	70.8	81.50	1.79	1.17	0.08	27.56
285	IE2939	89.5	179.84	4.36	1.23	0.00	-9.54	785	IE5418	69.2	29.84	0.14	0.67	0.12	-9.98
286	IE2941	83.5	19.20	1.56	1.03	0.01	-11.03	786	IE5419	69.7	56.25	2.02	1.07	0.14	-62.73
287	IE2945	82.2	2.00	0.52	0.63	0.10	14.61	787	IE5421	66.8	36.22	-1.06	0.93	0.04	-26.07
288	IE2953	80.6	29.14	1.87	0.70	0.16	54.24	788	IE5424	70.8	177.69	4.70	1.40	0.93	111.30
289	IE2954	82.6	95.72	3.71	1.10	0.03	16.54	789	IE5429	72.8	103.90	1.61	0.87	0.02	-7.00
290	IE2956	71.4	250.56	-5.97	0.83	0.04	32.63	790	IE5435	70.2	27.36	0.45	1.13	0.02	7.00
291	IE2957	71.6	483.32	6.71	0.60	0.13	9.09	791	IE5442	69.0	32.80	0.14	1.03	0.09	-41.12
292	IE2962	81.4	25.41	1.60	1.40	0.13	-55.73	792	IE5457	67.1	55.63	2.70	1.13	0.34	68.69
293	IE2968	74.0	50.53	1.54	1.00	0.13	58.71	793	IE546	61.8	17.92	1.60	1.23	0.01	-8.05
294	IE2971	79.9	46.54	2.58	1.10	0.04	-27.12	794	IE5472	67.8	63.04	2.93	1.00	0.25	75.24
295	IE2983	81.3	72.06	3.21	1.13	0.05	22.05	795	IE5475	68.5	40.27	0.86	0.80	0.12	57.22
296	IE2992	77.0	8.90	-1.12	0.90	0.03	28.61	796	IE5480	67.7	31.24	1.68	1.27	0.08	-47.68
297	IE2996	72.7	38.12	0.77	1.53	0.72	59.59	797	IE5485	68.7	48.08	2.25	0.63	0.16	59.75
298	IE2997	73.2	41.13	-0.10	1.00	0.09	45.15	798	IE5488	64.5	7.69	-0.02	1.17	0.04	-34.12
299	IE2999	73.2	37.72	1.28	0.83	0.44	107.87	799	IE5491	69.2	110.41	3.62	1.30	0.09	4.47
300	IE3000	71.0	58.60	1.33	1.03	0.02	20.56	800	IE5492	66.8	42.94	1.73	0.83	0.00	4.02
301	IE3015	76.4	47.53	2.41	1.00	0.00	0.00	801	IE5494	69.2	82.14	2.33	1.13	0.05	22.05
302	IE3022	85.2	101.06	3.60	1.10	0.19	48.12	802	IE5495	69.2	56.76	1.43	1.30	0.19	48.12
303	IE3025	77.8	304.84	-6.49	0.90	0.43	103.85	803	IE5496	69.1	87.03	2.97	0.73	0.08	47.68
304	IE3028	69.6	73.71	1.08	0.87	0.10	-37.10	804	IE5502	69.4	82.14	2.59	1.03	0.16	64.22
305	IE3038	75.7	83.29	3.24	1.17	0.21	44.10	805	IE5517	68.5	69.51	2.90	0.70	0.19	-48.12
306	IE3045	74.2	9.82	-0.97	0.93	0.12	50.66	806	IE5519	72.9	145.20	3.55	0.77	0.02	23.10
307	IE3046	77.9	36.73	2.29	0.97	0.24	81.80	807	IE5525	68.3	54.24	1.10	0.63	0.16	-15.49
308	IE3062	85.9	76.39	2.75	1.43	0.44	-108.92	808	IE5537	62.2	16.58	-1.20	0.70	0.19	72.27
309	IE3066	67.6	77.96	-2.07	0.77	0.02	23.10	809	IE5542	66.7	157.69	4.73	1.30	0.28	36.05
310	IE3070	72.2	70.08	2.21	0.73	0.30	89.85	810	IE5545	73.3	116.72	2.86	0.90	0.25	75.24
311	IE3073	77.1	8.64	1.11	0.60	0.13	-19.52	811	IE5563	72.3	100.33	1.92	0.73	0.09	-14.00
312	IE3075	72.7	24.72	-1.73	1.00	0.09	-45.15	812	IE5578	65.3	30.87	-1.15	0.90	0.01	15.05
313	IE3077	69.7	71.74	-0.71	0.73	0.06	1.05	813	IE5584	66.6	51.89	1.90	0.97	0.30	84.78
314	IE3094	68.4	47.20	-0.71	1.10	0.19	48.12	814	IE5591	62.1	7.62	-0.46	1.07	0.01	11.03
315	IE3096	67.0	87.88	-1.88	0.73	0.06	31.14	815	IE5597	61.8	7.52	-0.61	0.90	0.25	-75.24
316	IE3101	62.3	184.16	-2.24	1.33	0.14	-18.63	816	IE5620	61.8	11.46	1.28	1.13	0.06	35.61
317	IE3104	63.1	166.45	0.59	1.30	0.37	51.10	817	IE563	62.6	8.25	0.48	0.70	0.19	70.78
318	IE3106	66.7	85.00	0.19	1.07	0.04	12.51	818	IE5635	69.9	171.73	4.73	0.80	0.04	27.12
319	IE3111	71.4	65.14	1.41	0.83	0.09	49.17	819	IE5647	70.0	78.64	-0.41	1.03	0.00	-9.54
320	IE3114	69.1	62.41	-2.15	1.23	0.06	-36.66	820	IE5653	65.8	27.89	1.17	0.83	0.14	-42.61

S.no	Accession	Days t0 50% Flowering (days)			Plot yield (tn ha^{-1})			S.no	Accession	Days t0 50% Flowering (days)			Plot yield (tn ha^{-1})		
		Mean	b	S^{2}d	Mean	b	S^{2}d			Mean	b	S^{2}d	Mean	b	S^{2}d
321	IE3119	67.0	98.08	-1.74	0.87	0.01	8.05	821	IE5672	70.8	180.60	4.43	0.80	0.13	-19.52
322	IE3120	66.6	80.05	0.22	0.97	0.02	24.59	822	IE5689	75.0	205.49	3.34	0.93	0.01	19.07
323	IE3124	70.8	48.37	0.74	1.17	0.14	29.05	823	IE5711	66.5	88.02	-2.49	1.00	0.16	-60.19
324	IE3127	77.5	74.01	3.02	1.27	0.30	59.15	824	IE5733	58.8	4.44	-0.69	1.07	0.64	116.37
325	IE3128	78.7	29.74	2.01	1.10	0.03	16.54	825	IE5736	66.5	157.86	4.73	1.13	0.01	-8.05
326	IE3129	78.2	23.66	1.83	0.97	0.02	-20.56	826	IE5748	64.4	38.92	-1.59	1.10	0.00	0.00
327	IE3130	75.4	1.03	0.35	0.83	0.04	-12.51	827	IE5782	62.9	4.21	0.42	1.03	0.20	-69.73
328	IE3134	75.3	8.84	1.04	1.17	0.08	27.56	828	IE5788	61.7	2.23	-0.46	0.73	0.14	-29.05
329	IE3135	72.4	12.36	0.70	0.97	0.20	69.73	829	IE5791	62.6	18.70	1.62	0.70	0.04	-2.98
330	IE3136	76.4	135.31	4.32	0.93	0.09	49.17	830	IE5794	62.3	14.50	1.43	0.47	0.14	18.63
331	IE3157	80.7	18.61	-0.96	0.83	0.14	-42.61	831	IE5806	59.3	26.84	-1.96	1.17	0.06	-31.14
332	IE3165	74.6	10.69	-0.10	0.93	0.01	-11.03	832	IE581	56.5	80.26	2.64	1.03	0.01	-11.03
333	IE3169	79.8	62.12	2.98	0.63	0.10	14.61	833	IE5812	64.4	41.12	1.96	1.03	0.20	-69.73
334	IE3174	80.3	17.44	1.43	0.67	0.24	-40.08	834	IE5813	64.2	22.75	0.40	1.27	0.52	-119.95
335	IE3175	75.0	2.34	-0.57	0.77	0.01	8.05	835	IE5817	62.4	1.70	0.02	0.67	0.24	-53.64
336	IE3176	82.0	26.76	1.53	0.90	0.21	73.75	836	IE5831	63.1	10.92	0.23	0.70	0.12	-33.08
337	IE3187	80.4	49.70	2.20	1.23	0.04	-6.56	837	IE5845	66.6	55.74	1.90	0.80	0.12	-33.08
338	IE3194	82.3	43.03	1.18	0.93	0.04	-26.07	838	IE5862	61.6	20.32	-1.24	0.70	0.28	-63.17
339	IE3196	84.5	73.97	-0.10	1.13	0.02	7.00	839	IE5870	69.7	153.76	4.21	1.17	0.14	42.61
340	IE3199	77.4	12.52	-0.67	0.70	0.27	85.82	840	IE5873	66.5	90.91	-2.62	0.83	0.04	-26.07
341	IE3203	77.1	62.41	2.88	1.10	0.03	16.54	841	IE5875	60.3	0.56	0.20	0.80	0.13	58.71
342	IE3207	83.1	63.00	1.36	1.47	0.36	-86.87	842	IE5876	62.0	4.20	0.23	0.97	0.02	-20.56
343	IE3208	85.4	81.33	2.30	0.90	0.04	30.10	843	IE5877	57.4	39.86	-2.37	0.93	0.30	80.76
344	IE3223	79.8	74.45	3.25	0.57	0.20	63.77	844	IE588	63.3	143.10	4.52	0.83	0.22	-57.66
345	IE3225	80.8	91.32	-2.56	1.00	0.07	-31.59	845	IE5896	62.3	40.93	-2.23	1.37	0.17	-43.21
346	IE3238	73.0	16.10	1.04	0.67	0.08	20.12	846	IE593	67.4	54.49	0.56	0.73	0.04	32.63
347	IE3248	71.2	7.32	0.31	2.17	1.84	43.94	847	IE5945	65.1	122.44	-3.53	0.87	0.06	-35.61
348	IE3254	70.9	21.07	1.20	0.93	0.36	-86.27	848	IE595	68.7	243.03	5.85	0.57	0.12	50.21
349	IE3255	70.4	59.45	2.21	0.70	0.13	-19.52	849	IE5956	64.9	86.17	-2.59	0.77	0.10	53.19
350	IE3257	73.2	18.42	1.36	0.80	0.09	-4.47	850	IE5960	63.0	50.53	2.68	0.70	0.07	42.17
351	IE3270	72.4	2.47	-0.35	0.97	0.25	-79.27	851	IE5961	67.7	43.77	1.92	1.30	0.09	-40.68
352	IE3278	76.1	64.33	2.97	0.73	0.05	16.09	852	IE5968	68.4	70.61	2.35	0.60	0.21	69.29
353	IE3280	73.2	0.91	0.24	0.80	0.39	-78.22	853	IE5992	64.9	24.54	-0.53	1.00	0.03	-28.61
354	IE3287	73.5	19.81	1.01	1.27	0.04	-32.63	854	IE5999	62.6	6.73	0.50	1.03	0.00	5.51
355	IE3291	72.5	13.51	1.19	1.13	0.04	-21.61	855	IE6	59.2	27.21	-1.97	0.97	0.36	-94.32
356	IE3308	71.5	7.03	0.05	0.97	0.12	54.68	856	IE600	61.9	253.56	5.88	0.57	0.08	20.12
357	IE3313	71.7	28.33	1.57	1.07	0.36	86.27	857	IE6012	61.8	86.89	-3.20	0.53	0.10	29.65
358	IE3317	71.7	21.28	-1.34	1.07	0.01	-19.07	858	IE6013	61.5	352.30	6.98	0.60	0.13	55.73
359	IE3329	68.9	39.70	1.21	0.93	0.01	-11.03	859	IE6020	67.7	70.39	1.69	0.60	0.13	9.09
360	IE3330	70.5	42.04	0.84	1.07	0.01	-19.07	860	IE6025	69.7	122.34	3.13	1.03	0.00	5.51
361	IE3334	73.9	55.47	2.43	1.27	0.66	90.74	861	IE6029	69.9	65.50	-0.44	0.77	0.24	-40.08
362	IE3338	72.4	14.29	1.16	1.00	0.21	73.75	862	IE603	70.4	150.02	4.17	1.30	0.07	-42.17
363	IE3339	78.1	54.84	2.80	1.03	0.00	-9.54	863	IE6033	69.5	82.62	-0.24	1.20	0.21	-73.75
364	IE3340	75.1	17.76	-1.49	0.73	0.06	31.14	864	IE6055	65.6	38.60	1.27	0.60	0.16	-5.96
365	IE3357	103.8	2145.96	-11.45	1.30	0.12	33.08	865	IE6059	67.1	36.70	0.83	0.73	0.30	-59.15
366	IE3358	72.6	3.09	-0.29	1.17	0.14	-61.24	866	IE6072	66.4	39.66	2.24	0.97	0.02	-20.56
367	IE336	75.7	24.57	1.83	1.17	0.44	-107.87	867	IE6074	65.0	57.24	-1.94	0.77	0.05	38.14
368	IE3363	72.3	3.66	0.35	1.23	0.06	8.49	868	IE6082	66.7	108.52	3.13	0.70	0.13	-19.52
369	IE3364	71.2	54.61	-2.64	0.90	0.01	-1.49	869	IE6088	70.3	107.50	1.94	1.07	0.20	-65.71
370	IE3366	70.8	64.41	2.14	0.83	0.02	17.58	870	IE61	65.2	24.54	-0.53	0.90	0.01	13.56
371	IE3391	72.8	6.87	-0.53	1.13	0.01	-8.05	871	IE610	66.4	98.58	3.47	0.73	0.22	77.78
372	IE3392	72.9	16.29	1.31	1.33	0.10	23.54	872	IE6112	67.3	96.22	3.09	1.00	0.04	-30.10
373	IE3400	74.1	2.23	0.46	1.00	0.01	13.56	873	IE6117	67.1	66.37	1.45	0.77	0.02	-7.00
374	IE3412	74.1	11.97	1.09	1.30	0.09	4.47	874	IE6122	65.6	39.13	1.29	1.07	0.01	-19.07
375	IE3413	74.4	4.87	0.78	1.23	0.65	112.34	875	IE6127	64.3	23.80	0.49	0.87	0.26	-67.20
376	IE3431	73.2	17.76	1.32	1.30	0.27	-85.82	876	IE613	64.6	101.92	3.60	0.73	0.09	-14.00
377	IE3434	77.6	70.87	3.18	1.60	0.36	-81.36	877	IE6149	66.6	66.20	-1.18	0.73	0.30	-59.15
378	IE3443	78.4	49.33	2.61	1.03	0.00	-9.54	878	IE615	66.7	89.32	2.82	1.07	0.04	26.07
379	IE3446	69.5	134.14	3.29	1.43	0.70	-137.53	879	IE6154	67.5	92.16	1.84	0.77	0.30	45.75
380	IE3449	72.8	0.57	0.04	1.07	0.04	26.07	880	IE6165	65.4	78.46	2.31	0.70	0.13	9.09
381	IE3450	74.6	40.36	2.33	1.07	0.22	57.66	881	IE6167	65.4	74.96	2.25	0.73	0.06	1.05
382	IE3455	69.3	54.04	-2.52	0.87	0.05	38.14	882	IE6175	64.7	62.14	2.33	0.97	0.00	-4.02
383	IE3470	70.7	37.72	1.28	1.03	0.02	20.56	883	IE6221	65.4	66.56	2.12	0.63	0.16	-15.49
384	IE3475	74.7	29.74	1.96	1.03	0.05	-38.14	884	IE6227	67.4	74.24	2.04	0.90	0.19	72.27

S.no	Accession	Days t0 50% Flowering (days)			Plot yield (tn ha^{-1})			S.no	Accession	Days t0 50% Flowering (days)			Plot yield (tn ha^{-1})		
		Mean	b	S^2d	Mean	b	S^2d			Mean	b	S^2d	Mean	b	S^2d
385	IE3477	70.5	15.84	0.55	1.00	0.03	-16.54	885	IE6229	64.7	63.39	-0.57	1.40	0.28	36.05
386	IE3478	70.3	28.12	-1.14	0.97	0.01	-19.07	886	IE6235	64.3	40.08	1.97	0.90	0.13	-46.64
387	IE3482	71.1	10.80	0.12	0.73	0.08	-27.56	887	IE6236	66.8	43.56	1.80	0.77	0.17	-52.15
388	IE3483	70.4	26.17	1.28	1.00	0.31	76.73	888	IE6239	67.7	58.58	1.33	0.77	0.05	38.14
389	IE3484	75.0	9.14	1.14	0.87	0.10	53.19	889	IE6240	64.7	44.41	1.55	0.67	0.16	66.75
390	IE3485	72.0	9.88	0.10	0.87	0.06	-8.49	890	IE6241	64.4	41.79	1.87	1.07	0.25	71.22
391	IE3489	71.1	24.06	0.37	1.30	0.27	-85.82	891	IE6251	64.2	42.90	1.98	1.03	0.20	-69.73
392	IE3492	71.3	18.84	1.06	1.23	0.17	52.15	892	IE6252	64.4	55.56	1.67	0.87	0.02	-7.00
393	IE3502	73.7	2.09	-0.11	1.00	0.01	-15.05	893	IE6255	66.1	60.52	1.71	0.80	0.28	-63.17
394	IE3504	72.9	6.69	-0.58	1.37	0.12	-44.70	894	IE6258	68.4	62.41	0.22	1.00	0.09	-45.15
395	IE3509	74.6	0.69	0.27	1.03	0.02	7.00	895	IE6280	64.4	44.31	-0.29	0.80	0.04	27.12
396	IE3510	74.1	1.34	0.28	0.83	0.09	46.19	896	IE629	65.3	101.37	3.27	0.87	0.05	-22.05
397	IE3515	73.3	0.19	0.13	1.33	0.34	41.57	897	IE6294	66.8	72.10	0.60	1.00	0.36	90.29
398	IE3529	75.8	5.11	0.85	1.13	0.10	37.10	898	IE6300	65.4	56.14	1.15	1.13	0.01	-8.05
399	IE3531	73.8	10.36	-0.62	0.97	0.65	128.44	899	IE6313	71.5	278.70	5.16	1.10	0.43	91.78
400	IE3533	65.1	170.76	-4.34	0.77	0.12	-9.98	900	IE6321	67.3	75.72	2.69	0.60	0.07	25.63
401	IE3537	63.8	201.34	3.25	1.20	0.07	-43.66	901	IE6326	63.7	30.50	-0.17	0.90	0.04	-2.98
402	IE3538	64.2	100.96	-2.98	1.03	0.05	-38.14	902	IE633	63.7	45.56	1.84	1.23	0.10	37.10
403	IE3543	62.4	140.85	0.62	1.13	0.10	23.54	903	IE6332	68.1	116.85	2.82	0.70	0.07	25.63
404	IE3547	70.0	42.19	1.70	0.87	0.50	113.39	904	IE6337	69.6	118.52	3.19	0.77	0.06	-8.49
405	IE3559	72.3	7.09	-0.35	0.90	0.01	15.05	905	IE6350	68.7	79.99	1.43	0.77	0.10	-23.54
406	IE3566	73.8	21.63	1.69	1.07	0.04	12.51	906	IE6352	68.9	152.53	3.38	1.10	0.13	-58.71
407	IE3575	73.4	14.89	1.23	0.73	0.09	-14.00	907	IE6358	69.5	152.57	2.64	0.57	0.17	65.26
408	IE3581	74.1	19.56	1.39	1.13	0.17	52.15	908	IE6362	68.3	94.14	2.58	1.43	0.16	-3.58
409	IE3587	73.8	66.80	2.79	0.97	0.02	-20.56	909	IE6387	68.9	102.88	0.53	1.10	0.19	48.12
410	IE3600	73.5	6.51	-0.67	1.00	0.09	45.15	910	IE6396	60.0	84.42	-2.70	0.47	0.14	18.63
411	IE3604	70.1	27.43	0.83	0.90	0.07	31.59	911	IE641	60.4	258.70	6.08	0.80	0.07	43.66
412	IE3612	72.5	8.80	0.62	0.83	0.08	47.68	912	IE6416	69.0	127.00	1.51	1.30	0.19	-70.78
413	IE3613	72.3	13.58	1.16	0.97	0.00	9.54	913	IE6417	64.3	47.85	1.52	1.73	0.76	-134.55
414	IE3614	71.4	11.69	-0.24	1.20	0.07	-42.17	914	IE642	69.5	128.02	3.23	0.83	0.25	79.27
415	IE3628	73.5	6.02	0.66	0.93	0.09	49.17	915	IE6420	66.4	94.36	1.68	0.93	0.04	-26.07
416	IE3635	71.2	9.92	0.28	1.07	0.02	23.10	916	IE6421	67.3	139.75	3.54	0.80	0.03	28.61
417	IE3636	71.0	8.41	0.27	0.87	0.01	8.05	917	IE6426	71.4	184.62	3.42	0.93	0.00	-9.54
418	IE3637	73.5	25.74	1.89	1.40	0.07	-10.58	918	IE6428	70.8	102.61	1.76	0.63	0.30	-45.59
419	IE3643	75.2	4.16	0.77	1.30	0.79	-146.02	919	IE6432	70.6	160.05	2.44	1.03	0.16	-56.17
420	IE3652	75.7	17.54	1.52	0.87	0.02	-7.00	920	IE6435	68.4	87.50	0.69	1.00	0.57	-106.83
421	IE3653	74.1	2.81	0.14	0.87	0.06	-35.61	921	IE6436	64.4	60.36	1.72	1.43	0.44	-108.92
422	IE3654	74.8	2.56	0.45	0.77	0.04	21.61	922	IE6440	62.7	35.83	0.75	0.77	0.10	53.19
423	IE3655	72.6	3.52	-0.71	0.90	0.03	12.07	923	IE6443	66.7	79.96	2.19	1.10	0.13	-58.71
424	IE3656	70.7	25.27	1.27	1.20	0.04	-27.12	924	IE6447	66.3	85.36	0.68	1.23	0.46	-111.90
425	IE3657	74.0	1.04	0.31	0.80	0.19	-34.57	925	IE6451	69.5	161.70	2.87	0.63	0.22	74.80
426	IE3661	73.8	21.16	1.67	0.93	0.00	4.02	926	IE6455	73.5	430.65	7.08	0.67	0.06	-8.49
427	IE3663	74.8	4.00	0.73	0.93	0.04	-26.07	927	IE6464	67.6	109.62	0.01	0.77	0.37	-82.25
428	IE3667	75.7	12.26	1.31	1.43	0.56	-123.97	928	IE6466	66.5	100.21	2.84	0.93	0.02	-24.59
429	IE3670	73.8	1.46	0.41	1.13	0.02	20.56	929	IE6472	68.4	122.79	0.65	0.73	0.14	-29.05
430	IE3676	77.0	36.12	2.27	1.30	0.27	49.61	930	IE6473	67.2	63.44	0.59	0.70	0.19	-34.57
431	IE3687	76.6	14.44	1.44	0.80	0.39	-78.22	931	IE6479	65.7	100.84	3.06	1.27	0.05	-16.09
432	IE3693	79.1	70.77	3.04	0.73	0.12	-0.44	932	IE6482	67.2	102.01	0.49	0.80	0.07	-18.03
433	IE3694	75.3	1.86	0.48	0.90	0.19	-48.12	933	IE6484	65.5	138.36	3.50	1.17	0.04	12.51
434	IE3697	72.3	1.27	0.28	0.67	0.08	20.12	934	IE6486	65.2	56.30	-0.61	0.73	0.21	-44.10
435	IE3698	70.7	40.41	1.90	1.07	0.01	11.03	935	IE6488	61.6	29.19	0.78	0.87	0.26	-67.20
436	IE3699	73.9	18.97	1.49	0.67	0.17	65.26	936	IE6491	64.6	44.59	1.65	0.77	0.24	-53.64
437	IE3704	74.5	9.01	1.10	1.20	0.03	-12.07	937	IE6495	64.0	84.65	2.53	1.00	0.25	-75.24
438	IE3705	77.9	44.12	2.37	0.60	0.16	54.24	938	IE6510	65.8	94.32	1.85	1.03	0.09	-41.12
439	IE3706	75.5	8.81	0.96	0.93	0.01	-11.03	939	IE6512	68.7	143.32	0.99	0.80	0.19	-48.12
440	IE3711	78.1	71.29	2.97	1.13	0.01	-8.05	940	IE6514	64.6	84.25	1.40	1.10	0.04	30.10
441	IE3721	74.7	9.37	0.28	0.90	0.43	103.85	941	IE6528	65.8	76.57	1.91	0.87	0.05	-22.05
442	IE3722	76.0	18.36	1.41	1.00	0.31	88.80	942	IE6533	73.5	555.61	7.91	0.90	0.43	-91.78
443	IE3723	74.5	6.02	0.63	0.87	0.06	-8.49	943	IE6537	84.9	602.58	3.53	1.10	0.03	16.54
444	IE3727	70.2	1.77	0.32	1.13	0.20	-69.73	944	IE6541	84.4	578.08	3.21	0.90	0.25	75.24
445	IE3733	70.8	11.54	1.12	0.80	0.07	-18.03	945	IE6546	83.9	572.76	2.39	0.90	0.07	-31.59
446	IE3734	71.2	13.44	-1.35	0.63	0.12	-0.44	946	IE6549	68.1	377.46	-5.08	0.67	0.04	6.56
447	IE3738	72.0	47.14	2.28	0.87	0.37	-82.25	947	IE6550	53.5	7.12	0.13	1.03	0.17	-68.24
448	IE3744	73.8	12.04	1.04	0.83	0.21	-44.10	948	IE6553	62.7	90.12	3.31	0.67	0.06	36.66

S.no	Accession	Days t0 50% Flowering (days)			Plot yield (tn ha^{-1})			S.no	Accession	Days t0 50% Flowering (days)			Plot yield (tn ha^{-1})		
		Mean	b	S^2d	Mean	b	S^2d			Mean	b	S^2d	Mean	b	S^2d
449	IE3745	74.9	15.48	0.92	0.67	0.09	5.07	949	IE667	63.0	71.14	-1.32	0.70	0.09	-4.47
450	IE3746	75.1	26.26	1.73	0.83	0.08	-27.56	950	IE678	59.4	17.52	0.98	0.93	0.02	-24.59
451	IE3753	76.1	14.17	-0.09	1.23	0.10	-53.19	951	IE680	57.9	25.72	-1.21	0.93	0.09	-14.00
452	IE3758	70.6	5.22	0.85	0.83	0.08	-27.56	952	IE694	56.3	52.60	2.39	0.50	0.16	54.24
453	IE3766	73.2	10.60	0.83	0.97	0.00	9.54	953	IE712	61.8	23.41	0.80	1.23	0.02	-23.10
454	IE3769	75.4	74.92	2.87	0.97	0.01	-19.07	954	IE726	59.6	22.09	-0.46	0.77	0.01	8.05
455	IE3778	73.6	18.52	1.22	0.97	0.12	54.68	955	IE739	62.4	123.22	3.87	0.83	0.44	-87.76
456	IE3779	73.8	33.97	2.08	1.13	0.05	22.05	956	IE777	64.2	80.71	-0.54	1.20	0.09	-45.15
457	IE3780	74.2	30.08	2.01	0.97	0.01	8.05	957	IE795	64.9	115.85	3.48	1.17	0.08	-47.68
458	IE3790	75.8	62.08	2.62	1.07	0.25	-79.27	958	IE797	66.3	100.12	0.82	0.50	0.13	39.19
459	IE3802	76.3	103.77	3.63	1.20	0.12	33.08	959	IE798	62.0	42.06	0.49	0.77	0.10	-37.10
460	IE3803	74.3	9.44	0.73	1.00	0.01	15.05	960	IE8	60.2	9.85	0.06	1.10	0.16	-60.19
461	IE3804	74.2	12.52	1.09	1.17	0.32	-92.83	961	IE804	61.9	37.66	0.36	1.03	0.36	-86.27
462	IE3808	71.6	6.22	-0.52	1.03	0.00	5.51	962	IE808	62.5	41.86	0.91	0.97	0.24	-53.64
463	IE3817	70.5	23.16	1.78	1.00	0.03	-28.61	963	IE815	62.4	43.64	-0.50	1.23	0.12	9.98
464	IE3821	75.0	27.80	1.56	1.03	0.00	5.51	964	IE817	62.4	26.77	1.08	0.87	0.06	-35.61
465	IE3825	69.8	12.00	-1.22	0.87	0.02	-7.00	965	IE821	66.2	163.32	3.99	1.17	0.02	-17.58
466	IE3826	67.7	10.29	0.89	0.93	0.01	19.07	966	IE829	61.8	124.96	-3.36	0.73	0.09	-14.00
467	IE3827	76.2	128.30	4.23	0.73	0.05	16.09	967	IE847	58.6	163.29	4.84	0.93	0.14	-42.61
468	IE3855	71.4	3.52	-0.29	1.37	0.12	0.44	968	IE848	69.8	217.01	4.49	0.93	0.00	4.02
469	IE3861	74.2	155.23	4.70	1.07	0.01	-19.07	969	IE858	67.6	123.85	0.14	0.93	0.04	-26.07
470	IE3885	73.8	16.12	1.18	0.70	0.28	-36.05	970	IE864	65.8	50.44	0.97	1.03	0.00	5.51
471	IE3894	75.0	29.56	1.64	1.50	0.49	-112.94	971	IE872	62.6	43.77	0.28	1.10	0.03	-28.61
472	IE3901	75.6	47.94	2.13	1.03	0.02	-24.59	972	IE886	62.2	16.51	0.71	0.90	0.21	73.75
473	IE3910	76.6	65.17	2.91	0.97	0.01	11.03	973	IE888	64.3	65.02	1.72	0.83	0.08	47.68
474	IE3913	70.5	1.11	-0.07	0.87	0.10	53.19	974	IE895	66.6	116.17	2.72	0.77	0.01	8.05
475	IE3930	72.5	9.56	0.62	1.63	0.42	14.45	975	IE897	65.2	56.26	-0.65	0.77	0.10	-23.54
476	IE3935	66.9	9.40	0.17	1.27	0.06	-31.14	976	IE899	64.2	45.17	2.13	0.73	0.12	-0.44
477	IE3940	73.4	10.56	0.88	1.43	0.56	71.66	977	IE9	62.3	47.06	0.21	1.07	0.08	-47.68
478	IE3942	70.9	16.89	1.52	1.13	0.10	37.10	978	IE900	64.2	79.69	2.60	1.13	0.00	5.51
479	IE3945	73.8	16.54	1.37	1.07	0.12	54.68	979	IE905	63.7	84.72	2.58	1.00	0.01	15.05
480	IE3947	69.9	1.22	0.39	1.40	0.13	-39.19	980	IE906	64.5	81.90	2.45	0.90	0.00	0.00
481	IE3952	71.7	5.42	-0.53	1.07	0.04	-34.12	981	IE907	64.4	73.97	2.31	0.87	0.10	-37.10
482	IE3973	77.1	220.08	5.61	1.50	0.52	39.03	982	IE912	63.1	32.26	0.77	1.17	0.14	42.61
483	IE3974	71.8	50.92	2.67	0.77	0.26	83.29	983	IE913	68.2	142.65	2.05	1.07	0.04	-34.12
484	IE3987	71.6	12.31	1.33	1.10	0.31	76.73	984	IE914	65.5	188.42	4.38	1.07	0.00	9.54
485	IE3993	76.4	21.31	1.03	0.73	0.08	-27.56	985	IE924	68.2	235.12	4.67	0.93	0.00	4.02
486	IE4005	72.3	7.32	0.78	1.23	0.46	83.73	986	IE927	63.1	55.25	0.01	0.97	0.00	-5.51
487	IE4011	74.0	25.65	1.73	0.87	0.12	-50.66	987	IE928	64.8	107.70	-0.48	1.10	0.12	33.08
488	IE4017	71.9	7.58	0.71	1.13	0.02	20.56	988	IE929	59.1	10.66	-0.18	0.93	0.02	-24.59
489	IE4020	71.7	14.02	1.41	1.43	0.26	-78.82	989	IE930	60.2	26.17	0.31	1.03	0.20	65.71
490	IE4022	73.1	22.45	1.76	1.03	0.12	-54.68	990	IE942	59.8	41.94	2.11	1.20	0.04	-27.12
491	IE4023	75.7	86.46	3.21	1.20	0.03	-12.07	991	IE947	59.8	26.96	1.23	0.93	0.01	19.07
492	IE4024	72.6	11.96	0.57	0.97	0.01	-19.07	992	IE954	63.9	92.19	2.66	0.83	0.08	-27.56
493	IE4028	70.3	21.86	1.74	0.87	0.10	53.19	993	IE955	63.0	49.48	2.09	1.00	0.01	-13.56
494	IE4035	72.7	40.53	2.39	0.97	0.06	-35.61	994	IE96	65.0	67.59	1.44	0.90	0.04	-2.98
495	IE4036	71.1	9.96	1.19	1.17	0.02	-17.58	995	IE968	63.4	82.81	2.00	1.40	0.28	36.05
496	IE4044	75.3	91.51	3.61	0.77	0.05	38.14	996	IE971	64.9	111.40	2.06	0.80	0.03	12.07
497	IE4047	73.6	10.36	0.68	1.27	0.21	44.10	997	IE972	66.2	169.65	3.75	1.37	0.25	-73.31
498	IE4053	73.9	11.22	1.22	0.60	0.13	9.09	998	IE984	67.3	117.82	1.09	1.20	0.07	-42.17
499	IE4057	75.1	30.65	1.66	1.20	0.04	-27.12	999	IE990	63.2	67.08	0.52	0.80	0.03	12.07
500	IE4059	68.1	40.09	-2.36	0.97	0.04	-34.12	1000	IE991	64.9	139.64	3.04	1.03	0.01	19.07