FORMATION OF CORE SET IN RICE (*Oryza sativa* L.) SHORT DURATION GERMPLASM ACCESSIONS

By

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(2010-11-153)

THESIS

Submitted in partial fulfilment of the
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2012

DECLARATION

I hereby declare that the thesis entitled **"Formation of core set in rice (*Oryza sativa* L.) short duration germplasm accessions"** is a bonafide record of research work done by me during the course of research and the thesis has not previously formed the basis for the award to me of any degree, diploma, associateship, fellowship or other similar title, of any other university or society.

Place: Vellanikkara

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CERTIFICATE

Certified that the thesis entitled **"Formation of core set in rice (*Oryza sativa* L.) short duration germplasm accessions"** is a record of research work done independently by **Mr. Pawan Saini** under my guidance and supervision and that it has not previously formed the basis for the award of any degree, diploma, associateship, fellowship to him.

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Pawan Saini

Dedicated to Rice Science

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ABBREVIATIONS

%	Per cent
ABD	Augmented Blocks Design
ANOVA	Analysis of Variance
ARS	Agricultural Research Station
ASV	Alkali Spreading Value
AUP	Adjusted Unbiased Prediction
BC	Base Collection
C	Core set
CC	Core collection
CGIAR	Consultative Groups on International Agricultural Research
CIAT	International Center for Tropical Agriculture
CIMMYT	International Maize and Wheat Improvement Center
CIP	International Potato Center
cm	Centimeter
CR	Coincidence Rate
CRRI	Central Rice Research Institute
DRR	Directorate of Rice Research
g	Gram
GA	Genetic advance
GCV	Genotypic coefficient of variation
GG	Genetic gain
GRIN	Germplasm Resources Information Network
h^2	Heritability
HCC	Heuristic Core Collection
IBPGR	International Board for Plant Genetic Resource
ICAR	Indian Council of Agricultural Research
ICRISAT	International Crop Research Institute for Semi Arid Tropics

IITA	International institute for tropical Agriculture
IRGC	International Rice Gene bank Collection
IRRI	International Rice Research Institute
KAU	Kerala Agricultural University
MD	Mean Difference
mm	Millimitre
NBPGR	National Bureau of Plant Genetic Resources
PCA	Principal Component Analysis
PCV	Phenotypic coefficient of variation
PGC	Pattambi Germplasm Collection
POP	Package of Practice
RARS	Regional Agricultural Research Station
RHS	Royal Horticultural Society
RRS	Rice Research Station
SSR	Simple Sequence Repeats
TGMS	Temperature sensitive genetic male sterility
UPGMA	Unweighted Pair-Group Method Arithmetic Average
USDA	United State Department of Agriculture
VD	Variance Difference
VR	Variable Rate
WARDA	West African Rice Development Association
χ^2	Chi-square

Introduction

1. INTRODUCTION

Rice popularly known as 'Global grain' is the staple food for over half the world's population. It occupies almost one-fifth of the total land area covered under cereals. Rice is a major food crop cultivated in the country and also the staple food for a large segment of the Indian population. Grown in an area of 418.5 lakh hectares during 2009-10, it recorded a production of 891.3 lakh tonnes and a productivity of 2130 kg/ha, accounting for 40.85 per cent of total food grain produced in the country (Farm Guide, 2012).

Rice occupies the prime place among the food crops cultivated in Kerala. In 2009-10, the net area of rice in Kerala was 2.34 lakh hectares. This accounted for 8.77 per cent of total cropped area in the state with an annual production of 5.98 lakh tones and a productivity of 2556 kg /ha (Farm Guide, 2012). The undulating topography, the sloppy terrain, high rainfall, the criss-crossing rivers and their deltaic formations, the backwater systems and saline water intrusion have all resulted in a variety of heterogeneous waterlogged ecosystems where rice alone could be cultivated (Sasidharan *et al.,* 2002). Diversity of cropping systems, the edaphic and climatic variations found among and within different regions, as well as among farmers within these regions have resulted in a cafeteria of diverse genotypes.

Germplasm encompasses the total gene pool of a species and forms the raw material for any crop improvement program (Brown, 1989a). Germplasm collections furnish the richest source of variability. Furthermore, these collections preserve the genetic diversity of a cultivated species and serve as a genetic bank from which valuable genes can be extracted (Dilday *et al.,* 1999). Plant breeding being a continuous process these diverse genetic resources remains a critical input.

However, the extent of variation in the germplasm collections and their accessibility to biologists and breeders are essential factors affecting their utilization

in crop improvement programme. Frankel and Brown (1984) proposed the concept of "core collection" (CC) as a collection that encompasses a representative sample of the entire collection with minimum repetitiveness and maximum genetic diversity of a crop species and its relatives. With the core collection, it is convenient to study and utilize germplasm resources. Establishment of CC has proven to be a favored approach to facilitate efficient exploration of novel variation from genetic resources (Brown 1989a, Ellis *et al.*, 1998; Holbrook *et al.*, 2000; Malvar *et al.*, 2004).

Kerala Agricultural University (KAU), holds a rice germplasm collection of over 1000 accessions of varying duration assembled since its inception in 1972. The full spectrum of genetic resources in the collection includes wild species, natural hybrids between cultigens and wild relatives, primitive cultivars or land races, traditional varieties, pureline selections of farmer's varieties, elite varieties of hybrid origin and other breeding materials including mutants and hybrid derivatives (Kumary and Francies, 2003). Collection, conservation and cataloguing of accessions collected from time to time has been done under plan projects as well as projects *viz.*, NATP project on Plant Bio-diversity. A detailed comprehensive and accurate characterization of the collection is wanting. In addition, selection of an appropriate genotype for breeding programmes from this vast diverse collection often proves difficult and in turn becomes an obstacle to the effective and efficient utilization of the germplasm in crop improvement programmes. The concept of forming core collection serves as a very effective alternative from the point of enhancing the utility of this conserved germplasm, as it captures, the complete diversity of the entire collection it was derived from.

In light of above facts, the present investigation was carried out with following objectives.

- To assess the variability in the germplasm accessions
- To constitute a representative core set
- To evaluate the representativeness of core set *vis* a *vis* base collections

Review of Literature

2. REVIEW OF LITERATURE

Most germplasm collections consist of a large number of entries meant to preserve the genetic diversity of the particular species for future needs. However, fruitful utilization of this diversity for crop improvement programmes require, systematic cataloguing, evaluation and characterization of the collection. In practice, plant breeders are interested in having fairly small numbers of genotypes which possess, or are likely to possess the characters needed in their breeding programmes. Formation of core collections – a subset of the germplasm collection improves accessibility of these collections to users.

An attempt has been made to present a brief review of literature related to different aspects of the study undertaken. The review is categorized under the following themes:

2.1 Variability studies

2.1.1 Studies on variability and varietal classification based on qualitative characters

2.1.2 Studies on variability in quantitative characters

2.2 Germplasm collections

2.3. Core collection

2.3.1 Development of the concept of core collection

2.3.2 Core collections in crops other than rice

2.3.3 Core collections in rice

2.1 Variability studies

2.1.1 Studies on variability and varietal classification based on qualitative characters

The earliest noteworthy attempt at a detailed classification of rice varieties based on agronomical and physiological characteristics was that of Kikkawa (1912). Graham (1913) classified the Indian rice varieties based on the variability in leaf sheath colour and grain dimensions.

Hector (1930), exploited the variability with respect to anthocyanin pigmentation of leaf sheath, apiculus and stigma colour in his classification of Bengal rice. Variability in anthocyanin colouration along with grain characteristics has been used in the classification of rice varieties by Sethi and Saxena (1930); Ram and Chetty (1934) and Ram and Ekbote (1936).

Variation in morphological characters in various parts of plants has traditionally been used to distinguish one cultivar from other (Simmonds and Shepherd, 1955). Rosta (1975), grouped the rice varieties based on differences in leaf blade length, width, leaf colour, colour of ligule, colour of auricle and colour of flowers.

Chauhan and Nanda (1984) suggested that variability in kernel colour and appearance of milled grains were major identification characters of rice varieties. Naidu *et al.* (1986) classified 20 rice varieties as slender, medium and bold classes based on grain length to breadth ratio.

Grouping of 85 rice varieties based on differences in colour of hulled grain, vitreous characters, length, shape, profile value (width), 100 grain weight, presence or absence of pearl spots and shape of pearl spot was done by Vanangamudi *et al.* (1988).

In a study on 28 Gora rice genotypes for their variability in nine agro-morphological characters, Sinha *et al.* (1990), observed maximum variability for secondary branching per panicle. Grain shape, size, weight and fertility were the least variable characters in Gora rice genotypes.

Variations in rice hybrids for grain characters such as number of panicles, grains per panicle, grain yield, grain weight and shape were reported by Geetha *et al.*, 1994.

Caldo *et al.* (1996), analyzed diversity for phenotypic traits of 78 improved rice varieties with 14 quantitative traits and 27 qualitative traits by multivariate analysis. High variability was found for the characters, maturity, plant height and culm length whereas variability was low in leaf width and grain width.

According to Thimmanna *et al.* (2000), the variability in characters such as leaf length and width, pubescence of leaf, colour, leaf angle, ligule shape and colour, auricle colour, internode colour, panicle type, secondary branching, exertion, awning, seed length and width and 100 grain weight can be used in differentiating the parental lines of rice hybrids.

Zafar *et al.* (2004) evaluated 124 rice accessions for seven quantitative characters. Most of the accessions were with intermediate panicle type (47) followed by open panicle (44), whereas 33 (26.62%) accessions were found to possess compact panicle. A total of forty five (36.29 %) accessions were found with awns, whereas significant proportion (42.74%) was without awn. Awns were present in 20.96% of the accessions. Awn color also exhibited wide variation ranging from straw to different shades of brown color. Altogether 47 (37.90%) lines were found with erect leaf. A significant proportion (43.55%) was having drooping type leaves. Majority of the lines were partly exerted, whereas the proportion of well-exerted accession was only 6.45%. No accession was found with enclosed panicle. Not much variation was

observed for ligule and auricle colour in the present germplasm. Seed coat colour exhibited great variability ranging from different shades of brown to a variable range of purple colour.

Many studies have estimated the genetic variability of rice genotypes and concluded that traits like plant height and days to heading contributed to genetic divergence and important in the choice of parents for hybridization programme (Bose and Pradhan, 2005; Le and Yang, 2005; Madhavilatha and Suneetha, 2005; Singh *et al.*, 2006a).

Variation in six TGMS lines were observed by Ramakrishna *et al.* (2006), with respect to leaf sheath colour, panicle type, panicle exsertion, ligule shape and colour, auricle colour and apiculus pigmentation. However, no variation in ligule shape was observed among all the genotypes. The leaf sheath colour ranged from light green to purple. Panicle type ranged from open to intermediate and all panicles were well exserted. Both green and purple auricle colour, purple and white ligule was observed. Only two TGMS lines showed purple pigmentation on apiculus and stigma.

High variability in seven cultivars of *Navara*, a traditional medicinal rice of Kerala was reported by Joseph *et al.* (2007). They reported that these cultivars differed significantly with respect to thirty qualitative traits. The entries differed from one another and none of the entries were similar in all respects.

Characterization of 36 aromatic rice cultivars by Hien *et al.* (2007) for 22 morphological characters revealed that the cultivars were polymorphic except to ligule colour. Grain size, grain shape, culm strength, plant height and secondary branching contributed the highest mean diversity indices.

Twenty thermo-sensitive genetic male sterile (TGMS) lines from the PhilRice-UPLB hybrid rice program were evaluated for diversity on the basis of 24 agro-morphological traits using the Shannon-Weaver diversity index. High

polymorphism was observed in auricle and apiculus colour. Monomorphism was observed in the lines for leaf blade pubescence, leaf angle, colour of ligule, collar, internode and seed coat, panicle type and lemma and palea pubescence out of 19 qualitative traits studied. The mean Shannon-Weaver diversity indices were H' = 0.44 for all qualitative traits and H' = 0.66 for only those that showed polymorphism, indicating a moderate level of diversity among the 20 TGMS lines (Alcasid *et al.*, 2008).

Bora *et al.* (2008), reported high variability in rice varieties characterized on the basis of hulled and unhulled grain characters like grain length, grain colour, grain width, decorticated grain length, decorticated grain width, decorticated grain colour, L/B ratio and 1000 grain weight.

On assessment of genetic diversity in 50 rice genotypes based on 15 qualitative traits Banumathy *et al.* (2012), reported existence of highly significant differences among the 50 genotypes studied. According to them the genotypes differed with respect to leaf and lemma palea pubescence, leaf and culm angle, colour of apiculus, stigma and lemma. The genotypes grouped into two clusters of 11 genotypes and 39 genotypes based on these traits.

2.1.2 Studies on variability in quantitative characters

Crop improvement depends heavily on the magnitude of genetic variability available for manipulation. Total phenotypic variability expressed by a genotype or a group of genotypes can be apportioned into genotypic and environmental components.

The character wise chronological report of reviews of literature on phenotypic coefficient of variation (**PCV**), genotypic coefficient of variation (**GCV**), heritability ($\mathbf{h^2}$) and genetic gain in rice is presented in Table 1.

Table 1. Genetic variability, heritability and genetic gain in rice and other cereals

Sl. No.	Character	PCV (%)	GCV (%)	h^2 (%)	Genetic gain (%)	Reference
1.	Seedling shoot length (cm)	High	High	High	-	Khan *et al.*, 2002
2.	Seedling root length (cm)	High	High	Moderate	-	Khan *et al.*, 2002
		Low	Low	High	High	Ali *et al.*, 2009
3.	Seedling vigour index	High	High	High	High	Sujay, 2007
		High	Moderate	High	High	Prasad *et al.*, 2011
4.	Plant height (cm)	High	High	High	High	Manickavelu *et al.*, 2006; Nair and Rosamma, 2007; Nayak, 2008; Sadeghi, 2011
		High	Moderate	High	High	Girish *et al.*, 2006; Prabha *et al.*, 2009
		High	Moderate	Low	Low	Meenakumari *et al.*, 2012
		Moderate	Moderate	High	High	Nayak, 2008
		Moderate	Moderate	Moderate	High	Chauhan, 1996
		Moderate	Moderate	High	High	Nayak *et al.*, 2004; Sankar *et al.*, 2006; Singh *et al.*, 2006b; Jaiswal *et al.*, 2007; Padmaja *et al.*, 2008; Sedeek *et al.*, 2009; Prasad *et al.*, 2009; Sharma and Sharma, 2007; Singh *et al.*, 2011; Selvaraj *et al.*, 2011; Prasad *et al.*, 2011; Rani *et al.*, 2012; Mallikarjuna *et al.*, 2012; Nithya *et al.*, 2012; Babu *et al.*, 2012b
		Moderate	Low	High	Moderate	Kole *et al.*, 2008; Chakraborty and Chakraborty, 2010; Babu *et al.*, 2012a
		Moderate	Moderate	Moderate	Moderate	Salini *et al.*, 2012
		Moderate	Low	Moderate	Moderate	Reddy *et al.*, 2012
		Moderate	Low	Low	Low	Manickavelu *et al.*, 2006
		Low	Low	High	Moderate	Prasad *et al.*, 2001; Laxuman *et al.*, 2010; Subbaiah *et al.*, 2011; Akinwale *et al.*, 2011; Seyoum *et al.*, 2012
		Low	Low	Moderate	Moderate	Can and Lang, 2002; Singh *et al.*, 2007
5.	Culm length (cm)	Moderate	Moderate	High	High	Reddy, 2000
		Low	Low	High	Moderate	Sumalatha, 2010
6.	Stem thickness (mm)	Moderate	Moderate	Moderate	Moderate	Ayele, 2011
7.	Leaf blade width (cm)	High	Moderate	High	Low	Sadeghi, 2011
		Moderate	Moderate	High	High	Padmaja *et al.*, 2008; Prabha *et al.*, 2009
		Moderate	Moderate	High	Low	Singh *et al.*, 2011
8.	Leaf blade length (cm)	High	High	High	Moderate	Sadeghi, 2011
		Moderate	Moderate	High	High	Padmaja *et al.*, 2008; Prabha *et al.*, 2009
		Moderate	Moderate	High	Low	Singh *et al.*, 2011

Table 1. Genetic variability, heritability and genetic gain in rice and other cereals (contd...)

Sl. No.	Character	PCV (%)	GCV (%)	h^2 (%)	Genetic gain (%)	Reference
9.	Days to heading	High	High	High	High	Nair and Rosamma, 2007
		-	-	High	-	Singh and Shirisha, 2003
		High	High	High	Moderate	Sharma and Sharma, 2007
		High	Moderate	High	Moderate	Sadeghi, 2011
		Moderate	Moderate	High	High	Sankar *et al.*, 2006; Jaiswal *et al.*, 2007; Sedeek *et al.*, 2009; Selvaraj *et al.*, 2011; Rani *et al.*, 2012
		Low	Low	High	Low	Khan *et al.*, 2009; Prasad *et al.*, 2001 Nayak *et al.*, 2004 Singh *et al.*, 2006b Kole *et al.*, 2008 Chakraborty and Chakraborty, 2010 Akinwale *et al.*, 2011 Shehzad *et al.*, 2011 Seyoum *et al.*, 2012
		Low	Low	Moderate	Low	Manickavelu *et al.*, 2006; Chauhan, 1996
		Low	Low	High	Moderate	Manickavelu *et al.*, 2006; Girish *et al.*, 2006; Padmaja *et al.*, 2008; Prasad *et al.*, 2009; Singh *et al.*, 2007; Laxuman *et al.*, 2010; Subbaiah *et al.*, 2011; Singh *et al.*, 2011; Prasad *et al.*, 2011; Nithya *et al.*, 2012; Salini *et al.*, 2012; Babu *et al.*, 2012a; Babu *et al.*, 2012b; Reddy *et al.*, 2012
10.	Tillers per plant	High	High	High	High	Nair and Rosamma, 2007; Padmaja *et al.*, 2008; Selvaraj *et al.*, 2011; Rani *et al.*, 2012
		High	High	Moderate	High	Girish *et al.*, 2006; Reddy *et al.*, 2012
		High	High	High	Moderate	Can and Lang, 2002
		High	Moderate	High	High	Kole *et al.*, 2008
		High	Moderate	Moderate	High	Singh *et al.*, 2007; Akinwale *et al.*, 2011
		High	High	Moderate	Low	Singh *et al.*, 2011
		Moderate	Moderate	Moderate	Moderate	Karim *et al.*, 2007
		Moderate	Low	High	Moderate	Singh *et al.*, 2006b; Sedeek *et al.*, 2009
		Moderate	Low	Moderate	Moderate	Nayak *et al.*, 2004
		Low	Low	High	-	Khan *et al.*, 2009
		Low	Low	Moderate	Low	Seyoum *et al.*, 2012
11.	Spikelets per panicle	High	High	High	High	Chauhan, 1996; Prasad *et al.*, 2009
		High	High	High	Moderate	Sharma and Sharma, 2007
		High	Moderate	Moderate	High	Singh *et al.*, 2007

Table 1. Genetic variability, heritability and genetic gain in rice and other cereals (contd...)

Sl. No.	Character	PCV (%)	GCV (%)	h^2 (%)	Genetic gain (%)	Reference
12.	Productive tillers per plant	High	High	High	High	Sankar *et al.*, 2006; Jaiswal *et al.*, 2007; Singh *et al.*, 2007; Nair and Rosamma, 2007; Nayak, 2008; Padmaja *et al.*, 2008; Sadeghi, 2011; Prasad *et al.*, 2011; Selvaraj *et al.*, 2012; Rani *et al.*, 2012
		High	High	Moderate	High	Manickavelu *et al.*, 2006; Nayak, 2008; Chakraboty and Chakraboty, 2010
		High	High	Low	High	Meenakumari *et al.*, 2012
		High	Moderate	High	High	Laxuman *et al.*, 2010
		High	Moderate	High	Low	Singh *et al.*, 2011
		High	Moderate	Low	Moderate	Salini *et al.*, 2012
		Moderate	Moderate	High	High	Prasad *et al.*, 2001
		Moderate	Moderate	High	Moderate	Babu *et al.*, 2012a
		Moderate	Moderate	High	Low	Sharma and Sharma, 2007
		Moderate	Low	Low	Low	Akinwale *et al.*, 2011
		Low	Low	Low	Low	Seyoum *et al.*, 2012
13.	Panicle length (cm)	High	Moderate	High	High	Manickavelu *et al.*, 2006
		High	Moderate	High	Low	Sadeghi, 2011
		Moderate	Moderate	Moderate	Moderate	Girish *et al.*, 2006
		Moderate	Moderate	High	Moderate	Jaiswal *et al.*, 2007; Sharma and Sharma, 2007
		Moderate	Moderate	High	High	Sankar *et al.*, 2006; Nair and Rosamma, 2007; Prabha *et al.*, 2009; Nayak, 2008; Sedeek *et al.*, 2009; Prasad *et al.*, 2011; Rani *et al.*, 2012
		Moderate	Low	Moderate	Moderate	Salini *et al.*, 2012; Reddy *et al.*, 2012
		Moderate	Low	High	Moderate	Padmaja *et al.*, 2008
		Moderate	Low	Low	Low	Manickavelu *et al.*, 2006
		Low	Low	High	High	Selvaraj *et al.*, 2011; Meenakumari *et al.*, 2012; Babu *et al.*, 2012b
		Low	Low	High	Low	Prasad *et al.*, 2001; Singh *et al.*, 2007; Kole *et al.*, 2008; Khan *et al.*, 2009; Prasad *et al.*, 2009; Chakraborty and Chakraborty, 2010; Singh *et al.*, 2011; Babu *et al.*, 2012a; Seyoum *et al.*, 2012
		Low	Low	High	Moderate	Nayak *et al.*, 2004; Laxuman *et al.*, 2010; Subbaiah *et al.*, 2011; Nithya *et al.*, 2012
		Low	Low	Moderate	Low	Akinwale *et al.*, 2011; Chauhan, 1996
		Low	Low	-	-	Basita *et al.*, 2008; Shahidullah *et al.*, 2009
		Low	Low	Low	Low	Francies *et al.*, 2012

Table 1. Genetic variability, heritability and genetic gain in rice and other cereals (contd...)

Sl. No.	Character	PCV (%)	GCV (%)	h^2 (%)	Genetic gain (%)	Reference
14.	Grains per panicle	High	High	High	High	Nayak *et al.*, 2004; Girish *et al.*, 2006;Sankar *et al.*, 2006; Jaiswal *et al.*, 2007; Nair and Rosamma, 2007; Padmaja *et al.*, 2008; Prabha *et al.*, 2009; Sadeghi, 2011; Subbaiah *et al.*, 2011
		High	Moderate	High	High	Laxuman *et al.*, 2010
		High	Moderate	Moderate	High	Manickavelu *et al.*, 2006
		Moderate	Moderate	High	High	Prasad *et al.*, 2001;Kole *et al.*, 2008;Akinwale *et al.*,2011; Selvaraj *et al.*, 2011; Rani *et al.*, 2012; Sedeek *et al.*, 2009
		Moderate	Moderate	Moderate	Moderate	Francies *et al.*, 2012
		Moderate	Moderate	High	Moderate	Sharma and Sharma, 2007
		Moderate	Low	Moderate	Moderate	Seyoum *et al.*, 2012
		Low	Low	High	-	Khan *et al.*, 2009
		-	Low	High	-	Shehzad *et al.*, 2011
15.	Test weight of grain (g)	High	High	High	High	Prasad *et al.*, 2001; Jaiswal *et al.*, 2007; Karim *et al.*, 2007
		High	High	High	Moderate	Sadeghi, 2011
		Moderate	Moderate	High	High	Prasad *et al.*, 2011; Chauhan, 1996; Nair and Rosamma, 2007; Laxuman *et al.*, 2010
		Moderate	Moderate	High	Moderate	Nayak *et al.*, 2004
		Moderate	Moderate	High	Low	Sarkar *et al.*, 2007
		Moderate	Low	Low	Low	Akinwale *et al.*, 2011
		Low	Low	High	Moderate	Sedeek *et al.*, 2009; Babu *et al.*, 2012a
16.	Grain length (mm)	High	Moderate	High	Low	Prasad *et al.*, 2009
		High	High	High	Low	Sujay, 2007
		Low	Low	High	High	Salgotra *et al.*, 2005
		Low	Low	High	Moderate	Girish *et al.*, 2006; Vanaja and Babu, 2006; Nair and Rosamma, 2007; Veerabadhiran *et al.*, 2009; Rathi *et al.*, 2010; Nayak *et al.*, 2004
		Low	Low	Moderate	Low	Francies *et al.*, 2012
17.	Grain width (mm)	High	High	High	Low	Prasad *et al.*, 2009
		Moderate	Moderate	High	High	Rathi *et al.*, 2010
		Low	Low	High	Low	Sujay, 2007
		Low	Low	Moderate	Low	Francies *et al.*, 2012
18.	Grain thickness (mm)	High	High	High	High	Nair and Rosamma, 2007
19.	Decorticated grain length (mm)	Moderate	Moderate	High	High	Jaiswal *et al.*, 2007; Prabha *et al.*, 2009
		Moderate	Moderate	High	Low	Sarkar *et al.*, 2007
		Low	Low	High	Moderate	Babu *et al.*, 2012a
20.	Decorticated grain width (mm)	Moderate	Moderate	High	High	Prabha *et al.*, 2009

Table 1. Genetic variability, heritability and genetic gain in rice and other cereals (contd...)

Sl. No.	Character	PCV (%)	GCV (%)	h^2 (%)	Genetic gain (%)	Reference
21.	Straw yield (g)	High	High	High	High	Nair and Rosamma, 2007
		High	High	Moderate	High	Chauhan, 1996
22.	Grain yield (g)	High	High	High	High	Chauhan, 1996; Nayak *et al.*, 2004; Nair and Rosamma, 2007; Sharma and Sharma, 2007; Girish *et al.*, 2006; Sedeek *et al.*, 2009; Prabha *et al.*, 2009; Selvaraj *et al.*, 2011; Babu *et al.*, 2012a
		High	High	Moderate	High	Karim *et al.*, 2007
		High	High	High	Moderate	Can and Lang, 2002
		High	High	Moderate	High	Manickavelu *et al.*, 2006; Singh *et al.*, 2007
		High	Moderate	-	-	Basita *et al.*, 2008
		High	Moderate	Moderate	High	Laxuman *et al.*, 2010
		High	Moderate	Low	High	Manickavelu *et al.*, 2006
		High	High	High	Moderate	Singh *et al.*, 2011
		High	High	High	Low	Can and Lang, 2002; Sadeghi, 2011
		Moderate	Moderate	High	High	Kole *et al.*, 2008; Subbaiah *et al.*, 2011
		Moderate	Low	Moderate	Moderate	Seyoum *et al.*, 2012
		Moderate	Moderate	High	High	Veerabadhiran *et al.*, 2009
		Low	Low	High	-	Khan *et al.*, 2009

2.2 Germplasm collection

The sum total of hereditary material or genes present in a species is known as the germplasm of that species. Therefore germplasm is the total gene pool of a species consisting of landraces, advanced breeding lines, popular cultivars, wild and weedy relatives. Nikolai Ivanovich Vavilov in 1951, was the first to recognize the importance of genetic diversity for crop improvement and organized extensive germplasm collections of various crops from their 'centers of origin' and distribution for conservation (Brown, 1989a). Exploitation of the genetic diversity stored in germplasm collections or gene banks by their introduction into the breeding programs represents the best way to increase the diversity in cultivated crops (Tanksley and McCouch 1997).

The emphasis on importance of preserving germplasm has led to collection and maintenance of very large germplasm collection. However, although the representativeness of collection can be achieved through collection size, according to Mayor *et al.*, 1997, the accessibility and usefulness of collection is invariably related to size.

The research centers of the Consultative Groups on International Agricultural Research (CGIAR) hold in trust more than 5,00,000 samples of crop germplasm. This vast collection includes the world's staple crops (Fuccillo *et al.*, 1997). More than 400,000 rice germplasm accessions are conserved in gene banks around the world (Hamilton and Raymond 2005). International Rice Research Institute (IRRI) is home to the International Rice Gene Bank, the world's largest repository of rice genetic diversity, containing about 110,000 different types of rice from all over the world. This represents 18 per cent of the CGIAR germplasm holdings. With more than 20,300 samples sent to the gene bank for long-term conservation every year, this germplasm is the world's most genetically diverse collection of rice with more than 110 countries represented (Jackson, 1995; 1997; www.irri.org). Two other CGIAR

centers' – The International Institute for Tropical Agriculture (IITA) in Nigeria and West African Rice Development Association (WARDA) in Benin also maintain collections of rice smaller than the International Rice Gene bank Collection (IRGC) (Jackson *et al.*, 1997).

Since, India is the primary centre of origin of cultivated rice (*O. sativa* L.), it obviously conserves a very high genetic diversity within its diverse eco-geographic demarcation. Presently, National Bureau of Plant Genetic Resources (NBPGR), New Delhi holds more than 95,000 accessions of rice (Rao *et al.*, 2012). The gene banks of ICAR institutes [Central Rice Research institute (CRRI), Cuttack, Orissa and Directorate of Rice Research (DRR), Hyderabad] and State Agricultural Universities also play an important role in conserving rice biodiversity in the country.

The Regional Agricultural Research Station (RARS), Pattambi under the Kerala Agricultural University has taken efforts from time to time for the collection and conservation of rice biodiversity available in the state. The collection holds over 1000 rice varieties mainly from different parts of Kerala. Tremendous variation exists in the collection for various agronomic, grain and kernel quality characteristics (Kumary and Francies, 2003).

2.3 Core collection

A core collection has been defined as a collection which contains, with a minimum of repetitiveness, the maximum possible genetic diversity of a crop species and its wild relatives. Such a collection is not intended to replace existing gene bank collection, but, to make the variation contained within such collection more accessible to users.

2.3.1 Development of the concept of core collection

The large numbers of accessions accumulated in the gene banks are often poorly described. Their use for breeding purpose could be greatly increased if more

information on the amount and kind of variation in these collections is available. However, in most cases, such information is not available. This poses difficulty in effective utilization of germplasm for plant breeders and other research workers. In addition, the sheer size of many collections has frequently been cited as a barrier to increased utilization of collections (Holden, 1984).

Recognizing this, Frankel and Brown (1984), proposed development of core collections as a way out to alleviate the problem. According to them, core collections would represent "minimum repetitiveness, the genetic diversity of a crop species and its relatives". These might include sets that represent the broad genetic variation available for a total crop genome. The accessions or entries excluded from the sample would be retained as the reserve collection. Frankel's ideas on core collections, aimed at: (a) enhancing the management of germplasm collections, especially large ones such as that at IRRI and (b) facilitating the study and use of the conserved germplasm.

Frankel and Brown (1984) and Brown (1989 a and b), outlined procedures to develop core collection by using information on origin and characteristics of the accessions. According to them the guiding principles to constitute a core collection are i) the entire collection is a large taxonomic entity, ii) the core collection has a greatly reduced size, iii) the core is a true representative of the entire collection and iv) the core too is nearly as diverse as the entire collection

Several sampling methods to select entries have been suggested, ranging from random sampling to stratified sampling based on known groups with sample size constant, logarithmic or proportional to the group size (Brown *et al.*, 1987; Brown 1989b; Erskine and Muehlbauer, 1991).

The clustering of accessions based in multivariate techniques was suggested by Zeuli and Qualset (1987), to form groups, the members of which are likely to be genetically similar. Accordingly, the accessions of USDA durum wheat were divided

into groups based on their country of origin. Some countries with contrasting agro-ecological conditions grouped together. The results showed that country of origin is not a reliable basis for stratification.

Peeters and Martinelli (1989) also proposed that country of origin is a reliable unit of grouping and indicator of genetic diversity and this may provide a useful approach to those exploring the development of groups for a particular collection.

However, Brown (1989b), argued that the most effective strategies should involve a hierarchical stratification of the whole collection into groups of accession which share common taxonomic, geographical, ecological or generic characteristics. In cases of larger groups where there are chances of redundancy, representation in proportion to the logarithm of group size is more conservative. Based on the studies on barley and *Glycine*, he concluded that for smaller groups with less chances of redundancy, representation in proportion of group size is more appropriate. Similarly, Erskine and Muehlbauer (1991), found proportional strategy to be better than taking constant number from each group while developing a core collection in lentil germplasm. In an another study on composing a core collection of cultivated barley collected in China, Hintum (1995) found that proportional and logarithmic allocation scored better than constant representation.

Vaughan (1991), used the evolution database of world rice (*Oryza sativa* L.) collection, conserved at the International Rice Research Institute (IRRI), to compare different sampling strategies for choosing the core. A frequent source of resistance to different rice pests like brown plant hopper, green leafhopper and white backed, plant hopper and diseases, bacterial blight and rice blast was captured in the core. The results indicated stratified selection as more reliable than random and sequential selection, in retention of these characters.

In contrast to above strategy, Peeters *et al.* (1993) and Holbrook *et al.* (1993), reported that phenotypic similarity for a limited set of characters is a better indicator of genetic and ecological similarity than country of origin.

Several researchers have reported that for effective stratification of the collections, reliable characterization data along with passport data with information on country of origin should be available (Zeuli, and Qualset, 1993; Diwan *et al.*, 1994; Mathews and Ambrose, 1994 and Hamon *et al.*, 1995) to make the grouping of accessions based on phenotypic similarity and their country of origin more effective.

Combined use of agro-ecological and morphological characterization for stratification was used to establish the CIAT *Phaseolus vulgaris* core collection (Tohme *et al.*, 1995). Similarly, Hintum (1995) advocated the use of hierarchical approach for splitting the entire collection into smaller and smaller groups within groups. In his study, using a set of Chinese barley landraces with reliable passport data, stratification based on collection site was compared with stratification based on qualitative and quantitative characters. The collection site data proved best for clustering; followed by qualitative data. Clustering based on quantitative data did not improve sampling strategies.

When a complete data set for a germplasm collection is available, principal component analysis and cluster analysis are excellent tools for grouping of accessions by degree of similarity (Basigulp *et al.*, 1995). Similarly study was carried out by Bisht *et al.* (1999), to stratify the germplasm accessions of Indian sesame into diversity groups, based on well defined passport and characterization data using principal components score strategy.

Schoen and Brown (1995) developed two new sampling strategies for constructing diverse and representative core collections in cases of unequal diversity and differentiation among accessions occurring mostly in wild crop relatives.

Several other studies have been made to evaluate different sampling strategies for establishing a core collection in different crops like durum wheat in which random sampling strategy, random-systematic sampling strategy according a) to chronology of entry of the accessions into the collection, b) stratified by country of-origin were used (Zeuli and Qualset, 1993).

Methods of developing rice core collections were evaluated by Li *et al.* (2004), based on the predicted genotypic values for 992 rice varieties with 13 quantitative traits were predicted by the Adjusted Unbiased Prediction (AUP) method. Six hierarchical methods were combined with random, preferred and deviation sampling to develop 18 core collection of rice germplasm. The core collections which used predicted genotypic values had more genetic diversity than those based on phenotypic values.

Several variations in the adoption of approaches and procedures have been apparent from various core collections that have been developed so far. The basic idea in each of these studies was to make a better use of the germplasm, selecting a set of accessions, with different objectives in mind mostly to represent the broad genetic variation available for a total crop genome or species, a geographical region and entire germplasm maintained by a gene bank.

The common features observed in most of the studies were the need for a germplasm reference collection, stratification of the collection following hierarchical or non-hierarchical strategies, multivariate or principal component analysis and a sampling of 5-10 per cent from the defined groups following different sampling strategies as described by Brown (1989a), so that the core sample represent the genetic spectrum in the whole collection.

Different methods were proposed by Hu *et al.* (2000) in cotton for constructing core collections using stepwise clustering combined with three sampling strategies based on genotypic values and also evaluating representatives of core

collection. Of the different methods studied random sampling represented the genetic diversity structure of the initial collection whereas preferred sampling kept the accessions with special or valuable characteristics in the initial collections and deviation sampling retained the larger genetic variability of the initial collection. Finally they concluded that for better representation of core collection, cluster methods should be combined with different sampling strategies. The search using the PowerCore was heuristic. The core set was generated via this search by calculating the Mean Difference (MD, %), Variance Difference (VD, %), Coincidence Rate (CR, %) and Variable Rate (VR, %) for continuous variables and computing a frequency distribution for each variable (Hu *et al.*, 2000).The core collections based on genotypic values retained larger genotypic values and had superior representatives than those based on phenotypic values.

2.3.2 Core collections in crops

The first core collection established was that of perennial *Glycine* by Brown *et al.* (1987). The core consisted of 111 accessions developed from a collection of 1400 accession of twelve different species of *Glycine* at Canberra, Australia. Grouping was made initially, at species level and then eco-geographic factors were used to select the entries for the core. The proportion of accessions selected from each category (species x state) varied from less than 5-100% in order to achieve some representation. The core so developed included at least a few accessions of each species and geographic coverage of each Australian State. Preference was given to the accessions already used in research and included known morphological, cytological and isozyme variation with in species.

Moody *et al.* (1988) developed a core collection of wheat with a specific objective of estimating variation for tolerance to soil boron toxicity in the Australian wheat (*Triticum* spp.) collection. Geographical and soil data was used to select

genotypes. This approach of developing core collections with primary objectives promoted better evaluation, utilization and understanding of genetic variation.

Hamon and Van Stolen (1989) established a core collection from 2283 okra (*Abelmoschus esculentus*) collection in the joint ORSIOM/IBPGR project, using passport and characterization data of West African accessions. The core collection of 189 accessions was developed primarily to have a manageable collection scaled down to the needs of the breeder including the widest possible range of variability. The data on quantitative characters like date of flowering, plant height and number of internodes and qualitative descriptors like stem colour, leaf shape and fruit position was analyzed using univariate and multivariate methods to determine the correlations between characters and geographical distribution of variability.

The structure of variation in 67 barley (*Hordeum vulgare*) landraces from Syria and Jordan was investigated by using various spike characters from the landraces grown in a favourable environment in Syria (Weltzein, 1989). Factor analysis was used to identify trait complexes that accounted for major proportions of the total variation among landraces. The landraces were then clustered into nine distinct groups based on their similarity for all traits as well as geographical similarity of the collection. The samples were proportionally chosen from each cluster to form the core.

Hamon and Noirot (1990), proposed a core collection of okra (*Abelmoschus* spp.) using quantitative plant characterization data. They found that the selection of accessions based on multivariate analysis maximized the variation in the core in comparison to the original collection.

To develop a core collection, Mackay (1990), used specific traits like pasting quality of bread wheat, heat shock on bread quality and the spectral quality of anthocyanin across altitudes, in a range of *Triticum* spp. Accessions, including wild

and cultivated diploids, tetraploids and hexaploids. He used ecogeoraphical data for selection of accessions to include a rational amount of genetic variation in the core.

The European cooperative program for conservation and exchange of crop genetic resources nominated a working group, to report a proposal on the development of a core collection of *Hordeum* spp. (Bothmer *et al.*, 1990). The strategy of the proposal was to include less than 2000 accessions consisting of cultivars, landraces, wild species and genetic stocks. The characters included for creating Dendrogram of variation were growth habit, ear type and pedigree data for cultivars, eco-geographical data. The use of eco-geographical data was specifically mentioned. The inclusion of genetic and cytogenetic markers stocks in the core was also recommended to increase the quality of core for further research.

Holbrook *et al.* (1993) established a core set of 831 accessions from 7432 groundnut germplasm accessions by using the data on country of origin and by the amount of available morphological data. Random sampling was used to select 10 per cent from each group. They examined data of six phenotypic traits and found that the genetic variation expressed for each trait in the entire collection has been preserved in core set.

From a collection of 3000 durum wheat accessions, selection of a core sample was done by applying five different strategies. The core was further evaluated using four qualitative and eight quantitative spike characters (Zeuli and Qualset, 1993). Each strategies (random, random systematic according to chronology of entries into the collection, stratified by country of origin, stratified by log frequency by country of origin and stratified by canonical variables) generated about 500 accessions for the core sample. All the strategies produced representative sample from the whole collection, however stratified canonical sample increased phenotypic variances. They suggested multivariate approach as extremely useful though requires extensive data from the whole collection.

Crossa *et al.* (1993), developed maize (*Zea mays*) core collection, by sub dividing the entire germplasm into non-overlapping groups, based on racial complex and selected eco-geographical criteria. Within each race, accessions were stratified by region. Cluster analysis on morphological and agronomic characters identified groups of similar accessions. Similarly, the practical importance for maintaining germplasm in maize was reported by Crossa *et al.* (1995) taking an example of race *Tuxpeno*, for which 848 accessions were available from 23 races and 3 sub races. The selection of 175 accessions based on cluster analysis, principal component analysis, eco-geographical data, lodging and adaptation data assessed in multi-location trials was used to develop the core.

Radovic and Jelovac (1994) suggested a different approach to identify the divergent population for the selection of a core sample. Hierarchy was established using the combining ability of the testers. Seven per cent of the 902 maize populations at Yugoslav maize gene bank formed the core consisting of 72 entries. Eighteen morphological traits were used to determine the differences between the entire population and the core.

Balfourier and Charmet (1994), established a core collection from 547 natural populations of perennial ryegrass (*Lolium perenne*). The core consisting of 42 entries was developed on the basis of multivariate analysis, to preserve the diversity considering agronomic characteristics and eco-geographical stratification.

A core collection of 211 accessions for annual *Medicago* species was developed by evaluating 1240 accessions (40% of the total collection) based on 16 agronomic and morphological traits (Diwan *et al.*, 1994). The collection maintained at U. S. National Plant Germplasm System consisted of 36 species of this crop, which was used to develop the core. Accessions within species were grouped by cluster analysis based on unweighted pair group method and arithmetic averages. One accession per cluster was selected for each species to represent the greatest diversity

in geographical regions. The selected core was reevaluated and found to represent the variability of the germplasm collection maintaining the stability between evaluation years.

Mathews and Ambrose (1994), selected a representative core collection of 157 accessions (six per cent of John Innes *Pisum* collection) using passport data, cross reference with morphological data and descriptive statistics of group formed, based on species and sub-species, ecotypes and landraces, cultivars and genetic stocks.

The genetic organization of the coffee gene pool was critically investigated by Hamon *et al.* (1995), to develop the core according to genetic history and available genetic knowledge. A new method, Principal Component Score Strategy, was used on data obtained for cultivated *Coffea liberica*, a well studied species, for developing a core collection using quantitative data. The use of several different strategies, rather than a single one, to establish a core collection was suggested, depending upon the gene pool as well as the level of knowledge. Further Noirot *et al.*, (1995) studied the importance of principal component scoring for sampling stratification and choice of sample size. They recommended the use of quantitative data, but with small changes could be also for qualitative data, to effectively maximize the sample diversity.

Basigulp *et al.* (1995) developed a core collection of 200 entries from the U. S. collection of perennial alfalfa (*Medicago sativa*) plant introductions. The sample was taken from 1100 plant introductions collected from 47 countries, based on passport data from the Germplasm Resources information Network (GRIN) system. Eight methods were compared for the developing the core by non-parametric tests. Two methods, combined cluster analysis based on principal component within each cluster and direct selection of entries within each geographical group, were found best for the designating the core collection, which retained the greatest variability for all traits.

Corderio *et al.* (1995) suggested the use of different criteria for construction of a Brazilian core collection of cassava (*Manihot esculanta* Crantz). These included stratification of the collection into groups based on category (landraces or improved materials), origin (grouping accessions according to agroecological classification of origins) and characters of importance to breeders (selected according to heritability and reliability of data).

A core collection was established at ICRISAT by stratifying the world sorghum collection of 33100 accessions geographically and taxonomically into sub groups (Rao and Rao, 1995). Accessions in each subgroup were then clustered into closely related groups based on characterization data, using principal component analysis. A proportional sampling strategy resulted in a core collection of 3475 accessions (approximately 10 per cent of the entire collection).

Diwan *et al.* (1995) developed a core collection for U. S. National germplasm of annual *Medicago* spp., comprising eleven methods differing in their use of passport and evaluation data. The core developed by cluster analysis based on evaluation data represented the collection better than the core designed solely based on passport data. Further, random logarithmic selection of accessions generated better core collection than proportional method. In contrary to other studies, 5-10 per cent sample size for core collection was found to be insufficient to represent the entire collection.

A barley core collection of 2000 accessions was established by Knupffer and Van Hintum (1995) from entire *Hordeum* gene pool, consisting of landraces, improved cultivars and wild relatives from the primary (*H. vulgare* and diploid *H. spontaneum* complex), secondary (*H. bulbosum*) and tertiary gene pools (including 30 different species of *Hordeum*). The core collection was a collaborative international effort that included germplasm maintained at several institutes, representing the entire gene pool of the crop. Brown (1995), termed this kind of core as 'synthetic core'

wherein the accessions are assembled from various collaborative germplasm collections, which is more aid to germplasm use than to gene bank management.

A core sample was established by Tohme *et al.* (1995) from 24000 accessions, available from the world common bean (*phaseolus vulgaris* L.) collection, maintained at the Centro International de Agricultura Tropical (CIAT). A three-step process was followed, firstly by prioritizing the regions giving weight to traditional bean growing areas. Secondly, germplasm was classified according to agro-ecological origin. The third step was based on morpho-physiological data of growing habit, seed colour and seed size. The environmental parameters like length of growing season, photoperiod, soil type and moisture regime yielded 54 agro-ecological classes. A random selection within these agro-ecological classes resulted in a core collection of 1000 accessions identified from primary centers, an additional 300 from secondary centers along with 40 cultivars, 40 bred lines and 40 genetic stocks.

Grauke and Thompson (1995), evaluated pecan [*Carya illnoinensis* (Wangenh) K. Koch] germplasm collection and designated a core subset of 26 cultivars using stratified sampling procedures. Cultivars were selected with reference to geographic origin.

The effect of different methods on the representativeness of selected accessions for the core was examined by Galwey (1995), using data from Cambridge (UK) *Phaseolus* bean germplasm collection. Generally, different selection strategies yielded very similar outcomes in term of representativeness and diversity. However, the use of passport, taxonomic and eco-geographical data helped to ensure that the core collection is representative of the whole collection as well as the whole plant taxon under consideration.

A hierarchical clustering procedure with incremental sum of square as the fusion strategy and Euclidean distance as the dissimilarlity measure was used by Crossa *et al.* (1995), for classifying 175 maize accessions of the *Tuxpeno* race

complex. Multivariate methods were used to study the phenotypic diversity and to select a core collection. Accessions were randomly selected from each group by cluster analysis.

Mahajan *et al.* (1996), proposed a technique to establish a representative core set of South Asian okra (*Abelmoschus esculentus*) germplasm collection, maintained at the National Bureau of Plant Genetic Resources (NBPGR), using characterization data. A total of 260 representative accessions with diverse geographical background were selected for the study. A non-hierarchical cluster analysis was performed using Euclidean distance based on nine quantitative descriptors. The incremental sum of square was used as clustering criterion. Principal component for quantitative data was used to select the accessions from groups. Shannon-Weaver diversity index for qualitative data was also used to design a representative core sample of 53 accessions.

A core collection was developed by Pederson *et al.* (1996) from U.S. white clover germplasm collection for cyanogenesis that confers resistance to many species of leaf feeding insects and molluscs. A simple technique of geographic stratification and random selection was used to develop the core that was representative for total cyannogenesis and distribution of cyanogenic plants in the entire collection.

Taba *et al.* (1998) evaluated Caribbean maize (*Zea mays* L.) accessions from the CIMMYT maize germplasm bank to design a core subset based on morphological and agronomic characters. The sequential strategy proposed earlier by Franco *et al.* (1997) was used to stratify the entire collection. A pattern of phenotypic diversity of the accessions in each cluster was also established by canonical discriminant analysis. The selection of entries for the core was based on yield (mg/ha), ear rot (%) and moisture (%) calculated for each accession. The upper 20 per cent of the accessions representing the phenotypic diversity within clusters with high selection indices were chosen for the subset.

The Spanish National Germplasm Bank holds a collection of about 2000 barley accessions. The core collection was constituted by three groups of germplasm: successful old varieties (15); entries in common with previously existing barley core collections (15); and 2-row (8) and 6-row (122) entries from the BNG (Banco Nacional de Germoplasma), for a total of 160 entries. Several agronomic characters, such as days to flowering, days to maturity, length of grain filling period, plant height at maturity, grain yield, test weight and 1000 kernel weight were recorded (Igartua *et al.*, 1998).

A procedure for establishing a sesame core collection was systematically studied by Xiurong *et al.* (1999) representing over 4000 accessions and genetic diversity for the crop in China. Different hierarchical clustering procedures were used with data on 14 traits, grouping the accessions into seven ecotypes. 453 randomly selected accessions formed the core collection with good representativeness, confirmed by Zymogram characteristics.

Balfourier *et al.* (1999) compared different sampling strategies for developing a core sample in large sized natural populations of perennial ryegrass (*Lolium perenne* L.) and medic *Medicago truncatula* Gaertn.), for their ability to restore the spatial or geographic structure of the initial collection, their capacity to capture the phenotypic diversity of the whole collection and their effect in conservation of neutral alleles. The comparisons of two species found spatial structure of diversity to represent the best core collection, although there was a minimal effect on the mean number of neutral alleles.

Several methods of developing core collections using agronomic data for *Poa pratensis* L. was studied by Johnson *et al.* (1999). From a total collection of 228 accessions, a core collection representing 10 per cent of the collection was developed using random sampling, hierarchical cluster analysis (Ward's or UPGMA), and stratification by broad geographic regions using agronomic data. The core developed

from cluster analysis resulted in increased variances and range of agronomic traits, turf quality and seed production, compared to the core developed without cluster analysis.

A method was developed by Skinner *et al.* (1999) to develop a core collection by maximizing the diversity, measured as mean Euclidean distance, from within groups of accessions defined by species, sub species and geographic origin. The effectiveness of the method was tested on a collection of annual *Medicago* evaluated at the Australian *Medicago* Resource Center in Adelaide, South Australia. A core collection of 1705 accessions (10.4 per cent) was obtained by grouping sequentially, such that species formed group first followed by sub species within each species and geographical origin within each species-sub species group. The core represented 74 per cent of the extreme values of 27 characters, covering entire range in most cases.

Holbrook (1999) developed a core collection for the U.S. *Arachis hypogaea* germplasm collection consisting over 7000 accessions with great amount of genetic diversity. The collection was first studied by country of origin and then grouped into nine sets based on morphological characters using multivariate approach. The random selection procedure resulted in a core sample of 831 accessions representing the entire range of genetic variation present in the original collection.

A Peruvian sweet potato core collection was developed by Huaman *et al.* (1999) on the basis of morphological, eco-geographical and disease and pest reaction data. The entire collection was grouped into distinct clusters following Unweighted Pair-Group Method using an Arithmetic average (UPGMA) based on the above morphological descriptors. The sampling was based on square root of the number of accessions for each cluster, which resulted in a core collection consisting of 85 accessions. This sampling was further validated by partial assessment of the core resistance to diseases and pests, tolerance to salt, storage root dry matter content and vegetative period.

Tabare *et al.* (1999) developed a core collection of maize germplasm of Brazil. Core collection was established using a two-level sampling strategy and thee hundred accessions was selected, representing the genetic variability of the base collection.

Pengally and Maass (2001) constructed a core collection of 47 accessions of *Lablab purpurus* (L.) from two sets of germplasm collections of 249 accessions using a common set of morphological and agronomic attributes data collected from two different locations.

Upadhyaya and Ortiz (2001) established a mini core set from the core set promoting utilization of chickpea genetic resources in crop improvement. They used two stage strategy to select a chickpea mini core set consisting of only about one per cent of the entire collection held at ICRISAT genebank (16991 accessions).

A core collection was formed in chickpea (*Cicer arietinum*) based on evaluation by Upadhyaya *et al.* (2002 a) for 7 morphological descriptors (flower colour, plant colour, growth habit, seed colour, seed shape, dots on seed testa and seed testa texture) and 15 agronomic characteristics [days to flower, flowering duration (days), plant height (cm), plant width (cm), apical primary branches (No.), apical secondary branches (No.), basal primary branches (No.), basal secondary branches (No.), tertiary branches (No.), days to maturity, pods per plant (No.), seeds per plant (No.), 100-seed weight (g), plant yield (g), plot yield (kg/ha)].

A mini core set of peanut was developed by Upadhyaya *et al.* (2002 b) and was evaluated for morphological, agronomic and quality traits in the rainy and post rainy seasons. Wards method of clustering was used to separate core collection accessions into groups of similar accessions. A minicore set consisting of 184 accessions was selected. Newman keul's test for means; Levene's test for variance and chi-square test for frequency distribution analysis for different traits indicated that the variation in the core collection has been preserved in the mini core set also.

Reddy *et al.* (2005), reported the development of a core collection consisting of 1290 lines from 12,153 pigeon pea germplasm based on 14 qualitative morphological traits while Zhao *et al.* (2005) developed a core collection of annual wild soyabean (*Glycine soja*) from 6172 accessions based on 21 descriptors.

In a study, Swamy *et al.* (2006), characterized ground nut core collection of 504 accessions. Fourteen morphological traits were studied for assessing morphological variation within the core collection. Shannon-Weaver diversity index revealed that flower colour and leaf hairyness were monomorphic in nature. All the traits except growth habit, pod beak and pod reticulation in var. *festigiata* and pod beak in var. *vulgaris* exhibited low diversity.

World-wide wheat diversity 3,942 accessions originating from 73 countries were analyzed with a set of 38 genomic simple sequence repeat (SSR) markers. A final core of 372 accessions was selected with M strategy (Balfourier *et al.*, 2007).

In a study, Gowda *et al.* (2007), evaluated germplasm collection involving 4511 accessions of finger millet for different morpho-agronomic characters over the years. A core set of 551 accessions was formed using evaluated data by cluster analysis and PCA scoring. The core set formed was true representative of the entire collection and the procedure followed in its formation was appropriate as the statistical analysis indicated that core set did not differ significantly from entire collection of 4511 accessions. They found total diversity present in the entire collection was completely captured in core set.

A core set of 38 accessions was developed by Yuan *et al.* (2008) using Ward's method of clustering based on 12 qualitative traits and 5 quantitative traits from 122 Sweet osmanthus accessions. The means were compared using t- test, frequency distribution using χ^2 test, and Shannon Weaver diversity index. The Shannon Weaver diversity index for 17 descriptors indicated that genetic variation available for these traits in the entire collection has been preserved in the core set.

Cho *et al.* (2008) developed a core set of 260 accessions of Korean soybean from 2765 accessions using molecular profiling followed by UPGMA clustering. The core set was also assessed for phenotypic diversity with seven quantitative traits and three qualitative traits.

Gowda *et al.* (2008) evaluated 895 accessions of little millet for 10 quantitative and 11 qualitative traits and using that evaluated data formulated a core set of 55 accessions using a software Powercore (v.1.0). The mean, range, variance, frequency distribution, Shannon-Weaver diversity index (H) and phenotypic correlation values of core set and whole collection under study did not differ significantly, indicating that the core set represents the entire collection of 895 accessions and the entire diversity has been captured very well in the core set.

Around 6,390 accessions of cultivated peanut (*Arachis hypogaea* L.) have been collected in China. Jiang *et al.* (2008) developed a core collection of 576 accessions based on 15 morphological and biochemical data. Comparison between the newly selected Chinese peanut core collection and the introduced mini core collection consisting of 184 lines established at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) indicated that there were wider diversities in the var. *hirusta* than in *vulgaris* for leaf length, leaf width, seed length, seed width in the Chinese core collection.

Dean *et al.* (2008) reported that the US germplasm collection for peanuts was selectively reduced to a mini core or "core of the core" collection composed of 112 of the 7432 accessions in the whole collection. This reduction was based on morphological characteristics. Of these samples, 108 were available from a single location of one growth year. These samples were analyzed for total amino acid content, fatty acid content, tocopherols and folic acid content.

Yao *et al.* (2008) constructed a core collection of 124 maize landraces from Wuling Mountain region in China based on the genetic clustering from 42 microsatellite (SSR) markers with a combination of their geographic origin and germplasm characteristics. Four evaluating parameters for maize landrace core collection, including mean difference percentage (MD), variance difference percentage (VD), coincidence rate of range (CR) and variable rate of coefficient of variation (VR) were assessed with 20 quantitative traits.

Gowda *et al.* (2009) formulated a core set numbering 50 accessions from 729 accessions of barnyard millet. Evaluated data on both quantitative and qualitative traits were subjected to a new statistical analysis called Powercore (v.1.0) to form core set. The genetic variability of the core set was compared with the entire collection of 729 accessions. the mean, range, variance, frequency distribution, Shannon Weaver diversity index (H) and phenotypic correlation values calculated for core set and whole collection of 729 accessions were at par with each other and did not differ significantly. They suggested that, new method in formation of core set by using statistical analysis PowerCore is useful in retaining in most of the diversity present in the collection of barnyard millet germplasm.

Haradari (2009), evaluated 1000 accessions of finger millet for 11 quantitative and 12 qualitative characters and using that evaluated data formulated a core set of 77 accessions using Powercore (v.1.0) software. The mean, range, variance, frequency distribution, Shannon-Weaver diversity index (H) and phenotypic correlation values of core set and whole collection under study did not differ significantly, indicating that the core set represents the entire collection of 1000 accessions and the entire diversity has been captured very well in the core set.

A core collection of 2247 accessions was developed from 37,000 sorghum accessions by Upadhyaya *et al.* (2009). A sorghum mini core (10% accessions of the core or 1% of the entire collection) was developed from the existing core collection.

The core collection was evaluated for 11 qualitative and 10 quantitative traits in an augmented design using three control cultivars. The hierarchical cluster analysis of data using phenotypic distances resulted in 21 clusters. From each cluster, about 10% or a minimum of one accession was selected to form a mini core that comprised 242 accessions. The data in the mini core and core collections were compared using statistical parameters such as homogeneity of distribution for geographical origin, biological races, qualitative traits, means, variances, phenotypic diversity indices, and phenotypic correlations. These tests revealed that the mini core collection represented the core collection, which can be evaluated extensively for agronomic traits including resistance to biotic and abiotic stresses to identify accessions with desirable characteristics for use in crop improvement research and genomic studies.

Kottapalli *et al.* (2010) developed a Valencia core from USDA collection using 26 morphological descriptors. One hundred and twelve genotypes from the Valencia core were genotyped with 36 SSR markers generating 500 polymorphic loci.

A core set of finger millet germplasms (662 accessions) based on origin and data on fourteen quantitative traits was developed by Upadhyaya et al. (2010) from the entire global collection of 5940 accessions held in the genebank at ICRISAT, India. The principle component analysis (PCA) was performed on the accessions from each region. The comparison of mean, variance, frequency distribution, Shannon-Weaver diversity index (H') and phenotypic correlations indicated that the core set represents the entire collection. These tests indicated that sampling was optimal and the diversity has been captured very well in the core set.

Upadhyaya *et al.* (2011) constructed a core collection of proso-millet (*Panicum miliaceum* L.) using 833 accessions based on geographic information and 9 qualitative and 11 quantitative traits conserved at ICRISAT gene bank. The entire

germplasm collection was stratified into five groups based on races and data on 20 morpho-agronomic traits were used for clustering following Ward's method. About 10% was randomly selected from each of 10 clusters to constitute a core collection of 106 accessions.

2.3.3 Core collections in rice

Liang *et al.* (2004) studied the distribution of genetic diversity between *Oryza sativa* L. *indica, O. sativa* L. ssp. *Japonica* covering different ecological zones in Yunnan. Accessions were morphologically evaluated and also screened with specific markers of *indica/japonica* subspecies to form the Yunnan landrace rice core collection comprising of 113 accessions. The genetic diversity of *japonica* was higher than that of *indica* and the ecological zone with the highest and smallest genetic diversity lay in south-east and north-east Yunnan respectively. This diversity distribution was consistent at morphological and isozyme levels with studies on the entire Yunnan rice resources and core collection. The main conclusions were that the landrace rice core collection in Yunnan genetically represents the entire landrace rice resources in Yunnan.

Rice molecular markers developed in the granule bound starch synthase gene (Waxy) that controls grain amylose content and the soluble starch synthase IIa (Alk) gene that controls alkali spreading value (ASV) were used to characterize a core subset of rice germplasm that was maintained by the USDA-ARS National Small Grains Collection. The core subset comprising about 1600 accessions represented about 10 per cent of the selections from which it was derived derived from (17,000 accessions in the rice NSGC collection) (Mc Clung *et al.*, 2004).

The Rice Germplasm Collection of Embrapa, Brazil consists of approximately 10,000 accessions. Shannon Diversity Index (a measure of genetic diversity) was computed and the final Brazilian rice core collection consisted of 550 accessions representing rice collections from three strata: (a) landraces from Brazil (VT) (b)

breeding materials from Brazil (LCM) and (c) introductions (LCI) (Abadie *et al.*, 2005).

Pkenia *et al.* (2006) assessed the genetic potential for 990 rice lines for 26 quality traits and formed core collection employing Mahalanobis distance to calculate the genetic distance among the accessions. Twenty four core collections were developed by using eight hierarchical clustering methods, combined with random, preferred and deviation sampling at a sample proportion of 15%. These core collections were compared with others constructed at sample proportion range of 10% and 20%. The core collection developed using a sample size of 15% retained the highest degree of diversity and was stable for all the cluster methods and hence the best in developing a core collection of rice quality traits.

Yan *et al.* (2007) developed a core set of rice from 1790 entries collected from 114 countries. The formed core set was evaluated with respect to country of origin, frequency distribution for fourteen of descriptors and correlation coefficients. They conclude that the diversity of entire collection was preserved in core set.

In 2009, Jia *et al.*, developed the USDA rice core collection, including using a stratified random sampling method to represent the entire NSGC collection including over 18,000 accessions by characterizing the collection for sheath blight (*Rhizoctonia solani*) resistance in comparison with common checks, resistant Jasmine 85 and susceptible Lemont.

Weiguo *et al.* (2010) developed an allele-mining core set in rice (*Oryza sativa* L.) from an allelic diversity of collection of 4046 rice accessions. Using a heuristic approach, an allele-mining set of 162 accessions was successfully developed on the basis of SSR marker data. The core set accounting for about 4.0% of the entire collection, captured all of the alleles (482) retained in the entire collection, exhibiting 100% coverage of alleles with minimum redundancy.

A rice mini core collection consisting of 217 accessions to represent the USDA core and whole collections that include 1,794 and 18,709 accessions, respectively was developed by Xiaobai *et al.* (2010). Genetic structure and diversity were analyzed using both genotypic (128 molecular markers) and phenotypic (14 numerical traits) data. A model based clustering analysis resulted in lowland rice including three groups, aus (39 accessions), indica (71) and their admixtures (5), upland rice including temperate japonica (32), tropical japonica (40), aromatic (6) and their admixtures (12) and wild rice (12) including *glaberrima* and four other species of *Oryza*. Group differentiation was analyzed using both genotypic distance using 128 molecular markers and phenotypic (Mahalanobis) distance D^2 from 14 traits.

Zhang *et al.* (2011) constructed a core collection using 4,310 Chinese accessions of *Oryza sativa* L. using 36 SSR markers and phenotypic characterization. Thirty-four discrete morphological traits and the 16 quantitative traits were studied. Based on the most effective scheme selected from 229 sampling schemes, the core collection comprising 1.7% (932) of the accessions in the basic collection, retained more than 85% of both the SSR and phenotypic variations thus providing a rational framework for intensive surveys of natural variation in complex traits in rice genetic resources and hence utilization of variation in rice breeding.

Xiao-ling *et al.* (2011) constructed a nested core collection from of 2262 rice accessions to determine the appropriate sample size to represent the genetic diversity of rice landrace collection based on 34 qualitative traits and 15 quantitative traits. The result showed that 50-225 nested core collections, whose sampling rate was 2.2%-9.9%, were sufficient to maintain the maximum genetic diversity of the initial collection.

The rice base collection in India preserved in national gene bank consists of more than 95,000 accessions. The collection was stratified geographically by

grouping adjacent states with similar agro-climates. Data on 13 quantitative characters was used to group the germplasm accessions into 25 diverse clusters. The number of accessions in each cluster ranged from 3-78. From each cluster approximately 15-18% of accessions were randomly selected to constitute a mini core of 182 accessions (Rao *et al.*, 2012).

Materials and Methods

3. MATERIALS AND METHODS

The present investigation was carried out during *kharif* 2011-2012 in the Department of Plant Breeding and Genetics, College of Horticulture, Kerala Agricultural University (KAU), Vellanikkara P.O., Thrissur. 680 656 located 40 m above MSL at an altitude of $10^0$31' N latitude and $76^0$13' E longitude and experiencing humid tropical climate.

3.1 Experimental Material

The material for the present study comprised of one hundred and sixty (160) short duration germplasm accessions of rice (*Oryza sativa* L.) and three checks [Ptb 39 (Jyothy), Ptb 50 (Kanchana) and Ptb 55 (Harsha)] procured from 1) Regional Agricultural Research Station (RARS), KAU, Pattambi, Palakkad, 2) Rice Research Station (RRS), Moncompu, Thekkekara P.O., Alappuzha and 3) Agricultural Research Station (ARS), Mannuthy, Thrissur. The list of 160 germplasm accessions henceforth referred to as 'Base collection' is given in Table 2.

3.2 Methods

3.2.1 Layout of experiment

The experiment was laid out in an Augmented Blocks Design with 16 compact blocks accommodating a total of 160 short duration germplasm accessions and three checks. Each block comprised of 10 accessions (unreplicated) and three checks.

Each entry was sown in two rows of 3 m length at spacing of 20 cm x 15 cm. Recommended agronomic practices as per package of practices of Kerala Agricultural University (2007) were followed during crop growth period to raise a good crop.

Table 2. List of germplasm accessions in Base collection

Sl. No.	Accessions	PGC No.	IC No.	Sl. No.	Accessions	PGC No.	IC No.
1.	Annapoorna	1	263549	41.	Ptb 43 (Swarna Prabha)	54	263602
2.	Ptb 36 (Rohini)	2	263550	42.	Ptb 42 (Suvarnamodan)	55	263603
3.	Ptb 38 (Triveni)	3	263551	43.	Cul 25333	56	263604
4.	Ptb 39 (Jyothi)	4	263552	44.	Japan violet	57	263605
5.	Ptb 45 (Matta Triveni)	5	263553	45.	PM-701	58	263606
6.	ADT 37-11	6	263554	46.	PM-706	59	263607
7.	Ptb 46 (Jayathy)	7	263555	47.	PM-709	60	263608
8.	Bhagya	8	263556	48.	PM-713	61	263609
9.	Onam	9	263557	49.	PM-715	62	263610
10.	Ptb 49 (Kairaly)	11	263559	50.	PM-716	63	263611
11.	Ptb 50 (Kanchana)	12	263560	51.	PM-717	64	263612
12.	Thulasi	14	263562	52.	PM-2601	65	263613
13.	Dular	15	263563	53.	M1-14390	70	263618
14.	Supriya	16	263564	54.	Kargi	71	263619
15.	IR 36	17	263565	55.	Reymuthika	72	263620
16.	Kunju Kunju	18	263566	56.	Karangi	73	263621
17.	Harswa	19	263567	57.	Sabalai	74	263622
18.	IR-1552	20	263568	58.	Sihot	75	263623
19.	Cul 12814	26	263574	59.	R-320-300	78	263626
20.	Cul 8755	27	263575	60.	ASD17	83	263631
21.	Cul 8757	28	263576	61.	ASD (Peringotukurussi)	84	263632
22.	Cul 8759	29	263577	62.	ADT 36	85	263633
23.	Cul 8709	31	253679	63.	ADT 37-1	86	263634
24.	Cul 8714	33	263581	64.	ADT40	87	263635
25.	Cul 8716	34	263582	65.	Basmati supper	90	263638
26.	Cul 8723	36	253584	66.	TKM 6	91	263639
27.	Sulochana (Sel.)	37	263585	67.	Mo 8 (Aruna)	92	263640
28.	T(N) 1	38	263586	68.	Makom (Mo 9)	93	263641
29.	Cul 3	39	263587	69.	Cul 8711	95	-
30.	IR100	41	263589	70.	Cul 1727 / Navara	96	263644
31.	ASD 18	43	263591	71.	Panki	98	263646
32.	MOU 3	44	263592	72.	Cul 90-01	99	263647
33.	CO 37	45	263593	73.	Cul 90-03	100	263648
34.	Abhaya	46	263594	74.	Cul 210-22	101	263649
35.	ASD (Kongad)	47	263595	75.	Cul 210-29	104	263652
36.	ASD 16	48	263596	76.	Cul A4-1-1	105	263653
37.	Ptb 7 (Parambuvattan)	49	263597	77.	Cul A4-4-1	107	263655
38.	Ptb 10 (Thekkencheera)	50	263598	78.	Cul C2-1	108	264656
39.	Ptb 23 (Cheriya Aryan)	51	263599	79.	Cul C2-2	110	263658
40.	Ptb 30 (Chuvannamodan)	52	263600	80.	IVT 33	115	263663

Table 2. List of germplasm accessions in Base collection contd...

Sl. No.	Accessions	PGC No.	IC No.	Sl. No.	Accessions	PGC No.	IC No.
81.	IVT 109	117	263665	121.	F5-23-2	172	-
82.	JM-20-18	118	263666	122.	F6-11-1-1	173	-
83.	JM-20-5	119	263667	123.	IET18045	174	-
84.	JM-20-21	120	263668	124.	IET18886	177	-
85.	JM-20-8	121	263669	125.	OR-1885-16-34	178	-
86.	JM-10-7	122	263670	126.	IET17284	180	-
87.	JM-20-19	123	263671	127.	IET17467	181	-
88.	JM-10-32	124	263672	128.	IET18318 Sel1	186	-
89.	JM-10-31	125	263673	129.	IET18318 Sel2	187	-
90.	AM-10-24	126	263674	130.	PC-1 (Mavundiri)	188	-
91.	AM-10-5	127	263675	131.	CSR 10	191	-
92.	AM-20-27	128	263676	132.	CSR 3	192	-
93.	AM-30-8	129	263677	133.	CSR 23	193	-
94.	AM-30-5	130	263678	134.	CSR 27	194	-
95.	AM-10-7	133	263681	135.	MTU1010	195	-
96.	AM-30-31	134	263682	136.	Dhandori	196	-
97.	Kalyani II	137	263685	137.	Early samba	197	-
98.	IVT 14	138	263686	138.	Indira Sugandhi Dhar	198	-
99.	Cul 10-1-1 (Ahalya)	139	263687	139.	Kasturi	199	-
100.	Cul 210-25 (Varsha)	141	263689	140.	Cul C3-2 KM	200	-
101.	Cul A4-1-2	142	263690	141.	HS-16	-	-
102.	Cul 90-02	144	263692	142.	HS-1	-	-
103.	Cul 90-04	145	263693	143.	HS-13	-	-
104.	Cul 90-05	146	263694	144.	Ptb 35 (Annapurrna)	-	-
105	IVT 32	148	263696	145.	Manupriya	-	-
106.	IVT 42	149	263697	146.	Parambuvattan	-	-
107.	IVT116	150	263698	147.	Karuthamodan	-	-
108.	SBRP 2	152	263700	148.	Karanavara	-	-
109.	SBRP 3	153	263701	149.	Kalladiaryan	-	-
110.	SBRP 4	154	263702	150.	Chuvannamodan	-	-
111.	SBRP 5	155	263703	151.	Thottacheera	-	-
112.	DV-85	156	263704	152.	Karuthadukkan	-	-
113.	Moncompu 519	157	263705	153.	Chomala	-	-
114.	Cul 9410-3-Sel 1	165	-	154.	Njavara 11-2	-	-
115.	Cul 9410-3-Sel 1	166	-	155.	Cul KAUM 20	-	-
116.	Cul 9410-3-Sel 2	167	-	156.	Mo 21(Prathyasha)	-	-
117.	F3-11-3	168	-	157.	Mo 19 (Krishnanana)	-	-
118.	F5-14-1	169	-	158.	Cul M 20	-	-
119.	F5-17-1-1	170	-	159.	Mo 15 (Remanika)	-	-
120.	F5-23-1	171	-	160.	Mo 7 (Karthika)	-	-

3.2.2 Characterization and evaluation of rice accessions

The accessions in Base collection were classified according to their place of origin. They were traitized and data on sixty-five traits were recorded as per descriptor of rice (Rani *et al.*, 2004; IRRI, 2007). The descriptor included forty one qualitative traits and twenty four quantitative traits.

3.2.3 Formation of core set

The data recorded on Base collection were analyzed and a subset of 37 accessions referred to as 'core set' was formed using the software 'Power Core' (v.1.0) developed by Genetic Resource Division, Rural Development Administration, Republic of Korea.

'PowerCore' software uses the NET Frame work version 1.1 environment and is freely available for the MS windows platform (http://genebank.rda.go.kr/'powercore'/). This new method is widely used for the establishment of core and allele mining set by the Advanced M (Maximization) strategy implemented through a modified Heuristic Algorithm. The design concept and implementation strategy of 'PowerCore' and the validation on the outcome in comparison with other methods has been well described by Kim *et al.* (2007). 'PowerCore' by default classifies the continuous variables into different categories based on Sturges's rule (Sturges, 1926), which is described as: $K = 1 + \log_2 n$, where n = number of observed accessions. However, the software also allows modifying this rule to make desired number of classes for the continuous variables. Once classification of the continuous variables is performed, the software takes into account all classes, without omission of any of its variables. Thus, it possesses the capability to cover all the distribution ranges of each class. It minimizes the loss of useful alleles and effectively selects accessions with highest diversity reducing the repeated alleles.

3.2.4 Comparison of core set with Base collection

The accessions both in Base collection and formulated core set were classified according to their place of origin and the frequencies compared.

The frequencies of descriptor data pertaining to each qualitative traits were assessed both in Base collection and core set and their ratios compared. Chi-square test (χ^2) was applied to test whether the expected frequencies of accessions under different descriptors were observed in the

core set formed. Estimates of mean, range, coefficient of variability and variance with respect to quantitative traits in the two populations were determined. One Sample't' and Levene's test, respectively, were used to compare mean data and test the homogeneity of variance of both populations and determine whether the core set formed, reflected the diversity present in the Base collection.

Shannon and Weaver diversity index (H) was estimated using the frequency distribution for quantitative traits and qualitative traits. The index gives the measure of phenotypic diversity present in the Base collection and core set for each trait studied.

3.2.5 Recording of observations

Observations were recorded on ten healthy plants chosen at random in each accession. Observations on sixty-five descriptors comprising of forty one qualitative traits (Rani *et al.*, 2004) and twenty four quantitative traits (Rani *et al.*, 2004; IRRI, 2007) were recorded as per descriptor of rice.

3.2.5.1 Qualitative traits

Observations pertaining to various plant parts (Fig. 1, 2 and 3) were recorded on ten healthy plants chosen at random in each accession. A visual rating or scoring was adopted for assessment of qualitative traits as per guidelines prescribed in the Descriptor of rice enumerated in Table 3 (Rani *et al.*, 2004). The Royal Horticultural Society (RHS) colour chart was used to assess the colour traitistics.

Table 3. Descriptor for qualitative traits (Rani *et al.*, 2004)

Sl. No.	Traits	Recording of observation	Score	Classified as
1.	Coleoptile colour	First leaf through coleoptile / second leaf visible (less than 1 cm)	1 2 3	Colourless Green purple
2.	Basal leaf sheath colour	Booting (early boot stage)	1 2 3 4	Green Light purple Purple lines Purple
3.	Leaf: Intensity of green colour	Booting (early boot stage)	3 5 7	Light Medium Dark
4.	Leaf: Anthocyanin colouration	Booting (early boot stage)	1 9	Absent Present
5.	Leaf: Distribution of anthocyanin	Booting (early boot stage)	1 2 3 4	On tips only On margins only In blotches only Uniform
6.	Leaf sheath: Anthocyanin colouration	Booting (early boot stage)	1 9	Absent Present
7.	Leaf sheath: Intensity of anthocyanin colouration	Booting (early boot stage)	1 3 5 7 9	Very weak Weak Medium Strong Very strong
8.	Leaf: Pubescence of blade surface	Booting (early boot stage)	1 3 5 7 9	Absent Weak Medium Strong Very strong
9.	Leaf auricles	Booting (early boot stage)	1 9	Absent Present
10.	Leaf: Anthocyanin colouration of auricles	Booting (early boot stage)	1 2 3	Colourless Light purple Purple
11.	Leaf: Collar	Booting (early boot stage)	1 9	Absent Present
12.	Leaf: Anthocyanin colouration of collar	Booting (early boot stage)	1 9	Absent Present
13.	Leaf: Ligule	Booting (early boot stage)	1 9	Absent Present

Table 3. Descriptor for qualitative traits (Rani *et al.*, 2004) **contd...**

Sl. No.	Traits	Recording of observation	Score	Classified as
14.	Ligule shape (Fig.4)	Booting (early boot stage)	1 2 3	Truncate Acute Split
15.	Leaf: Colour of ligule	Booting (early boot stage)	1 2 3	Green Light purple Purple
16.	Flag leaf attitude (Early stage) (Fig.5)	Beginning of anthesis	1 3 5 7	Erect Semi-erect Horizontal Deflexed
17.	Flag leaf attitude (Late stage) (Fig.5)	Ripening (terminal spikelets ripened)	1 3 5 7	Erect Semi-erect Horizontal Deflexed
18.	Culm: Attitude (Fig.6)	Booting (early boot stage)	1 3 5 7	Erect Semi-erect Open Spreading
19.	Lemma: Anthocyanin colouration of keel	Anthesis half-way	1 3 5 7 9	Absent or very weak Weak Medium Strong Very strong
20.	Lemma: Anthocyanin colouration of area below apex	Anthesis half-way	1 3 5 7 9	Absent or very weak Weak Medium Strong Very strong
21.	Lemma: Anthocyanin colouration of apex	Anthesis half-way	1 3 5 7 9	Absent or very weak Weak Medium Strong Very strong
22.	Spikelet: Colour of stigma	Anthesis half-way	1 2 3 4 5	White Light green Yellow Light purple Purple
23.	Stem: Anthocyanin colouration of nodes	Milk development	1 9	Absent Present
24.	Stem: Intensity of anthocyanin colouration of nodes	Milk development	3 5 7	Weak Medium Strong
25.	Stem: Anthocyanin colouration of internodes	Milk development	1 9	Absent Present

Table 3. Descriptor for qualitative traits (Rani *et al.*, 2004) **contd...**

Sl. No.	Traits	Recording of observation	Score	Classified as
26.	Panicle: Curvature of main axis (Fig.8)	Ripening (terminal spikelets ripened)	1 3 5 7	Straight Semi-straight Drooping Deflexed
27.	Spikelet: Density of pubescence of lemma	Beginning of anthesis - Dough development	1 3 5 7 9	Absent Weak Medium Strong Very strong
28.	Spikelet: Colour of tip of lemma	Dough development - Ripening (terminal spikelets ripened)	1 2 3 4 5 6	White Yellowish Brown Red Purple Black
29.	Lemma palea colour	Dough development- Ripening (terminal spikelets ripened)	0 1 2 3 4 5 6 7 8 9	Straw Gold and gold furrows on straw background Brown spots on straw Brown furrows on straw Brown (tawny) Reddish to light purple Purple spots on straw Purple furrows on straw Purple Black
30.	Panicle: Awns	Ripening (terminal spikelets ripened)	1 9	Absent Present
31.	Panicle: Colour of awns (late observation)	Ripening (terminal spikelets ripened)	1 2 3 4 5 6 7 8 9	Yellowish white Yellowish brown Brown Reddish brown Light red Red Light purple Purple Black
32.	Panicle: Distribution of awns	Ripening (terminal spikelets ripened)	1 3 5	Tip only Upper half only Whole length
33.	Panicle: Presence of secondary branching (Fig.9)	Ripening (terminal spikelets ripened)	1 9	Absent Present
34.	Panicle: Secondary branching (Fig.10)	Ripening (terminal spikelets ripened)	1 2 3	Weak Medium Strong

Table 3. Descriptor for qualitative traits (Rani *et al.*, 2004) **contd...**

Sl. No.	Traits	Recording of observation	Score	Classified as
35.	Panicle: Attitude of branches (Fig.11)	Ripening (terminal spikelets ripened)	1 3 5 7 9	Erect Erect to semi-erect Semi-erect Semi-erect to spreading Spreading
36.	Panicle: Exsertion (Fig.12)	Ripening (terminal spikelets ripened)	3 5 7	Partly exserted Mostly exserted Well exserted
37.	Time of maturity	Ripening (terminal spikelets ripened)	1 3 5 7 9	Very early Early Medium Late Very late
38.	Leaf: Senescence	Caryopsis hard (can no longer be dented by thumbnail and over 90% of spikelets ripened)	3 5 7	Early Intermediate Late
39.	Sterile lemma: Colour	Caryopsis hard (can no longer be dented by thumbnail and over 90% of spikelets ripened)	1 2 3 4	Straw Gold Red Purple
40.	Decorticated grain: Shape	Caryopsis hard (can no longer be dented by thumbnail and over 90% of spikelets ripened)	1 2 3 4 5 6	Short slender Short bold Medium slender Long bold Long slender Extra long slender
41.	Decorticated grain: Colour	Caryopsis hard (can no longer be dented by thumbnail and over 90% of spikelets ripened)	1 2 3 4 5 6 7 8 9	White Light brown Variegated brown Dark brown Light red Red Variegated purple Purple Dark purple

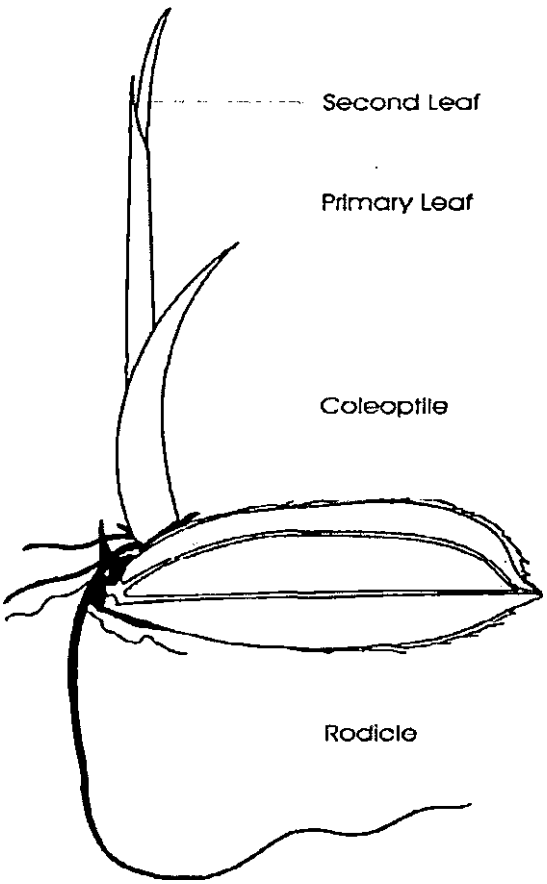


Fig.1 : Parts of young germinating seedling in rice

(Source: Rani *et al.*, 2004)

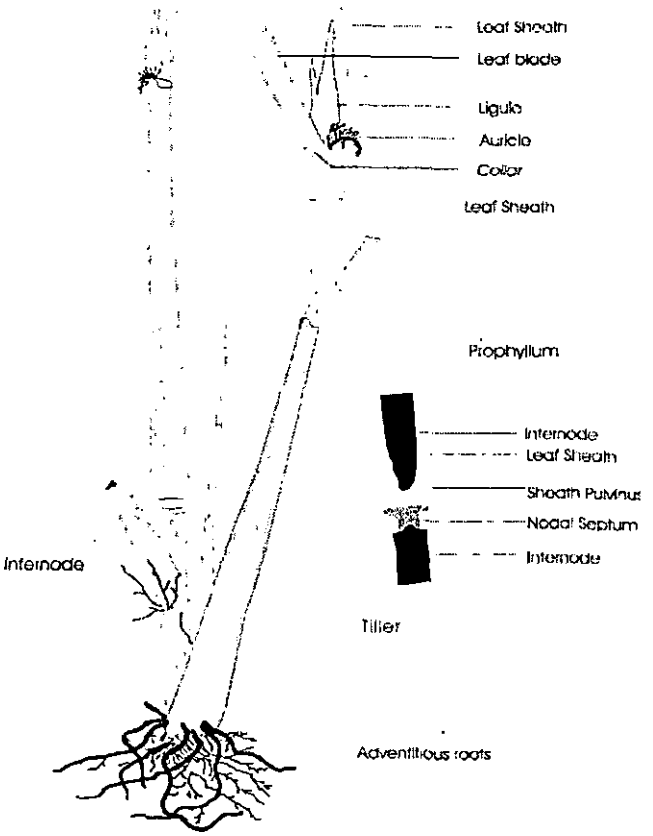


Fig. 2: Parts of a primary tiller and its secondary tiller in rice

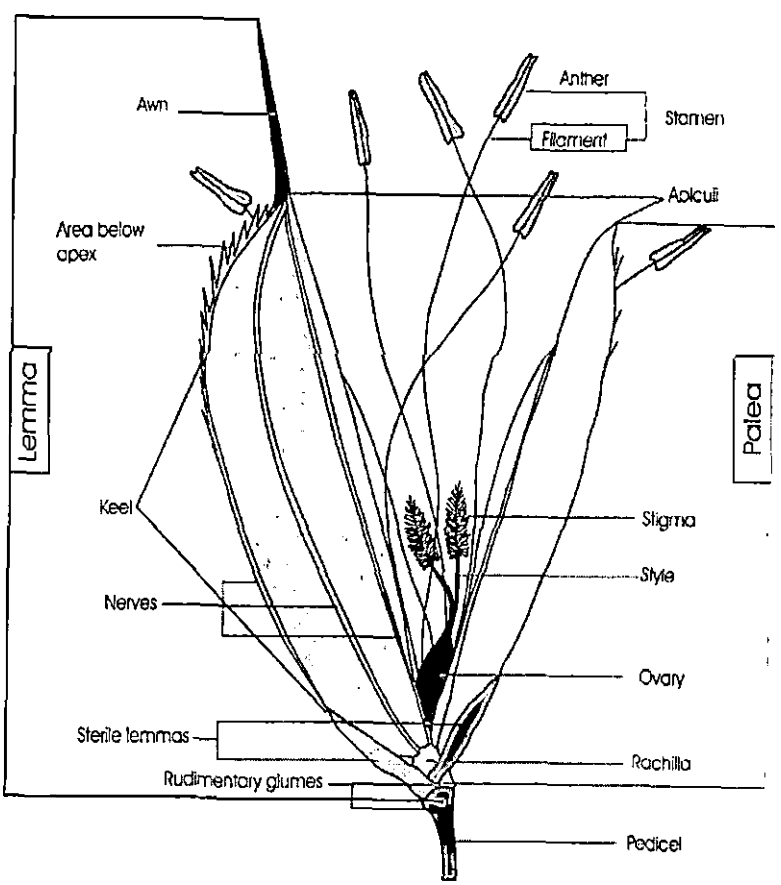


Fig. 3: Parts of a spikelet in rice

(Source: Rani *et al.*, 2004)

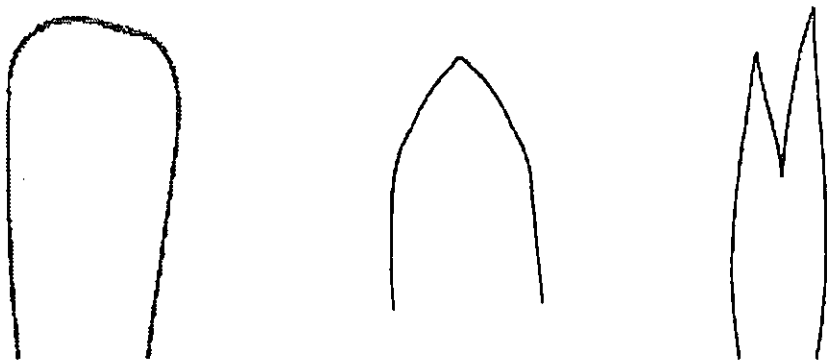


Fig. 4: Shape of ligule in rice

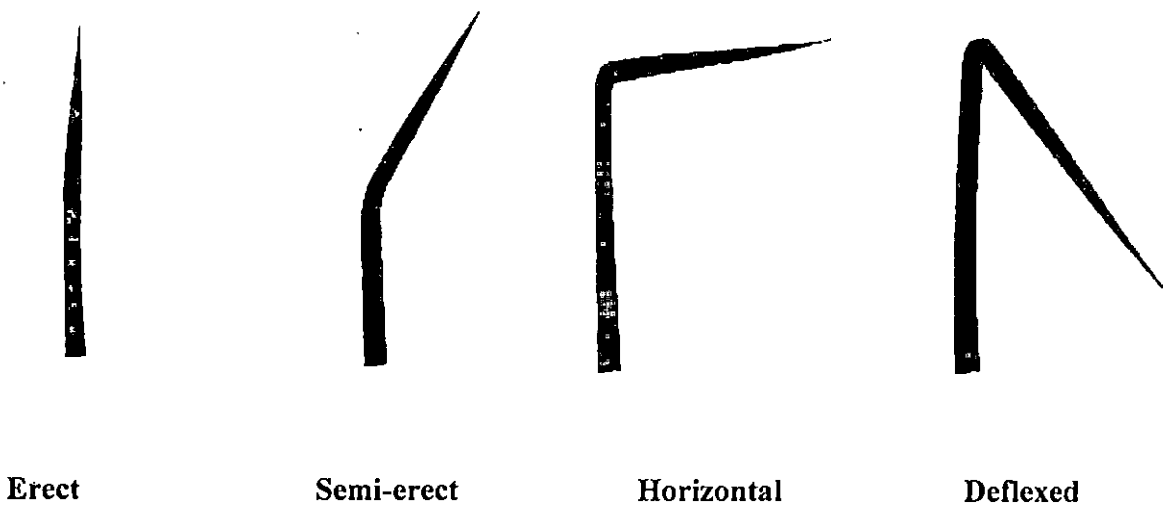
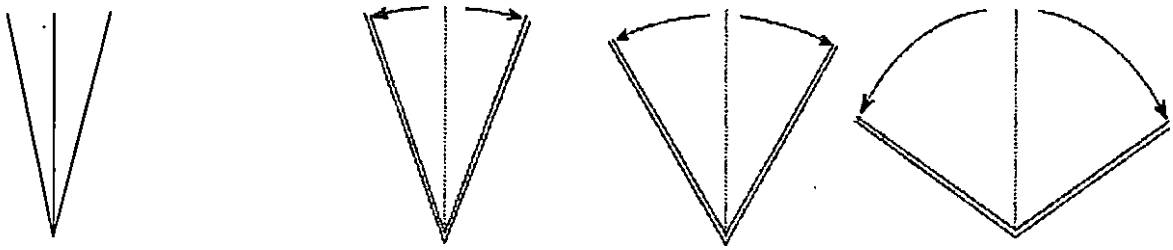


Fig.5: Flag leaf attitude in rice

(Source: Rani *et al.*, 2004)



Erect **Intermediate** **Open** **Spreading**

Fig.6: Culm attitude

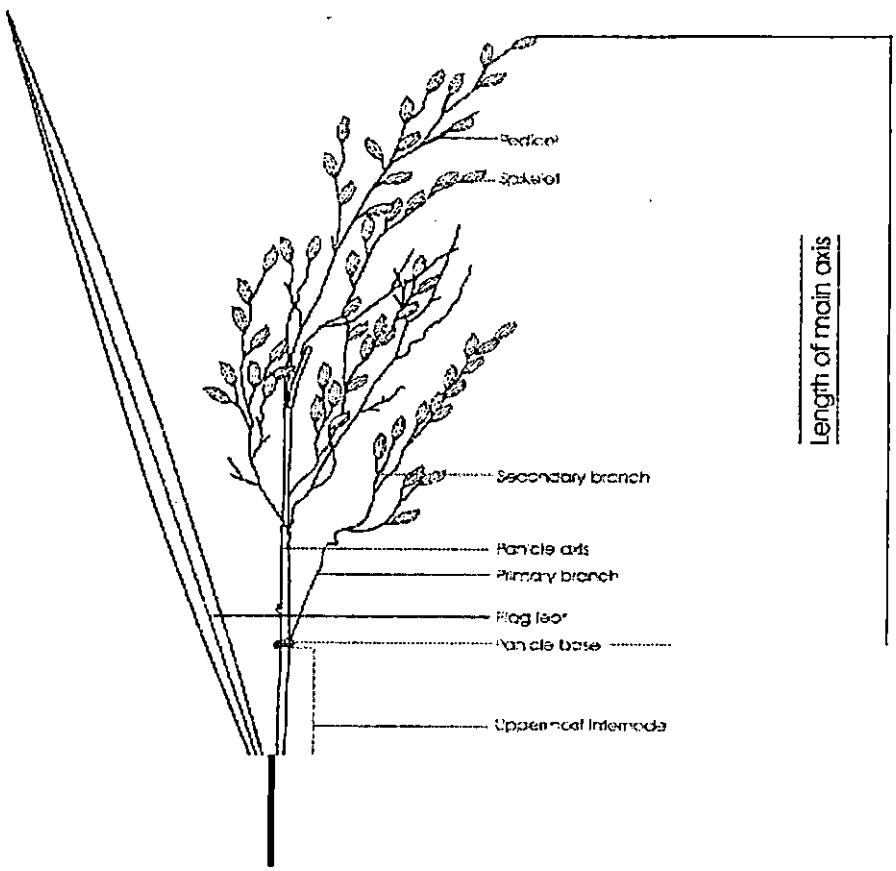


Fig. 7: Parts of a panicle in rice

(Source: Rani *et al.*, 2004)

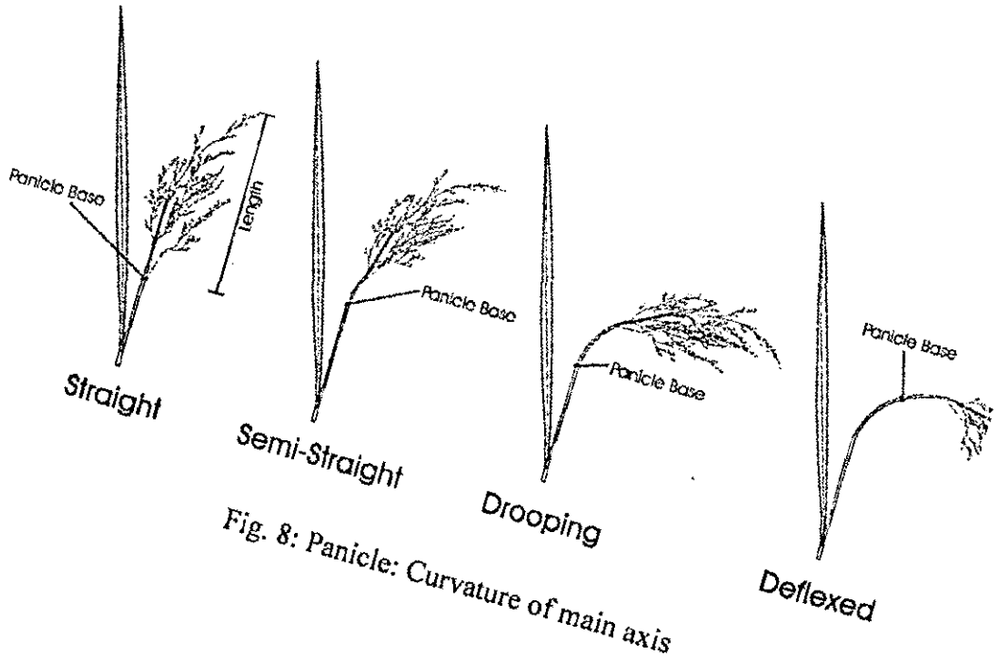


Fig. 8: Panicle: Curvature of main axis

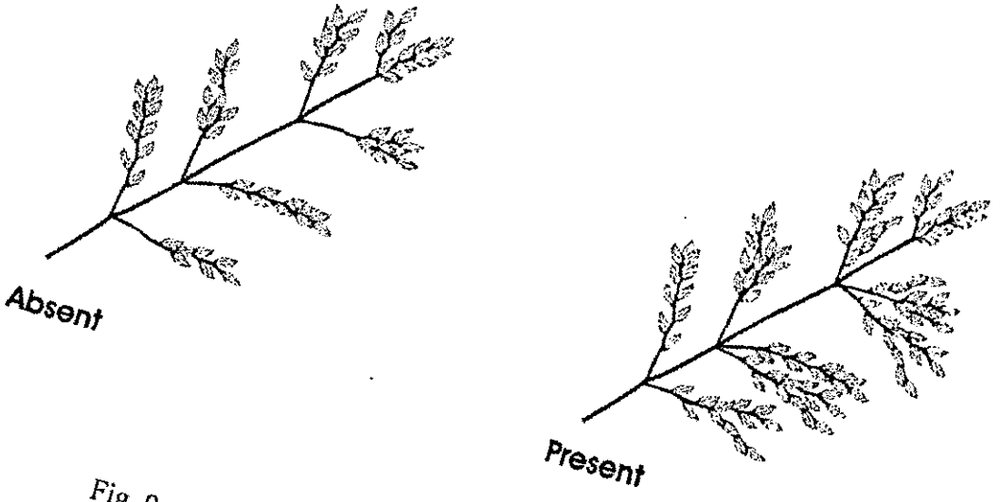


Fig. 9: Panicle: Presence of secondary branching

(Source: Rani *et al.*, 2004)

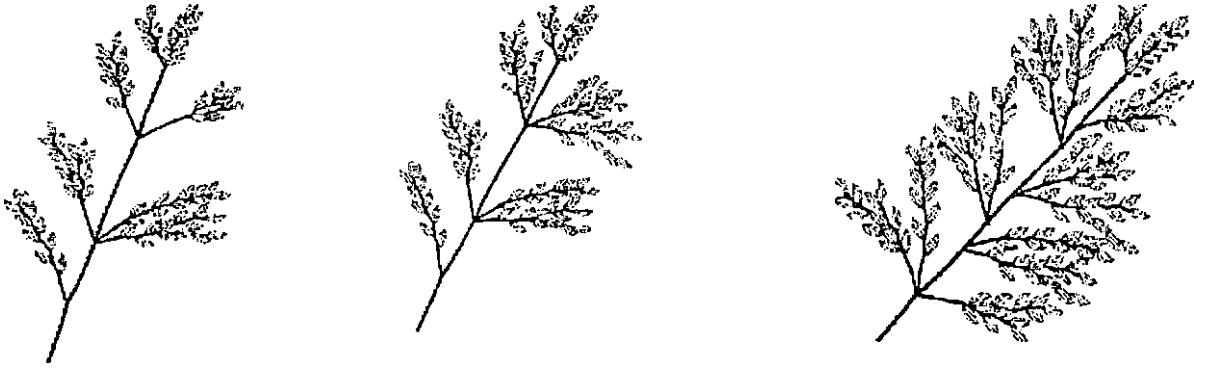
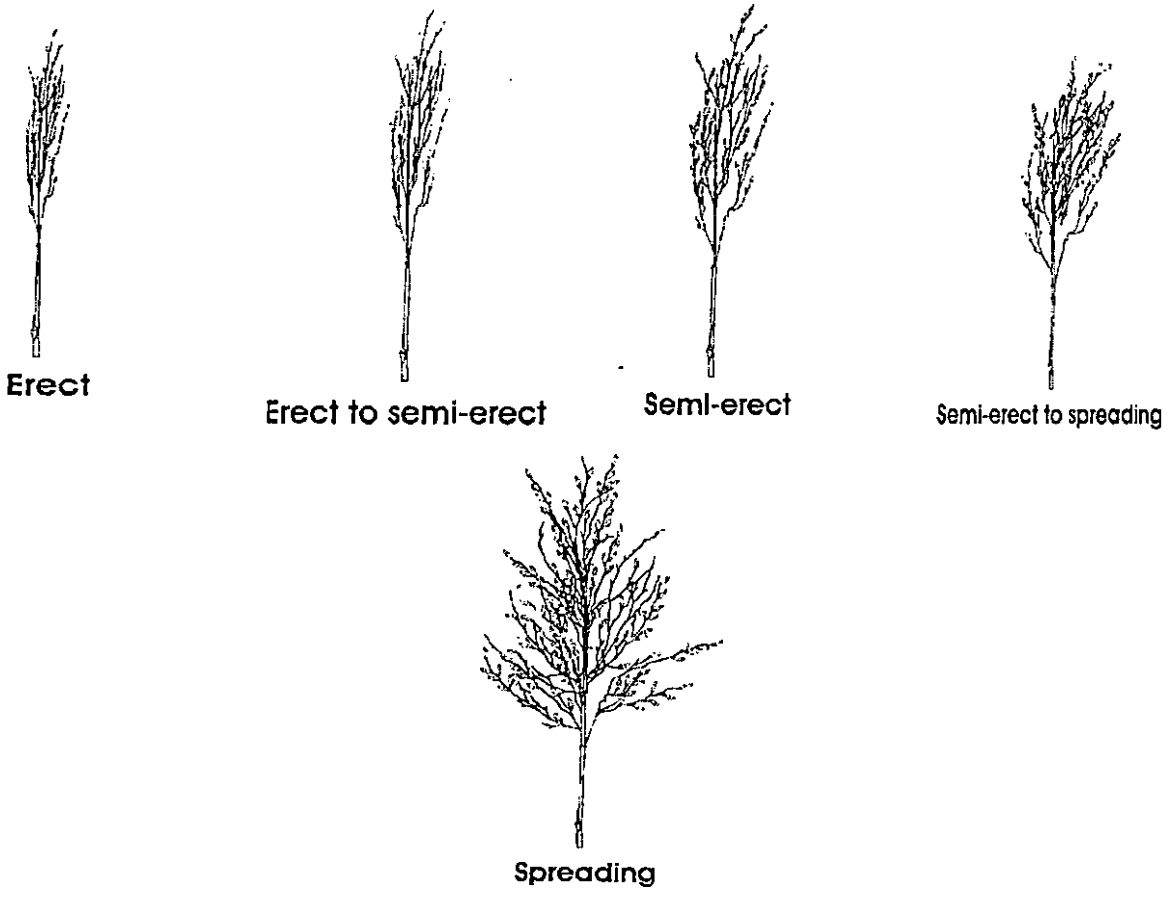
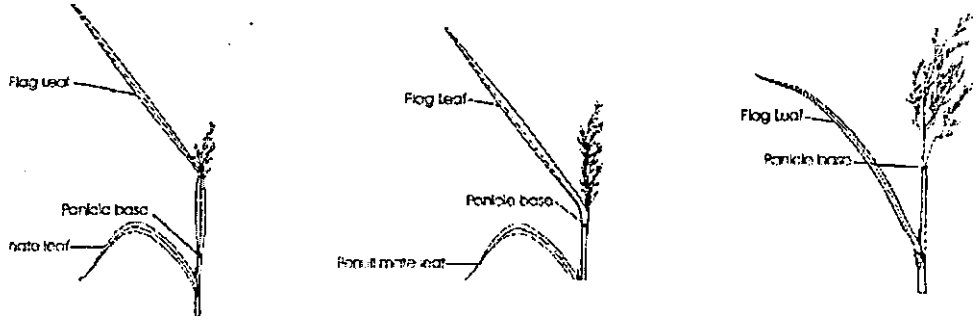


Fig. 10: Panicle: Secondary branching



(Source: Rani *et al.*, 2004)

Fig 11: Panicle: Attitude of branching



Partly exserted (<80%) | **Mostly exserted (81-99%)** | **Well exserted (100%)**

Fig.12: Panicle exsertion

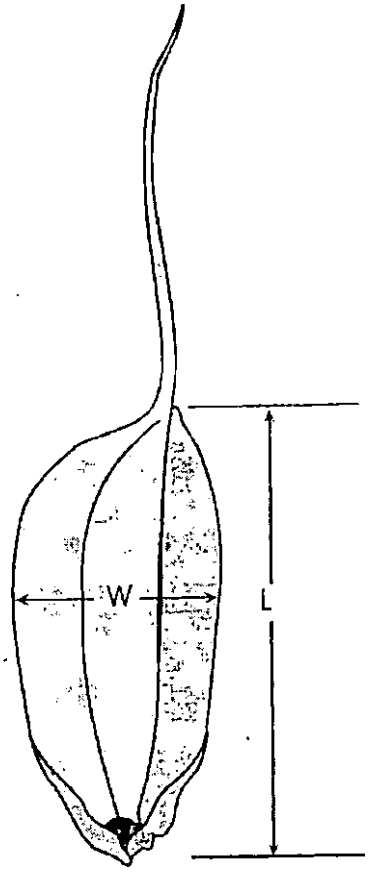


Fig 13: Grain: Length and width

L: Length; W: Width

(Source: Rani *et al.*, 2004)

3.2.5.2 Quantitative traits

Quantitative traits were recorded by making actual measurements on ten randomly chosen plants and average values computed. Observations on grain and decorticated grains were recorded on ten seeds each from the ten randomly selected plants and the average values computed. Following were the observations recorded in both Base collection and core set.

1. Seedling shoot length (cm)

Measured from the base of the shoot to the tip of the tallest leaf blade at five leaf stage (20 days after sowing - seedling stage) expressed in centimeters.

2. Seedling root length (cm)

Measured from the base of the root to the tip of the longest root at five leaf stage (20 days after sowing - seedling stage) expressed in centimeters.

3. Seedling vigour index

The vigour index was calculated as follows

Seedling vigour = Shoot length/ Root length

4. Total seedling biomass (g)

Seedling are cut, dried in an oven at 110^0 C for 24 hours and weighed expressed in grams.

5. Plant height (cm)

Measured from the ground level to the tip of the flag leaf at milk development stage and expressed in centimeter.

6. Culm length (cm)

Measured from the ground level to the base of the panicle at milk development stage and expressed in centimeter.

7. Stem thickness (mm)

Measured from the outer diameter of culm at the mid portion with the help of vernier calipers at milk development stage and expressed in centimeter.

8. Time of heading

Actual number of days from sowing to 50 per cent of the plants are heading is computed as time of heading.

9. Leaf blade width (cm)

Width of leaf blade of the penultimate leaf (i.e. highest leaf below the flag leaf) on the main culm was measured at the widest portion at booting stage and expressed in centimeter.

10. Leaf blade length (cm)

Length of leaf blade of penultimate leaf (i.e. highest leaf below the flag leaf) on the main culm was measured from the ligule to the tip of the blade at booting stage and expressed in centimeter.

11. Total tillers per plant

The total number of grain bearing and non-bearing tillers were counted at milk development stage.

12. Productive tillers per plant

The total numbers of grain bearing tillers were counted at milk development stage.

13. Panicle length (cm)

Length of main axis of panicle measured from the panicle base to the tip (Fig 7) was measured and expressed in centimeter.

14. Spikelets per panicle

Number of spikelets per panicle was counted on three randomly selected panicles from each of the ten representative plants at milk development stage and the average computed.

15. Grains per panicle

Number of filled grains per panicle was counted at maturity on three randomly selected panicles from each of the ten representative plants at caryopsis hard stage and the average computed.

16. Test weight of grain (g)

Random sample of 1000 well-developed, whole grains, dried to 13 per cent moisture content was weighed from each of the ten representative plants after harvest and the average computed and expressed in grams.

17. Grain length (mm)

The longitudinal distance from the base of the lower most sterile lemma to the tip (apiculus) of the lemma or palea (Fig. 13) whichever is longer was measured and expressed in millimeter. In the case of awned varieties length is measured to a point comparable to the tip of the apiculus (excluding awns) and expressed in millimeters.

18. Grain width (mm)

The distance across the fertile lemma and palea (Fig. 13) of the well-developed, whole grains, dried to 13 per cent moisture content was measured at the broadest point and expressed in millimeters.

19. Grain thickness (mm)

Dorsi-ventral thickness of the well-developed, whole grains, dried to 13 per cent moisture content was measured at thickest point and expressed in millimeters.

20. Decorticated grain length (mm)

Longitudinal dimension from the base to the tip of well-developed, dehusked whole grains, dried to 13 per cent moisture content was measured and expressed in millimeters.

21. Decorticated grain width (mm)

Measured as the distance across the broadest point of dehusked, well-developed, whole grains, dried to 13 per cent moisture content and expressed in millimeters.

22. Decorticated grain thickness (mm)

Dorsi-ventral thickness of the well-developed, dehusked whole grains, dried to 13 per cent moisture content was measured at thickest point and expressed in millimeters.

23. Straw yield per plant (g)

Total straw yield from ten representative plants was weighed and the average value expressed in gram.

24. Grain yield per plant (g)

Total grain yield from ten representative plants was weighed and the average value expressed in gram.

3.3 Statistical analysis

The data of mean values for all the trait were analyzed for their variance as outlined by Sapra and Agarwal (1991). Analysis was done using "Augmen" computer programme.

3.3.1 Variability studies

3.3.1.1 Analysis of variance (ANOVA)

Source of variation	Degrees of freedom	Sum of square	'F' value
Blocks	(b-1)	B	B/SS(e)
Checks Varieties	(v-1)	SS(v)	SS(v)/SS(e)
Genotypes (U. R. varieties)	(V-1)	SS(VS)	SS(VS)/SS(e)
Genotypes v/s Checks	1	SS(V)	SS(V)/SS(e)
Error	(v-1) (b-1)	SS(e)	

Where V= number of accessions tested

v= number of check varieties

b= number of blocks

The significance was tested by referring to the table given by Fisher (1936).

3.3.1.2 Estimation of genetic parameters

A. Genotypic and phenotypic variances

These were estimated according to the method suggested by Lush (1940)

Genotypic variance (σ^2_g) = accessions variance- error from checks/no of blocks

Phenotypic variance (σ^2_p) = σ^2_g + MSS (error)

B. Coefficient of variation

The components namely, phenotypic, genotypic and environmental variances were used for estimation of coefficient of variation at both phenotypic and genotypic levels for all the traits were computed by following the formula as suggested by Burton and De vane (1953).

Phenotypic coefficient of variation (PCV)

$$PCV(\%) = \frac{\sigma_P}{\overline{X}} \times 100$$

Genotypic coefficient of variation (GCV)

$$GCV(\%) = \frac{\sigma_g}{\overline{X}} \times 100$$

Where $\overline{X}$ = grand mean of the trait

σ_P = phenotypic standard deviation

σ_g = genotypic standard deviation

The PCV and GCV were classified as suggested by Subramanian and Menon (1973) into low (0-10%), moderate (10.1-20%) and high (>20%).

C. Heritability (h^2)

Heritability (Broad sense) for all the traits were computed by the formula suggested by Lush (1945).

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

Where,

h^2 = heritability (broad sense)

σ^2_g = genotypic variance

σ^2_p = phenotypic variance

Heritability was classified as suggested by Robinson *et al.* (1949) in to low (0-30%), moderate (30.1-60%) and high (>60%).

D. Genetic Advance (GA)

Genetic advance was estimated according to the formula given by Johnson *et al.* (1955).

$$GA = h^2.K.\sigma_p$$

Where,

h^2 = heritability

σ_p = phenotypic standard deviation

K = standardized selection differential at given intensity and it is 2.06 at 5 per cent intensity of selection.

E. Genetic gain

Genetic gain = $(GA / \overline{X}) \times 100$

Where, GA = Genetic advance ;

$\overline{X}$ = General mean

Genetic gain was categorized as suggested by Johnson *et al.*, (1955) as low (0-10%), moderate (10.1-20%) and high (>20%).

3.3.2 One sample't' test

The means of the entire collection and core set were compared by one sample't' test. Let xi (I = 1,2,3.....n) be a random sample of size 'n' from a normal population with mean 'μ' and variance σ^2. Then one sample't' test is defined by the statistic:

$$T = \frac{\overline{X} - \mu}{s/\sqrt{n}}$$

Where,

$$\overline{X} = \frac{1}{N}\sum_{i=1}^{n} xi \quad \text{is the core mean}$$

$$S^2 = \frac{1}{N-1}\sum_{i=1}^{n} (xi-x)^2 \quad \text{is an unbiased estimate}$$

of the population variance σ^2 and it follows't' distribution with (n-1) degrees of freedom.

3.3.3 Homogeneity test for variance

The homogeneity of variances between the base accessions and the core set was tested by Levene's test (Levene, 1960) which is given by the statistic:

$$F = \frac{V_1}{V_2}$$

Where,

$$V_1 = \frac{1}{n_1 - 1} \sum_{i=1}^{n} (xi - \bar{x})^2$$ is the entire variance

$$V_2 = \frac{1}{n_2 - 1} \sum_{i=1}^{n} (y_i - \bar{y})^2$$ is the core variance

It follows F – distribution with (V_1, V_2) degrees of freedom where $V_1 = (n_1-1)$ and $V_2 = (n_2-1)$.

3.3.4 Goodness of fit test

Goodness of fit test was used for testing the significance of the discrepancy between theory and experiment and is known as chi-square (χ^2) test of goodness of fit. It is given by,

$$\chi^2 = \sum_{I=1}^{n} \left[\frac{(f_i - e_i)^2}{e_i} \right]$$

Follows chi - square distribution with (n-1) degrees of freedom.

Where,

$i = 1,2,3.....n$

f_i = set of observed (experimental) frequencies

e_i = set of expected (theoretical) frequencies

3.3.5 Shannon – Weaver diversity index (H)

The diversity index (H) of Shannon -Weaver (1949) was estimated and used as a measure of phenotypic diversity in the entire collection and core set for each trait. The Shannon – Weaver diversity index (H) was estimated using:

$$H = \sum_{i=1}^{n} p_i \log_e p_i$$

Where,

n = Number of phenotypic classes

p_i = The proportion of individuals of a given species to the total number of individuals in the community

Genetic diversity (%)

The diversity percentage can be computed as

$$\text{Diversity per cent} = \frac{\text{Core set mean}}{\text{Base collection mean}} \times 100$$

Results

4. RESULT

The results of the present investigation "Formation of core set in rice (*Oryza sativa* L.) short duration germplasm accessions" conducted during *Kharif* 2011 are presented under the following headings:

4.1 Characterization and evaluation of Base collection

4.1.1 Geographical distribution of accessions in Base collection

4.1.2 Variability studies in Base collection

4.1.2.1 Variability studies in Base collection for qualitative traits

4.1.2.2 Variability studies in Base collection for quantitative traits

4.2 Formation of core set

4.3 Comparisons of core set *vs* Base collection

4.3.1 Geographical distribution of accessions in core set *vs* Base collection

4.3.2 Variability in core set *vs* Base collection

4.3.2.1 Frequency distribution of qualitative traits in core set *vs* Base collection

4.3.2.2 Variability in quantitative traits in core set *vs* Base collection

4.3.3 Diversity in core set *vs* Base collection

4.1 Characterization and evaluation of Base collection

4.1.1 Geographical distribution of accessions in Base collection

Geographical distribution of accessions in Base collection is presented in Table 4; Fig.14. All accessions were from Asia. The collection comprised of accessions from India (156 accessions; 97.5%) and Philippines [4 accessions- PGC

Table 4: Geographical distribution of accessions in Base collection

Sl. No.	Continent	Country	State		No. of accessions	Per cent distribution
1.	Asia	India				
			a)	Andhra Pradesh (DRR)	7	4.375
			b)	Haryana (CSSRI)	4	2.5
			c)	Odisha	2	1.25
			d)	Maharashtra	6	3.75
			e)	Kerala	124	77.5
			f)	Tamil Nadu	11	6.875
			g)	Utter Pradesh	1	0.625
			h)	Paschim Banga	1	0.625
A)		**Total (India)**			**156**	**97.5**
2.		**Philippines**				
			a)	International Rice Research Institute (IRRI), Manila	4	2.5
B)		**Total (Philippines)**			**4**	**2.5**
		Grand total		(A) + (B)	**160**	**100**

Fig. 14. Geographical distribution of accessions in Base collection

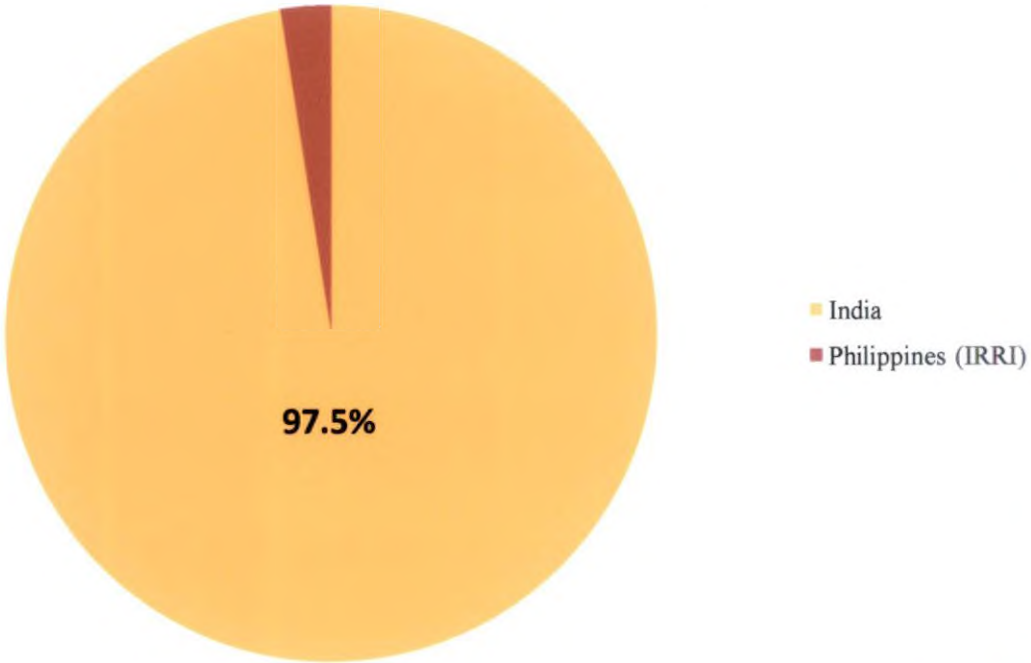
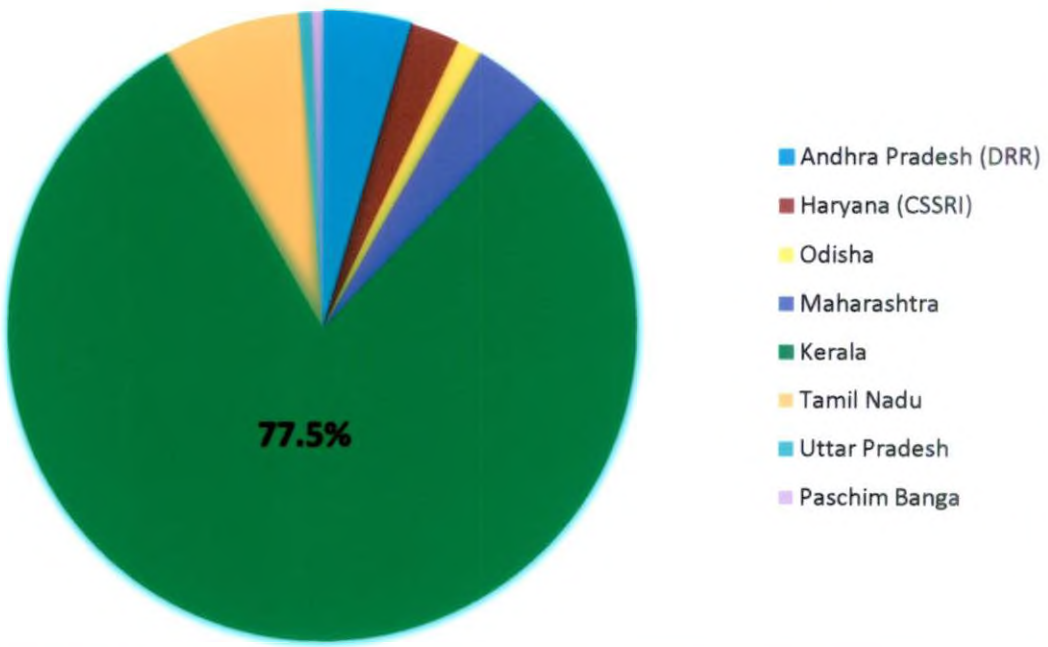


Fig. 15. Geographical distribution of accessions in Base collection from India



17 (IR 36), PGC 20 (IR 1552), PGC 41 (IR100) and PGC 38 [T(N)1]; 2.5%]. The majority of accessions in Indian collection (Fig.15) were from Kerala (124 accessions; 77.5%) followed by those from Tamil Nadu (11 accessions; 6.875%), Andhra Pradesh (7 nos.; 4.375 %), Maharashtra (6 nos.; 3.75%), Haryana (4 nos.; 2.5%), Odisha (2 nos.; 1.25 %) and one each (0.625% each) from Uttar Pradesh and Paschim Banga.

4.1.2 Variability studies in Base collections

4.1.2.1 Variability studies in Base collection for qualitative traits

Rice accessions were characterized with respect to 41 qualitative traits (Table 3) as per Rani *et al.*, 2004. The frequency distribution of accessions in each descriptor state (sub-group) with respect to each trait was assessed (Table 5).

1. **Coleoptile: Colour**

   Out of 160 accessions, 136 (85%) possessed colourless coleoptile while 24 accessions (15%) possessed purple coleoptile. No accessions had green coleoptile.

2. **Basal leaf: Sheath colour**

   Majority of accessions (135 nos.; 84.4%) showed green basal leaf sheath colour. Twelve accessions (7.5%) had light purple leaf sheath followed by 13 accessions (8.1%) with purple lines on leaf sheath.

3. **Leaf: Intensity of green colour**

   The intensity of greenness in leaf varied between dark green colour (65 accessions; 40.6%) to light green (18 accessions; 11.3%). Seventy-seven accessions (48.1%) possessed medium green leaves.

Table 5. Frequency distribution of qualitative traits in Base collection

Sl. No.	Descriptor	Descriptor state	Score code	No. of accessions	Per cent
1.	Coleoptile: colour	Colourless	1	136	85.00
		Green	2		
		Purple	3	24	15.00
2.	Basal leaf: Sheath colour	Green	1	135	84.4
		Light purple	2	12	7.5
		Purple line	3		
		Purple	4	13	8.1
3.	Leaf: Intensity of green colour	Light	3	18	11.3
		Medium	5	77	48.1
		Dark	7	65	40.6
4.	Leaf: Anthocyanin colouration	Absent	1	137	85.6
		Present	9	23	14.4
5.	Leaf: Distribution of anthocyanin colouration	On tips only	1	1	4.34
		On margins only	2	18	78.26
		In blotches only	3	2	8.69
		Uniform	4	2	8.69
6.	Leaf sheath: Anthocyanin colouration	Absent	1	137	85.6
		Present	9	23	14.4
7.	Leaf sheath: Intensity of anthocyanin colouration	Very weak	1	137	85.6
		Weak	3	19	11.87
		Medium	5	2	1.25
		Strong	7		
		Very strong	9	2	1.25
8.	Leaf: Pubescence of blade surface	Absent	1	4	2.5
		Weak	3	53	33.1
		Medium	5	100	62.5
		Strong	7	3	1.9
		Very strong	9		
9.	Leaf: Auricles	Absent	1		
		Present	9	160	100
10.	Leaf: Anthocyanin colouration of auricles	Colourless	1	157	98.1
		Light purple	2		
		Purple	3	3	1.9
11.	Leaf: Collar	Absent	1		
		Present	9	160	100
12.	Leaf: Anthocyanin colouration of Collar	Absent	1	157	98.1
		Present	9	3	1.9
13.	Leaf: Ligule	Absent	1		
		Present	9	160	100
14.	Leaf: Shape of ligule	Truncate	1		
		Acute	2		
		Split	3	160	100

Table 5. Frequency distribution of qualitative traits in Base collection (contd...)

Sl. No.	Descriptor	Descriptor state	Score code	No. of accessions	Per cent
16.	Flag leaf: Attitude of blade (Early observation)	Erect Semi-erect Horizontal Deflexed	1 3 5 7	160	100
17.	Flag leaf: Attitude of blade (Late observation)	Erect Semi-erect Horizontal Deflexed	1 3 5 7	50 109 1	31.25 68.13 0.62
18.	Culm: Attitude	Erect Semi-erect Open Spreading	1 3 5 7	130 25 5	81.3 15.6 3.1
19.	Lemma: Anthocyanin colouration of keel	Absent or very weak Weak Medium Strong Very strong	1 3 5 7 9	157 2 1	98.1 1.3 0.6
20.	Lemma: Anthocyanin colouration of area below apex	Absent Weak Medium Strong Very strong	1 3 5 7 9	157 2 1	98.1 1.3 0.6
21.	Lemma: Anthocyanin colouration of apex	Absent Weak Medium Strong Very strong	1 3 5 7 9	136 13 7 4	85 8.125 4.4 2.5
22.	Spikelet: Colour of stigma	White Light green Yellow Light purple Purple	1 2 3 4 5	136 24	85 15
23.	Stem: Anthocyanin colouration of nodes	Absent Present	1 9	137 23	85.6 14.4
24.	Stem: Intensity of anthocyanin colouration of nodes	Weak Medium Strong	3 5 7	156 1 3	97.5 0.6 1.9
25.	Stem: Anthocyanin colouration of internodes	Absent Present	1 9	137 23	85.6 14.4
26.	Panicle: Curvature of main axis	Straight Semi-straight Drooping Deflexed	1 3 5 7	160	100

Table 5. Frequency distribution of qualitative traits in Base collection (contd...)

Sl. No.	Descriptor	Descriptor state	Score code	No. of accessions	Per cent
27.	Spikelet: Density of pubescence of lemma	Absent	1		
		Weak	3	38	23.8
		Medium	5	114	71.3
		Strong	7	8	5.0
		Very strong	9		
28.	Spikelet: Colour of tip of lemma	White	1		
		Yellowish	2	136	85.0
		Brown	3		
		Red	4		
		Purple	5	24	15.0
		Black	6		
29.	Lemma and Palea colour	Straw	0	9	5.6
		Gold and gold furrows on straw background	1	32	20.0
		Brown spots on straw	2	25	15.6
		Brown furrows on straw	3	76	47.5
		Brown (Tawny)	4	14	8.8
		Reddish to light purple	5	3	1.9
		Purple spots on straw	6		
		Purple furrows on straw	7		
		Purple	8	1	0.6
		Black	9		
30.	Panicle: Awns	Absent	1	148	92.5
		Present	9	12	7.5 .
31.	Panicle: Colour of awns	Yellowish white	1	11	91.66
		Yellowish brown	2		
		Brown	3		
		Reddish brown	4		
		Light red	5		
		Red	6	1	8.33
		Light purple	7		
		Purple	8		
		Black	9		
32.	Panicle: Distribution of awns	Tip only	1	3	2.5
		Upper half only	3	2	16.66
		Uniform	5	7	58.33
33.	Panicle: Presence of secondary branching	Absent	1		
		Present	9	160	100
34.	Panicle: Secondary branching	Weak	1		
		Strong	2	160	100
		Clustered	3		

Table 5. Frequency distribution of qualitative traits in Base collection (contd...)

Sl. No.	Descriptor	Descriptor state	Score code	No. of accessions	Per cent
35.	Panicle: Attitude of branches	Erect	1		
		Erect to semi-erect	3	8	5.0
		Semi-erect	5	149	93.1
		Semi-erect to spreading	7	3	1.9
		Spreading	9		
36.	Panicle: Exsertion	Partly exserted	3		
		Mostly exserted	5		
		Well exserted	7	160	100
37.	Time of maturity	Very early	1	3	1.9
		Early	3	123	76.9
		Medium	5	32	20.0
		Late	7	2	1.3
		Very late	9		
38.	Leaf: Senescence	Early	3		
		Intermediate	5	155	96.9
		Late	7	5	3.1
39.	Sterile Lemma: Colour	Straw	1	155	96.9
		Gold	2		
		Red	3	1	0.6
		Purple	4	4	2.5
40.	Decorticated grain: Shape	Short slender	1	3	1.9
		Short bold	2	136	85.0
		Medium slender	3	5	3.1
		Long bold	4	12	7.5
		Long slender	5	4	2.5
		Extra long slender	6		
41.	Decorticated grain: Colour	White	1	47	29.4
		Light brown	2	3	1.9
		Variegated brown	3		
		Dark brown	4	1	0.6
		Light red	5	44	27.5
		Red	6	65	40.6
		Variegated purple	7		
		Purple	8		
		Dark purple	9		

4. Leaf: Anthocyanin colouration

Anthocyanin colouration on leaf was absent in 137 accessions (85.6%) while 23 accessions (14.75 %) had anthocyanin pigmentation on leaves.

5. Leaf: Distribution of anthocyanin colouration

Out of the 23 accessions with anthocyanin colouration on leaves, two accessions exhibited uniform anthocyanin colouration on leaf whereas one (4.34%) showed very weak anthocyanin colouration (on leaf tips only). Eighteen accessions (11.3%) possessed anthocyanin pigmentation on leaf margins, while 2 accessions (1.3%) had pigmentation in blotches only.

6. Leaf sheath: Anthocyanin colouration

Leaf sheath anthocyanin colouration was absent in 137 accessions (85.6%) and present in 23 accessions (14.4%).

7. Leaf sheath: Intensity of anthocyanin colouration

The intensity of anthocyanin colouration in leaf sheath was very weak in most accessions (137 accessions; 85.6%). The colour intensity was weak in 19 accessions (11.87%), while two accessions each (1.25% each) exhibited medium and very strong intensity of anthocyanin colouration in leaf sheath.

8. Leaf: Pubescence of blade surface

The pubescence of leaf blade was medium in 100 accessions (62.5%), weak in 53 accessions (33.1%) and strong in three accessions (1.9%). It was absent in four accessions (2.5%).

9. Leaf: Auricles

All the 160 accessions in the Base collection possessed auricles.

10. Leaf: Anthocyanin colouration of auricles

Out of the 160 accessions, 157 accessions (98.1%) showed colourless auricles whereas the auricle was purple coloured in three accessions (1.9%).

11. Leaf: Collar

All the 160 accessions (100%) possessed a clear cut leaf collar.

12. Leaf: Anthocyanin colouration of Collar

In majority of accessions (157 accessions; 98.1%) anthocyanin colouration was absent in leaf collar whereas it was pigmented in three accessions (1.9%).

13. Leaf: Ligule

In all the 160 accessions, ligule was found to be present.

14. Leaf: Shape of ligule

All the 160 accessions possessed split type of ligule.

15. Leaf: Colour of ligule

Green colour ligule was observed in 157 accessions (98.1%) while in three accessions (1.9%) it was purple coloured.

16. Flag leaf: Attitude of blade (Early observation)

In the early stage (booting stage), the attitude of flag leaf was erect in all the 160 accessions.

17. Flag leaf: Attitude of blade (Late observation)

In the late stage (maturity stage), semi-erect flag leaf was observed in 109 accessions (68.13%), erect flag leaf in 50 accessions (31.25%). Horizontal flag leaf was observed only in one accession (0.62%).

18. Culm: Attitude

Culm attitude was erect in 130 accessions (81.3%); followed by 25 accessions (15.6%) with semi-erect and five accessions with open type culm attitude.

19. Lemma: Anthocyanin colouration of keel

Anthocyanin colouration of lemma keel was very weak in 157 accessions (98.1%). It was weak in two accessions (1.3%) and medium in one accession (0.6%).

20. Lemma: Anthocyanin colouration of area below apex

The anthocyanin colouration of lemma below apex was absent in 157 accessions (98.1%), weak in two accessions (1.3%) and medium in one accession (0.6%).

21. Lemma: Anthocyanin colouration of apex

Anthocyanin colouration of lemma apex was strong in four accessions (2.5%), medium in seven accessions (4.4%) and weak in 13 accessions (8.125%). It was absent in 85.0% of the accessions.

22. Spikelet: Colour of stigma

Only two types of stigma colour *viz.*, white and purple were observed in the Base collection. Majority of accessions (136 accessions; 85.0%) exhibited

white stigma while 24 accessions (15.0%) had purple stigma.

23. Stem: Anthocyanin colouration of nodes

Anthocyanin colouration on nodes was absent in 137 accessions (85.6%) and present in 23 accessions (14.4%).

24. Stem: Intensity of anthocyanin colouration of nodes

The intensity of anthocyanin colouration of nodes was weak in 156 accessions (97.5%). It was strong in three accessions (1.9%) and medium in one accession.

25. Stem: Anthocyanin colouration of internodes

Twenty-three accessions (4.4%) exhibited anthocyanin colouration on internodes while it was absent in the rest (137 accessions; 85.6%).

26. Panicle: Curvature of main axis

The curvature of main axis of panicle was semi-straight in all the 160 accessions in the Base collection.

27. Spikelet: Density of pubescence of lemma

Pubescence of lemma on spikelet was weak in 38 accessions (23.8%). Majority (114 accessions; 71.3%) of accessions possessed medium pubescence on spikelet surface whereas eight accessions (5%) exhibited strong pubescence.

28. Spikelet: Colour of tip of lemma

The colour of apiculus was yellowish in 136 accessions (85%) and purple in 24 accessions (15%).

29. Lemma and Palea colour

Majority of accessions (76 accessions; 47.5%) had brown furrows on straw coloured lemma and palea while 32 accessions (20%) had gold and gold furrows on straw background. The colour of lemma and palea in the rest varied between brown spots on straw (25 and 15.6%), brown (14 and 8.8%), straw (9 and 5.6%), reddish to purple (3 and 1.9%) and purple (1 and 0.6%).

30. Panicle: Awns

Awns were absent in 148 accessions (92.5%) and present in 12 accessions (7.5%).

31. Panicle: Colour of awns

The colour of awns in the 12 accessions could be grouped into yellowish and red. Eleven accessions (91.66%) showed yellowish awns and only one accession possessed red awns (8.33%).

32. Panicle: Distribution of awns

Out of the 12 accessions with awns, the distribution of awns were restricted to tip of panicle in three accessions (25.0%) whereas it was found in upper half only in two accessions (16.66 %). The awns were distributed throughout the panicle in the rest (7 accessions; 58.33%).

33. Panicle: Presence of secondary branching

Secondary branching in panicles was present in all the accessions in Base collection.

34. Panicle: Secondary branching

All the 160 accessions showed strong secondary branching.

35. Panicle: Attitude of branches

Attitude of panicle branching varied between erect to semi-erect (8 accessions; 5%) and semi-erect to spreading (3 accessions; 1.9%). However, in majority of accessions (149 accessions; 93.1%) it was semi-erect.

36. Panicle: Exsertion

Well exserted panicles were observed all the accessions in Base collection.

37. Time of maturity

Three accessions (1.9%) matured very early. However most accessions (123 accessions; 76.9%) were early in maturity, followed by 32 accessions (20%) of medium maturity and two accessions of late in maturity.

38. Leaf: Senescence

In five accessions (3.1%), the leaf senescence was observed to occur late. However, in majority of the accessions (155 accessions; 96.9%) intermediate leaf senescence was noticed.

39. Sterile Lemma: Colour

The colour of sterile lemma varied between straw (155 and 96.9%), red (1 and 0.6%) and purple (4 and 2.5%).

40. Decorticated grain: Shape

Short bold grains were found in majority of accessions (136 accessions; 85%) whereas it was short slender in three accessions (1.9%), medium slender in

five accessions (3.1%), long bold in 12 accessions (7.5%) and long slender in four accessions (2.5%).

41. Decorticated grain: Colour

Colour of decorticated grain varied from white (47 accessions; 29.4%) to light brown (3 accessions; 1.9%), dark brown (1 accessions; 0.6%), light red (44 accessions; 27.5%) and red (65 accessions; 40.6%).

4.1.2.2 Variability studies in Base collection for quantitative traits

Analysis of variance (Table 6) revealed that highly significant difference existed between accessions in Base collection for all the 24 traits studied. The mean values of various traits pertaining to individual accessions in the Base collection are presented in Appendix I. The estimates of range, population mean, variance and genetic parameters viz., phenotypic and genotypic coefficient of variation (PCV and GCV respectively), heritability (h^2) , genetic advance (GA) and genetic gain (genetic advance as per cent of mean) for various traits studied are presented in Table 7 and Fig.16.

1. Seedling shoot length (cm)

The shoot length of seedling ranged from 17.1 cm PGC 33 (Cul 8714) to 42.5 cm (Thottacheera) and the mean value was 26.76 cm. The PCV and GCV were 42.02 per cent and 41.75 per cent, respectively. Seedling shoot length recorded a heritability of 98.71 per cent, a GA of 22.87 per cent and genetic gain of 85.46 per cent.

2. Seedling root length (cm)

The mean seedling root length was 5.32 cm. Root length varied between 2.77 cm in accession Cul M20 to 8.61 cm in accession PGC 171 (F5-23-1). PCV and GCV were 213.20 and 212.61 per cent, respectively. The values of heritability, GA and

Table 6. Analysis of variance for quantitative traits in Base collection

Source of variation	df	Seedling shoot length (cm)	Seedling root length (cm)	Seedling vigour index	Total seedling biomass (g)	Plant height (cm)	Culm length (cm)	Stem thickness (mm)	Days to heading	Leaf blade width (cm)
Blocks	15	2.25	0.45	0.35	0.07	10.45	29.6	0.2	0.9	0.13
Checks	2	47.84**	3.86**	0.71**	1.38**	15.03**	290.63**	0.12**	294.14**	0.00
Genotypes (Unreplicated)	159	1999.52**	2049.37**	1973.79**	1893.66**	1980.94**	1984.91**	1809.08**	1982.28**	2239.3**
Genotypes v/s Checks	1	4457.28**	30154.13**	32098.87**	39239.06**	4204.88**	93838.94**	30234.58**	83467.81**	40568.43**
Error	30	1.62	0.71	0.56	0.11	10.11	44.4	0.25	0.52	0.15

Table 6. Analysis of variance for quantitative characters in Base collection

Source of variation	df	Leaf blade length (cm)	Total tillers per plant	Productive tillers per plant	Panicle length (cm)	Spikelet per panicle	Grain per panicle	Test weight of grain (g)	Grain length (mm)	Grain width (mm)
Blocks	15	10.11	1.18	1.18	0.12	288.61	384.14	0.07	0.07	0.01
Checks	2	3.92**	16.45**	16.45**	0.33**	308.94**	92.2**	0.06*	4.67**	0.28**
Genotypes (Unreplicated)	159	3331.63**	3178.35**	1923.56**	1855.04**	1626.38**	2938.49**	2198.31**	2300.98**	2372.67**
Genotypes v/s Checks	1	56181.47**	19**	24145.57**	3403.37**	583061.3**	214061.1**	6650.66**	31635.76**	46426.86**
Error	30	23.51	1.62	1.62	0.12	246.84	231.14	0.09	0.04	0.01

***P= 0.05 and P ** =0.01**

Table 6. Analysis of variance for quantitative traits in Base collection (contd...)

Source of variation	df	Grain thickness (mm)	Decorticated grain length (mm)	Decorticated grain width (mm)	Decorticated grain thickness (mm)	Straw yield per plant (g)	Grain yield per plant (g)
Blocks	15	0.01	0.07	0.01	0.01	1183.03	6.66
Checks	2	0.03	6.96**	0.28**	0.02	1327.05**	434.74**
Genotypes (Unreplicated)	159	1968.46**	748.6**	1068.7**	778.29**	1140.67**	806.73**
Genotypes v/s Checks	1	44005.57**	6599.34**	1500.35**	12235.05**	1114.2**	17312.27**
Error	30	0.00	0.04	0.01	0.01	1170.11	4.32

***P= 0.05 and P ** =0.01**

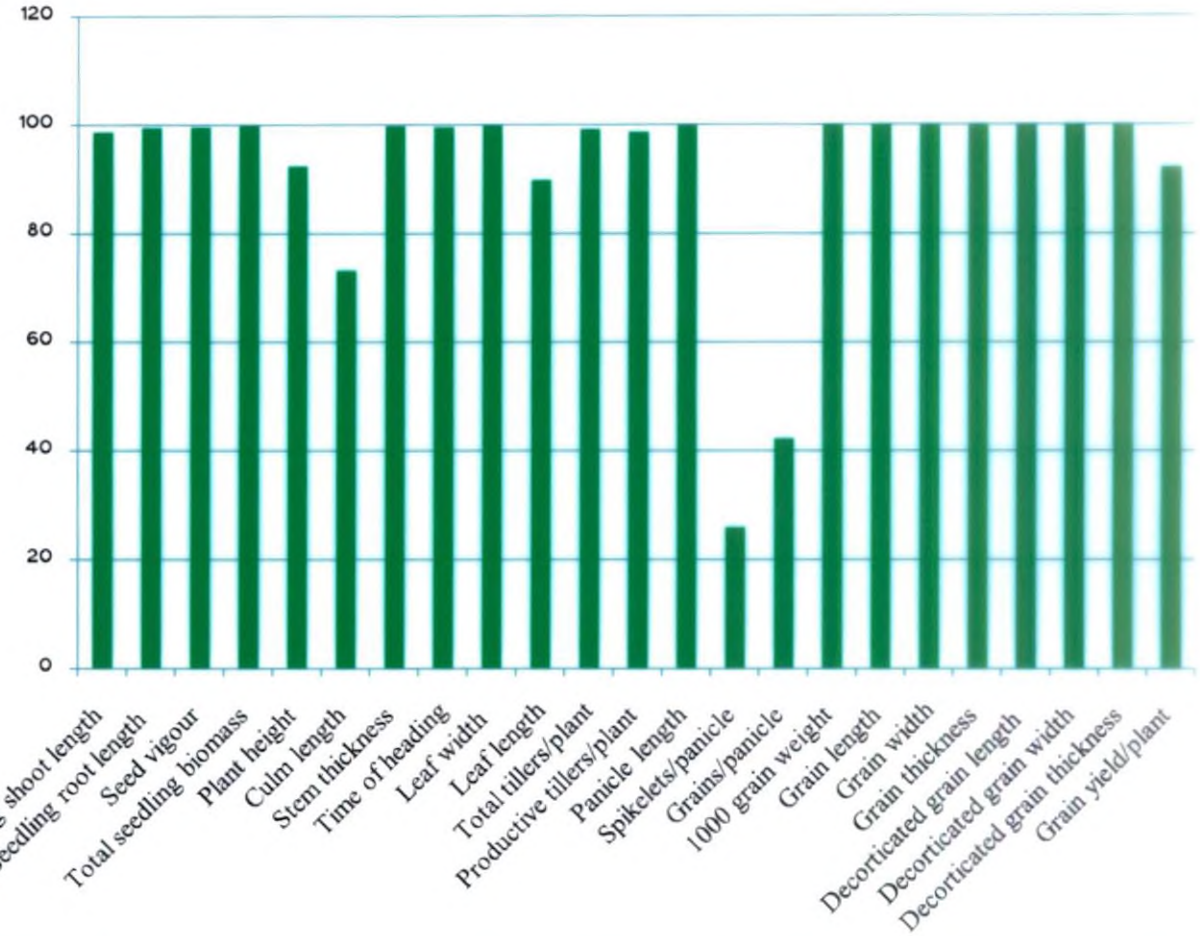
Table 7. Genetic parameters for quantitative traits in Base collection

Sl. No.	Traits	Mean±SE	Range		Variance		Coefficient of Variability		h^2 (Broad sense) (%)	Genetic Advance	GA as per cent of means
			Minimum	Maximum	PV	GV	PCV (%)	GCV (%)			
1	Seedling shoot length (cm)	26.762±0.3518	17.1	42.5	126.48	124.86	42.02	41.75	98.71	22.87	85.46
2	Seedling root length (cm)	5.322±0.8060	2.77	8.61	128.75	128.04	213.20	212.61	99.44	23.25	436.78
3	Seedling vigour index	5.209±0.9907	3.05	8.83	123.88	123.32	213.67	213.18	99.54	22.83	438.17
4	Total seedling biomass (g)	0.801±0.0205	0.27	1.83	118.45	118.34	1358.13	1357.51	99.90	22.40	2795.16
5	Plant height (cm)	181.03±0.6371	82.75	279.27	133.28	123.17	9.19	8.83	92.41	21.98	17.49
6	Culm length (cm)	89.6571±1.2956	61.83	140.17	165.68	121.28	14.35	12.28	73.20	19.41	21.64
7	Stem thickness (mm)	4.1092±0.0642	2.40	6.83	113.30	113.05	259.03	258.75	99.77	21.88	532.44
8	Days to heading	84.97±0.703	64	118	124.38	123.86	13.12	13.09	99.58	22.88	26.92
9	Leaf blade width (cm)	1.627±0.0265	1.30	3.52	140.09	139.94	727.29	726.90	99.89	24.36	1496.62
10	Leaf blade length (cm)	43.231±0.6128	25.92	67.48	230.26	206.75	35.10	33.26	89.79	28.07	64.92
11	Total tillers per plant	12.707±0.1960	9.1	29.6	200.16	198.54	162.49	161.83	99.19	28.91	332.02
12	Productive tillers per plant	8.707±0.1960	5.1	25.6	121.74	120.12	126.72	125.87	98.66	22.43	257.57

Table 7. Genetic parameters for quantitative traits in Base collection **(contd...)**

Sl. No.	Traits	Mean±SE	Range		Variance		Coefficient of Variability		h^2 (Broad sense) (%)	Genetic Advance	GA as per cent of means
			Minimum	Maximum	PV	GV	PCV (%)	GCV (%)			
13	Panicle length (cm)	25.177±0.2391	15.71	50.21	116.05	115.93	42.78	42.76	99.89	22.17	88.05
14	Spikelets per panicle	156.049±3.1573	73.1	281.6	333.06	86.22	11.69	5.95	25.88	9.73	6.23
15	Grains per panicle	95.304±3.1897	4.5	223.2	400.34	169.20	20.99	13.64	42.26	17.42	18.27
16	Test weight of grain (g)	22.715±0.0309	21.38	23.65	137.47	137.38	51.61	51.6	99.93	24.14	106.26
17	Grain length (mm)	6.935±0.0634	4.291	9.250	143.84	143.80	172.92	172.90	99.97	24.70	356.13
18	Grain width (mm)	1.260±0.0247	0.222	2.476	148.30	148.29	966.42	966.39	99.99	25.08	1990.70
19	Grain thickness (mm)	0.3765±0.0173	0.016	1.348	123.02	123.02	2946.00	2946.00	100	22.85	6068.76
20	Decorticated grain length (mm)	4.435±0.0634	1.79	6.750	46.83	46.78	154.27	154.20	99.91	14.08	317.52
21	Decorticated grain width (mm)	0.260±0.0247	0.778	1.476	66.80	66.79	3142.44	3142.2	99.98	16.83	6472.44
22	Decorticated grain thickness (mm)	0.326±0.0173	0.034	1.298	48.65	48.64	2136.31	2136.08	99.97	14.37	4399.88
23.	Straw yield per plant (g)	26.713±2.0966	14.88	45.94	-	-	-	-	-	-	-
24.	Grain yield per plant (g)	22.031±0.6886	7.628	48.979	54.47	50.15	33.49	32.14	92.06	14.00	63.53

Fig. 16. Heritability (%) for quantitative traits in Base collection



genetic gain were 99.44 per cent, 23.25 per cent and 436.78 per cent was observed for seedling root length.

3. Seedling vigour index

The seedling vigour index varied between 3.05 PGC 27 (Cul 8755) to 8.83 (PGC 71: Kargi) with a mean value of 5.21. The PCV and GCV were 213.67 and 213.18 per cent, respectively. The heritability of this trait was 99.54 per cent, GA of 22.83 per cent and genetic gain of 438.17 per cent was observed for seedling vigour index.

4. Total seedling biomass (g)

The mean total seedling biomass recorded in the Base population was 0.801 g. It ranged between 0.27 g in PGC 38 [T(N) 1] to 1.83 g in PGC 194 (CSR 27). The PCV and GCV were 1358.13 and 1357.51 per cent, respectively. The heritability estimates of 99.90 per cent with GA of 22.40 per cent and genetic gain of 2795.16 per cent was observed for total biomass.

5. Plant height (cm)

The mean plant height recorded in the Base population was 181.03 cm. It ranged from 82.75 cm [PGC 150 (IVT 116)] to 279.27 cm [PGC 60 (PM-709)]. The PCV and GCV were 9.19 and 8.83 per cent, respectively. Heritability estimate of 92.41 per cent, GA of 21.98 per cent and genetic gain of 17.49 per cent was observed for plant height.

6. Culm length (cm)

The culm length ranged from 61.83 cm [PGC 29 (Cul 8759)] to 140.17 cm [PGC 72 (Reymuthika)] with a mean value of 89.65 cm. The PCV and GCV were 14.35 and 12.28 per cent, respectively. It showed heritability of 73.20 per cent with

GA of 19.41 per cent and genetic gain of 21.64 per cent was observed for culm length.

7. Stem thickness (mm)

The mean stem thickness in the Base population was 4.10 mm. It varied between 2.40 mm in PGC 145 (Cul 90-04) to 6.83 mm in PGC 91 (TKM 6). The PCV and GCV were 259.03 and 258.75 per cent, respectively. Stem thickness recorded a heritability of 99.77 per cent, GA of 21.88 per cent and genetic gain of 532.44 per cent.

8. Days to heading

Days to heading in Base collection ranged from 64 days to 118 days with a mean value of 84.97 days. The accession PGC 115 (IVT 33) was the earliest to flower, while Mo 19 (Krishnanjana)] flowered late at 118 days. The PCV and GCV were 13.12 and 13.09 per cent. Estimates of heritability, GA and genetic gain for days to flowering were 99.58 per cent, 22.88 per cent and 26.92 per cent.

9. Leaf blade width (cm)

The mean leaf width in the Base population was 1.62 cm and it range from 1.30 cm in PGC 96 (Cul 1727/Navara) to 3.52 cm in PGC 108 (Cul C2-1). The PCV and GCV were 727.29 and 726.90 per cent, respectively. Leaf blade width recorded heritability of 99.89 per cent, GA of 24.36 per cent and genetic gain of 1496.62 per cent.

10. Leaf blade length (cm)

The leaf length varied between 25.92 cm in PGC 26 (Cul 12814) to 67.48 cm in Cul KAUM 20 with a mean 43.23 cm. The PCV and GCV were 35.10 and 33.26 per cent, respectively. This trait recorded heritability of 89.79 per cent, GA of 28.07 per cent and genetic gain of 64.92 per cent.

11. Total tillers per plant

The mean total tillers per plant recorded were 12.70 and ranged from 9.1 [PGC 58 (PM-701)] to 29.6 [PGC 83 (ASD 17)]. The PCV and GCV were 162.49 and 161.83 per cent, respectively. Total tillers per plant recorded heritability of 99.19 per cent with GA of 28.91 per cent and genetic gain of 332.02 per cent.

12. Productive tillers per plant

Number of productive tillers per plant ranged from 5.1 to 25.6 with a mean value of 8.70. PGC 58 (PM-701) and PGC 83 (ASD 17) respectively recorded the lowest and highest number of productive tillers per plant. The PCV and GCV were 126.72 and 125.87 per cent, respectively. The heritability, GA and genetic gain estimates for productive tillers per plant were 98.66 per cent, 22.43 per cent and 257.57 per cent.

13. Panicle length (cm)

The mean panicle length recorded in Base collection was 25.17 cm. It ranged from 15.71 cm [PGC 74 (Sabalai)] to 50.21 cm [PGC 95 (Cul 8711)]. The PCV and GCV were 42.78 and 42.76 per cent, respectively. Panicle length recorded heritability, GA and genetic gain as 99.89 per cent, 22.17 per cent and 88.05 per cent.

14. Spikelets per panicle

The spikelets per panicle ranged from 73.1 to 281.6 in PGC 115 (IVT 33) and PGC 7 [Ptb46 (Jayathi)] respectively. The mean value for this trait in the Base collection was 156.04. The PCV and GCV were 11.69 and 5.95 per cent, respectively. The heritability estimate of this trait was 25.88 per cent, GA of 9.73 per cent and genetic gain of 6.23 per cent.

15 Grains per panicle

The grains per panicle ranged from 4.5 (Karuthamodan) to 223.2 {PGC 7 [Ptb46 (Jayathi)}. The mean value for this trait in the Base collection was 95.30. The PCV and GCV were 20.99 and 13.64 per cent, respectively. Grains per panicle exhibited heritability of 42.26 per cent with GA of 17.42 per cent and genetic gain of 18.27 per cent.

16. Test weight of grain (g)

The 1000 grain weight ranged from 21.38 g (Chomala) to 23.65 g [PGC 73 (Karangi)]. The mean value for this trait in the Base collection was 22.71 g. The PCV and GCV were 51.61 and 51.6 per cent, respectively. The heritability of 99.93 per cent, GA of 24.14 per cent and genetic gain of 106.26 per cent was observed for 1000 grain weight.

17. Grain length (mm)

The grain length ranged from 4.291mm [PGC 72 (Reymuthika)] to 9.250 mm [PGC 199 (Kasturi)]. The mean value for this trait in the Base collection was 6.93 mm. The PCV and GCV were 172.92 and 172.90 per cent, respectively. The heritability, GA and genetic gain estimates for grain length was as 99.97 per cent, 24.70 per cent and 356.13 per cent.

18. Grain width (mm)

The grain width ranged from 0.222 mm [PGC 199 (Kasturi)] to 2.476 mm Mo 7 (Karthika). The mean value for this trait in the Base collection was 1.260 mm. The PCV and GCV were 966.42 and 1966.39 per cent, respectively. The values of Heritability, GA and genetic gain for this trait were 99.99 per cent, 25.08 per cent and 1990.70 per cent.

19. Grain thickness (mm)

The grain thickness ranged from 0.016 mm [PGC 193 (CSR 23)] to 1.348 mm Mo7 (Karthika). The mean value for this trait in the Base collection was 0.376 mm. The PCV and GCV were 2946.00 and 2946.00 per cent, respectively. Grain thickness showed heritability of 100 per cent with GA of 22.85 per cent and genetic gain of 6068.76 per cent.

20. Decorticated grain length (mm)

The decorticated grain length ranged from 1.79 mm [PGC 72 (Reymuthika)] to 6.750 mm [PGC 199 (Kasturi)]. The mean value for this trait in the Base collection was 4.435 mm. The PCV and GCV were 154.27 and 154.20 per cent, respectively. The heritability, GA and genetic gain estimates for decorticated grain length were 99.91 per cent, 14.08 per cent and 317.52 per cent.

21. Decorticated grain width (mm)

The decorticated grain width ranged from 0.778 mm [PGC 199 (Kasturi) to 1.476 mm Mo7 (Karthika). The mean value for this trait in the Base collection was 0.260 mm. The PCV and GCV were 3142.44 and 3142.2 per cent, respectively. The heritability, GA and genetic gain values for decorticated grain width were of 99.98 per cent, 16.83 per cent and 6472.44 per cent.

22. Decorticated grain thickness (mm)

The decorticated grain thickness ranged from 0.034 mm [PGC 193 (CSR 23)] to 1.298 mm Mo7 (Karthika). The mean value for this trait in the Base collection was 0.326 mm. The PCV and GCV were 2136.31 and 2136.08 per cent, respectively. The observed heritability, GA and genetic gain for decorticated grain thickness were of 99.97 per cent, 14.37 per cent and 4399.88 per cent.

23. Straw yield per plant (g)

The mean straw yield per plant recorded in Base collection was 26.71 g. It ranged from 14.88 g in accession (HS-13) to 45.94 g in PGC 199 (Kasturi).

24. Grain yield per plant (g)

The mean grain yield per plant recorded in Base collection was 22.03 g. It ranged from 7.62 g (Karuthamodan) to 48.97 g [PGC 18 (Kunju Kunju)]. The PCV and GCV were 33.49 and 32.14 per cent, respectively. This trait showed heritability of 92.06 per cent with GA of 14.00 per cent and genetic gain of 63.53 per cent.

4.2. Formation of core set

A subset (core set) of the Base collection (160 accessions) was formed based on 24 quantitative traits using the Power Core (v.1.0) software. The details on formation of core set and list of accessions in the core set are given in Table 8.

The core set formed comprised of 34 accessions (21.25 per cent) of the entire collection. The resultant core set had a mean difference (MD) of 6.98 per cent, 41.99 per cent variance difference (VD), 128.37 per cent variable rate (VR) and 96.34 per cent coincidence rate (CR).

The accessions in the core set included traditional rice varieties (Thottacheera, Karuthadukkan, Chomala), pureline selections of land races [PGC 49 (Ptb7:Parambuvattan), PGC 50 (Ptb10 : Thekkencheera)], high yielding varieties [Ptb 35 (Annapurna), PGC 7 (Ptb 46: Jayathy), PGC PGC 9 (Onam), PGC 14 (Tulasi), Mo7 (Karthika) etc], several breeding lines [PGC 28 (Cul 8757), PGC 33 (Cul 8714), PGC 145 (Cul 90-04), PGC 167 (Cul 9410-3- Sel 2)] to name a few.

Table 8. Details pertaining to core set

Accessions in core set

Sl. No.	Accessions	PGC No.	IC No.	Sl. No.	Accessions	PGC No.	IC No.
1.	Ptb 46 (Jayathy)	7	263555	18.	Cul 90-04	145	263693
2.	Onam	9	263557	19.	SBRP 3	153	263701
3.	Thulasi	14	263562	20.	SBRP 4	154	263702
4.	Dular	15	263563	21.	Moncompu 519	157	263705
5.	Cul 8757	28	263576	22.	Cul 9410-3-Sel 2	167	-
6.	Cul 8714	33	263581	23.	IET 18886	177	-
7.	Ptb 7 (Parambuvattan)	49	263597	24.	IET 18318 Sel 2	187	-
8.	Ptb 10 (Thekkencheera)	50	263598	25.	CSR 27	194	-
9.	Kargi	71	263619	26.	Indira Sugandhi Dhar	198	-
10.	Reymuthika	72	263620	27.	Kasturi	199	-
11.	Karangi	73	263621	28.	Ptb 35 (Annapurna)	-	-
12.	TKM 6	91	263639	29.	Thottacheera	-	-
13.	Cul 8711	95	-	30.	Karuthadukkan	-	-
14.	Panki	98	263646	31.	Chomala	-	-
15.	IVT 33	115	263663	32.	Cul KAUM 20	-	-
16.	IVT 109	117	263665	33.	Cul M 20	-	-
17.	AM-10-24	126	263674	34.	Mo 7 (Karthika)	-	-

Core set formation

Sl. No.	Particulars	Entries
1.	Number of accessions	160
2.	Number of variables	24
3.	Core set	
a)	Non-heuristic search	44
b)	Maximum possible entries	160
c)	PowerCore	34
4.	Mean difference (MD)	6.98
5.	Coincidence rate (CR)	96.34
6.	Variance difference (VD)	41.99
7.	Variable rate (VR)	128.37

4.3 Comparison of core set *vs.* Base collection

4.3.1 Geographical distribution of accessions in core set *vs* Base collection

A comparison of geographical distribution of accessions in core set and Base collection is presented in Table 9; Fig. 17.

χ^2 probabilities for frequency distribution of accessions based on geographic origin in the core set and Base collection were non significant for all the 9 geographic locations ($P = 0.01$). The overall χ^2 (5.36 at df 8) was also non significant ($P = 0.01$).

The collection in Base collection comprised of accessions from India (156 accessions; 97.5%) and Philippines (4 accessions; 2.5%). However, in the core set only accessions from India was represented. Similar to Base collection (124 accessions; 77.5%), the majority of accessions in core set (26 accessions; 76.47%) were from Kerala. With respect to distribution of accessions from other states, unlike Base collection the states of Uttar Pradesh and West Bengal were not represented in core set. In core set, there were accessions from Maharashtra (3 accessions and 8.88%), Andhra Pradesh (2 accessions and 5.88%) and one each from Haryana, Odisha and Tamil Nadu (2.94% each). However, in Base collection, accessions from Tamil Nadu (11 accessions; 6.875%) were more in number compared to those from Andhra Pradesh (7 nos.; 4.375 %), Maharashtra (6 nos.; 3.75%), Haryana (4 nos.; 2.5%), Odisha (2 nos.; 1.25 %) and one each (0.625% each) from Uttar Pradesh and Paschim Banga.

4.3.2 Variability in core set *vs* Base collection

4.3.2.1 Frequency distribution of qualitative traits in core set *vs* Base collection

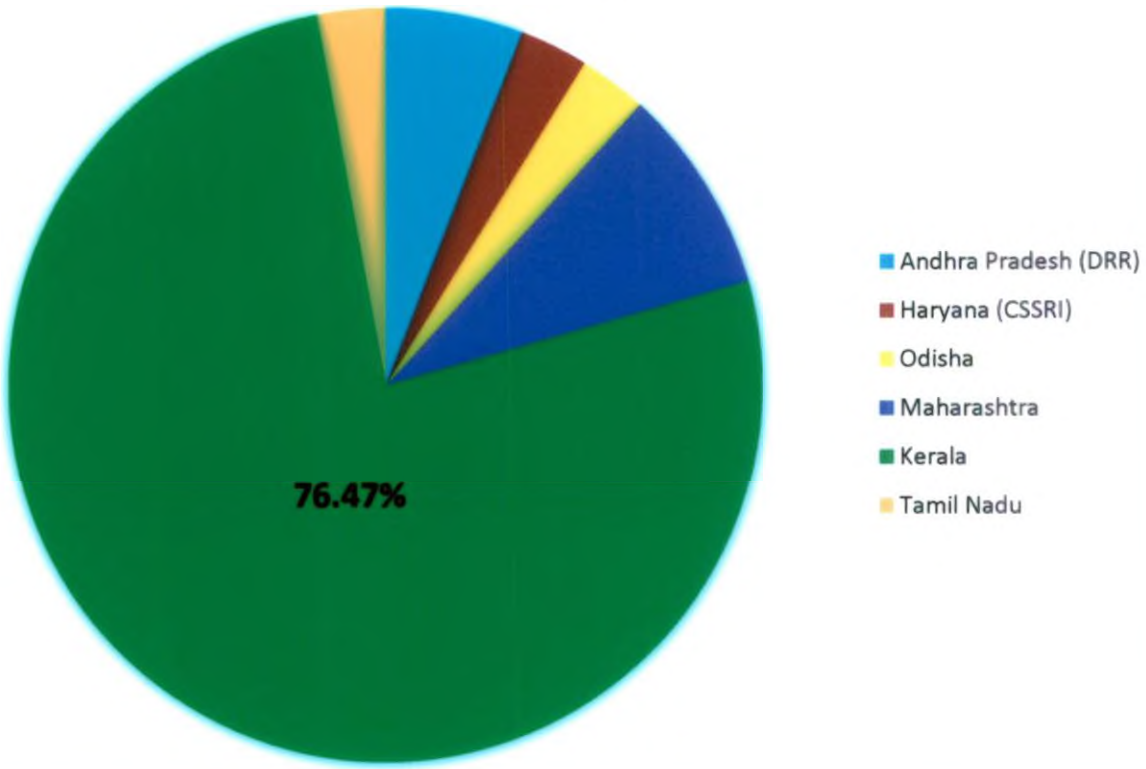
Rice accessions in core set were characterized with respect to 41 qualitative traits as per Rani *et al.*, 2004. A comparison of frequency distribution of accessions in

Table 9: Geographical distribution of accessions in core set *vs* Base collection

Sl. No.	Continent	Country	State		Accessions		Per cent distribution	Core set	Per cent distribution
					No.	χ^2			
1.	Asia	India							
			a)	Andhra Pradesh (DRR)	7	0.176	4.375	2	5.88
			b)	Haryana (CSSRI)	4	0.026	2.5	1	2.94
			c)	Odisha	2	0.777	1.25	1	2.94
			d)	Maharashtra	6	0.333	3.75	3	8.83
			e)	Kerala	124	0.004	77.5	26	76.47
			f)	Tamil Nadu	11	0.765	6.875	1	2.94
			g)	Uttar Pradesh	1	0.212	0.625	0	0
			h)	Paschim Banga	1	0.212	0.625	0	0
A)		**Total (India)**			**156**		**97.5**	**34**	**100**
2.		**Philippines**							
			a)	International Rice Research Institute (IRRI), Manila	4	0.85	2.5	0	0
B)		**Total (Philippines)**			**4**		**2.5**	**0**	**0**
C)		**Overall**		(A) + (B)	**160**	**5.36^{NS}**	**100**	**34**	**100**

χ^2: (P=0. 01) at df 8; (P= 0.05) at df 8

Fig. 17. Geographical distribution of accessions in core set



various subclasses of each of the 41 qualitative traits studied in core set and Base collection is presented in (Table 10; Plate 1-14).

1. **Coleoptile: Colour**

In Base collection, 136 (85%) possessed colourless coleoptile while 24 accessions (15%) possessed purple coleoptile. No accessions had green coleoptile. However, in core set out, of 25 accessions (73.52%) showed colourless coleoptile colour followed by 9 accessions (26.48%) exhibiting purple pigmentation of coleoptile.

2. **Basal leaf: Sheath colour**

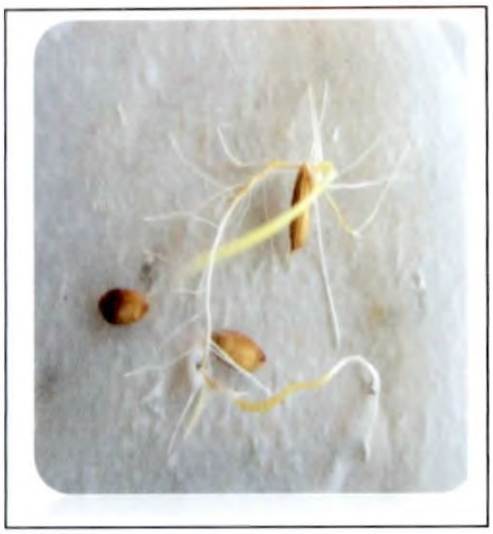
Majority of accessions in Base collection (135 nos.; 84.4%) showed green basal leaf sheath colour. Twelve accessions (7.5%) had light purple leaf sheath followed by 13 accessions (8.1%) with purple lines on leaf sheath. In core set 25 accessions (73.52%) showed green basal leaf sheath colour, followed by five accessions (14.70%) with light purple and four accessions (8.82%) with purple basal leaf sheath.

3. **Leaf: Intensity of green colour**

The intensity of greenness in leaf in Base collection varied between dark green colour (65 accessions; 40.6%) to light green (18 accessions; 11.3%). Seventy-seven accessions (48.1%) possessed medium green leaves. In core set, 21 accessions (61.74%) with medium green colour, followed by four accessions (11.76%) with light green colour and 9 accessions (26.47%) observed with dark green colour.

4. **Leaf: Anthocyanin colouration**

Anthocyanin colouration on leaf in Base collection was absent in 137



Colourless

Purple

Plate 1: Coleoptile colour

Green

Light Purple

Purple

Plate 2: Basal leaf sheath colour

accessions (85.6%) while 23 accessions (14.75 %) had anthocyanin pigmentation on leaves. In core set 26 accessions (76.47%) showed very weak anthocyanin colour on tips only, followed by eight accessions (23.53%) on margins only.

5. Leaf: Distribution of anthocyanin colouration

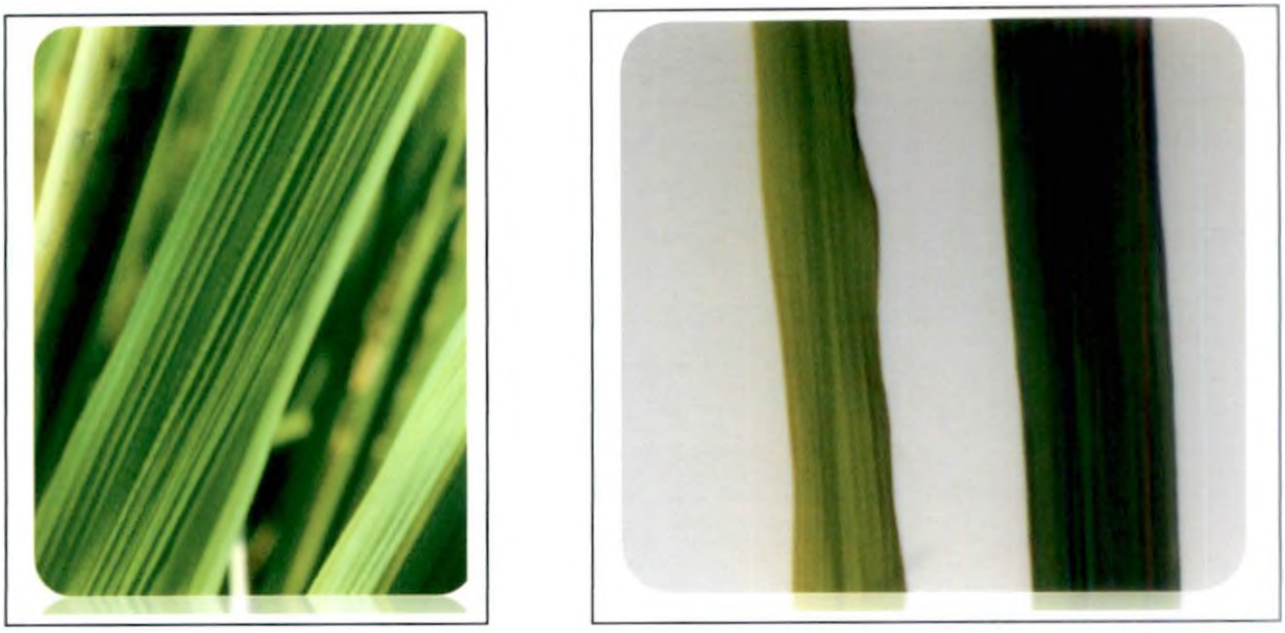
Out of the 23 accessions with anthocyanin colouration on leaves, two accessions exhibited uniform anthocyanin colouration on leaf whereas only one (4.34%) showed very weak anthocyanin colouration (on leaf tips only). Eighteen accessions (11.3%) possessed anthocyanin pigmentation on leaf margins only, while two accessions (1.3%) had pigmentation in blotches. In core set, eight accessions (88.88%) showed anthocyanin pigmentation on leaf margins and only, one accession (11.11%) had anthocyanin pigmentation on tips.

6. Leaf sheath: Anthocyanin colouration

Leaf sheath anthocyanin colouration in Base collection was absent in 137 accessions (85.6%) and present in 23 accessions (14.4%). In core set, leaf sheath anthocyanin colouration was absent in 26 accessions (76.47%) and present in eight accessions.

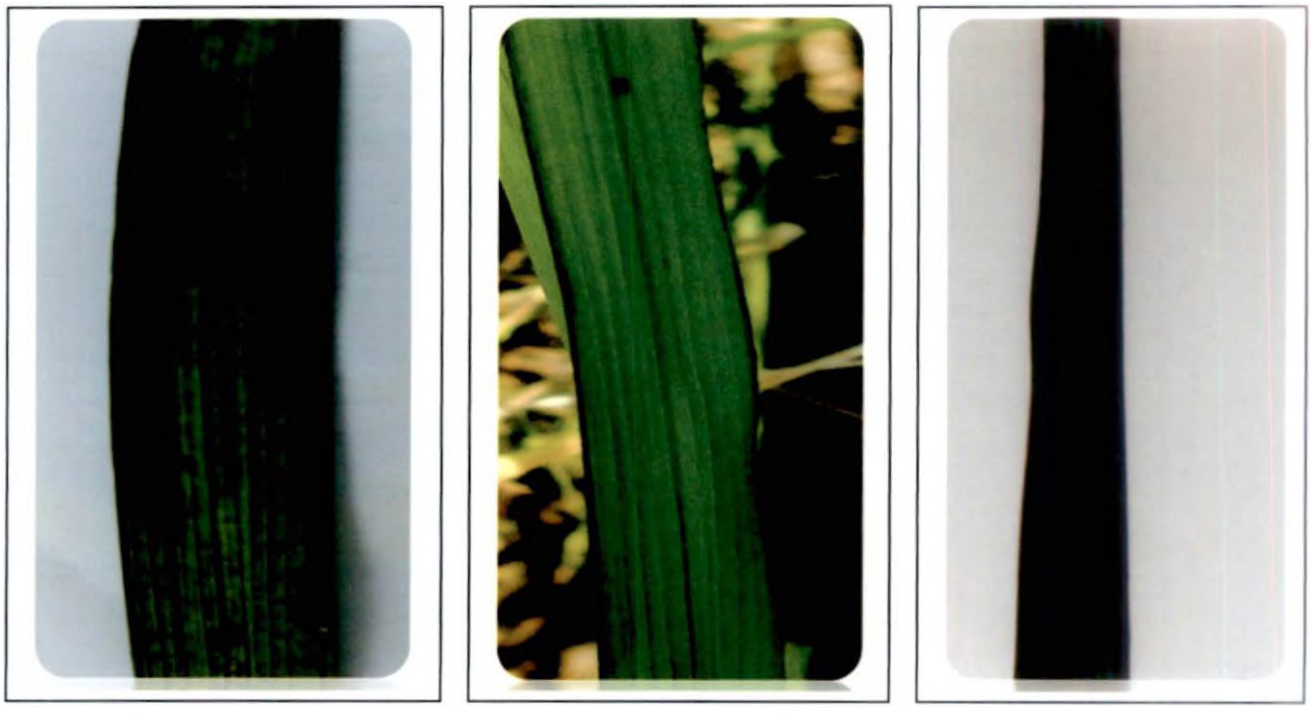
7. Leaf sheath: Intensity of anthocyanin colouration

The intensity of anthocyanin colouration in leaf sheath in Base collection was very weak in most accessions (137 accessions; 85.6%). The colour intensity was weak in 19 accessions (11.87%), while two accessions each (1.25% each) exhibited medium and very strong intensity of anthocyanin colouration in leaf sheath. In core set, very weak intensity of anthocyanin colouration in leaf sheath was observed in 29 accessions (85.29%), followed by weak intensity in three accessions (8.83%), and medium in two accessions (5.88%).



Green Pale green Dark green

Plate 3: Leaf: Intensity of green colour



Purple Blotch Purple Margin Purple

Plate 4: Leaf: Distribution of anthocyanin

Table 10. Frequency distribution of qualitative traits in core set *vs* Base collection

Sl. No.	Descriptor	Descriptor state	Score code	B	C	χ^2
1.	Coleoptile: colour	Colourless Green Purple	1 2 3	136 24	25 9	2.613^{NS}
2.	Basal leaf: Sheath colour	Green Light purple Purple line Purple	1 2 3 4	135 12 13	25 5 4	2.485^{NS}
3.	Leaf: Intensity of green colour	Light Medium Dark	3 5 7	18 77 65	4 21 9	2.512^{NS}
4.	Leaf: Anthocyanin colouration	Absent Present	1 9	137 23	26 8	1.750^{NS}
5.	Leaf: Distribution of anthocyanin colouration	On tips only On margins only In blotches only Uniform	1 2 3 4	1 18 2 2	1 8	2.128^{NS}
6.	Leaf sheath: Anthocyanin colouration	Absent Present	1 9	137 23	26 8	1.750^{NS}
7.	Leaf sheath: Intensity of anthocyanin colouration	Very weak Weak Medium Strong Very strong	1 3 5 7 9	137 19 2 2	29 3 2	3.573^{NS}
8.	Leaf: Pubescence of blade surface	Absent Weak Medium Strong Very strong	1 3 5 7 9	4 53 100 3	2 7 25	3.629^{NS}
9.	Leaf: Auricles	Absent Present	1 9	 160	 34	-
10.	Leaf: Anthocyanin colouration of auricles	Colourless Light purple Purple	1 2 3	157 3	34	0.647^{NS}
11.	Leaf: Collar	Absent Present	1 9	 160	 34	-
12.	Leaf: Anthocyanin colouration of Collar	Absent Present	1 9	157 3	34	0.647^{NS}
13.	Leaf: Ligule	Absent Present	1 9	 160	 34	-

- : Chi square not performed; NS : Non-significant

Table 10. Frequency distribution of qualitative traits in core set *vs* Base collection (contd...)

Sl. No.	Descriptor	Descriptor state	Score code	B	C	χ^2
14.	Leaf: Shape of ligule	Truncate Acute Split	1 2 3	 160	 34	-
15.	Leaf: Colour of ligule	Green Light purple Purple	1 2 3	157 3	34	0.647^{NS}
16.	Flag leaf: Attitude of blade (Early observation)	Erect Semi-erect Horizontal Deflexed	1 3 5 7	160	34	-
17.	Flag leaf: Attitude of blade (Late observation)	Erect Semi-erect Horizontal Deflexed	1 3 5 7	50 109 1	12 22	0.404^{NS}
18.	Culm: Attitude	Erect Semi-erect Open Spreading	1 3 5 7	130 25 5	24 10	4.418^{NS}
19.	Lemma: Anthocyanin colouration of keel	Absent or very weak Weak Medium Strong Very strong	1 3 5 7 9	157 2 1	34	0.647^{NS}
20.	Lemma: Anthocyanin colouration of area below apex	Absent Weak Medium Strong Very strong	1 3 5 7 9	157 2 1	34	0.647^{NS}
21.	Lemma: Anthocyanin colouration of apex	Absent Weak Medium Strong Very strong	1 3 5 7 9	136 13 7 4	25 5 3 1	2.851^{NS}
22.	Spikelet: Colour of stigma	White Light green Yellow Light purple Purple	1 2 3 4 5	136 24	26 8	1.481^{NS}
23.	Stem: Anthocyanin colouration of nodes	Absent Present	1 9	137 23	26 8	1.750^{NS}

- : Chi square not performed; NS : Non-significant

Table 10. Frequency distribution of qualitative traits in core set *vs* Base collection (contd...)

Sl. No.	Descriptor	Descriptor state	Score code	B	C	χ^2
24.	Stem: Intensity of anthocyanin colouration of nodes	Weak Medium Strong	3 5 7	156 1 3	34	0.867^{NS}
25.	Stem: Anthocyanin colouration of internodes	Absent Present	1 9	137 23	26 8	1.750^{NS}
26.	Panicle: Curvature of main axis	Straight Semi-straight Drooping Deflexed	1 3 5 7	160	34	-
27.	Spikelet: Density of pubescence of lemma	Absent Weak Medium Strong Very strong	1 3 5 7 9	38 114 8	8 25 1	0.277^{NS}
28.	Spikelet: Colour of tip of lemma	White Yellowish Brown Red Purple Black	1 2 3 4 5 6	136 24	26 8	1.481^{NS}
29.	Lemma and Palea colour	Straw Gold and gold furrows on straw background Brown spots on straw Brown furrows on straw Brown (Tawny) Reddish to light purple Purple spots on straw Purple furrows on straw Purple Black	0 1 2 3 4 5 6 7 8 9	9 32 25 76 14 3 1	4 7 7 11 3 2	5.395^{NS}
30.	Panicle: Awns	Absent Present	1 9	148 12	28 6	3.430^{NS}
31.	Panicle: Colour of awns	Yellowish white Yellowish brown Brown Reddish brown Light red Red Light purple Purple Black	1 2 3 4 5 6 7 8 9	11 1	5 1	0.281^{NS}

- : Chi square not performed; NS : Non-significant

Table 10. Frequency distribution of qualitative traits in core set *vs* Base collection (contd...)

Sl. No.	Descriptor	Descriptor state	Score code	B	C	χ^2
32.	Panicle: Distribution of awns	Tip only	1	3	1	1.5^{NS}
		Upper half only	3	2		
		Uniform	5	7	5	
33.	Panicle: Presence of secondary branching	Absent	1			-
		Present	9	160	34	
34.	Panicle: Secondary branching	Weak	1			-
		Strong	2	160	34	
		Clustered	3			
35.	Panicle: Attitude of branches	Erect	1			2.014^{NS}
		Erect to semi-erect	3	8	1	
		Semi-erect	5	149	31	
		Semi-erect to spreading	7	3	2	
		Spreading	9			
36.	Panicle: Exsertion	Partly exserted	3			-
		Mostly exserted	5			
		Well exserted	7	160	34	
37.	Time of maturity	Very early	1	3	1	0.988^{NS}
		Early	3	123	24	
		Medium	5	32	8	
		Late	7	2	1	
		Very late	9			
38.	Leaf: Senescence	Early	3			0.612^{NS}
		Intermediate	5	155	32	
		Late	7	5	2	
39.	Sterile Lemma: Colour	Straw	1	155	34	1.091^{NS}
		Gold	2			
		Red	3	1		
		Purple	4	4		
40.	Decorticated grain: Shape	Short slender	1	3	1	4.328^{NS}
		Short bold	2	136	25	
		Medium slender	3	5	1	
		Long bold	4	12	4	
		Long slender	5	4	3	
		Extra long slender	6			
41.	Decorticated grain: Colour	White	1	47	12	1.765^{NS}
		Light brown	2	3		
		Variegated brown	3			
		Dark brown	4	1		
		Light red	5	44	7	
		Red	6	65	15	
		Variegated purple	7			
		Purple	8			
		Dark purple	9			

- : Chi square not performed; NS : Non-significant

8. Leaf: Pubescence of blade surface

In Base collection, pubescence of leaf blade was medium in 100 accessions (62.5%), weak in 53 accessions (33.1%) and strong in three accessions (1.9%). It was absent in four accessions (2.5%). Weak leaf blade pubescence was noticed in seven accessions (20.58%), medium in 25 accessions (73.52%) and absent in four accessions (5.88%) in core set.

9. Leaf: Auricles

All the 160 accessions 100%) in the Base collection as well as core set possessed auricles.

10. Leaf: Anthocyanin colouration of auricles

In Base collection 157 accessions (98.1%) showed colourless auricles whereas the auricle was purple coloured in three accessions (1.9%). Thirty four accessions (100%) possessed colourless auricles in core set.

11. Leaf: Collar

Both in core set and Base collection, all the accessions (100%) possessed a clear cut leaf collar.

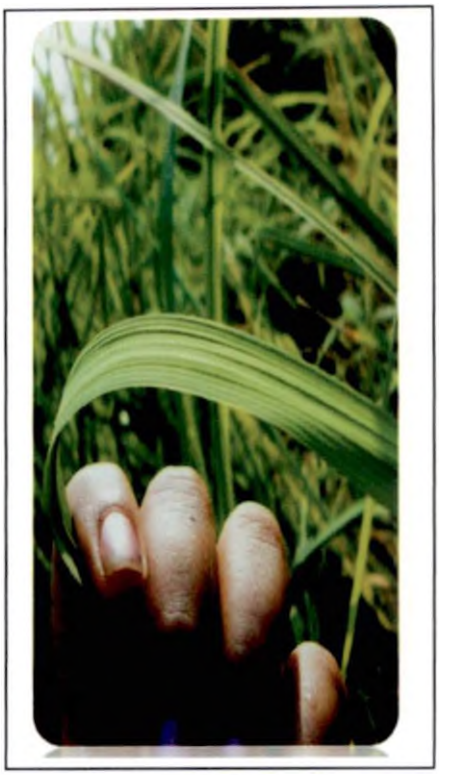
12. Leaf: Anthocyanin colouration of Collar

In majority of accessions (157 accessions; 98.1%) anthocyanin colouration was absent in leaf collar in Base collection whereas it was pigmented in three accessions (1.9%). In core set, anthocyanin colouration on leaf collar was absent in all the 34 accessions (100%).

13. Leaf: Ligule

Both in core set and Base collection, all the accessions (100%) possessed ligule.

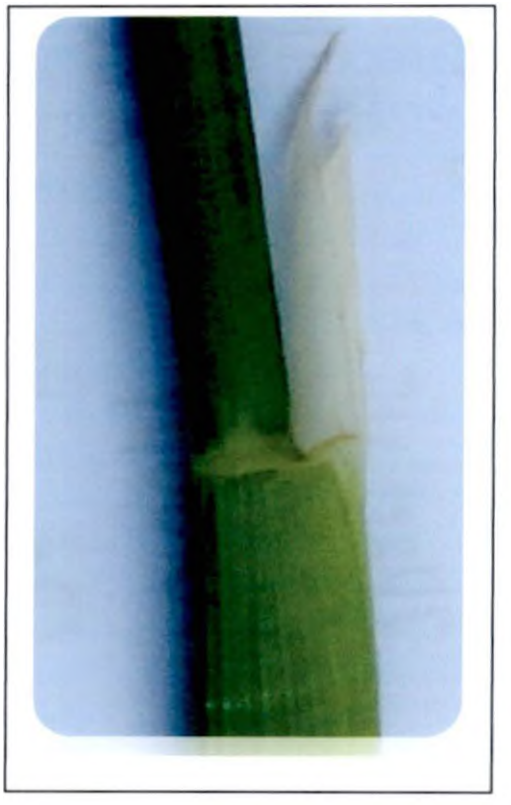
Strong



Medium

Weak

Plate 5: Leaf: Pubescence of blade



Colourless

Purple

Plate 6: Leaf: Anthocyanin colouration of auricles

14. Leaf: Shape of ligule

All the accessions possessed split type of ligule in both Base collection and core set (100%).

15. Leaf: Colour of ligule

In Base collection, green colour ligule was observed in 157 accessions (98.1%) while in three accessions (1.9%) it was purple coloured. In core set, green colour ligule observed in all accessions.

16. Flag leaf: Attitude of blade (Early observation)

In Base collection, the attitude of flag leaf was erect in all the 160 accessions the early stage (booting stage). In core set, the attitude of flag leaf was erect in all the 34 accessions (100%) in the early stage (booting stage).

17. Flag leaf: Attitude of blade (Late observation)

In Base collection, in the late stage (maturity stage), semi-erect flag leaf was observed in 109 accessions (68.13%) and erect flag leaf in 50 accessions (31.25%). Horizontal flag leaf was observed only in one accession (0.62%). In core set, in the late stage (maturity stage), 12 accessions (35.29%) were observed with erect flag leaf, followed by 22 accessions (64.70%) with semi-erect flag leaf.

18. Culm: Attitude

In Base collection, culm attitude was erect in 130 accessions (81.3%); followed by 25 accessions (15.6%) with semi-erect and five accessions with open type culm attitude. Culm attitude was erect in 24 accessions (70.58%); followed by 10 accessions (29.42%) with semi-erect culm attitude in core set.

Erect Semi-erect Horizontal

Plate 7: Flag leaf: Attitude of blade (early observation)

Green Purple

Plate 8: Lemma: Anthocyanin colouration of apex

19. Lemma: Anthocyanin colouration of keel

In Base collection, anthocyanin colouration of lemma keel was very weak in 157 accessions (98.1%). It was weak in two accessions (1.3%) and medium in one accession (0.6%). In core set, anthocyanin colouration of lemma keel was very weak in 34 accessions (100%). At the apex of lemma, anthocyanin colouration was observed in 25 accessions (73.53%), it was weak in four accessions (11.76%), medium in three accessions (8.82%) and strong in one accession (2.94%).

20. Lemma: Anthocyanin colouration of area below apex

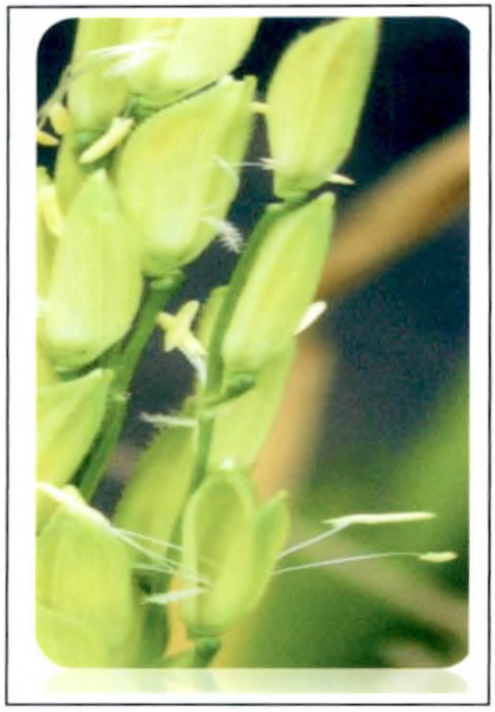
The anthocyanin colouration of lemma below apex in Base collection was absent in 157 accessions (98.1%), weak in two accessions (1.3%) and medium in one accession (0.6%). In core set, lemma anthocyanin colouration below apex was absent in 34 accessions (100%).

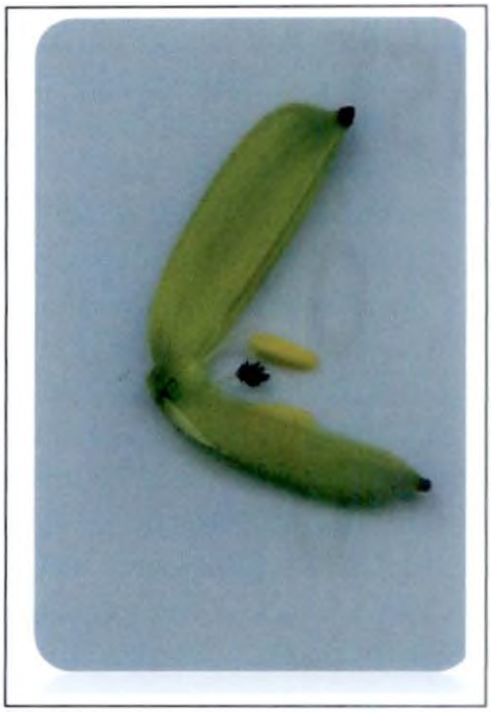
21. Lemma: Anthocyanin colouration of apex

Anthocyanin colouration of lemma apex was strong in four accessions (2.5%), medium in seven accessions (4.4%) and weak in 13 accessions (8.125%). It was absent in 85.0% of the accessions. In core set, anthocyanin colouration was absent in 25 accessions (73.52%), medium in three accessions (8.82%), weak in five accessions (14.71%) and strong in one accession (2.94%).

22. Spikelet: Colour of stigma

Only two types of stigma colour *viz.*, white and purple were observed in the Base collection. Majority of accessions (136 accessions; 85.0%) exhibited white stigma while 24 accessions (15.0%) had purple stigma. In core set, majority of genotypes (26 and 76.47%) exhibited white and only eight (23.53%) accessions had purple stigma colour.





White **Purple**

Plate 9: Spikelet: Colour of stigma

Plate 10: Plant habit: Pigmentation

Green

Purple

Plate 11: Panicle colour

Partially enclosing spikelet

Fully enclosing spikelet

Plate 12: Sterile lemma

23. Stem: Anthocyanin colouration of nodes

In Base collection, anthocyanin colouration on nodes was absent in 137 accessions (85.6%) and present in 23 accessions (14.4%). In core set, Anthocyanin colouration on stem nodes was absent in 26 accessions (76.47%) and present in eight accessions (23.53%).

24. Stem: Intensity of anthocyanin colouration of nodes

The intensity of anthocyanin colouration of nodes in Base collection was weak in 156 accessions (97.5%). It was strong in three accessions (1.9%) and medium in one accession. All the 34 accessions in core set were having weak intensity of anthocyanin on nodes.

25. Stem: Anthocyanin colouration of internodes

Twenty-three accessions (4.4%) exhibited anthocyanin colouration on internodes while it was absent in the rest (137 accessions; 85.6%) in Base collection. In core set, anthocyanin colouration on stem internodes was observed eight accessions (23.53%) and 26 accessions (76.47%) did not showed anthocyanin colouration on internodes.

26. Panicle: Curvature of main axis

The curvature of main axis of panicle in both Base collection and core set was semi-straight in all the accessions.

27. Spikelet: Density of pubescence of lemma

In Base collection, pubescence of lemma on spikelet was weak in 38 accessions (23.8%). Majority (114 accessions; 71.3%) of accessions possessed medium pubescence on spikelet surface whereas eight accessions (5%) exhibited strong pubescence. In core set, density of pubescence of

lemma on spikelet was weak in eight accessions (23.53%), followed by medium density of pubescence in 25 accessions (76.53%) and strong in one accession (2.94%).

28. Spikelet: Colour of tip of lemma

The colour of apiculus in Base collection was yellowish in 136 accessions (85%) and purple in 24 accessions (15%). The apiculus colour was yellowish in 26 accessions (76.47%) and purple in eight accessions (23.53%) in core set.

29. Lemma and Palea colour

In Base collection, majority of accessions (76 accessions; 47.5%) had brown furrows on straw coloured lemma and palea while 32 accessions (20%) had gold and gold furrows on straw background. The colour of lemma and palea in the rest varied between brown spots on straw (25 and 15.6%), brown (14 and 8.8%), straw (9 and 5.6%), reddish to purple (3 and 1.9%) and purple (1 and 0.6%). In core set, a wide range of lemma and palea was observed in germplasm accessions *viz.,* straw, gold and gold furrows on straw backgrounds, brown spots on straw, brown furrows on straw, brown (tawny), and reddish to light purple, purple. Majority of genotypes (11 and 32.35%) exhibited brown furrows on straw followed by gold and gold furrows on straw background (7 and 20.58%) followed by brown spots on straw (7 and 20.58%), brown (3 and 8.82%), straw (4 and 511.76%), reddish to purple (2 and 5.88%).

30. Panicle: Awns

In Base collection, awns were absent in 148 accessions (92.5%) and present in 12 accessions (7.5%). In core set, awns were absent in 28 accessions (82.35%) and present in six accessions (23.53%).

Absent

Present

Plate 13: Panicle: Awn

Semi-erect to spreading

Semi-erect

Plate 14: Panicle: Attitude of branches

31. Panicle: Colour of awns

In Base collection, the colour of awns in the 12 accessions could be grouped into yellowish and red. Eleven accessions (91.66%) showed yellowish awns and only one accession possessed red awns (8.33%). In core set, two types of awns colour was observed yellowish (5 and 14.70%) and red (1 and 2.94%).

32. Panicle: Distribution of awns

In Base collection, 12 accessions with awns, the distribution of awns were restricted to tip of panicle in three accessions (25.0%) whereas, it was found in upper half only in two accessions (16.66 %). The awns were distributed throughout the panicle in the rest (7 accessions; 58.33%). In core set, distribution of panicle awns was observed in all three categories *viz.*, tip only (1 and 16.66%), and uniform awns in five accessions (83.33%).

33. Panicle: Presence of secondary branching

Both in core set and Base collection, all the accessions possessed secondary branching.

34. Panicle: Secondary branching

All the accessions (100%) in Base collection and core set showed strong secondary branching.

35. Panicle: Attitude of branches

Attitude of panicle branching in Base collection varied between erect to semi-erect (8 accessions; 5%) and semi-erect to spreading (3 accessions; 1.9%). However in majority of accessions (149 accessions; 93.1%) it was semi-erect. In core set, attitude of panicle branches was noticed as erect to semi-erect (1 and 2.94%), semi-erect (31 and 91.17%) and semi-erect to spreading (2 and 5.88%).

36. Panicle: Exsertion

Both in core set and Base collection, all the accessions (100%) possessed well exserted panicles.

37. Time of maturity

In Base collection, three accessions (1.9%) matured very early. However most accessions (123 accessions; 76.9%) were early in maturity, followed by 32 accessions (20%) of medium maturity and two accessions of late in maturity. In core set, one accession (2.94%) matured very early, while 24 accessions (70.58%) were early in maturity, followed by eight accessions (23.53%) of medium maturity, one accession (2.94%) of very early in maturity and only one accession (2.94%) of late in maturity.

38. Leaf: Senescence

In Base collection, five accessions (3.1%) the leaf senescence was observed to occur late. However, in majority of the accessions (155 accessions; 96.9%) intermediate leaf senescence was noticed. In core set, two accessions (5.88%) the leaf senescence was observed to occur late. In majority of accessions (32 accessions; 94.11%) intermediate leaf senescence was noticed.

39. Sterile Lemma: Colour

The colour of sterile lemma in Base collection varied between straw (155 accessions and 96.9%), red (1 and 0.6%) and purple (4 accessions and 2.5%). In core set, the sterile lemma colour was observed as straw in all the accessions.

40. Decorticated grain: Shape

Short bold grains were found in majority of accessions (136 accessions; 85%) whereas it was short slender in 3 accessions (1.9%), medium slender in five accessions (3.1%), long bold in 12 accessions (7.5%) and long slender in four accessions (2.5%). In core set, majority of accessions observed short bold (25 accessions; 73.53%). Whereas, it was short slender in one accession (2.94%), medium slender one accession (2.94%), long bold in four accessions (11.76%) and long slender in three accessions (8.83%).

41. Decorticated grain: Colour

Colour of decorticated grain in Base collection varied from white (47 accessions; 29.4%) to light brown (3 accessions; 1.9%), dark brown (1 accessions; 0.6%), light red (44 accessions; 27.5%) and red (65 accessions; 40.6%). In core set, decorticated grain colour was observed as white (12 and 35.30%), light red (7 and 20.59%) and red (15 and 44.11%).

The chi-square (χ^2) values for frequency distribution of accessions in various subclasses of the qualitative traits studied with respect to Base collection and core set was non-significant. The chi-square test (χ^2) was not performed with respect to traits leaf auricle, leaf collar, leaf ligule, shape of ligule, attitude of flag leaf blade (early observation), curvature of main axis of panicle, presence and nature of secondary branching in panicles and panicle exsertion, as all the accessions grouped into single classes with respect to these traits.

4.3.2.2 Variability in quantitative traits in core set *vs* Base collection

Comparison of statistical parameters viz., mean, range and variance with respect to 24 quantitative traits in both core set and Base collection are presented in Table 11; Fig.18 and 19 along with the results on (i) One sample t-test for comparison

of mean of the two populations (core set and Base collection) and (ii) homogeneity test (F test) for comparison of variance of quantitative traits in both population.

The results of One sample t-test for comparison of mean of core set (C_M) and Base collection (B_M) revealed that there was no significant difference between the two populations with respects each of the 24 quantitative traits. The difference in the range of variability in core set (C_R) and Base collection (B_R) was narrow for all the traits studied.

The results of One sample t - test for comparison of mean of core set (C_M) and Base collection (B_M) revealed that there was no significant difference between the two population with respect to mean values of the each of the 24 quantitative traits. On conduct of homogeneity test (F test) for comparison of variance of quantitative traits in both core set and Base collection, the F value estimate with respect each of the 24 quantitative traits proved non significant.

The core set evaluation indicated the presence of promising accessions which would be prove useful in further crop improvement programme (Table 12). PGC 115 (IVT 33), PGC 15 (Dular), PGC 33 (Cul 8714), PGC 9 (Onam), PGC 14 (Tulasi), PGC 50 [Ptb 10 (Thekkencheera)], PGC 72 (Reymuthika) and Thottacheera were promising for earliness.

PGC 91 (TKM 6), PGC 72 (Reymuthika), Thottacheera, PGC 98 (Panki), Karuthadukkan, PGC 50 [Ptb 10 (Thekkencheera)], PGC 153 (SBRP-3), PGC 73 (Karangi), PGC 19 (Dular) and PGC 154 (SBRP 4) were identified as very tall.

PGC 115 (IVT 33), PGC 28 (Cul 8757), PGC 117 (IVT 109), PGC 33 (Cul 8714), PGC 126 (Cul AM 10-24), Karuthadukkan, Chomala, PGC 50 [Ptb 10 (Thekkencheera)], Thottacheera and PGC 49 [Ptb 7 (Parambuvattan)], were promising for productive tillers.

Table 11. Comparison of mean, range and variance for the quantitative traits in core set *vs* Base collection

Sl. No	Traits	Mean ±SE		T test	Range		Variance		F test
		Base	Core set		Base	Core set	Base	Core set	
1	Seedling shoot length (cm)	26.76±0.352	28.18±1.046	1.578^{NS}	17.12-42.50	17.11-42.49	19.80	37.21	8.901^{NS}
2	Seedling root length (cm)	5.32±0.806	5.40±0.2345	0.385^{NS}	2.77-8.61	2.77-8.04	1.19	1.87	3.310^{NS}
3	Seedling vigour index	5.20±0.9907	5.44±0.2486	0.966^{NS}	3.05-8.83	3.26-8.68	1.57	2.10	1.996^{NS}
4	Total seedling biomass (g)	0.80±0.0205	0.85±0.0558	0.992^{NS}	0.27-1.83	0.43-1.83	0.67	0.11	3.145^{NS}
5	Plant height (cm)	181.03±1.6345	180.14±1.7376	1.657^{NS}	82.75-279.27	102.58-176.03	64.96	102.66	4.223^{NS}
6	Culm length (cm)	89.65±1.2956	95.92±3.2952	1.964^{NS}	61.83-140.17	68.4-140.20	268.58	369.19	1.549^{NS}
7	Stem thickness (mm)	4.10±0.0642	4.19±0.1661	0.515^{NS}	2.40-6.83	2.40-6.83	0.66	0.94	1.504^{NS}
8	Days to heading	84.97±0.703	85.00±1.698	0.018^{NS}	64-118	64-115	79.11	98.06	0.719^{NS}
9	Leaf blade width (cm)	1.62±0.0265	1.71±0.0838	1.223^{NS}	1.30-3.52	1.30-3.28	0.11	0.24	5.449^{NS}
10	Leaf blade length (cm)	43.23±0.6128	45.30±1.4048	1.402^{NS}	25.92-67.48	30.25-67.48	60.09	67.10	0.008^{NS}
11	Total tillers per plant	12.70±0.1960	13.46±0.6941	1.422^{NS}	9.10-29.60	9.50-29.60	6.15	16.38	8.742^{NS}
12	Productive tillers per plant	8.70±0.1960	9.46±0.6941	1.422^{NS}	5.10-25.60	5.50-25.60	6.15	16.38	8.742^{NS}
13	Panicle length (cm)	25.17±0.2391	26.29±0.8535	1.714^{NS}	15.71-50.21	17.92-50.21	9.15	24.77	2.974^{NS}
14	Spikelets per panicle	156.04±3.1573	166.02±8.766	1.255^{NS}	73.10-281.60	73.10-281.60	1594.98	2612.63	4.170^{NS}
15	Grains per panicle	95.30±3.1897	105.01±8.924	1.208^{NS}	4.52-223.20	9.42-223.20	1627.85	2707.92	4.534^{NS}
16	Test weight of grain (g)	22.71±0.0309	22.67±0.0844	-0.490^{NS}	21.38-23.65	21.38-23.65	0.15	0.24	2.444^{NS}
17	Grain length (mm)	6.77±0.0634	6.77±0.1781	1.334^{NS}	4.29-9.25	4.29-9.25	0.64	1.08	2.353^{NS}
18	Grain width (mm)	1.26±0.0247	1.21±0.0781	-0.703^{NS}	0.22-2.48	0.22-2.48	0.11	0.21	6.902^{NS}
19	Grain thickness (mm)	0.38±0.0173	0.44±0.0520	1.439^{NS}	0.02-1.35	0.03-1.35	0.05	0.09	4.902^{NS}
20	Decorticated grain length(mm)	4.27±0.0634	4.27±0.1781	1.334^{NS}	1.79-6.75	1.79-6.75	0.64	1.08	2.353^{NS}
21	Decorticated grain width(mm)	1.13±0.0247	1.13±0.0781	-0.703^{NS}	0.78-1.48	0.78-1.48	0.11	0.21	6.902^{NS}
22	Decorticated grain thickness(mm)	0.33±0.0173	0.39±0.0520	1.439^{NS}	0.34-1.30	0.02-1.30	0.05	0.09	4.902^{NS}
23	Straw yield per plant (g)	26.71±2.0966	37.85±9.5825	1.763^{NS}	14.88-45.94	16.81-43.37	703.36	3122.08	10.302^{NS}
24	Grain yield per plant (g)	22.03±0.6886	21.83±1.6224	-0.123^{NS}	7.63-48.98	8.00-46.967	75.87	89.50	1.077^{NS}

^{NS}: Non-significant ; ^{S}: Significant

Fig.18. Estimates of mean for seedling traits in core set *vs* Base collection

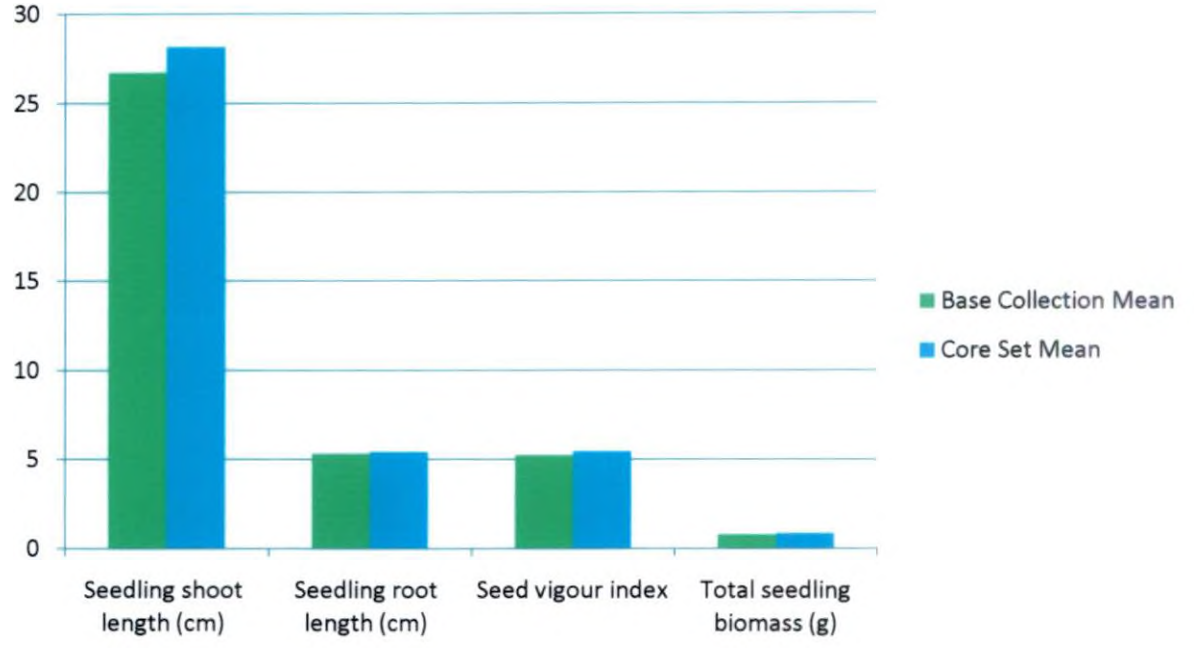


Fig.19. Estimates of mean for grain dimensions in core set *vs* Base collection

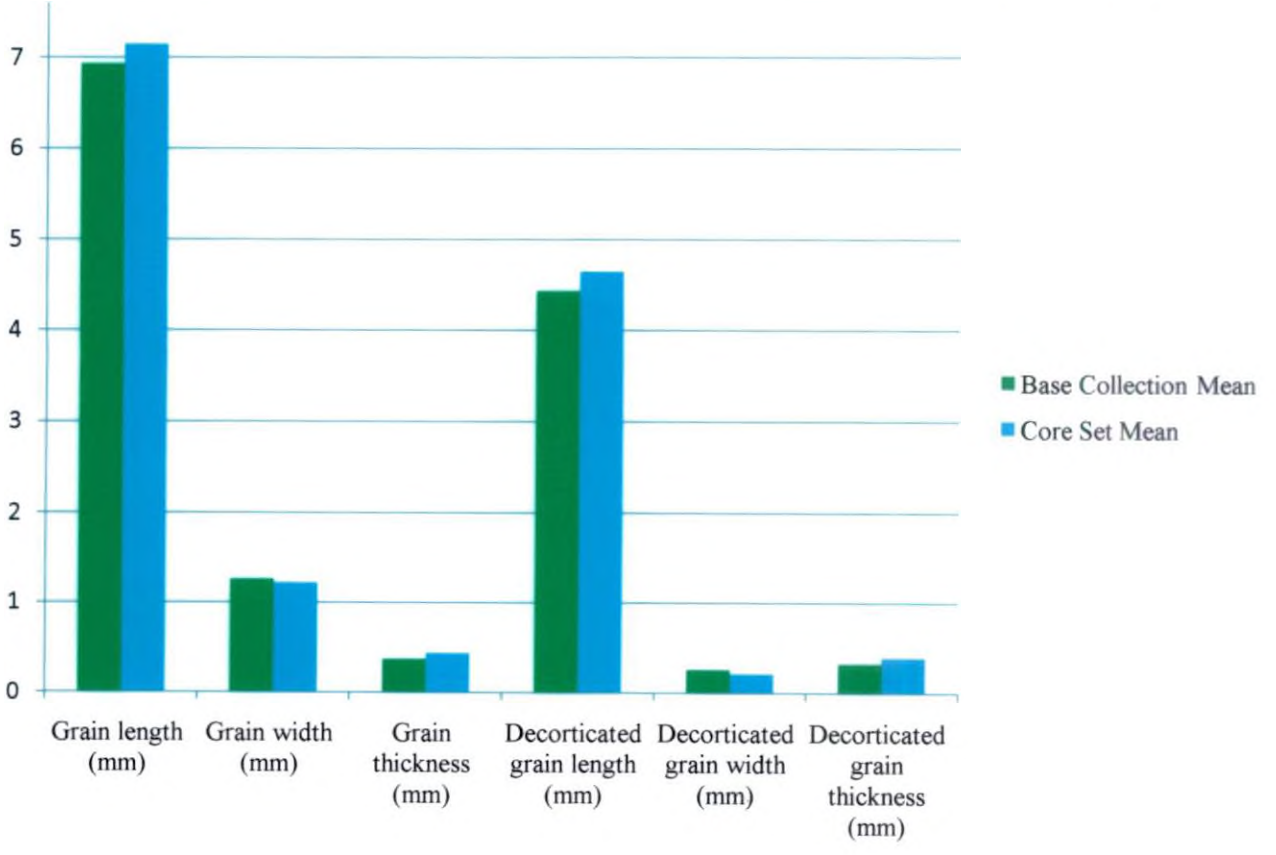


Table 12. Grain yield and other economic traits of genotypes in core set

PGC No.	Name	Plant Height (cm)	Culm Length (cm)	Stem Thickness (mm)	Days to Heading	Leaf Width (cm)	Leaf Length (cm)	Total tillers / plant	Productive tillers / plant	Panicle Length (cm)	Grains/ panicle	Test Weight of Grain (g)	Grain Length (mm)	Grain Width (mm)	Straw Yield / Plant (g)	Grain Yield / Plant (g)
7	Ptb 46 (Jayathy)	120.18	75.9	5.51	86	2.94	36.28	11.7	7.7	28.97	223.2	22.52	6.85	1.75	22.55	31.99
9	Onam	117.49	81.87	3.46	76	1.61	38.29	10.9	6.9	29.04	98	22.77	7.13	1.98	19.85	39.38
14	Tulasi	107.66	71.58	3.76	76	1.55	45.12	12.8	8.8	24.29	128.9	23.19	8.77	1.97	21.17	22.87
15	Dular	141.68	106.4	3.33	75	3.07	44.32	11.5	7.5	26.21	38.2	22.92	7.25	1.68	16.80	22.50
28	Cul 8757	116.48	84.61	3.36	85	1.5	46.39	22.2	18.2	24.49	134.2	23.35	7.80	1.11	30.85	46.96
33	Cul 8714	102.58	68.42	4.07	76	1.54	43.86	18.3	14.3	28.27	92.1	22.41	7.02	1.11	21.56	36.09
49	Ptb 7 (Prambuvattan)	132.46	101.53	5.32	81	1.44	45.27	13.9	9.9	25.61	127.5	22.60	6.61	1.30	21.02	32.44
50	Ptb 10 (Thekkencheera)	152.8	117.95	4.92	76	1.36	43.87	14.4	10.4	26.79	37.3	22.78	6.56	1.56	34.13	25.04
71	Kargi	111.95	81.98	2.88	76	1.52	34.11	13.7	9.7	17.92	82.1	22.02	5.89	1.19	20.21	9.32
72	Reymuthika	171.75	140.17	3.66	88	1.67	46.07	9.5	5.5	28.06	146.2	22.14	4.29	1.16	27.34	13.84
73	Karangi	141.21	108.32	3.63	81	1.64	42.85	11.1	7.1	22.52	22	23.64	6.30	0.98	21.47	30.78
91	TKM 6	176.02	129.9	6.83	84	1.54	58.42	11.1	7.1	31.93	170.5	22.3	8.03	0.81	26.44	10.74
95	Cul 8711	125.08	87.15	3.79	83	1.53	46.4	12.1	8.1	50.21	105.2	22.46	6.93	0.97	20.09	25.47
98	Panki	162.15	137.52	5.02	96	1.86	59.57	10.8	6.8	27.13	98.6	22.60	6.76	1.51	43.37	12.99
115	IVT 33	125.11	99.85	3.23	64	1.3	39.41	29.6	25.6	24.31	9.4	22.01	7.58	0.99	19.95	17.31
117	IVT 109	103.74	76.26	4.18	81	1.52	36.58	18.4	14.4	23.11	28.1	22.59	7.65	1.16	23.15	27.39
126	AM 10-24	124.01	93.91	4.25	83	1.5	36.96	18.1	14.1	23.99	96.1	22.93	7.30	1.28	25.48	29.17
145	Cul 90-04	111.64	84.33	2.39	81	3.28	36.06	13	9	25.54	72.8	22.53	5.92	1.15	18.35	25.25
153	SBRP-3	145.45	109.99	4.42	91	1.35	54.07	10.4	6.4	25.45	79.1	23.54	7.63	1.32	24.43	18.37
154	SBRP-4	141.26	105.42	5.20	91	1.38	55.85	10.1	6.1	26.07	109.4	23.48	8.15	1.29	20.90	18.56
157	Moncumpu 519	121.32	73.19	4.58	88	1.61	57.04	11.3	7.3	24.29	165	22.76	8.09	0.79	22.04	13.79
167	Cul 9410-3-Sel 2	134.02	86.24	4.28	90	1.62	43.62	10.9	6.9	25.57	163.5	22.84	8.07	1.02	18.77	22.96
177	IET 18886	131.05	98.7	3.75	94	1.5	53.15	11.7	7.7	27.66	90.4	23.18	8.81	1.42	24.15	18.20
187	IET 18318-Sel 2	118.58	85.51	4.17	91	1.84	46.74	12	8	23.44	152.3	21.93	6.37	0.46	24.32	17.02
194	CSR 27	123.51	90.41	4.31	86	1.65	40.37	11	7	28.03	163.9	22.97	7.63	1.16	27.04	31.90
198	Indira Sugandhidhar	120.95	86.9	5.32	99	1.67	41.65	11.5	7.5	25.14	154.9	22.27	7.5	0.77	20.482	16.56
199	Kasturi	129.16	92.46	6.14	78	1.54	39.64	11.5	7.5	28.21	129.8	22.44	9.25	0.22	45.94	14.49
	Ptb 35(Annapurna)	117.88	78.22	3.20	81	2.55	49.01	11.3	7.3	25.36	199.8	22.61	6.33	1.43	22.68	32.76
	THOTTACHEERA	163.61	126.98	3.74	76	1.48	49.71	14.4	10.4	25.42	96.3	22.55	7.04	1.43	25.85	15.22
	KARUTHADUKKAN	157.338	124.53	4.23	82	1.62	47.04	16.5	12.5	28.6	111	23.09	7.84	1.41	23.40	9.69
	CHOMALA	131.78	100.83	3.64	78	1.77	36.54	16.5	12.5	23.32	66	21.37	5.28	0.37	22.55	8.00
	Cul KAUM-20	138.31	79.33	5.15	115	1.39	67.48	11.3	7.3	25.07	42.5	23.09	5.57	1.03	24.44	15.1
	Cul M-20	111.81	86.85	2.82	96	1.5	30.25	12.3	8.3	22.31	85.6	22.32	7.39	0.89	22.87	15.07
	Mo 7 (Karthika)	103	88.39	3.78	106	1.37	48.38	11.9	7.9	21.56	50.7	22.76	7.33	2.47	21.22	14.69

Longer length of panicle was observed in PGC 95 (Cul 8711), PGC 91 (TKM 6), PGC 9 (Onam), PGC 7 [Ptb 46 (Jayathi)]), Karuthadukkan, PGC 33 (Cul 8714), PGC 199 (Kasturi), PGC 72 (Reymuthika), PGC 194 (CSR 27) and PGC 15 (Dular).

The grains per in the core set was high for PGC 7 [Ptb 46 (Jayathi)]), Ptb 35 (Annapurna), PGC 91 (TKM 6), PGC 157 (Moncompu 519), PGC 194 (CSR 27), PGC 167 (Cul 9410-3-Sel2), PGC 191 (Kasturi), PGC 72 (Reymuthika) and PGC 28 (Cul 8757).

PGC 73 (Karangi), PGC (Cul 8757), PGC 49 [Ptb 7 (Parambuvattan)], Karuthadukan, PGC 194 (CSR 27), PGC 157 (Moncompu 519), PGC 194 (CSR 27), PGC 126 (Cul AM 10-24), PGC 15 (Dular), PGC 167 (Cul 9410-3-Sel2), PGC 50 [Ptb 10 (Thekkencheera)] and PGC 9 (Onam) were identified for high test weight.

4.3.3 Phenotypic diversity in core set *vs* Base collection

The Shannon – Weaver diversity index (H') calculated to compare the diversity for the 65 traits (41 qualitative traits) and (24 quantitative traits) in the Base germplasm and core set are presented in the Table 13. This index is used in genetic studies as a measure of both allelic richness and allelic evenness. A low H' indicates an extremely unbalanced frequency of classes for an individual trait and a lack of genetic diversity. Shannon - Weaver index (H') for the 65 traits studied is presented in Table 13.

The H' indices for all the traits in core set (C) were similar to that in Base collection (B) accessions. Among the qualitative traits lemma and palea colour had highest H' value in both Base collection and core set (B =1.75, C =2.05). However the H' value was zero for presence / absence of auricles, collar and ligules in leaf, shape of ligule, attitude of flag leaf blade (early observation), exsertion of panicle, presence and nature of secondary branching in panicle and curvature of main axis of

Table 13. Diversity index (H') in core set *vs* Base collection

Sl. No.	Trait	Diversity index (H') [Shannon-Weaver Index]		Diversity (%)
		Base collection	Core set	
Qualitative traits				
1.	Coleoptiles colour	1.202	1.285	106.90
2.	Basal leaf: Sheath colour	1.265	1.391	109.96
3.	Leaf: Intensity of green colour	1.519	1.479	97.36
4.	Leaf: Anthocyanin colouration	1.195	1.267	106.02
5.	Leaf: Distribution of anthocyanin colouration	1.386	1.635	117.96
6.	Leaf sheath: Anthocyanin colouration	1.196	1.267	105.93
7.	Leaf sheath: Intensity of anthocyanin colouration	1.240	1.251	100.88
8.	Leaf: Pubescence of blade surface	1.432	1.365	95.32
9.	Leaf: Auricles	0.000	0.000	0
10.	Leaf: Anthocyanin colouration of auricles	1.041	0.000	0
11.	Leaf: Collar	0.000	0.000	0
12.	Leaf: Anthocyanin colouration of collar	1.041	0.000	0
13.	Leaf: Ligule	0.000	0.000	0
14.	Leaf: Shape of ligule	0.000	0.000	0
15.	Leaf: Colour of ligule	1.041	0.000	0
16.	Flag leaf: Attitude of blade (Early observation)	0.000	0.000	0
17.	Flag leaf: Attitude of blade (Late observation)	1.330	1.325	99.62
18.	Culm: Attitude	1.279	1.300	101.64
19.	Lemma: Anthocyanin colouration of keel	1.046	0.000	0
20.	Lemma: Anthocyanin colouration of area below apex	1.046	0.000	0
21.	Lemma: Anthocyanin colouration of apex	1.281	1.431	111.70
22.	Spikelet: Colour of stigma	1.201	1.267	105.49
23.	Stem: Anthocyanin colouration of nodes	1.195	1.267	106.02
24.	Stem: Intensity of anthocyanin colouration of nodes	1.058	0.000	0
25.	Stem: Anthocyanin colouration of internodes	1.195	1.267	106.02
26.	Panicle: Curvature of main axis	0.000	0.000	0
27.	Spikelet: Density of pubescence of lemma	1.375	1.337	97.23
28.	Spikelet: Colour of tip of lemma	1.202	1.267	105.40

Table 13. Diversity index (H') in core set *vs* Base collection (contd...)

Sl. No.	Trait	Diversity index (H') [Shannon-Weaver Index]		Diversity (%)
		Base	Core set	
29.	Lemma and Palea colour	1.747	2.046	117.11
30.	Panicle: Awns	1.123	1.224	108.99
31.	Panicle: Colour of awns	1.098	1.823	166.02
32.	Panicle: Distribution of awns	1.517	1.211	79.82
33.	Panicle: Presence of secondary branching	0.000	0.000	0
34.	Panicle: Secondary branching	0.000	0.000	0
35.	Panicle: Attitude of branches	1.134	1.166	102.82
36.	Panicle: Exsertion	0.000	0.000	0
37.	Time of maturity	1.328	1.411	106.25
38.	Leaf: Senescence	1.062	1.102	103.76
39.	Sterile Lemma: Colour	1.069	0.000	0
40.	Decorticated grain: Shape	1.030	1.477	143.39
41.	Decorticated grain: Colour	1.675	1.580	94.32
	Mean ± SE	0.964±0.082	0.840±0.106	84.25
Quantitative traits				
1.	Seedling shoot length (cm)	3.519	3.689	104.83
2.	Seedling root length (cm)	2.182	2.326	106.59
3.	Seedling vigour index	2.208	2.269	102.76
4.	Total seedling biomass (g)	2.018	2.170	107.53
5.	Plant height (cm)	2.201	2.385	108.35
6.	Culm length (cm)	2.174	2.244	103.21
7.	Stem thickness (mm)	2.169	2.244	103.45
8.	Days to heading	2.057	2.108	102.47
9.	Leaf blade width (cm)	1.562	1.686	107.93
10.	Leaf blade length (cm)	2.180	2.197	100.77
11.	Total tillers per plant	1.691	1.832	108.33
12.	Productive tillers per plant	1.691	1.832	108.33
13.	Panicle length (cm)	1.502	1.617	107.65
14.	Spikelet per panicle	2.157	2.310	107.09
15.	Grain per panicle	2.141	2.310	107.89
16.	Test weight of grain (g)	2.099	2.224	105.95
17.	Grain length (mm)	2.078	2.257	108.61
18.	Grain width (mm)	1.872	2.153	115.01
19.	Grain thickness (mm)	1.909	2.141	112.15
20.	Decorticated grain length (mm)	2.078	2.257	108.61
21.	Decorticated grain width (mm)	1.872	2.153	115.01
22.	Decorticated grain thickness (mm)	1.909	2.141	112.15
23.	Straw yield per plant (g)	1.046	1.166	111.47
24.	Grain yield per plant (g)	2.192	2.177	99.31
	Mean ± SE	2.021±0.087	2.162±0.088	107.32
	Overall mean ± SE	1.4920.528	1.501±0.660	100.54

panicle, in both the populations. In core set, anthocyanin colouration of auricles, collar, ligule, keel and area below apex of lemma, sterile lemma and nodes also recorded a value of (0.00).

Among all the quantitative traits, seedling shoot length recorded the highest H' index in both Base collection and core set (B=3.519, C=3.689). Similarly, straw yield per plant recorded the lowest H' index in both Base collection and core set (B=1.046, C=1.166).

The average H' values for 41 qualitative traits were 0.840 ± 0.106 and 0.96 ± 0.082 in core set and Base collection respectively. The average of H' values for 24 quantitative traits in core set were 2.162 ± 0.087 and that in Base collection was 2.021±0.088. The overall mean of H' values for all the 65 traits were 1.501±0.660 and 1.492±0.528 in core set and Base collection, respectively. The total per cent of diversity in core set over Base collection with respect to qualitative traits was 87.08 compared to 107.32 per cent in quantitative traits. The overall diversity per cent in core set over Base collection, considering both quantitative and qualitative traits, was 100.54%.

Discussion

5. DISCUSSION

Germplasm is the total gene pool of a species consisting of landraces, advanced breeding lines, popular cultivars, wild and weedy relatives. It forms the raw material for any crop improvement program. The basic requirement for success of plant breeding programs is the availability of variation in plant species. Germplasm collection contains a vast reservoir of genetic variability, which would help to broaden the genetic base of the cultivars. Knowledge on nature and extent of genetic variation, diversity available in the germplasm helps the breeder to plan sound breeding programmes. However, identification of potential parental material from the diverse collections is often tedious, owing to the huge size of germplasm collections. This could be overcome if a subset of genotypes or the core set that has funneled out or retained the maximum diversity in the original base population can be drawn. The core set will thereby help the breeder to pin-point and effectively select the appropriate genotype based on the objective of the crop improvement programme.

In the present investigation, the short duration germplasm collection held in KAU comprising of 160 accessions (Base collection) were evaluated for 41 qualitative traits and 24 quantitative traits as per descriptor of rice (Rani *et al.*, 2004; IRRI, 2007). Results of the present investigations are discussed under the following headings:

5.1 Characterization and evaluation of Base collection

5.1.1 Geographical distribution of accessions in Base collection

5.1.2 Variability studies in Base collection

5.1.2.1 Variability studies in Base collection for qualitative traits

5.1.2.2 Variability studies in Base collection for quantitative traits

5.2 Formation of core set

5.3 Comparison of core set *vs* Base collection

5.3.1 Geographical distribution of accessions in core set *vs* Base collection

5.3.2 Variability in core set *vs* Base collection

5.3.2.1 Frequency distribution of qualitative traits in core set *vs* Base collection

5.3.2.2 Variability in quantitative traits in core set *vs* Base collection

5.3.2.3 Diversity in core set *vs* Base collection

5.1 Characterization and evaluation of Base collection

5.1.1 Geographical distribution of accessions in Base collection

The short duration germplasm collection (160 accessions; Base collection) held in KAU comprised of accessions from within and outside the country. However, majority were from India and all the four accessions {(IR 36), PGC 20 (IR 1552), PGC 41 (IR100) and PGC 38 [T(N)1} from outside the country were from IRRI, Philippines. More than 3/4th of the Indian collection was from Kerala. Accessions from the neighbouring states viz., Tamil Nadu, Andhra Pradesh and Maharashtra constituted the major group from outside the state. Accessions from north India (Haryana and Uttar Pradesh) and eastern part of the country (Odisha and Paschim Banga) have also found a place in collection. The geographical distribution of accessions in the Base collection reflects the emphasis laid on assembling the variability of germplasm within the state.

5.1.2 Variability studies in Base collections

5.1.2.1 Variability studies in Base collection for qualitative traits

Characterization of Base collection with respect to 41 qualitative traits as per Rani *et al.*, 2004 pointed out that there was no variability among the 160 accessions with respect to nine traits viz., presence of leaf auricle, collar and ligule, shape of ligule, attitude of flag leaf blade (early observation), curvature of main axis of panicle, presence and nature of secondary branching in panicles and panicle exsertion. Hence, these traits are not useful in grouping of accessions in the Base collection studied.

The accessions in the Base collection could be categorized based on the presence of anthocyanin pigmentation and the gradation in pigmentation found in various plant parts *viz.,* coleoptile, basal leaf sheath, leaves, nodes, internodes, auricles, ligule, lemma, stigma and awns. Therefore, the above traits can be used as a basis for distinguishing and grouping of accessions for further evaluation. Several workers have exploited the variability with respect to anthocyanin pigmentation for classification of genotypes (Thimmanna *et al.*,2000; Zafar *et al.*, 2004; Ramakrishna *et al.*, 2006; Hien *et al.*, 2007; Alcasid *et al.*, 2008 and Banumathy *et al.*, 2012).

The Base collection could be grouped into distinct classes based on the presence of wide variability with respect to pubescence of leaf surface, attitude of flag leaf (late observation), culm attitude, time of maturity, distribution of awns on panicle, colour of lemma and palea and sterile lemma, shape and colour of decorticated grain. Vanangamudi *et al.* (1988); Sinha *et al.* (1990); Caldo *et al.* (1996); Thimmanna *et al.* (2000); Zafar *et al.* (2004); Hien *et al.* (2007); Alcasid *et al.* (2008); Bora *et al.* (2008) and Banumathy *et al.* (2012) have reported the usefulness of the above traits in grouping of genotypes.

5.1.2.2 Variability studies in Base collection for quantitative traits

Analysis of variance for 24 quantitative traits revealed highly significant differences among 160 germplasm accessions in Base collection for all the traits. The presence of such wide variability in yield and yield components in rice have been reported by earlier workers (Girish *et al.*, 2006; Sankar, 2006; Vanaja and Babu, 2006; Karim *et al.*, 2007; Padmaja *et al.*, 2008; Chakraborty and Chakraborty, 2010; Rathi *et al.*, 2010; Subbaiah, 2011; Akinwale *et al.*, 2011; Sadeghi, 2011; Selvaraj *et al.*, 2011 and Seyoum *et al.*, 2012). The results indicated that the Base collection under present study was highly diverse and provides ample scope for selection of superior and desirable genotypes for further crop improvement in rice.

The phenotypic coefficient of variation (PCV) was higher as compared to genotypic coefficient of variation (GCV) indicating the influence of environment on expression of these traits. High PCV and GCV were recorded for all the traits except plant height, culm length, days to heading, spikelets per panicle and grains per panicle. Plant height had recorded low PCV and low GCV (Laxuman *et al.*, 2010; Akinwale *et al.*, 2011; Seyoum *et al.*, 2012) whereas; culm length and days to heading recorded only moderate values. Similar results with respect to culm length and days to heading was reported by Reddy (2000); Sedeek *et al.* (2009); Selvaraj *et al.* (2011) and Rani *et al.* (2012). Spikelets per panicle had recorded moderate PCV and low GCV which is in contrast to the findings of Sharma and Sharma (2007) and Prasad *et al.* (2009). In accordance to the reports of Laxuman *et al.* (2010), high PCV and low GCV for grains per panicle in the Base collection indicated high influence of environment on expression of this trait.

High heritability coupled with high genetic gain obtained for all traits except plant height, spikelets per panicle and grains per panicle indicated that the traits are governed by additive gene action offering scope for improvement of these traits through direct selection. Similar high estimates of heritability and genetic gain with

respect to various plant and grain traits have been reported (Ali *et al.*, 2009; Reddy, 2000; Padmaja *et al.*, 2008; Prabha *et al.*, 2009; Selvaraj *et al.*, 2012).

However, both plant height and grains per panicle had recorded moderate genetic gain while the heritability of this trait varied from high (plant height) to moderate (grains per panicle) indicating moderate response to selection. Occurrence of high heritability and moderate genetic gain for plant height have been reported by Laxuman *et al.* (2010); Akinwale *et al.* (2011); Babu *et al.* (2012b) and Seyoum *et al.* (2012). The results on grains per panicle as evident in the study are in confirmation with the reports of Francies *et al.* (2012) and Seyoum *et al.* (2012).

The low heritability and genetic gain observed in spikelets per panicle indicated that the trait is highly influenced by environment and the ineffectiveness of selection for improvement of this trait. This is in contradiction with the result of Sharma and Sharma (2007) and Prasad *et al.* (2009) who reported high heritability and genetic gain for spikelets per panicle.

5.2 Formation of core set

Appropriate choice of parental genotypes is essential for effective and efficient plant breeding programmes. The utilization of germplasm collections could be enhanced by deployment of useful diversity in core set. In addition to this, formation of core collection is also an area of much interest in the field of allele mining. A core set is a subset of the entire accession in a germplasm. This set, captures most of the available genetic diversity of the species (Brown, 1989a). In the present investigation, based on the data on 24 quantitative traits, a core set of 34 accessions was formed from the Base collection (160 short duration accessions) held in the germplasm collection of KAU using software called PowerCore (v.1.0).

The core set formed, represented 21.25 per cent of the Base collection. Brown (1989a) had proposed that an ideal core collection size should be about 10 per cent of

the total collection that would maintain over 70 per cent of the alleles over the collection. However, according to Xiao-ling *et al.* (2011) the ratio of a core collection to its initial collection may be smaller when the size of the initial collection is larger and larger when the size of its initial collection is relatively smaller, because, a larger size collection may have more repetition of resources. The immense value of core collection in crop improvement programs have been emphasized by several workers as it can be evaluated extensively and more economically for desirable traits due to its reduced size (Weiguo *et al.*, 2010; Xiaobai *et al.*, 2010; Zhang *et al.*, 2011; Rao *et al.*, 2012).

The mean difference (MD) per cent, variance difference (VD) per cent, the coincidence rate (CR) per cent and the Variable rate (VR) per cent are designed to comparably evaluate the property of core collection and Base collection. Over the entire 24 qualitative traits, the MD per cent was far less than the significance level of 20 per cent as suggested by Hu *et al.* (2000). The MD per cent of the core set was similar to the average of the core collection developed by Kim *et al.* (2007) and Agrama *et al.* (2009). The VD per cent of the core was larger than that reported by Kim *et al.* (2007) and Agrama *et al.* (2009) as the variance of 22 out of 24 traits was greater in the core set than that in the base collection.

The VR per cent of the core set was larger than that reported by Kim *et al.* (2007). The VR per cent compares the coefficient of variation values of the 24 quantitative traits measured in the core set with the base collection and determines how well the variance is being represented in the core set. According to Hu *et al.* (2000), more than 100 per cent of VR per cent is required for a core collection to be a representative of original collection. Since, VR per cent of the core set was 128.37 per cent, the core set of 34 accessions can be considered a true representative of the base collections from which it has originated. The CR per cent over the 24 traits was high (96.34 per cent), indicating homogenous distribution of quantitative traits in the core set and base collection. According to Kim *et al.* (2007), a CR per cent larger

than 80 indicated homogenous distribution of ranges for the traits studied in core set are well represented when compared to the core collection. The CR per cent in the core collection was similar to the findings of Hu *et al.* (2000) and Agrama *et al.* (2009).

According to Hu *et al.* (2000); Kim *et al.* (2007) and Agrama *et al.* (2009), core collection with low MD% (<20%) and VD%, large CR% (>80%) and VR% (>100%) were considered to provide a good representation of the genetic diversity of the initial collection. Therefore, this core set could be considered as a sound representation of the genetic diversity found in the short duration rice germplasm accessions held in KAU.

The core set comprised of traditional rice varieties (Thottacheera, Karuthadukkan, Chomala), pureline selections of land races {PGC 49 [Ptb 7 (Parambuvattan)], PGC 50 [Ptb 10 (Thekkencheera)]}, high yielding varieties [Ptb 35 (Annapurna), PGC 7 [Ptb 46 (Jayathy)], PGC 9 (Onam) , PGC 14 (Tulasi), Mo7 (Karthika) etc] and several breeding lines [PGC 28 (Cul 8757), PGC 33 (Cul 8714), PGC 145 (Cul 90-04), PGC 167 (Cul 9410-3 Sel 2)] to name a few. It also included varieties from outside the state of Kerala.

Incidentally, PGC 49 [Ptb 7(Parambuvattan)] and traditional rice varieties Thottacheera, Karuthadukkan and Chomala are varieties recommended for uplands of Kerala. PGC 50 [Ptb 10 (Thekkencheera)] a pureline selection from land race Thekkencheera, is resistant to gall midge, BPH, stem borer and has high photosynthetic efficiency. It has been used repeatedly as donor for various traits in rice breeding programmes nationwide (Kumary and Francies, 2003).

Ptb 35 (Annapurna) is reported to be the first short duration dwarf variety released in Asia through hybridization and selection. It was released from Regional Agricultural Research Station, KAU, Pattambi in 1966 from a cross T(N)1 / Ptb 10. PGC 7 [Ptb 46 (Jayathy)] is a white kernelled high yielding variety released from the

same station. It had out-yielded the international check IR 36 at 43 locations over 18 countries including East Asia, South Asia, North Africa, and Latin America in the International Rice Testing Programme of 1983-84 (Karunakaran and Rosamma, 2003).

5.3 Comparison of core set *vs* Base collection

An attempt was made to compare the core set and the Base collection with respect to geographical distribution and variability pertaining to the 41 qualitative traits and 24 quantitative traits. Frequencies for distribution of accessions in the core set and Base collection based on geographical origin and all the qualitative traits were tested by χ^2. A homogeneity test for variance (F test) and a One sample t-Test for means were applied to test for significant differences between the estimates of each quantitative trait in core set and Base collection. The phenotypic diversity in the core set and Base collection was also assessed using Shannon- Weaver diversity index.

5.3.1 Geographical distribution of accessions in core set *vs* Base collection

$\chi 2$ probabilities for frequency distribution of accessions in the core set and Base collection based on geographic origin were non significant for all the 9 geographic locations ($P = 0.01$) . This indicated representative similarity and that each location was represented adequately. The overall $\chi 2$ was also non significant ($P = 0.01$).

The core set comprising of 34 accessions contained entries from within India alone unlike the Base collection which had 4 accessions from IRRI, Philippines. As in Base collection, the core set too comprised of entries from within and outside the state of Kerala. Predominance of accessions from Kerala was found both in core set and Base collection. This reflected the emphasis laid on assembling the variability in germplasm within the state. In contrast to Base collection, the core set included accessions only from the states of Kerala, Tamil Nadu, Andhra Pradesh, Maharashtra,

Odisha and Haryana. None of the accessions from Uttar Pradesh and Paschim Banga were represented in the core set. The number of accessions from Maharashtra and Andhra Pradesh in core set was greater than those from Tamil Nadu, Haryana and Odisha.

Incidentally, in core set, accessions from Tamil Nadu were less in number compared to Base collection. This large exclusion of accessions from Tamil Nadu might be due to the redundancy or greater similarity in accessions owing to close geographical origin. Slight dissimilarity in distribution of accessions according to their geographic origin in the Base collection and core set may be attributed to closeness in geographic location from which the accessions in the Base collection were collected. Brocke *et al.* (2003) had cited farmers' seed management and regional exchange activities as a reason for regional similarity.

Rabbani *et al.* (1998) had reported absence of association between classification of genotypes based on morphological traits and geographic origin. Shafaeddin (2002) also found no relationship between the genetic diversity and geographical classification when all quantitative traits were considered. Burnham *et al.* (2002) assumed that a distinct genetic diversity did exist within South Korean soybean landraces but it was not dependent on the geographical relationship of the eight provinces.

5.3.2 Variability in core set *vs* Base collection

5.3.2.1 Variability for qualitative traits in core set *vs* Base collection

Qualitative traits are useful for grouping of accessions, as they show high heritability and stable expression. Further, if qualitative traits show association with yield components, it can serve as a marker in selection process. The goodness of fit of frequency distribution of accessions in core set and Base collection with respect to

various subclasses of each of the 41 qualitative traits studied was tested using chi-square test (χ^2).

χ^2 probabilities for frequency distribution of accessions in the subclasses of all 41 qualitative traits were non significant. This indicated that the core set and Base collection were on par with respect to the frequency distribution of accessions in the sub-classes of all the 41 qualitative traits. Uniform distribution of classes in the core set and Base collection in turn indicated that the sampling technique to constitute the core set was appropriate and that the core set represented the Base collection for qualitative traits. This also pointed out that the core set had captured the variability in the Base collection with respect to all the 41qualitative traits.

As there was no variation in Base collection with respect to nine traits viz., leaf auricle, leaf collar, leaf ligule, shape of ligule, attitude of flag leaf blade (early observation), curvature of main axis of panicle, presence and nature of secondary branching in panicles and panicle exsertion, the core set too was monomorphic for these traits. Hence, these traits cannot be used for grouping of accessions in the Base collection studied. In groundnut, Swamy *et al.* (2006) also found monomorphism for flower color and leaf hairiness. According to Rani *et al.* (2004) the collection of varieties should be divided into groups to facilitate the assessment of distinctness and the traits which are suitable for grouping purposes are those which do not vary, or vary only very slightly, within a variety.

As in Base collection, the accessions in core s*et al*so could be categorized based on the presence of anthocyanin pigmentation and the gradation in pigmentation found in various plant parts viz., coleoptile, basal leaf sheath, leaves, nodes, internodes, auricles, ligule, lemma, stigma and awns. However, accessions with anthocyanin pigmentation in auricles, collar, ligule, Lemma – keel and area below apex where not included in the core set. This may be because the core set has been formed on the basis of 24 quantitative traits studied and not based on 41 qualitative

traits. Such slight differences in frequencies between the core collection and original population has been reported by Upadhyaya *et al.* (2002a) and Cho *et al.* (2008). According to Yan *et al.* (2007) lower correlation for some of the descriptors do not necessarily indicate that the core collection is not representative of the original collection it was derived from.

5.3.2.2 Variability for quantitative traits in core set *vs* Base collection

There existed a large variation among the accessions within the core set and Base collection for the 24 quantitative traits studied. In both core set and Base collection, high level of genetic variation was observed for grains per panicle, spikelets per panicle, culm length, straw yield per plant, days taken to heading , grain yield per plant, plant height and length of leaf blade. These traits could be utilized efficiently for tailoring new plant varieties. However, in both the populations, variability existed but was comparatively low for grain and decorticated grain dimensions, stem thickness and width of leaf blade.

One sample t-test was applied to test the homogeneity of means of each quantitative trait between the Base collection and core set and analyze if significant differences exist between them. The test revealed that the mean of the two populations did not differ significantly from each other. The results suggest that mean components of core set remains at par with the Base collection for all the traits studied and that the core set represented the Base collection for each of the 24 quantitative traits. Unlike the findings in the study, several workers (Yan *et al.*, 2007 and Agrama *et al.*, 2009) have reported differences between the mean performance of several traits in core collection and initial population from which it was derived from.

In general, higher values of variance for all the 41 quantitative traits were observed in core set when compared to the Base collection. This indicated that the core set retained a large variation in the Base collection. Variance values were

compared using Levene's test and we found no significant difference for all the traits under study. These results suggest that, core set is as diverse as the Base collection even at the individual trait level and it has captured the variance in the Base collection. The usefulness of core collection in capturing the diversity in original population has been well demonstrated and documented in several crops (Lasa *et al.*, 2001 and Ahmad *et al.*, 2008 in barley, Upadhyaya *et al.*, 2002b and Meena *et al.*, 2010 in chickpea, Swamy *et al.*, 2006 in groundnut, Cho *et al.*, 2008 in soybean Upadhyaya *et al.*, 2011 in bajra, Vymyslicky *et al.*, 2012 in alfalfa).

On the basis of mean performance for grain yield and other economic traits, seven diverse short duration superior genotypes, namely, PGC 28 (Cul 8757), PGC 49 [Ptb 7 (Parambuvattan)],), PGC 194 (CSR 27), PGC 50 [Ptb 10 (Thekkencheera)], PGC 126 (Cul AM- 10-24), PGC 9 (Onam) and PGC 33 (Cul 8714) could be identified. Each of these genotypes was exceptionally good for one or more traits, with an acceptable level for other traits. Therefore, the genotypes may be involved in crossing programs to recover transgressive segregates.

5.3.3 Phenotypic diversity in core set *vs* Base collection

The core set should include as much genetic diversity as possible. It provides the user a set of genetically distinct accessions. The grouping of similar genotypes depends on the level of dissimilarity among them. The Shannon-Weaver diversity index (H') (Shannon and Weaver, 1949) was used to measure and compare the phenotypic diversity for qualitative and quantitative traits in the core set and Base collection. The index is used in genetic studies as a convenient measure of both allelic richness and allelic evenness. The low (H') indicates an extremely unbalanced frequency of classes for an individual trait and a lack of genetic diversity.

The diversity index values (H') were variable among the traits in core set and Base collection.

Among morphological descriptors, lemma and palea colour recorded the highest index values (H') both in Base collection and core set. Variation in colour of awns was the maximum in core set presenting larger diversity than in Base collection. Clearly, there was a much higher proportion of variation in anthocyanin colour of awns, stigma, sterile lemma, lemma and palea colour, lemma apex, nodes, internodes and leaves, distribution of awns, decorticated grain shape and time of maturity, in core set than in Base collection. However, the diversity with respect to, anthocyanin pigmentation of leaf auricles, collar, ligule, keel, nodes, sterile lemma, keel and area below apex of lemma and the intensity of pigmentation in internodes in Base collection were not represented in core set. Base collection, presented larger diversity with respect to decorticated grain shape, distribution of awns in panicles, pubescence of leaf surface and lemma, attitude of flag leaf (late observation) and intensity of greenness in leaf.

In general, the average diversity estimate with respect to qualitative traits in core set was slightly less compared to the Base collection as the core set was formed on the basis of variation in quantitative traits. For most core collections constructed, phenotypic values of traits were used and representative evaluation was mainly based on them (Holbrook *et al.*, 1993; Li *et al.*, 2000; Xu *et al.*, 2004; Zhang *et al*, 2004). Clustering based on phenotypic values may not be accurate, because of environment effects and the core entries sampled are not perfect representation of the initial collection (Zhu 1993, Ji, 2000 and Yao *et al.*, 2008). They suggest the use of molecular markers to provide the repertoire for assessing genetic diversity at the DNA level. However, such DNA fingerprinting methodologies to develop minicore collections have been attempted only on a smaller population (the core collection) rather than the large original collection. Minicore collections have been developed in a number of crops such as rice (Ebana *et al.*, 2008; Xiaobai *et al.*, 2010 and Rao *et al.*, 2012) chickpea (Upadhyaya and Ortiz, 2001), groundnut (Upadhyaya *et al.*,

2002b), pigeonpea (Upadhyaya *et al.*, 2006), sorghum (Upadhyaya *et al.*, 2009), and finger millet (Upadhyaya *et al.*, 2010).

However, as the average H` for all 41 qualitative traits in the core set was comparable to that in the Base collection, it suggested that the core set has captured adequate diversity from the Base collection with respect to qualitative traits. It may be concluded that the genetic variation available in the Base collection has been almost preserved in the core set.

Among 24 traits, seedling shoot length had the highest index values (H') in both Base collection and core set. The H' indices and the per cent diversity of core set with respect to quantitative traits was slightly higher than Base collection except for grain yield, indicating that the core set is a true representative of diversity in Base collection. Theoretically, the diversity of a core collection will not exceed that of an initial collection from which the core is established. Interestingly, in the study, the polymorphism was higher in core set than in Base collection. The reason for this is attributed to the fact that a combination of traitistics has been used to choose the accessions in the core set, which may favour rare alleles with lower frequencies (Yao *et al.*, 2008). This implied that, there was a higher level of genetic diversity conserved in the core set and that the core set well represented the Base collection.

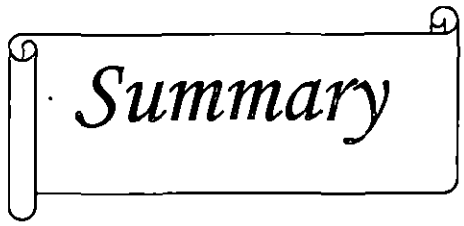
The overall mean of (H') values for the qualitative and quantitative traits in core set was similar to Base collection. The overall diversity per cent in core set over Base collection was 100.54 per cent. This indicated that the diversity present in the Base collection was well represented in the core set formed. This result is in accordance with the findings of Xiao-ling *et al.* (2011) in rice.

Summarizing these comparisons, we can conclude that the core set seems to be a good subset of the short duration germplasm accessions in rice held in Kerala Agricultural University and represents a good sample of the existing trait diversity in the Base collection.

5.3.4 Future line of work

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

- The diverse core set can be utilized for identifying promising parents in breeding programmes aiming at improving yield and yield attributes.
- The value of the core set can be enhanced by traitizing it for biochemical, milling and cooking qualities, biotic and abiotic stresses.
- Mini core formation using molecular markers can be attempted to further remove redundancy.


Summary

6. SUMMARY

Rice (*Oryza sativa* L.) is the staple food for over half the world's population. With 44.62 million hectares under rice, India ranks first in area under rice cultivation and second next to China, in rice production. Rice occupies the prime place among the food crops cultivated in Kerala. Diversity of cropping systems, the edaphic and climatic variations found among and within different regions have resulted in vast diversity of forms in rice crop in the state.

The genetic diversity of the particular species is preserved for future needs through germplasm collections. However, fruitful utilization of this diversity for crop improvement programmes, require, systematic cataloguing, evaluation and Characterization of the collection. In practice, plant breeders are interested in having fairly small numbers of genotypes which possess, or are likely to possess the traits needed in their breeding programmes. Formation of core collections – a subset of the germplasm collection improves accessibility of these collections to users.

Considering the above, an attempt was made in the present study to form a core set using PowerCore (v.1.0) software, based on the variability in 24 quantitative traits present in the 160 short duration germplasm accessions (Base collection) held under Kerala Agricultural University. The geographic distribution of accessions, variability and genetic diversity present in the base collection and core set with respect to 41 qualitative traits and 24 quantitative traits were compared to assess if the core set was a true representative of the Base collection.

The salient findings of the study are summarized below:

1. Of the 160 accessions in the Base collection, majority were from India. All four accessions {PGC 17 (IR 36), PGC 20 (IR 1552), PGC 41 (IR100) and PGC 38 [T(N)1} from outside the country were from IRRI, Philippines. More than seventy five per cent of the Indian collection was from Kerala.

2. Characterization of Base collection with respect to 41 qualitative traits pointed out that there was high variability among the 160 accessions with respect to all the traits studied except the nine traits *viz.*, leaf auricle, leaf collar, leaf ligule, shape of ligule, attitude of flag leaf blade (early observation), curvature of main axis of panicle, presence and nature of secondary branching in panicles and panicle exsertion. The above mentioned monomorphic traits are not useful in grouping of accessions in the Base collection studied. However, the high variability with respect to the pigmentation in different plant parts, pubescence of blade leaf surface, attitude of flag leaf and culm, presence and distribution of awns and decorticated grain shape was helpful in grouping of accessions.

3. Analysis of variance for 24 quantitative traits revealed highly significant differences among 160 germplasm accessions for all the traits.

4. The phenotypic coefficient of variation was high compared to genotypic coefficient of variation, indicating the influence of environment on expression of these traits. High PCV and low GCV for grains per panicle in the Base collection indicated higher influence of environment on expression of this trait.

5. High heritability coupled with high genetic gain obtained for all traits except plant height, spikelets per panicle and grains per panicle indicated that the traits are governed by additive gene action offering scope for improvement of these traits through direct selection.

6. A core set of 34 accessions was formed based on 24 quantitative traits using PowerCore (v.1.0) software from the Base collection (160 short duration accessions) held in the germplasm collection of KAU. The core set formed, represented 21.25 per cent of total accessions in the Base collection.

7. The core set comprised of traditional rice varieties (Thottacheera, Karuthadukkan, Chomala), pureline selections of land races [PGC 49 - Ptb 7(Parambuvattan), PGC 50 - Ptb 10 (Thekkencheera)], high yielding varieties [Ptb 35 (Annapurna), PGC 7 [Ptb 46 (Jayathy)], PGC 9 (Onam), PGC 14 (Tulasi), Mo7 (Karthika) etc] and several breeding lines [PGC 28 (Cul 8757), PGC 33 (Cul8714), PGC 145 (Cul 90-04), PGC 167 (Cul 9410-3 Sel 2)] of Kerala state.

8. The $\chi 2$ probabilities for frequency distribution of accessions in the core set and Base collection based on geographic origin were non significant for all the nine geographic locations (P = 0.01) indicating that each location was represented adequately.

9. The goodness of fit of frequency distribution of accessions in core set and Base collection with respect to various subclasses of each of the 41 qualitative traits studied was tested using chi-square test (χ^2). The results indicated that the core set and Base collection were on par with respect to the frequency distribution of accessions in the sub-classes of all the 41 qualitative traits.

10. One sample t-test applied to test the homogeneity of means of each quantitative trait (24 nos.) between the Base collection and core set revealed that the mean of the two populations did not differ significantly from each other.

11. Results of Levene's F test to compare the variance values of each of the 24 quantitative traits between core set and Base collection revealed that, core set was as diverse as the Base collection and that it has captured adequately the variance in the Base collection.

12. Shannon-Weaver diversity index (H') values for the 41 qualitative and 24 quantitative traits in core set was similar to Base collection and the overall diversity per cent in core set over Base collection was 100 per cent. This indicated that the diversity present in the Base collection was well represented in the core set formed.

The study revealed that the core set formed was a good subset of the short duration germplasm accessions in rice held in Kerala Agricultural University and represented a true sample of the existing trait diversity in the Base collection. Hence, this core set could be effectively utilized for crop improvement programmes in rice in future.

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Appendices

Appendix I : Estimates of mean for quantitative traits in the Base collection

Sl. No.	PGC No.	Accession	Seedling shoot length (cm)	Seedling root length (cm)	Seedling vigour index	Total seedling biomass (g)	Plant height (cm)	Culm length (cm)	Stem thickness (mm)	Days to heading	Leaf blade width (cm)	Leaf blade length (cm)	Total tillers per plant	Productive tillers per plant
1	1	Annapoorna	25.20	4.43	5.69	0.75	100.92	62.86	3.340	76	1.35	40.81	14.4	10.4
2	2	Ptb 36 (Rohini)	29.61	5.42	5.46	0.98	116.51	84.04	3.942	81	1.53	38.73	12.8	8.8
3	3	Ptb 38 (Triveni)	30.31	4.01	7.56	0.89	113.38	77.86	3.863	80	1.48	35.47	11.3	7.3
4	4	Ptb 39 (Jyothi)	26.81	4.55	5.89	1.03	115.43	82.65	3.355	86	1.45	41.92	13.0	9.0
5	5	Ptb 45 (Matta Triveni)	27.11	6.25	4.34	1.11	127.05	86.84	3.175	79	1.40	48.96	16.1	12.1
6	6	ADT 37-11	26.04	4.17	6.24	0.71	128.89	97.95	3.929	79	1.46	37.27	11.1	7.1
7	7	Ptb 46 (Jayathy)	23.76	4.86	4.89	0.72	120.18	75.90	5.515	86	2.94	36.28	11.7	7.7
8	8	Bhagya	27.13	4.07	6.67	0.61	130.80	85.59	2.894	86	1.41	40.90	11.9	7.9
9	9	Onam	23.60	3.34	7.07	0.58	117.49	81.87	3.463	76	1.61	38.29	10.9	6.9
10	11	Ptb 49 (Kairaly)	21.98	4.24	5.18	0.56	120.08	79.60	2.874	76	1.57	39.84	11.5	7.5
11	12	Ptb 50 (Kanchana)	23.25	4.06	5.73	0.58	111.41	77.21	3.810	80	1.45	43.85	16.9	12.9
12	14	Thulasi	24.31	5.00	4.86	0.62	107.66	71.58	3.762	76	1.55	45.12	12.8	8.8
13	15	Dular	30.19	6.04	5.00	0.73	141.68	106.40	3.332	75	3.07	44.32	11.5	7.5
14	16	Supriya	23.06	5.06	4.56	0.69	110.22	74.21	3.739	79	1.62	46.65	12.0	8.0
15	17	IR 36	23.83	5.95	4.01	1.04	113.10	73.52	3.870	86	1.55	42.64	14.4	10.4
16	18	Kunju Kunju	24.87	4.48	5.55	0.61	111.76	79.61	4.148	81	1.57	29.68	10.3	6.3
17	19	Harswa	27.10	5.34	5.07	1.03	107.85	70.70	3.939	75	1.54	38.30	13.4	9.4
18	20	IR-1552	27.46	3.48	7.89	0.86	103.63	67.02	3.481	76	1.44	34.94	9.9	5.9
19	26	Cul 12814	23.37	3.66	6.39	0.67	107.39	83.18	3.847	81	1.67	25.92	10.5	6.5
20	27	Cul 8755	25.44	5.06	5.03	0.84	114.60	74.51	3.678	86	1.74	43.73	12.0	8.0
21	28	Cul 8757	28.22	6.18	4.57	1.15	116.48	84.61	3.361	85	1.50	46.39	22.2	18.2
22	29	Cul 8759	22.53	5.28	4.27	0.96	95.00	61.83	3.993	85	1.55	35.45	12.7	8.7
23	31	Cul 8709	19.88	4.39	4.53	0.61	111.63	73.49	4.619	86	1.57	45.55	13.6	9.6
24	33	Cul 8714	17.11	3.08	5.56	0.43	102.58	68.42	4.077	76	1.54	43.86	18.3	14.3
25	34	Cul 8716	22.40	5.06	4.43	0.69	122.09	81.55	4.137	89	1.62	47.37	15.0	11.0
26	36	Cul 8723	22.89	7.49	3.06	0.74	112.42	81.73	3.934	76	1.63	42.46	13.7	9.7
27	37	Sulochana (Sel.)	25.96	4.97	5.22	0.65	136.37	108.97	2.943	76	1.38	45.16	14.6	10.6
28	38	T(N) 1	24.20	6.10	3.97	0.27	122.16	85.94	4.020	88	1.64	44.85	12.5	8.5
29	39	Cul 3	27.25	4.65	5.86	0.75	117.30	76.32	4.975	93	1.58	51.32	11.9	7.9
30	41	IR100	26.00	7.08	3.67	0.96	97.90	68.90	4.900	76	1.62	35.96	11.8	7.8
31	43	ASD 18	22.65	6.90	3.28	0.82	109.93	79.94	5.097	80	1.60	38.69	12.7	8.7
32	44	MOU 3	26.39	5.19	5.08	0.82	113.17	76.33	3.920	80	1.61	41.55	12.3	8.3
33	45	CO 37	23.56	4.05	5.82	0.48	124.18	86.75	4.763	87	1.58	37.10	13.8	9.8
34	46	Abhaya	26.93	6.72	4.01	0.94	112.69	80.13	4.593	90	1.64	36.03	12.0	8.0
35	47	ASD (Kongad)	26.60	5.24	5.08	0.71	106.22	77.80	4.163	78	1.68	41.76	10.7	6.7
36	48	ASD 16	29.30	5.80	5.05	1.33	127.21	84.13	4.952	81	1.50	44.71	10.4	6.4
37	49	Ptb 7 (Parambuvattan)	38.42	7.21	5.33	1.48	132.46	101.53	5.329	81	1.44	45.27	13.9	9.9
38	50	Ptb 10 (Thekkencheera)	36.25	7.08	5.12	1.43	152.80	117.95	4.922	76	1.36	43.87	14.4	10.4
39	51	Ptb 23 (Cheriya Aryan)	37.54	5.68	6.61	0.88	160.52	124.40	3.222	76	1.57	45.12	11.3	7.3
40	52	Ptb 30 (Chuvannamodan)	23.30	3.50	6.66	0.58	156.49	122.26	4.034	76	1.49	44.02	14.9	10.9

Appendix I : Estimates of mean for quantitative traits in the Base collection (contd....)

Sl. No.	PGC No.	Accession	Seedling shoot length (cm)	Seedling root length (cm)	Seedling vigour index	Total seedling biomass (g)	Plant height (cm)	Culm length (cm)	Stem thickness (mm)	Days to heading	Leaf blade width (cm)	Leaf blade length (cm)	Total tillers per plant	Productive tillers per plant
41	54	Ptb 43 (Swarna Prabha)	29.14	5.64	5.17	1.12	142.94	106.43	3.530	86	1.77	43.67	11.5	7.5
42	55	Ptb 42 (Suvarnamodan)	28.61	6.02	4.75	1.00	136.78	101.06	4.897	76	1.64	46.99	11.5	7.5
43	56	Cul 25333	23.75	7.36	3.23	0.88	118.10	83.31	3.705	92	1.66	42.17	11.3	7.3
44	57	Japan violet	28.55	5.72	4.99	1.45	98.76	67.65	3.222	76	1.53	36.02	12.5	8.5
45	58	PM-701	30.07	3.60	8.35	0.40	154.83	123.06	4.647	85	1.53	43.06	11.9	7.9
46	59	PM-706	36.18	5.23	6.92	1.28	151.83	118.46	5.116	84	1.52	45.21	13.1	9.1
47	60	PM-709	33.24	5.89	5.64	0.76	279.27	106.14	4.183	83	1.56	40.81	14.4	10.4
48	61	PM-713	33.54	5.25	6.39	0.84	131.63	92.87	3.394	86	1.45	42.25	16.4	12.4
49	62	PM-715	28.84	5.64	5.11	0.70	148.11	97.77	4.225	86	1.57	50.09	13.2	9.2
50	63	PM-716	29.37	5.10	5.76	0.61	130.52	89.61	2.803	86	1.52	52.81	10.6	6.6
51	64	PM-717	25.99	4.98	5.22	0.41	139.10	104.08	4.822	85	1.42	54.96	17.6	13.6
52	65	PM-2601	35.10	6.58	5.33	0.94	162.01	127.68	4.265	86	1.86	50.40	10.1	6.1
53	70	M1-14390	26.91	5.11	5.27	0.93	109.56	74.32	4.169	81	1.56	46.38	11.3	7.3
54	71	Kargi	37.94	8.04	4.72	1.31	111.95	81.98	2.886	76	1.52	34.11	13.7	9.7
55	72	Reymuthika	33.74	5.16	6.54	0.79	171.75	140.17	3.668	88	1.67	46.07	9.5	5.5
56	73	Karangi	34.91	5.46	6.39	1.01	141.21	108.32	3.638	81	1.64	42.85	11.1	7.1
57	74	Sabalai	25.24	3.98	6.34	0.91	98.36	71.73	3.976	76	1.67	29.11	9.1	5.1
58	75	Sihot	33.75	4.00	8.44	0.94	130.20	103.10	3.605	81	1.44	44.60	18.4	14.4
59	78	R-320-300	25.92	3.49	7.43	0.81	124.27	97.19	4.161	84	1.88	39.75	12.6	8.6
60	83	ASD17	24.03	4.58	5.25	0.58	105.44	77.15	3.568	83	1.50	29.25	11.7	7.7
61	84	ASD (Peringotukurussi)	24.91	3.56	7.00	0.59	120.69	80.81	3.905	81	1.57	48.88	10.8	6.8
62	85	ADT 36	24.32	4.26	5.71	0.64	116.48	80.42	4.082	85	2.89	38.88	12.3	8.3
63	86	ADT 37-1	24.61	4.63	5.32	0.63	124.20	94.20	4.211	81	1.86	39.19	12.3	8.3
64	87	ADT40	24.95	4.44	5.62	0.73	137.04	97.28	5.958	103	1.88	46.99	12.5	8.5
65	90	Basmati supper	27.63	6.19	4.46	1.00	115.83	84.26	4.571	94	1.54	34.64	12.0	8.0
66	91	TKM 6	31.92	6.29	5.07	0.66	176.02	129.90	6.833	84	1.54	58.42	11.1	7.1
67	92	Mo 8 (Aruna)	27.35	5.59	4.89	0.70	86.23	86.23	4.146	94	1.58	29.26	12.3	8.3
68	93	Makom (Mo 9)	27.08	5.44	4.98	0.89	112.02	82.40	4.078	91	1.53	30.65	13.4	9.4
69	95	Cul 8711	22.32	6.84	3.26	0.69	125.08	87.15	3.791	83	1.53	46.40	12.1	8.1
70	96	Cul 1727 / Navara	31.90	3.61	8.84	0.62	124.37	82.81	4.160	76	1.33	46.45	10.5	6.5
71	98	Panki	37.09	6.25	5.93	1.22	162.15	137.52	5.020	96	1.86	59.57	10.8	6.8
72	99	Cul 90-01	24.91	4.52	5.51	0.67	98.45	98.44	4.875	76	2.09	32.09	10.8	6.8
73	100	Cul 90-03	24.92	5.64	4.42	0.73	100.26	78.39	2.815	76	2.03	31.74	10.5	6.5
74	101	Cul 210-22	22.16	4.90	4.52	0.70	105.43	76.75	2.813	86	1.93	33.58	11.1	7.1
75	104	Cul 210-29	22.96	5.90	3.89	0.53	103.33	73.19	4.032	83	1.90	30.89	10.2	6.2
76	105	Cul A4-1-1	26.01	5.66	4.60	0.99	99.42	72.35	4.087	76	1.41	31.55	11.7	7.7
77	107	Cul A4-4-1	22.86	4.80	4.76	0.56	106.84	76.61	2.824	84	1.55	30.95	11.0	7.0
78	108	Cul C2-1	23.78	4.99	4.77	0.61	99.60	68.61	3.275	84	3.52	39.80	12.5	8.5
79	110	Cul C2-2	21.65	5.24	4.13	0.52	117.83	73.30	5.323	84	1.82	43.51	11.1	7.1
80	115	IVT 33	29.82	7.57	3.94	0.63	125.11	99.85	3.239	64	1.30	39.41	29.6	25.6

Appendix I : Estimates of mean for quantitative traits in the Base collection (contd....)

Sl. No.	PGC No.	Accession	Seedling shoot length (cm)	Seedling root length (cm)	Seedling vigour index	Total seedling biomass (g)	Plant height (cm)	Culm length (cm)	Stem thickness (mm)	Days to heading	Leaf blade width (cm)	Leaf blade length (cm)	Total tillers per plant	Productive tillers per plant
81	117	IVT 109	25.67	6.35	4.04	0.96	103.74	76.26	4.186	81	1.52	36.58	18.4	14.4
82	118	JM-20-18	17.35	4.02	4.32	0.39	109.73	79.30	3.635	86	1.63	33.26	15.3	11.3
83	119	JM-20-5	25.47	5.07	5.02	0.99	109.94	81.04	3.591	85	1.59	33.79	14.1	10.1
84	120	JM-20-21	23.16	4.51	5.14	0.63	111.44	79.37	3.645	84	1.60	34.96	13.6	9.6
85	121	JM-20-8	21.08	4.36	4.83	0.37	113.64	86.10	3.776	85	1.53	30.35	12.2	8.2
86	122	JM-10-7	21.94	6.63	3.31	0.58	117.28	88.36	4.199	85	1.69	36.52	13.5	9.5
87	123	JM-20-19	24.43	4.66	5.24	0.52	110.73	80.62	3.816	88	1.57	32.25	12.2	8.2
88	124	JM-10-32	23.23	5.40	4.30	0.93	109.57	80.14	3.919	86	1.54	34.11	15.8	11.8
89	125	JM-10-31	25.53	4.78	5.34	0.68	111.09	78.40	4.465	88	1.53	36.95	13.3	9.3
90	126	AM-10-24	27.67	3.89	7.11	0.66	124.01	93.91	4.253	83	1.50	36.96	18.1	14.1
91	127	AM-10-5	27.54	6.83	4.03	1.13	127.12	97.23	3.945	80	1.57	50.80	16.1	12.1
92	128	AM-20-27	28.39	5.79	4.90	0.85	125.08	100.75	3.360	83	1.42	48.00	11.1	7.1
93	129	AM-30-8	30.20	6.58	4.59	0.93	131.98	97.16	3.148	84	1.49	46.04	12.4	8.4
94	130	AM-30-5	29.20	5.10	5.73	0.70	132.62	97.56	2.821	85	1.53	49.31	11.4	7.4
95	133	AM-10-7	27.43	6.20	4.42	0.85	124.26	94.47	3.137	85	1.30	45.41	11.2	7.2
96	134	AM-30-31	27.41	4.81	5.70	0.78	116.13	89.42	4.967	85	1.30	46.23	13.7	9.7
97	137	Kalyani II	28.35	6.17	4.59	0.89	97.74	78.11	4.431	67	1.46	39.54	12.3	8.3
98	138	IVT 14	30.42	6.52	4.67	0.94	241.64	84.36	3.635	70	1.45	41.23	10.8	6.8
99	139	Cul 10-1-1 (Ahalya)	31.65	5.99	5.28	1.58	89.97	69.04	2.592	76	1.53	36.75	12.1	8.1
100	141	Cul 210-25 (Varsha)	22.41	5.55	4.04	0.84	108.28	81.15	3.391	81	1.72	38.43	10.7	6.7
101	142	Cul A4-1-2	27.98	5.03	5.56	0.97	108.54	74.56	3.799	80	1.73	42.01	15.3	11.3
102	144	Cul 90-02	25.56	6.58	3.88	0.80	111.59	80.74	3.831	78	1.82	40.64	12.7	8.7
103	145	Cul 90-04	23.11	5.61	4.12	0.87	111.64	84.33	2.399	81	3.28	36.06	13.0	9.0
104	146	Cul 90-05	26.57	4.75	5.59	0.73	110.16	83.05	4.510	84	1.64	41.82	10.9	6.9
105	148	IVT 32	21.62	6.48	3.34	0.72	147.36	108.39	4.630	81	1.54	40.94	10.9	6.9
106	149	IVT 42	25.29	7.11	3.56	1.17	88.96	63.27	3.578	81	1.46	37.94	13.0	9.0
107	150	IVT116	23.70	5.20	4.56	0.56	82.75	62.93	4.126	81	2.92	37.34	11.6	7.6
108	152	SBRP 2	29.52	4.14	7.13	0.50	147.47	112.74	4.223	91	1.45	59.34	9.3	5.3
109	153	SBRP 3	32.70	4.67	7.00	0.62	145.45	109.99	4.426	91	1.35	54.07	10.4	6.4
110	154	SBRP 4	33.75	3.98	8.48	0.51	141.26	105.42	5.206	91	1.38	55.85	10.1	6.1
111	155	SBRP 5	32.16	5.48	5.87	0.62	140.28	107.95	5.304	80	1.48	42.26	17.7	13.7
112	156	DV-85	32.91	5.64	5.84	0.66	155.99	122.79	3.975	81	1.59	42.58	14.7	10.7
113	157	Moncompu 519	26.83	6.25	4.29	0.93	121.32	73.19	4.589	88	1.61	57.04	11.3	7.3
114	165	Cul 9410-3-Sel 1	22.63	4.66	4.86	0.45	122.21	93.97	3.408	103	1.58	59.81	12.8	8.8
115	166	Cul 9410-3-Sel 1	23.58	4.18	5.64	0.51	131.91	84.45	4.123	87	1.57	48.37	12.0	8.0
116	167	Cul 9410-3-Sel 2	23.31	4.95	4.71	0.64	134.02	86.24	4.289	90	1.62	43.62	10.9	6.9
117	168	F3-11-3	21.02	4.50	4.67	0.43	124.69	89.18	4.168	86	1.66	44.00	11.2	7.2
118	169	F5-14-1	28.70	5.14	5.58	0.75	138.90	102.54	5.191	86	1.86	50.52	11.9	7.9
119	170	F5-17-1-1	24.00	7.03	3.41	0.89	141.18	93.03	3.835	84	1.68	55.76	10.2	6.2
120	171	F5-23-1	27.16	8.61	3.15	1.23	126.78	90.48	3.642	102	1.47	53.37	12.6	8.6

Appendix I : Estimates of mean for quantitative traits in the Base collection (contd....)

Sl. No.	PGC No.	Accession	Seedling shoot length (cm)	Seedling root length (cm)	Seedling vigour index	Total seedling biomass (g)	Plant height (cm)	Culm length (cm)	Stem thickness (mm)	Days to heading	Leaf blade width (cm)	Leaf blade length (cm)	Total tillers per plant	Productive tillers per plant
121	172	F5-23-2	26.34	6.66	3.95	0.81	124.95	97.36	4.255	101	1.39	44.64	11.4	7.4
122	173	F6-11-1-1	25.27	4.87	5.19	0.51	131.80	94.01	4.555	94	1.63	53.23	13.0	9.0
123	174	IET18045	19.90	4.30	4.63	0.37	109.66	83.38	3.000	94	1.56	42.53	11.5	7.5
124	177	IET18886	29.65	5.35	5.54	0.73	131.05	98.70	3.758	94	1.50	53.15	11.7	7.7
125	178	OR-1885-16-34	26.48	6.32	4.19	0.95	148.28	128.19	6.059	104	1.46	56.87	13.5	9.5
126	180	IET17284	24.16	6.59	3.67	0.78	127.15	102.62	5.957	95	1.71	48.01	12.5	8.5
127	181	IET17467	24.09	6.43	3.75	0.78	125.08	86.42	3.526	91	1.53	43.98	11.2	7.2
128	186	IET18318 Sel1	26.88	5.43	4.95	0.70	125.28	85.47	4.325	93	1.57	50.88	11.4	7.4
129	187	IET18318 Sel2	25.73	6.36	4.05	0.91	118.58	85.51	4.179	91	1.84	46.74	12.0	8.0
130	188	PC-1 (Mavundiri)	27.87	4.64	6.01	0.67	125.92	101.19	5.229	96	1.71	54.38	10.8	6.8
131	191	CSR 10	26.35	5.31	4.96	0.85	107.14	69.59	4.925	89	1.59	45.32	12.3	8.3
132	192	CSR 3	23.83	6.79	3.51	0.74	102.15	82.84	5.964	94	1.50	39.33	12.0	8.0
133	193	CSR 23	22.48	5.72	3.93	0.55	97.66	71.00	5.253	94	1.47	35.05	13.7	9.7
134	194	CSR 27	28.64	8.00	3.58	1.83	123.51	90.41	4.312	86	1.65	40.37	11.0	7.0
135	195	MTU1010	26.38	5.09	5.18	0.73	208.43	83.50	4.498	81	1.52	36.17	11.3	7.3
136	196	Dhandori	32.36	5.90	5.48	1.08	149.93	108.01	5.417	107	1.46	33.25	11.2	7.2
137	197	Early samba	24.50	5.12	4.79	0.66	137.64	106.05	4.704	91	1.56	49.05	12.9	8.9
138	198	Indira Sugandhi Dhar	21.97	4.20	5.23	0.45	120.95	86.90	5.322	99	1.67	41.65	11.5	7.5
139	199	Kasturi	23.28	5.51	4.23	0.73	129.16	92.46	6.147	78	1.54	39.64	11.5	7.5
140	200	Cul C3-2 KM	23.95	5.39	4.44	0.78	110.05	79.54	3.277	96	1.49	42.73	11.9	7.9
141		HS-16	26.28	6.91	3.80	1.01	115.72	72.65	4.464	76	1.47	37.83	15.2	11.2
142		HS-1	28.86	7.46	3.87	1.02	103.18	74.05	4.034	76	1.30	41.37	12.2	8.2
143		HS-13	26.92	4.55	5.92	0.71	102.17	71.99	6.303	76	1.44	46.20	10.2	6.2
144		Ptb 35 (Annapurrna)	23.42	5.49	4.27	0.56	117.88	78.22	3.209	81	2.55	49.01	11.3	7.3
145		Manupriya	27.94	5.16	5.41	0.86	158.23	109.69	4.017	76	1.37	57.60	17.0	13.0
146		Parambuvattan	33.60	5.00	6.72	1.00	152.00	106.23	4.402	81	1.39	52.83	15.0	11.0
147		Karuthamodan	35.97	5.73	6.28	1.42	150.68	109.44	2.813	76	1.55	58.74	11.5	7.5
148		Karanavara	30.23	4.39	6.89	0.64	160.57	114.00	3.704	76	1.63	55.48	12.1	8.1
149		Kalladiaryan	38.01	4.56	8.34	0.69	146.04	112.05	4.494	82	1.54	44.89	10.1	6.1
150		Chuvannamodan	31.43	4.12	7.63	0.73	144.27	108.04	3.026	78	1.46	42.04	15.1	11.1
151		Thottacheera	42.49	5.00	8.50	1.03	163.61	126.98	3.742	76	1.48	49.71	14.4	10.4
152		Karuthadukkan	31.36	3.61	8.69	0.53	157.34	124.53	4.238	82	1.62	47.04	16.5	12.5
153		Chomala	25.31	3.92	6.46	0.57	131.78	100.83	3.642	78	1.77	36.54	16.5	12.5
154		Njavara 11-2	21.24	4.63	4.59	0.63	138.31	100.31	3.622	115	1.49	56.18	14.3	10.3
155		Cul KAUM 20	22.95	4.76	4.82	1.20	214.71	79.33	5.155	115	1.39	67.48	11.3	7.3
156		Mo 21(Prathyasha)	22.25	5.86	3.80	0.85	107.79	78.06	5.187	106	1.45	54.12	11.9	7.9
157		Mo 19 (Krishnanana)	20.55	6.50	3.16	0.77	108.81	80.07	5.453	118	1.49	53.37	11.9	7.9
158		Cul M 20	20.65	2.77	7.45	0.84	111.81	86.85	2.827	96	1.50	30.25	12.3	8.3
159		Mo 15 (Remanika)	21.70	4.95	4.38	1.56	112.91	79.67	4.101	107	1.55	56.73	12.1	8.1
160		Mo 7 (Karthika)	20.19	4.70	4.30	0.96	103.00	88.39	3.780	106	1.37	48.38	11.9	7.9

Appendix I : Estimates of mean for quantitative traits in the Base collection (contd....)

Sl. No.	PGC No.	Accession	Panicle length (cm)	Spikelets /panicle	Grains / panicle	Test weight of grain (g)	Grain length (mm)	Grain width (mm)	Grain thickness (mm)	Decorticated grain length (mm)	Decorticated grain width (mm)	Decorticated grain thickness (mm)	Straw yield / plant (g)	Grain yield / plant (g)
1	1	Annapoorna	24.17	131.7	80.5	22.550	6.573	1.413	0.362	4.073	0.413	0.312	33.49	29.62
2	2	Ptb 36 (Rohini)	23.37	159.1	110.7	23.130	7.675	1.385	0.373	5.175	0.385	0.323	19.99	35.37
3	3	Ptb 38 (Triveni)	23.60	153.6	97.5	23.140	7.829	1.489	0.335	5.329	0.489	0.285	22.52	28.90
4	4	Ptb 39 (Jyothi)	23.40	165.4	100.1	22.960	7.891	1.484	0.558	5.391	0.484	0.508	21.94	28.72
5	5	Ptb 45 (Matta Triveni)	22.91	151.3	106.5	22.685	7.316	1.708	0.791	4.816	0.708	0.741	31.53	31.08
6	6	ADT 37-11	22.88	142.4	82.1	22.410	6.855	1.754	1.313	4.355	0.754	1.263	21.27	15.94
7	7	Ptb 46 (Jayathy)	28.97	281.6	223.2	22.525	6.855	1.754	0.721	4.355	0.754	0.671	22.56	31.99
8	8	Bhagya	28.05	179.1	127.8	23.110	7.377	1.914	0.881	4.877	0.914	0.831	24.78	46.24
9	9	Onam	29.04	159.0	98.0	22.770	7.131	1.980	0.819	4.631	0.980	0.769	19.86	39.38
10	11	Ptb 49 (Kairaly)	24.88	163.4	98.9	22.695	7.075	1.868	0.902	4.575	0.868	0.852	22.66	33.55
11	12	Ptb 50 (Kanchana)	23.24	121.0	53.2	23.055	7.224	1.726	0.880	4.724	0.726	0.830	30.66	43.19
12	14	Thulasi	24.29	188.8	128.9	23.195	8.772	1.977	1.005	6.272	0.977	0.955	21.18	22.88
13	15	Dular	26.21	102.6	38.2	22.920	7.253	1.684	0.858	4.753	0.684	0.808	16.81	22.51
14	16	Supriya	26.32	133.0	79.2	22.750	7.003	1.958	0.959	4.503	0.958	0.909	16.14	20.90
15	17	IR 36	24.83	155.5	97.4	22.980	8.357	1.293	0.574	5.857	0.293	0.524	25.82	44.65
16	18	Kunju Kunju	26.77	153.5	93.5	22.930	6.870	1.645	0.603	4.370	0.645	0.553	39.51	48.98
17	19	Harswa	24.88	157.1	97.9	22.745	6.620	1.902	0.705	4.120	0.902	0.655	21.33	15.77
18	20	IR-1552	27.57	96.8	58.1	22.890	7.395	1.107	0.281	4.895	0.107	0.231	18.28	16.81
19	26	Cul 12814	27.03	89.9	43.3	22.690	6.252	1.329	0.260	3.752	0.329	0.210	22.44	21.24
20	27	Cul 8755	22.88	179.9	130.6	22.775	6.339	1.122	0.243	3.839	0.122	0.193	25.47	23.04
21	28	Cul 8757	24.49	184.6	134.2	23.350	7.806	1.116	0.299	5.306	0.116	0.249	30.85	46.97
22	29	Cul 8759	23.95	147.6	102.3	22.715	6.678	1.211	0.358	4.178	0.211	0.308	18.34	36.83
23	31	Cul 8709	27.15	172.4	127.0	22.590	6.762	1.207	0.317	4.262	0.207	0.267	23.75	24.15
24	33	Cul 8714	28.27	141.4	92.1	22.410	7.028	1.116	0.258	4.528	0.116	0.208	21.57	36.10
25	34	Cul 8716	26.82	216.4	170.8	22.920	6.799	1.222	0.317	4.299	0.222	0.267	22.12	38.28
26	36	Cul 8723	24.83	211.3	166.6	22.875	6.972	1.187	0.287	4.472	0.187	0.237	25.74	43.69
27	37	Sulochana (Sel.)	27.16	101.5	39.3	21.620	5.718	1.245	0.217	3.218	0.245	0.167	24.59	8.91
28	38	T(N) 1	26.53	176.0	131.9	22.450	6.691	1.078	0.178	4.191	0.078	0.128	28.36	21.85
29	39	Cul 3	26.85	155.8	112.3	22.970	7.347	1.289	0.318	4.847	0.289	0.268	21.19	22.53
30	41	IR100	23.80	125.7	75.8	22.815	6.108	1.257	0.320	3.608	0.257	0.270	24.99	31.52
31	43	ASD 18	26.04	186.6	130.0	22.250	6.671	0.830	0.144	4.171	0.170	0.094	23.74	45.47
32	44	MOU 3	24.92	176.5	125.5	22.770	6.714	1.054	0.323	4.214	0.054	0.273	22.77	26.83
33	45	CO 37	22.23	123.8	68.0	22.260	7.857	0.992	0.323	5.357	0.008	0.273	24.07	19.00
34	46	Abhaya	22.92	187.5	123.7	22.265	7.769	0.552	0.158	5.269	0.448	0.108	21.03	28.93
35	47	ASD (Kongad)	23.19	162.0	100.4	22.535	6.116	1.365	0.235	3.616	0.365	0.185	22.08	31.02
36	48	ASD 16	24.65	197.9	149.0	22.450	5.960	1.424	0.243	3.460	0.424	0.193	19.66	17.01
37	49	Ptb 7 (Parambuvattan)	25.61	186.6	127.5	22.605	6.611	1.302	0.311	4.111	0.302	0.261	21.02	32.44
38	50	Ptb 10 (Thekkencheera)	26.79	103.3	37.3	22.785	6.563	1.567	0.511	4.063	0.567	0.461	34.14	25.04
39	51	Ptb 23 (Cheriya Aryan)	26.94	88.8	24.4	22.880	6.704	1.485	0.453	4.204	0.485	0.403	22.22	31.53
40	52	Ptb 30 (Chuvannamodan)	26.80	103.1	60.8	22.730	7.507	1.386	0.489	5.007	0.386	0.439	23.87	9.01

Appendix I : Estimates of mean for quantitative traits in the Base collection (contd....)

Sl. No.	PGC No.	Accession	Panicle length (cm)	Spikelets per panicle	Grains per panicle	Test weight of grain (g)	Grain length (mm)	Grain width (mm)	Grain thickness (mm)	Decorticated grain length (mm)	Decorticated grain width (mm)	Decorticated grain thickness (mm)	Straw yield per plant (g)	Grain yield per plant (g)
41	54	Ptb 43 (Swarna Prabha)	28.05	212.7	163.3	22.685	7.164	1.044	0.119	4.664	0.044	0.069	24.47	24.68
42	55	Ptb 42 (Suvarnamodan)	29.71	215.0	154.2	22.615	6.294	1.068	0.155	3.794	0.068	0.105	21.22	33.04
43	56	Cul 25333	28.34	162.4	104.8	23.415	7.627	1.271	0.409	5.127	0.271	0.359	21.08	23.48
44	57	Japan violet	22.96	113.2	56.0	22.400	6.065	1.354	0.196	3.565	0.354	0.146	23.23	8.15
45	58	PM-701	26.32	94.9	36.2	23.020	6.318	1.671	0.290	3.818	0.671	0.240	26.99	21.48
46	59	PM-706	26.60	145.7	93.0	22.795	6.488	1.510	0.304	3.988	0.510	0.254	22.21	20.32
47	60	PM-709	27.76	99.2	42.0	22.815	6.375	1.396	0.224	3.875	0.396	0.174	33.23	28.15
48	61	PM-713	26.94	107.9	48.7	22.770	6.823	1.086	0.165	4.323	0.086	0.115	28.17	10.75
49	62	PM-715	31.56	147.9	79.1	22.985	6.584	1.483	0.374	4.084	0.483	0.324	20.06	15.96
50	63	PM-716	28.37	137.4	74.0	22.695	6.123	1.348	0.251	3.623	0.348	0.201	37.76	8.85
51	64	PM-717	28.14	153.4	85.6	22.560	7.031	1.280	0.176	4.531	0.280	0.126	25.91	20.50
52	65	PM-2601	28.07	170.2	98.4	22.900	5.913	1.305	0.291	3.413	0.305	0.241	34.63	22.77
53	70	M1-14390	24.60	132.1	81.7	22.125	6.148	0.926	0.181	3.648	0.074	0.131	20.70	15.15
54	71	Kargi	17.92	148.0	82.1	22.020	5.892	1.190	1.155	3.392	0.190	1.105	20.22	9.32
55	72	Reymuthika	28.06	211.1	146.2	22.140	4.291	1.168	0.239	1.791	0.168	0.189	27.34	13.84
56	73	Karangi	22.52	92.7	22.0	23.645	6.304	0.982	0.144	3.804	0.018	0.094	21.47	30.78
57	74	Sabalai	15.71	97.7	34.5	22.680	6.215	1.346	0.254	3.715	0.346	0.204	19.26	9.64
58	75	Sihot	24.35	100.3	49.0	22.890	6.638	1.141	0.300	4.138	0.141	0.250	17.51	14.87
59	78	R-320-300	26.37	164.8	106.7	22.995	7.671	1.327	0.360	5.171	0.327	0.310	25.42	23.69
60	83	ASD17	22.49	97.5	26.8	22.800	6.587	1.330	0.339	4.087	0.330	0.289	23.33	19.80
61	84	ASD (Peringotukurussi)	26.24	239.1	181.7	22.925	6.115	1.329	0.234	3.615	0.329	0.184	27.14	29.32
62	85	ADT 36	27.10	159.0	91.7	22.540	6.942	1.009	0.175	4.442	0.009	0.125	23.64	20.50
63	86	ADT 37-1	24.87	276.7	216.3	22.255	5.196	1.350	0.316	2.696	0.350	0.266	25.00	27.65
64	87	ADT40	26.02	172.2	103.7	22.665	6.272	1.341	0.323	3.772	0.341	0.273	29.54	9.83
65	90	Basmati supper	22.89	182.4	115.9	22.995	6.562	1.427	0.386	4.062	0.427	0.336	22.60	20.97
66	91	TKM 6	31.93	224.2	170.5	22.300	8.037	0.814	0.240	5.537	0.186	0.190	26.45	10.75
67	92	Mo 8 (Aruna)	23.85	172.4	111.9	22.240	6.614	1.288	0.250	4.114	0.288	0.200	20.96	19.68
68	93	Makom (Mo 9)	27.23	191.1	135.6	22.435	7.279	1.201	0.259	4.779	0.201	0.209	31.24	19.06
69	95	Cul 8711	50.21	164.5	105.2	22.465	6.938	0.977	0.229	4.438	0.023	0.179	20.09	25.48
70	96	Cul 1727 / Navara	23.23	152.8	79.9	22.765	4.884	1.149	0.199	2.384	0.149	0.149	24.54	17.36
71	98	Panki	27.13	151.9	98.6	22.605	6.769	1.511	0.477	4.269	0.511	0.427	43.37	13.00
72	99	Cul 90-01	19.07	148.5	82.5	22.110	5.607	1.279	0.244	3.107	0.279	0.194	17.96	19.37
73	100	Cul 90-03	21.62	138.2	63.6	22.375	5.648	1.344	0.300	3.148	0.344	0.250	20.68	19.58
74	101	Cul 210-22	22.32	183.3	111.4	22.315	5.733	1.459	0.378	3.233	0.459	0.328	16.14	25.62
75	104	Cul 210-29	22.52	199.5	139.7	22.620	5.803	1.218	0.289	3.303	0.218	0.239	19.50	22.62
76	105	Cul A4-1-1	21.95	135.6	69.5	22.360	6.727	1.149	0.196	4.227	0.149	0.146	18.15	19.92
77	107	Cul A4-4-1	23.20	154.9	89.1	23.165	7.633	1.231	0.364	5.133	0.231	0.314	18.90	16.18
78	108	Cul C2-1	24.94	155.4	86.5	22.120	6.397	1.277	0.379	3.897	0.277	0.329	21.47	17.33
79	110	Cul C2-2	25.37	176.5	99.2	22.395	6.559	1.444	0.538	4.059	0.444	0.488	24.40	20.32
80	115	IVT 33	24.31	73.1	9.4	22.015	7.587	0.997	0.388	5.087	0.003	0.338	19.96	17.31

Appendix I : Estimates of mean for quantitative traits in the Base collection (contd....)

Sl. No.	PGC No.	Accession	Panicle length (cm)	Spikelets per panicle	Grains per panicle	Test weight of grain (g)	Grain length (mm)	Grain width (mm)	Grain thickness (mm)	Decorticated grain length (mm)	Decorticated grain width (mm)	Decorticated grain thickness (mm)	Straw yield per plant (g)	Grain yield per plant (g)
81	117	IVT 109	23.11	92.3	28.1	22.590	7.655	1.162	0.549	5.155	0.162	0.499	23.16	27.39
82	118	JM-20-18	23.78	130.0	64.4	23.130	7.655	1.162	0.539	5.155	0.162	0.489	17.21	27.73
83	119	JM-20-5	23.89	124.4	64.2	22.935	7.142	1.034	0.243	4.642	0.034	0.193	16.95	21.35
84	120	JM-20-21	23.92	156.6	95.7	22.970	7.923	1.167	0.264	5.423	0.167	0.214	19.50	22.47
85	121	JM-20-8	23.97	153.8	94.6	23.275	7.950	1.234	0.336	5.450	0.234	0.286	16.78	24.51
86	122	JM-10-7	26.83	142.4	70.9	23.090	7.258	1.193	0.271	4.758	0.193	0.221	25.18	26.20
87	123	JM-20-19	23.25	133.7	74.0	23.175	7.317	0.872	0.152	4.817	0.128	0.102	18.43	22.99
88	124	JM-10-32	24.64	157.7	98.4	23.050	8.070	1.327	0.491	5.570	0.327	0.441	26.68	28.04
89	125	JM-10-31	24.23	148.8	90.3	22.865	7.351	1.068	0.224	4.851	0.068	0.174	24.68	16.24
90	126	AM-10-24	23.99	153.2	96.1	22.935	7.309	1.285	0.500	4.809	0.285	0.450	25.48	29.17
91	127	AM-10-5	25.81	177.1	110.8	22.985	7.414	1.211	0.191	4.914	0.211	0.141	33.60	32.58
92	128	AM-20-27	24.90	154.0	82.9	22.790	7.741	1.258	0.299	5.241	0.258	0.249	16.23	22.55
93	129	AM-30-8	24.45	173.7	103.9	22.885	6.981	1.188	0.210	4.481	0.188	0.160	18.71	23.60
94	130	AM-30-5	25.36	157.1	95.6	22.610	6.881	1.180	0.230	4.381	0.180	0.180	19.19	18.73
95	133	AM-10-7	23.52	154.6	90.7	22.985	7.290	1.275	0.264	4.790	0.275	0.214	19.22	18.64
96	134	AM-30-31	23.20	137.0	79.1	23.225	7.638	1.244	0.363	5.138	0.244	0.313	24.72	18.05
97	137	Kalyani II	22.21	164.8	97.8	23.360	6.766	1.257	0.356	4.266	0.257	0.306	24.50	14.63
98	138	IVT 14	22.94	135.5	79.9	23.120	7.623	1.227	0.405	5.123	0.227	0.355	20.91	13.74
99	139	Cul 10-1-1 (Ahalya)	20.42	121.6	54.2	22.375	5.754	1.258	0.340	3.254	0.258	0.290	19.75	15.95
100	141	Cul 210-25 (Varsha)	23.22	94.7	42.1	22.580	5.269	1.142	0.320	2.769	0.142	0.270	20.08	28.15
101	142	Cul A4-1-2	25.88	212.5	142.4	22.455	5.738	1.293	0.244	3.238	0.293	0.194	18.88	27.34
102	144	Cul 90-02	24.98	173.9	109.7	22.400	6.007	1.121	0.286	3.507	0.121	0.236	24.72	34.43
103	145	Cul 90-04	25.54	149.8	72.8	22.530	5.922	1.159	0.422	3.422	0.159	0.372	18.35	25.25
104	146	Cul 90-05	23.61	165.8	83.7	23.105	7.740	1.095	0.524	5.240	0.095	0.474	22.91	30.09
105	148	IVT 32	23.92	159.6	80.9	22.860	7.683	1.209	0.474	5.183	0.209	0.424	24.13	26.38
106	149	IVT 42	22.79	112.0	47.1	22.365	6.755	1.315	0.464	4.255	0.315	0.414	20.72	16.83
107	150	IVT116	21.13	117.7	58.1	22.365	7.251	1.194	0.355	4.751	0.194	0.305	15.37	8.20
108	152	SBRP 2	25.19	141.5	73.4	23.365	7.870	1.338	0.548	5.370	0.338	0.498	27.10	17.55
109	153	SBRP 3	25.45	137.7	79.1	23.540	7.630	1.326	0.572	5.130	0.326	0.522	24.43	18.38
110	154	SBRP 4	26.07	172.4	109.4	23.480	8.159	1.299	0.517	5.659	0.299	0.467	20.91	18.56
111	155	SBRP 5	26.44	193.3	116.6	22.505	6.174	1.244	0.315	3.674	0.244	0.265	29.24	27.68
112	156	DV-85	25.00	106.0	41.6	22.960	6.878	1.240	0.435	4.378	0.240	0.385	25.79	12.87
113	157	Moncompu 519	24.29	223.3	165.0	22.760	8.099	0.796	0.257	5.599	0.204	0.207	22.05	13.79
114	165	Cul 9410-3-Sel 1	24.50	158.1	89.8	22.250	6.403	1.272	0.308	3.903	0.272	0.258	33.00	15.82
115	166	Cul 9410-3-Sel 1	27.25	248.5	182.9	22.865	7.930	1.057	0.196	5.430	0.057	0.146	27.87	17.23
116	167	Cul 9410-3-Sel 2	25.57	243.6	163.5	22.845	8.070	1.021	0.298	5.570	0.021	0.248	18.78	22.97
117	168	F3-11-3	24.91	210.6	131.6	22.380	5.317	1.263	0.412	2.817	0.263	0.362	19.09	20.67
118	169	F5-14-1	26.37	222.8	156.1	22.390	6.593	1.198	0.357	4.093	0.198	0.307	20.69	21.24
119	170	F5-17-1-1	30.29	226.6	167.1	22.740	6.698	1.383	0.383	4.198	0.383	0.333	24.98	20.03
120	171	F5-23-1	24.70	174.4	113.3	22.700	7.478	1.284	0.275	4.978	0.284	0.225	23.78	23.22

Appendix I : Estimates of mean for quantitative traits in the Base collection (contd....)

Sl. No.	PGC No.	Accession	Panicle length (cm)	Spikelets per panicle	Grains per panicle	Test weight of grain (g)	Grain length (mm)	Grain width (mm)	Grain thickness (mm)	Decorticated grain length (mm)	Decorticated grain width (mm)	Decorticated grain thickness (mm)	Straw yield per plant (g)	Grain yield per plant (g)
121	172	F5-23-2	23.93	194.2	126.7	22.780	7.415	1.525	0.457	4.915	0.525	0.407	39.42	17.40
122	173	F6-11-1-1	23.70	156.2	86.4	23.275	7.119	1.645	0.539	4.619	0.645	0.489	29.62	18.51
123	174	IET18045	24.26	190.0	131.0	21.635	6.722	0.628	0.179	4.222	0.372	0.129	25.24	18.73
124	177	IET18886	27.66	158.2	90.4	23.180	8.810	1.426	0.443	6.310	0.426	0.393	24.15	18.21
125	178	OR-1885-16-34	25.12	133.1	81.7	22.700	5.417	1.351	0.427	2.917	0.351	0.377	23.58	28.44
126	180	IET17284	23.93	141.9	85.7	23.000	7.583	0.668	0.186	5.083	0.332	0.136	24.76	33.99
127	181	IET17467	29.03	151.6	94.2	22.830	8.066	1.178	0.428	5.566	0.178	0.378	22.33	18.60
128	186	IET18318 Sel1	26.79	197.5	138.0	22.095	7.607	0.583	0.109	5.107	0.417	0.059	19.46	16.47
129	187	IET18318 Sel2	23.44	216.2	152.3	21.935	6.377	0.467	0.063	3.877	0.533	0.013	24.32	17.03
130	188	PC-1 (Mavundiri)	24.82	186.2	119.7	22.930	7.118	1.266	0.371	4.618	0.266	0.321	21.77	18.97
131	191	CSR 10	23.52	163.2	99.6	23.265	7.342	1.224	0.424	4.842	0.224	0.374	22.65	27.25
132	192	CSR 3	24.16	146.7	83.7	22.295	7.471	0.534	0.066	4.971	0.466	0.016	43.37	15.14
133	193	CSR 23	23.38	170.3	107.3	21.525	5.875	0.270	0.016	3.375	0.730	0.034	25.23	12.75
134	194	CSR 27	28.03	217.5	163.9	22.970	7.636	1.168	0.381	5.136	0.168	0.331	27.04	31.90
135	195	MTU1010	24.56	144.8	87.4	22.760	7.852	0.966	0.303	5.352	0.034	0.253	19.84	17.71
136	196	Dhandori	26.38	171.9	116.9	22.740	6.114	1.561	0.545	3.614	0.561	0.495	25.75	24.10
137	197	Early samba	25.09	142.1	83.6	22.480	7.570	1.056	0.253	5.070	0.056	0.203	25.51	19.63
138	198	Indira Sugandhi Dhar	25.14	207.5	154.9	22.275	7.500	0.775	0.193	5.000	0.225	0.143	20.48	16.57
139	199	Kasturi	28.21	189.9	129.8	22.445	9.250	0.222	0.128	6.750	0.778	0.078	45.94	14.50
140	200	Cul C3-2 KM	24.41	169.2	105.4	23.120	7.525	1.294	0.400	5.025	0.294	0.350	25.72	13.54
141		HS-16	22.62	101.9	36.5	23.185	7.500	1.362	0.532	5.000	0.362	0.482	16.94	14.94
142		HS-1	24.02	120.9	65.4	23.095	7.467	1.317	0.507	4.967	0.317	0.457	16.40	18.85
143		HS-13	23.23	143.2	82.5	22.440	6.696	1.300	0.257	4.196	0.300	0.207	14.88	10.33
144		Ptb 35 (Annapurna)	25.36	261.2	199.8	22.615	6.339	1.437	0.438	3.839	0.437	0.388	22.68	32.77
145		Manupriya	24.83	102.7	43.7	22.950	7.028	1.519	0.376	4.528	0.519	0.326	39.26	17.69
146		Parambuvattan	25.86	110.6	48.6	23.495	7.492	1.527	0.403	4.992	0.527	0.353	26.26	15.06
147		Karuthamodan	26.55	74.9	4.5	22.885	7.527	1.336	0.473	5.027	0.336	0.423	23.96	7.63
148		Karanavara	25.86	105.5	37.2	23.090	7.515	1.369	0.336	5.015	0.369	0.286	18.97	12.56
149		Kalladiaryan	24.58	122.1	66.1	22.730	6.551	1.342	0.405	4.051	0.342	0.355	23.66	11.97
150		Chuvannamodan	25.86	104.1	45.3	22.680	7.449	1.351	0.321	4.949	0.351	0.271	24.37	7.65
151		Thottacheera	25.42	158.9	96.3	22.555	7.046	1.437	0.458	4.546	0.437	0.408	25.85	15.23
152		Karuthadukkan	28.60	171.3	111.0	23.090	7.849	1.416	0.344	5.349	0.416	0.294	23.41	9.70
153		Chomala	23.32	114.1	66.0	21.375	5.283	0.373	0.032	2.783	0.627	0.018	22.56	8.01
154		Njavara 11-2	25.50	158.3	98.1	23.120	6.740	1.475	0.324	4.240	0.475	0.274	25.85	26.39
155		Cul KAUM 20	25.07	110.0	42.5	23.090	5.571	1.031	0.180	3.071	0.031	0.130	24.45	15.10
156		Mo 21(Prathyasha)	23.62	131.9	67.9	22.435	6.480	1.434	0.467	3.980	0.434	0.417	24.01	19.94
157		Mo 19 (Krishnanana)	26.46	147.6	91.9	22.675	6.802	1.312	0.279	4.302	0.312	0.229	24.96	15.61
158		Cul M 20	22.31	154.3	85.6	22.320	7.394	0.890	0.207	4.894	0.110	0.157	22.87	15.08
159		Mo 15 (Remanika)	24.57	144.2	81.9	22.135	6.988	1.856	0.882	4.488	0.856	0.832	19.41	20.20
160		Mo 7 (Karthika)	21.56	99.9	50.7	22.760	7.336	2.476	1.348	4.836	1.476	1.298	21.23	14.70

Abstract

FORMATION OF CORE SET IN RICE (*Oryza sativa* L.) SHORT DURATION GERMPLASM ACCESSIONS

By

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ABSTRACT OF THE THESIS

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ABSTRACT

Rice (*Oryza sativa* L.) popularly known as 'Global grain' is the staple food for over half the world's population. In Kerala, rice occupies the prime place among the food crops cultivated. Diversity of cropping systems, the edaphic and climatic variations found among and within different cropping regions have resulted in a cafeteria of variable genotypes.

Concerted efforts by breeders in Kerala Agricultural University to conserve the diversity in rice crop, have resulted in formation of a germplasm collection of over 1000 accessions. Such large variability, though essential for crop improvement programmes, reduces the accessibility of germplasm and poses difficulty in making effective choice of parental material for breeding programmes. The concept of core collection proposed by Frankel (1984) provides a solution to this problem. According to him, core collection is defined as a representative sample of the entire collection with minimum repetitiveness and maximum genetic diversity of a crop species and its relatives.

Considering the advantages in obtaining a subset that retains maximum diversity of the large germplasm collection, an effort was made to form a core set from a base collection of 160 short duration accessions (Base collection). The 160 accessions were raised in an Augmented Blocks Design, at College of Horticulture, Vellanikkara with 16 blocks during *kharif* 2011 -12. Each block comprised of 10 accessions (unreplicated) and 3 checks. The accessions were characterized and evaluated for 41 qualitative traits and 24 quantitative traits as per the descriptor of rice (Rani *et al.*, 2004; IRRI 2007).

Results revealed that wide variability existed in the Base collection for all the traits studied. A core set of 34 accessions was developed by using PowerCore (v.1.0) software based on 24 quantitative traits. The representativeness of diversity in base collection in the core set was evaluated through comparison of, i) estimates of mean for the quantitative trait through One sample't' test, and ii) Levene's F-test for variances. Chi-square test was employed to examine the parity in frequency distribution of morphological traits in the core set and Base collection. All the above tests proved that both the core set and Base collection did not differ significantly from each other. This indicated that variability in core set was on par with that found in the Base collection.

Shannon-Weaver diversity index between Base collection and the core set was compared to assess the extent of diversity present in the two populations. Results revealed that core set comprising of 34 accessions has captured 100.54% of total diversity of the Base collection (160 accessions) which it was derived from. Thus, the core set proved to be a true representative of the diversity present in the Base collection. The reduced number greatly enhances accessibility of germplasm collection for breeding programmes aiming at improving yield and yield contributing traits.