

STUDY ON CLASSIFICATION AND IDENTIFICATION OF FINE RICE CULTIVARS

A THESIS

BY

YAKOUB AHMED ISMAIL

Student No. 1705173

Semester, January-June, 2017-2018

Session: 2017-2018

MASTER OF SCIENCE (MS)

IN

GENETICS AND PLANT BREEDING



**DEPARTMENT OF GENETICS AND PLANT BREEDING
HAJEE MOHAMMAD DANESH SCIENCE AND TECHNOLOGY
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**HAJEE MOHAMMAD DANESH SCIENCE AND TECHNOLOGY
UNIVERSITY, DINAJPUR**

JUNE, 2018



**Dedicated
To
My Beloved
Parents**

STUDY ON CLASSIFICATION AND IDENTIFICATION OF FINE RICE CULTIVARS

ABSTRACT

This study was carried out to identify of fine germplasms collected from different regions of Bangladesh based on morphological traits for utilization in breeding programmes. A total of 20 varieties were characterized in this study. The plant morphological traits viz., plant height, panicle length, Number of tillers per plant, hundred grain weight, effective grain, non effective grain, internode distance, lodging, number of days to 50% flowering, days to maturity, grain length and width, breadth, showed most variation among the genotypes. Among the grain quality traits exhibited most variation among the evaluated genotypes. Twenty cultivars are grouped in to five clusters.

The cluster analysis of both quantitative morphological and grain quality traits revealed the grouping of genotypes into five clusters. Minimum number (1) of genotypes were included in cluster 3 and the maximum (9) in cluster1. Cluster 2, 4, and 5 consisted of 2, 4 and 4 genotypes respectively

Dendrogram using agglomerative clustering method representing distribution of 20 rice genotypes based on morphological and grain quality trait the highest cluster mean value was observed in cluster 1for plant height; panicle length in cluster iv, no of grains in cluster v, panicle weight in cluster iv ,hundred grain weight in cluster iv, effective grain in cluster v ,non effective grain in cluster iv, internode distance in cluster iv, days of heading in cluster I, 100 grain weight in cluster iv, grain length in

cluster ii. Grain breadth in cluster iii. Grain flatness in cluster iii. The differences among the studied rice genotypes, Jaistha Kathari has golden seed color days of maturity < 121 days of heading < 73 and lodging > 25. Sada Kathari is golden color days of maturity < 121 and days of heading > 73, lodging > 25. Seed color of Paijam is golden days of maturity < 100 and days of heading < 73. Seed color of Phinekathari is golden in color, days of heading > 62. Seed color golden in Katharivog, days of heading < 76, days of maturity > 130. seed color of Chinigura is golden in color, days of maturity < days of heading > 73. Seed color of Bolder is golden plant height > 102 lodging < 53. Seed color of Badshavog is golden in color, days of heading < 76, days of maturity > 130 Seed color of RANJIT is radish brown Seed color of RADHUNI PAGOL is light brown with golden in color. Buchinbigi is radish brown, days of maturity < 121, days of heading > 73, lodging > 25. Salna is golden in color, lodging > 83, days of heading is > 62. BR-34 seed color is brown, days of maturity is < 121, days of heading is > 73, lodging > 25. Malshira seed color is radish brown, days of heading is > 64. Binnipakri is radish brown, days of maturity < 100. Dhanchikon seed color is red, days of maturity > 117. The above these are the identifying characteristics of aromatic fine rice, which are described by CART analysis.

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All praises are due to “Almighty Allah” the supreme authority of this universe, which enabled me to complete the research work as well as to prepare this dissertation for the degree of Master of Science (MS) in Genetics and Plant Breeding.

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LIST OF ABBREVIATIONS

AEZ	=	Agro Ecological Zone
Atm.	=	Atmosphere
BADC	=	Bangladesh Agricultural Development Centre
BARI	=	Bangladesh Agricultural Research Institute
BBS	=	Bangladesh Bureau of Statistics
CART	=	Classification and Regression Tree
CIMMYT	=	International Maize and Rice Improvement center
cm	=	Centimeter
CV	=	Coefficient of variation
DAE	=	Department of Agricultural Extension
DAS	=	Days after Sowing
DNA	=	Deoxyribo Nucleic Acid
DUS	=	Distinctness, Uniformity and Stability
FAO	=	Food and Agriculture Organization
FAOSTAT	=	FAO Statistical Databases
FR	=	<u>Farmers' Rights</u>
g	=	Gram
GA	=	Genetic Advance
GAM	=	Genetic advance as percent of mean
GCV	=	Genotypic Coefficient of Variation
GCV	=	Genotypic Coefficient of Variation
GDP	=	Gross Domestic Product
GLM	=	General linear model
HI	=	Harvest Index
HSTU	=	Hajee Mohammad Danesh Science and Technology University
IBPGR	=	International Board for Plant Genetic Resources.
ICAR	=	Indian Council of Agricultural Research
IFPRI	=	International Food Policy Research Institute
LGB	=	Lower glume beak
m	=	Meter

ABBREVIATIONS (Contd.)

meq	=	Mili equivalent
mm	=	Millimeter
MP	=	Murate of Potash
NGOs	=	Non-Governmental Organizations
NIFA	=	Nuclear Institute for Food and Agriculture
No.	=	Number
NWFP	=	North-West Frontier Province
°C	=	Degree Celsius
PCV	=	Phenotypic Coefficient of Variation
PPV	=	Protection of Plant Varieties
RAPD	=	Randomly Amplified Polymorphic DNA
SD	=	Standard Deviation
TSP	=	Triple Super Phosphate
UPOV	=	Union for the Protection of New Varieties of Plants
USDA	=	United States Department of Agriculture
Viz	=	Namely
WRC	=	Rice Research Centre

CHAPTER I

INTRODUCTION

Rice is a monocotyledonous angiosperm. The genus, to which it belongs, *Oryza*, contains more than 20 species, only two of which are referred to as cultivated rice: *Oryza sativa*, (Watanabe, 1997) cultivated in South-east Asian countries, and *Oryza glaberrima* cultivated in West Africa. Rice was originally cultivated in tropical Asia, the oldest record dating 5000 years BC, but then extended also to temperate regions (Watanabe, 1997).

Rice is the most important staple food in Asia. More than 90% of the world's rice is grown and consumed in Asia, where 60% of the world's population lives. Rice accounts for between 35-60% of the caloric intake of three billion Asians (Guyer *et al.*, 1998). Over 150 million hectares of rice are planted annually, covering about 10% of the world's arable land. In 1999/2000, this amounted to some 600 million tonnes of rice seed, equal to 386 million tonnes of milled rice. With the world population estimated to increase from 6.2 billion in the year 2000 to about 8.2 billion in the year 2030, the global rice demand will rise to about 765 million tonnes, or 533 million tons of milled rice (FAO, 2002). For almost three decades since the Green Revolution, the rice yield growth rate was approximately 2.5% per year. During the 1990s, however, this has decreased to only 1.1% (Riveros and Figures, 2000).

Rice (*Oryza sativa* L.) is the main staple food and dominant crop in Bangladesh. It is grown on more than three fourths of the total cultivable land and dominates the cropping pattern throughout the country. IRRI (2011) reported that over the last thousand years, rice has been the dominant crop in Bangladesh and it currently accounts for 77% of agricultural land use. There are about 13 million farm families, who grow different types of rice, which includes traditional, modern, or hybrid rice varieties. Over 11.7 million hectares of land in Bangladesh is dedicated to rice production. It provides about 70% of direct human calorie intake, making it the most important food crop in Bangladesh. Ashrafuzzaman *et al.* (2009) reported that aromatic rice in Bangladesh covered 12.5% of total Aman rice cultivation. About 75% of the total cropped area and over 80% of the total irrigated area is planted to rice. Thus, rice plays a vital role in the livelihood of the people of Bangladesh. According

to World Bank (WB) food self-sufficiency in Bangladesh mostly depends on rice production (Barmon and Chaudhury, 2012). The Government of Bangladesh (GOB) is intent on achieving self-sufficiency in food grain production based on rice (GAIN Report, 2011). The total contribution of the rice production is about 70% of the total agricultural contribution to GDP (BBS, 2009). Bangladesh's rice production is estimated to reach 338.30 LMT (lac metric tons) in the fiscal year 2011-2012, up from about 335.41 LMT in 2010. The annual production was estimated 323.00 LMT in 2009-10 (Oryza, 2012). Locally adapted genotypes of rice have evolved by nature and human selection (Kaulet *et al.*, 1982). Among these land races, many of which are either fine grain or aromatic types (Ullah *et al.*, 2011). However, the area under local rice cultivars is not likely to change, covering approximately one-third of the cropping area during the rainy season (July-December) every year. The yield potential of local rice varies from 2.5 to 3.5 t/ha (Anon, 1997). It is well known that local rice is mostly non-responsive to nitrogenous fertilizer and yield reduction is caused by lodging in most cultivars. Although the nutritional quality, palatability, delectableness, taste, cooking quality and consumer demand are higher for local rice than for high yielding varieties but some architectural defects cause significant problems with assimilation and translocation during grain-filling stages of the local cultivars. Nevertheless, higher prices, export quality and a vital role in the global market warrant their higher production, hence the need to increase the yield potential of fine rice cultivars (Golam *et al.*, 2003).

Rice production in Bangladesh has almost doubled during the past three decades (BRRI, 2014). But we can't export the coarse rice after fulfillment of the demand due to high competition with other quality rice growing countries (Chowdhury, 1991). Breeding strategies, therefore, should be focused on to produce fine aromatic rice. Rice breeders of Bangladesh Rice Research Institute (BRRI), as well as national policy makers have given emphasis on fine and aromatic rice production. Aromatic rice has long been popular in the continent, and is now becoming more popular in Middle East, Europe and United States. There is a great opportunity to earn foreign currency by exporting aromatic rice, as the consumption area of aromatic rice throughout the world is large and price would be also high (Chowdhury and Bhuiyan, 1991). Furthermore, consumers in urban areas in our country also prefer fine and aromatic rice. Most of the aromatic rice germplasm that are available in Bangladesh are low yielding, photoperiod sensitive and are grown during Aman season (Transplanted rice) in the rain fed low land ecosystem (Begum *et al.*, 1993).

To date, farmers across the country are used to cultivate different local varieties or land races particularly in the unfavorable ecosystems. Local variety including aromatic rice genotypes occupied about 12.16% of the rice growing areas in Bangladesh (BBS, 2011). Many of these local varieties have some special characteristics such as aroma, better taste, and higher cooking quality which also provide additional value in socioeconomic aspects. Moreover, aromatic rice constitutes a special group of rice genotype well known in many countries across the world for their aroma and/or super fine grain quality (Singh, 2000).

Bangladesh has a stock of above 8,000 rice germless of which nearly 100 are aromatic (Hamid *et al.*, 1982). It is worthwhile to mention that Aromatic rice is closely related to the social and cultural heritages in Bangladesh. It is consumed during weddings and other festivals (Saker., 2002). Aromatic and fine rice germplasm native to Bangladesh generally have short bold and medium bold grain type with mild to strong aroma (Shahidullah, *et al.*, 2009). In Bangladesh, among the different aromatic rice varieties, Chinigura is the predominant one that covers more than 70% of rice farms in the northern district of Naogaon and Dinajpur. Other important aromatic rice varieties are Kalijira (predominantly grown in Mymensingh) and Kataribhog (mainly cultivated in Dinajpur) (Baqul., *et al.*, 1997). Most of the aromatic rice varieties in Bangladesh are of locally adapted, photoperiod-sensitive, and grown during Amman season under rainfed lowland ecosystem. The production cost of aromatic and fine rice is low compared to that of coarse rice. Therefore, the income potential is higher with aromatic fine rice cultivation, since its cultivation does not usually require additional expenditures. Aromatic rice has got paramount importance in breeding programmes in the countries, which are self-sufficient in their production. Preference is given for kernel length, size, shape, appearance and cooking quality characters especially kernel elongation ratio. As such the plant breeders should focus their attention towards the improvement of both Basmati types and aromatic short grain rice for quality and high yield potential. The global dependence on rice has led to the development of thousands of varieties with large genetic and morphological diversity. Therefore, the documentation of distinguishing characters is very essential to carry out the scientific study. Characterizing the genetic basis of variation in plants and linking it to the observable traits will provide an important framework for significantly increasing the efficiency of selections made in plant breeding

programmes. The need for a detailed examination of diagnostic characteristics thus has become imperative to maintain identity of released and notified varieties. Characterization of variety is useful to identify and avoid duplication. Qualitative traits being more stable over generations (Raut, 2003). Therefore, attention should be given for breeding high yielding quality aromatic rice varieties. Measurement of correlation coefficient helps identify the relative contribution of component characters towards yield (Panse, 1957). Moreover, the correlation between grain yield and a component character may sometimes be misleading due to an over estimation or underestimation for its association with other characters. Thus, yield components have influence on ultimate yield both directly and indirectly (Tukey, 1954). Splitting of total correlation into direct and indirect effects, therefore, would provide a more meaningful interpretation of such association. Path coefficient, which is a standard partial regression coefficient, specifies the cause and effect relationship and measures the relative importance of each variable (Wright, 1921). Therefore, correlation in combination with path coefficient analysis will be an important tool to find out the association and quantify the direct and indirect influence of one character upon another (Dewey and Lu, 1959).

Considering the above facts the present study has been undertaken with the following objectives

- A. To study the variability and similarity among the characters.
- B. To identify the cultivars with classification and regression tree (CART).

CHAPTER II

REVIEW OF LITERATURE

Sufficient information regarding the varieties of aromatic rice with morphological and physiological analyses is meager in the world literature. Improvement in yield and quality is normally achieved by selecting genotypes with desirable character combinations existing in the nature or by hybridization. The parents identify on the basis of variability analysis would be more promising. In this chapter an approach has been made to review some of available information related to the study. The literatures relevant to this study have been reviewed under the following heads:

2.1 Genetic variability

Breeding strategies should emphasize on fine and aromatic rice production. Most of the aromatic rice germplasm available in our country is average yielding, photoperiod sensitive and grown during Kharif season in Rainfed low land ecosystem. The quantitative measurement of individual character provides the basis for an interpretation of analysis of variance. The nature and extent of variability forms the basis for all crop improvement programmes. According to Allard (1960), yield is polygenically controlled quantitative character and is highly influenced by environment. Partitioning of observed variability into heritable and non-heritable components is very much essential to get a true indication of the genetic coefficient of variability.

Sawant *et al.* (1994) observed significant differences for all the traits, with high genotypic and phenotypic coefficients of variation for grains/panicle (GP), plant height (PH), ear bearing tillers/plant, 100-grain weight (GW) and grain yield/plant (GY). Heritability and genetic advance were high for PH, GP and GW. GY had low heritability with moderate genetic advance.

Ganesan *et al.* (1995) reported moderate amount of variability (10-20%) for days to panicle emergence, plant height and days to 50% flowering.

Mishra *et al.* (1996) reported that PCV and GCV estimates were high for grains per panicle whereas PCV was high for number of chaffs per panicle, 100-grain weight

and yield. Heritability estimates were high for all characters except number of tillers per hill, panicle length and number of chaffs per panicle indicating better scope for selection. However, genetic advance was low for most of the traits

Datke *et al.* (1997) evaluated 24 F6 lines of paddy rice. All lines showed significant differences for all the characters studied, except number of effective tillers/plant and straw yield/plant. GCV was high for grain yield/plant and low to moderate for the remaining traits. High heritability values were associated with high genetic advance with respect to days to 50% flowering, plant height, number of spikelets/panicle and grain yield/plant, indicating the presence of additive genes.

Chaudhary and Das (1998) reported high genotypic coefficient of variation for grain yield followed by grains per panicle. High heritability with high genetic advance was found for grains per panicle followed by grain yield.

Shridhara *et al.* (1999) observed high heritability and genetic advance coupled with large genetic variability for amylose content, milling recovery, kernel elongation ratio, total number of tillers and number of effective tillers.

Lalitha and Sreedhar (1999) estimated high heritability for amylose content, length/breadth ratio of grain and alkali value while they were moderate for grain yield per plant and volume expansion ratio and low for protein content and gel consistency.

Singh *et al.* (1999) observed range, phenotypic coefficient of variation and genotypic coefficient of variation were higher for all characters in F5 of Pankaj x Janki, except days to 50% flowering and 1000-grain weight. Heritability for all the characters were high, the highest (99.81) for days to 50% flowering (*Oryza longistaminata* x Jagannath) and the lowest for panicles/plant (Pankaj x Janaki). Heritability was comparatively higher in cross *Oryza longistaminata* x Jagannath for most of the characters studied. All crosses recorded high genetic advance for panicles/plant, grains/panicle and grain yield/plant, the highest values (47.18%) for grain yield/plant in cross *Oryza longistaminata* x Jagannath.

Sadhukhan and Chattopadhyay (2000) recorded high GCV and PCV values for grain yield per plant and number of grains per panicle. Test grain weight, plant height, length and length-width ratio of grain and grain length after cooking had moderate to high GCV and PCV values. Broad-sense heritability estimates were moderate to high

for all the characters studied. Yield per plant, test grain weight, plant height, number of grains per panicle, length-width ratio of grain, grain length after cooking and amylose content had high genetic gain as a percentage of the population mean.

Sarawgi *et al.* (2000) revealed relatively greater genetic variability among 128 rice lines, for gel length and gelatinization temperature. The heritable component of variation was relatively high in L/B ratio, milled grain length, gel length, normalized grain weight and gelatinization temperature. The heritability coupled with genetic advance was high for gel length, gelatinization temperature, L/B ratio, normalized grain weight and 100-milled grain weight.

Yadav (2000) studied genetic variability for yield and its components in 15 genotypes of rice. Appreciable amount of genotypic coefficient of variation, heritability and genetic advance were observed for total grains per panicle, total grains per plant and grain yield per plant. This indicated the role of additive genetic component controlling these traits and scope for selections.

Bidhan *et al.* (2001) observed high phenotypic and genotypic variances for grain yield, followed by number of filled grains per panicle. They recorded heritability which ranged from 50% (grain yield per hill) to 90% (grain breadth). Genetic advance as percent of mean was highest for number of filled grains per panicle (70.34), followed by grain yield (68.72). Number of filled grains per panicle, 1000-grain weight, grain length and breadth exhibited less environmental effect and high heritability coupled with moderate to high genetic advance.

Zen and Bahar (2001) reported high heritability of all plant characters and yield (76.98% -97.96%), heritability of filled spikelets per panicle was medium (37.29 percent). Plant height, productive tillers, spikelets per year, and yield had a wide genetic variability. Selection for those characters could be done at early generation.

Nayak *et al.* (2002) studied genetic variability, heritability and genetic advance for grain yield and yield contributing characters in 2000 scented rice genotypes and high estimates of GCV and PCV were observed for number of panicles/plant and grain yield/plant.

Mishra and Verma (2002) recorded higher magnitude of GCV for kernel elongation ratio, followed by sterility percentage, biological yield per plant, and grain yield.

Genetic advance as percentage of the mean was highest for kernel elongation ratio and lowest for grain yield per plant. Plant height, flag leaf area, number of ear-bearing tillers per plant, number of fertile spikelets per panicle, sterility percentage, 100-grain weight, head rice recovery percentage, spikelet density, kernel breadth after cooking, and kernel elongation ratio showed high heritability coupled with high genetic advance.

Singh *et al.* (2002) reported high genotypic and phenotypic variances for grain yield per plant, panicle weight, number of grains per panicle and number of branches per panicle, medium for panicle length, 1000-seed weight and low for panicle length and milling percent. High heritability with high genetic advance was recorded for number of grains per panicle followed by panicle weight and grain yield per plant.

Chaudhary and Motiramani (2003) observed a wide range of variation for most of the characters. Heritability in broad sense was very high for all the characters exhibited high heritability coupled with high genetic advance except harvest index.

Mishra *et al.* (2003) observed high genotypic variance for kernel elongation ratio followed by biological yield and grain yield per plant. Heritability in broad sense with genetic gain as percentage of mean was found to be higher for head rice recovery percentage followed by spikelets density, kernel breadth after cooking and kernel elongation ratio.

Nayak *et al.* (2003) recorded moderate to high genetic variability for all characters.

Patil *et al.* (2003) observed high heritability associated with high genetic advance for alkali spreading value, unfilled grain percentage, 1000-grain weight, grain yield per plant, brown rice length: breadth ratio, ear-bearing tillers, filled grains per panicle, kernel length: breadth ratio, paddy length: breadth ratio, kernel length: breadth ratio of cooked rice, brown rice length and paddy length.

Satish *et al.* (2003) observed high GCV and PCV values for spikelets/panicle, number of grains/panicle and grain yield/plant. High heritability along with high genetic advance was observed for number of spikelets/panicle, number of grains/panicle, grain yield/plant followed by other characters. Emphasis should be given on these characters while selecting scented rice varieties to improve grain yield.

Singharia *et al.* (2003) recorded larger PCV and GCV values for number of secondary branches, panicle and grains borne on primary branch and low for days to 50% flowering, panicle length, kernel length and kernel breadth. High heritability coupled with high genetic advance was recorded for 1000-seed weight, seeds per panicle and primary branch length indicating greater scope for yield improvement through selection.

Chaudhary *et al.* (2004) studied genetic variability, heritability and genetic advance for 17 quality and plant traits of 54 aromatic rice accessions. The phenotypic and genotypic coefficients of variation, heritability and genetic advance indicated that Selection of genotypes may be carried out for kernel length: breadth ratio, length: breadth ratio of cooked rice and alkali spreading value for quality traits in all the genotypes. All the traits exhibited high heritability coupled with high genetic advance and genetic variability.

Hasib *et al.* (2004) evaluated mean performance, variability, heritability and genetic advance for four selected lines in the F₆ generation. The difference between the value of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was low in all the 8 quantitative characters studied indicating the effect of the genetic factor in controlling these traits. High heritability, and moderate to low PCV, GCV and genetic advance were observed for all the traits.

Sarma and Bhuyan (2004) observed higher GCV and PCV values for the number of grains per panicle, followed by grain yield per plant and number of effective panicles per plant. Broad-sense heritability was highest for plant height followed by days to 50% flowering and number of effective panicles per plant. The highest genetic advance was observed for number of grains per panicle, followed by grain yield per plant and number of effective panicles per plant. Grains per panicle and the number of effective panicles per plant showed high heritability and genetic advance.

Sinha *et al.* (2004) observed high GCV for grain yield followed by test weight and panicles per plant. High heritability with high genetic advance was found for grain yield followed by test weight and panicles per plant.

Vivek *et al.* (2004) revealed a wide range of variation for all the characters among the genotypes. Grain yield per plant, biological yield per plant, number of tillers and

panicles per plant had high values of genetic coefficient of variation and phenotypic coefficient of variation. They reported high heritability with high genetic advance for grain yield per plant and biological yield per plant.

Elayaraja *et al.* (2005) observed high heritability associated with moderate to high genetic advance as a percent of mean for number of productive tillers, panicle length, number of grains per panicle, 100- grain weight and grain yield per plant in M2 generation.

Madhavalatha *et al.* (2005a) revealed high variability, heritability and genetic advance for number of grains per panicle, grain yield per plant, harvest index and kernel L/B ratio, while days to maturity, fertility percentage, hulling recovery and kernel elongation ratio had high heritability coupled with low genetic advance.

Nayak and Reddy (2005) reported maximum GCV and PCV values for grain yield followed by alkali spreading in the rabbi seasons and vice versa for the kharif seasons. Broad sense heritability was high for all the studied characters in both rabbi and kharif seasons. High genetic advance was also observed for alkali spreading value and grain yield in both seasons, while moderate genetic advance values were observed for head rice recovery, kernel length, length/breadth ratio and amylase content in both seasons indicating non-additive gene action.

Patil and Sarawgi (2005) reported the genetic and phenotypic coefficients of variation were high for number of unfilled grains per panicle, unfilled grain percentage, grain yield per plant, 1000-grain weight, number of ear-bearing tillers per plant, and number of filled grains per panicle. High heritability estimates coupled with high genetic gain were recorded for grain yield per plant, number of ear-bearing tillers per plant, number of filled grains per panicle, and unfilled grain percentage.

Panwar (2005) observed high heritability and genetic advance for grain yield per panicle, chaffy grains per panicle, grain yield per plant, filled grains per panicle and secondary branch number per panicle, indicating the effectiveness of selection for these characters.

Singh *et al.* (2005) revealed significant differences among the genotypes for all the characters. High estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were recorded for grain yield (t/ha), biological yield (t/ha) and harvest index (%).

Sarkar *et al.* (2005) recorded high GCV and PCV values for number of panicles per plant, number of tillers per plant, and grain yield per plant. The highest heritability value was registered for 1000-grain weight, followed by brown kernel length and grain length. The number of spikelets per panicle and number of grains per panicle showed high heritability along with high genetic advance.

Satyanarayana *et al.* (2005) reported high variability, heritability and genetic advance for number of grains per panicle, spikelet fertility, days to 50% flowering and plant height, while test weight recorded high variability and heritability, coupled with low genetic advance. The number of effective tillers per plant and panicle length recorded low heritability.

Saxena *et al.* (2005) observed high PCV and GCV values for number of unfilled spikelet's, seed yield per plant, biological yield per plant, number of filled spikelets, total number of spikelet's, and length: breadth ratio of rough rice. Broad-sense heritability was Also very high for number of filled spikelet's, 100-seed weight, plant height, total number of spikelet's and panicle length, indicating the possibility of improving such traits through selection. Seed yield per plant and number of unfilled spikelet's showed high genetic advance.

Vivek *et al.* (2005) reported high genotypic and phenotypic coefficient of variation for grain yield, followed by harvest index and biological yield. They observed high heritability coupled with high genetic advance which were also observed for grain yield, followed by harvest index and biological yield.

Singh *et al.* (2006) recorded a wide range of variation for all the traits. The highest genotypic and phenotypic coefficients of variation were recorded for grain yield. High heritability and high genetic advance were recorded for plant height, indicating the predominance of additive gene action for this trait.

Vanaja and Babu (2006) observed high broad sense heritability for all quality attributes. High heritability, high expected genetic gain, and moderate genotypic coefficient of variation were noted for alkali spreading value, L/B ratio of grain, milling percentage, amylase content, volume expansion ratio, and water uptake, implying the potential of these parameters to be used in breeding programmed.

Kumar *et al.* (2007) recorded high PCV, GCV coupled with high heritability estimates and high genetic advance as percentage of mean for number of filled grains per panicle, 100-grain weight, biomass per plant and grain yield per plant in the F₂ populations of the cross P₁, P₃. Similarly, the F₃ population of the cross P₂, P₁ exhibited high genetic parameters for number of productive tillers per plant and grain yield per plant.

Mustafa and Elsheikh (2007) observed a wide range of genetic variability among the genotypes for most of the characters. The highest genotypic coefficient of variation was recorded for grain yield, percent unfilled grains per panicle, number of grains per panicle and number of filled grains per panicle.

Karad and Pol (2008) observed high GCV values for number of mature and immature panicles mt.sq.-1, 1000 grain weight and plant height. The estimate of heritability together with genetic advance was high for 1000 grain weight, number of mature and immature panicles and plant height.

Kole *et al.* (2008) reported high PCV and GCV values for flag leaf angle and panicle number; moderate for grain number per panicle, straw weight, harvest index and grain yield per plant; and low for days to flower, plant height, panicle length, spikelet Number, spikelet fertility (%) and test weight. High heritability accompanied by high to moderate genetic advance for flag leaf angle, panicle number, grain number, straw weight and grain yield indicated the predominance of additive gene action for the expression of these characters.

Anbanandan *et al.* (2009) observed high PCV and GCV values for grain yield per plant for cross 1 followed by cross 2 in both F₃ and F₄ generations. Also, cross 1 and cross 2 recorded high heritability and genetic advance for number of productive tillers per plant, 1000-grain weight and grain yield per plant in both F₃ and F₄ generations.

Chandra *et al.* (2009) observed high PCV and GCV values for number of productive tillers per plant, number of grains per panicle, 1000-grain weight and grain yield per plant. High heritability along with high genetic advance was observed for plant height, number of grains/panicle and 1000-grain weight.

Khan *et al.* (2009) reported highly significant differences among 25 genotypes for all the morphological traits and six genotypes used for the grain quality studies also showed significant differences among grain quality traits except volume expansion ratio and grain elongation ratio. Broad sense heritability estimates were higher for morphological traits ranging from 67.37 to 98.24.

Sabesan *et al.* (2009) observed high values of heritability along with genetic advance for grain yield per plant, 100 grain weight, productive tillers per plant, grains per panicle, grain length, grain breadth, kernel length, panicle length and plant height.

Roy *et al.* (2009) observed large amount of variability in 1,000-seed weight, alkali spreading value, brown kernel L/B ratio and moderate variability in brown and cooked kernel length, amylase content and kernel elongation index. High heritability and genetic advance were noted for 1,000-seed weight, amylase content, alkali spreading value and brown kernel L/B, implying the potential of these parameters to be used in breeding programmers.

Jayasudha and Sharma (2010) observed high PCV and GCV values for grain yield per plant, harvest index, pollen fertility (%) and spikelet fertility (%). Characters like pollen fertility (%), spikelet fertility (%), days to 50% flowering and grain yield per plant showed high value of heritability coupled with high genetic advance.

Nandan *et al.* (2010) observed high heritability along with high genetic advance as percent of mean for number of effective tillers per plant, panicle weight, number of grains per panicle, number of spikelets per panicle, 1000 grain weight, and kernel length. Before cooking (KLBC), length breadth (L/B) ratio, water uptake ratio and grain yield per plant.

Abarshahr *et al.* (2011) observed broad-sense heritability varied from 0.05 for brown grain width to 0.99 for plant height and number of spikelets per panicle under optimum irrigation and from 0.1 for brown grain width to 0.99 for plant height. The lowest and highest phenotypic CV values were observed for panicle fertility percentage and paddy yield and genotypic CV was related to brown grain width and plant height, respectively.

Babu *et al.* (2011) observed high genotypic coefficient of variation for number of panicles/hill and high phenotypic coefficient of variation for number of panicles/hill and number of tillers/hill whereas plant height, number of tillers/hill, panicle length, flag leaf length and test weight showed high estimates of heritability. Number of panicles/hill and number of tillers/hill showed high genetic advance as percent of mean.

Fiyaz *et al.* (2011) observed significant differences among the genotypes for all the traits. High values of heritability and genetic advance were observed for total spikelet per panicle, 1000- grain weight and total biomass.

Pandey and Singh (2011) observed high PCV and GCV values for grains/panicle, grain yield/plant and gel consistency. Total tillers/plant and effective tillers/plant at maturity had moderate PCV, GCV and genetic advance coupled with moderate heritability. High heritability coupled with high genetic advance was observed for grains/panicle, grain yield/plant and GC.

Singh and Pandey (2011) reported high heritability and high genetic advance for the traits plant height, effective tillers per plant, spikelet's per panicle, filled grains per panicle, grain weight per panicle, specific leaf weight, test weight, kernel length cooked kernel length, leaf area index, grain length, L/B ratio and gelatinization temperature.

Yadav *et al.* (2011) reported high PCV and GCV values for seed yield, harvest index, biological yield, number of spikelets per panicle, flag leaf length, plant height and number of tillers. High heritability coupled with high genetic advance as percent of mean was registered for seed yield, harvest index, number of spikelet's per panicle, biological yield and flag leaf length.

2.2 Genetic Divergence

Genetic improvement in any crop mainly depends upon the amount of genetic variability present in the population. The importance of genetic diversity in crop plants was first realized by Darwin (1859) and the term “morphism” employing genetic morphs was given by Huxley (1955) which means the existence of distinct genetic forms in balance in a population. Mahalanobis's D2 analysis Mahalanobis's D2 analysis is a powerful tool in quantifying the degree of divergence between biological populations at genetic level and provides a quantitative measure of association between geographic and genetic diversity based on generalized distance (Mahalanobis, 1936).

Shanthi and Singh (2001) studied the genetic divergence by using Mahalanobis's D2 statistic and Tocher's method and grouped them into four clusters. The first cluster contained nine genotypes, the second containing six while third (MM-72) and fourth (MM-71) clusters were monogenic. The genotypes belonging to clusters II and III having greater cluster distance were recommended for inclusion in hybridization programmes as they were expected to produce good sergeants.

Surender Raju (2002) assessed the genetic divergence among 42 genotypes by Mahalanobis's D2 statistic and grouped them into 12 clusters. The characters 100-grain weight, volume expansion ratio, kernel length and days to 50 per cent flowering have contributed maximum to the genetic divergence.

Yadav *et al.* (2002) assessed the genetic divergence of 100 aromatic rice genotypes and grouped them into nine clusters. The pattern of distribution of genotypes within various clusters was random and independent of geographical isolation. Based on mean performance, genetic distance and clustering pattern, inter-crossing of genotypes Gam Poon, Khao Jao Hawam, Basmati Sufaid 187, KCN 80152, Abor Bora and Hara may be useful in creating wider variability for important agronomic and quality traits with high yielding sergeants.

Mishra *et al.* (2003) evaluated the nature and magnitude of the genetic diversity in 16 rice cultivars and their 72 F1 hybrids. The genotypes were grouped in 12 clusters based on the relative magnitude of multivariate D2 values. The highest number of genotypes was in cluster XII. The highest genetic distance was observed between

clusters III and VIII and lowest between cluster VII and VIII. No close correspondence was evidenced between geographical distribution and genetic divergence.

Das *et al.* (2004) studied genetic divergence in 50 landrace collections of rice and grouped them into 10 clusters. Days to 50 % flowering, seed yield per plant, grain length, kernel breadth and 100-kernel weight were identified as potential characters that can be used as parameters while selecting diverse parents in the hybridization programmers for yield and quality improvement.

Nayak *et al.* (2004) analyzed the nature and magnitude of genetic divergence among two hundred scented rice genotypes for ten quantitative traits and grouped the genotype into ten clusters. No relationship was found between the clustering pattern and geographical distribution. Days to 50 % flowering played a important role in the formation of clusters.

Madhavalatha and Suneetha (2005) evaluated 54 elite rice germplasm lines for their genetic diversity with regard to yield, yield components and quality traits. The genotype were grouped into nine clusters, a perusal of the results on cluster means revealed plant height and days to 50 per cent flowering, together accounted for 82.04 per cent of the total genetic divergence, indicating their importance in the choice of parents for hybridization programmed.

Senapati and Sarkar (2005) studied the genetic divergence in 40 tall indicia rice genotypes and clustered them into five groups. Majority of the genotypes (30) were included in cluster I. Cluster II was second with six genotypes, while cluster III had only two genotypes. Cluster IV and V were the mono genotypic clusters. Cluster IV showed Maximum genetic distance from cluster V suggested wide diversity between these groups. Panicle number per hill, panicle length, sterility percentage, yield per plot and 1000-grain weight was the chief contributors towards genetic divergence. Suman *et al.* (2005) grouped 114 rice genotypes into 10 clusters by using Mahalanobis D2 statistic. The maximum inter-cluster distance was observed between clusters V and X. Harvest index gave the highest contribution towards divergence followed by seed density and total number of tillers per plant. Geographical diversity did not relate to genetic diversity.

Deepak *et al.* (2006) studied genetic divergence among 50 aromatic rice accessions including five scented improved varieties and grouped them into 7 clusters. The cluster VI had the highest mean for seed yield per plant and for biological yield per plant. Inter cluster distance was recorded highest between cluster III and cluster IV. The conclusion drawn by the cluster analysis was that in the studied population high variability was observed between the genotypes in different clusters for different characters.

Mundhe *et al.* (2006) studied genetic diversity in 39 rice genotypes and grouped them into seven clusters. Intra-cluster distance was maximum in cluster III followed by cluster II and cluster I. Inter-cluster distance was maximum between cluster V and VII followed by cluster III and V, and cluster II and V. Ravinder *et al.* (2006) studied genetic divergence in 50 unscented rice genotypes for yield and grouped them to three and four clusters in normal and late-sown conditions, respectively. There was no relationship between clustering pattern and geographical distribution. Based on the high cluster mean and wide genetic distance, hybridization between superior genotypes of clusters Individuals (IR 36, Palman 579, BR 827, HKR 117, HKR 126, HKR 86-105, IR 64 and RP 2151-21-22) and cluster III (Govind and NDR 84) had been advocated to achieve high heterocyst and high yielding sergeants.

Singh *et al.* (2006) studied the genetic divergence in 52 traditional lowland rice genotypes by using Mahalanobis D2 statistics and grouped into six clusters. Clusters II, III, and IV exhibited high values for most of the characters. Plant height, followed by leaf angle and leaf area, highly contributed to the formation of clusters. Clusters II, IV, and V showed maximum inter-cluster distances and high values of plant height, Days to 50 percent flowering, panicle length, seed yield per plant and milling percent, may be used for initiating a hybridization programme.

Arivoli *et al.* (2007) evaluated a total of 23 rice genotypes, which were grouped into 11 clusters based on D2 analysis. Results revealed the presence of morphological differences between the genotypes. The characters like total number of grains per panicle, number of filled grain per panicle and plant height contributed maximum towards total genetic divergence.

Sandhyakishore *et al.* (2007) studied genetic divergence for different yield attributing traits in 70 rice genotypes and grouped them into nine different clusters. The mode of distribution of genotypes from different eco-regions into various clusters was at random indicating that geographical diversity and genetic diversity were not related.

Sarawgi and Bisne (2007) worked on genetic divergence in 81 scented rice genotypes. Based on D2 statistics genotypes were grouped into nine clusters. The genotypes from cluster II having desired mean for characters like hulling percentage, milling percentage and head rice recovery and panicle length; cluster VII having high value for kernel length and Lper B ratio and cluster V low value for Days to 50 percent flowering but highest value for seed yield Kg ha⁻¹.

Kumar *et al.* (2008) estimated genetic divergence in 30 genetically diverse genotypes of rice by using Mahalanobis D2 statistic and grouped them into eight clusters. The intercluster distance was highest between clusters V and VI. This indicates that the genotypes could be used in hybridization programmed and are likely to exhibit high heterocyst and possibility of throwing transgressive sergeants in subsequent generations.

Shahidullah *et al.* (2009) assessed the genetic divergence in 40 aromatic rice for grain quality and nutrition aspects. In multivariate analysis, genotypes were grouped into six clusters. The inter-cluster D2 value was maximum (26.53) between I and VI followed by 21.28 (between I and V). Majority of the local aromatic rice varieties with smaller kernels were included in the cluster I. The cluster III contains Elai, sarwati and sugandha-1 with long-slender kernel and 'very good' appearance. Thus, these varieties can be used in breeding programmed for improvement of germplasm. Mohanty *et al.* (2010) evaluated 40 rice genotypes using Mahalanobis's D2 analysis. The 40 rice genotypes were grouped into five clusters. The pattern of distribution of genotypes from different eco-geographical regions into various clusters was at random indicating that geographical diversity and genetic diversity were not related. The characters viz. leaf area at 90 DAS, Number of grains per panicle and Days to 50 percent flowering contributed maximum towards genetic divergence among the genotypes.

Padmaja *et al.* (2010) analyzed the genetic divergence in 150 genotypes of rice by using Mahalanobis D² statistics revealed the existence of considerable diversity among the genotypes. On the basis of D² values, the genotypes were categorized into 13 clusters. Cluster XI was the largest consisting of 28 genotypes, while cluster I contained only two genotypes. Cluster I showed maximum inter-cluster distance with cluster IX indicating that the genotypes from these clusters may be used as potential donors in hybridization programmed to obtain desirable recombinants.

Parikh *et al.* (2011) evaluated the 71 rice accessions to study the diversity pattern among the genotypes. The genotypes were grouped in to eight clusters. The mode of distribution of genotypes from different geographic regions in to various clusters was at random, indicating no association between geographical distribution of genotypes and genetic divergence. The inter-cluster distance, indicating wider genetic diversity among the accessions of different groups. Sharma *et al.* (2011) evaluated the genetic divergence using D² statistic in 63 rice genotypes and grouped them into eight different clusters, in which, cluster VII was the largest having 16 genotypes. Based on mean performance, genetic distances and clustering pattern, the genotypes; Pusa Basmati-1 and Taraori Basmati of cluster II, Sarju52, Narendra Usar-3 and Narendra-80 of cluster IV, Badshah Bhog, MTU-7029 and BPT5204 of cluster VI and Malviya-36, Kanakjeer and Super Basmati of cluster VIII proved to be promising for use in hybridization programmer. Vennila *et al.*, (2011) evaluated 41 rice genotypes for yield and yield attributing characters. The analysis of variance revealed significant differences among the genotypes for all the characters studied. Based on the genetic distance all the 41 genotypes were grouped into thirteen different clusters. The maximum inter-cluster distance was recorded between clusters III and XIII and the maximum intra-cluster distance was found in cluster XI followed by VI. The characters like number of grains per panicle, plant height, and grain length and grain breadth contributed maximum towards genetic diversity. Ovung *et al.* (2012) studied genetic divergence in 70 rice genotypes by considering 13 quantitative characters. The genotypes were grouped into nine clusters. The inter cluster distance was maximum between cluster VI and VII followed by cluster III and IX, Suggesting that the genotypes constituted in these clusters may be used as parents for future hybridization programmer. Traits like spikelets per panicle, plant height and biological yield were the major contributors to genetic divergence. Chakravorty *et al.* (2013) assessed

genetic divergence among 51 rice genotypes grouped them into 11 clusters. Cluster II was found to be the largest comprising 16 genotypes followed by cluster III having eight genotypes and cluster I included 7 genotypes. Cluster VI and XI had single genotype each. The characters viz. Culm diameter, Culm length, grain length contributed maximum towards genetic divergence. On the basis of cluster mean, intra and inter cluster distance and per se, cluster XI, X, XI, VI and VII may be used for their desirable characters in breeding programme of rice. Entries like, Sarkele aman, Annada and Jhingasal were selected which could be intercrossed to obtain high heterotic effect and also to recover desirable transgressive segregants. Lingaiah *et al.* (2014) studied Sixty four mid early group genotypes of rice for genetic diversity for yield and yield contributing characters. Sixty four genotypes were grouped into 11 clusters. The pattern of distribution of genotypes into different clusters was at random. Plant height contributed maximum towards genetic divergence followed by Days to 50 % flowering. The maximum inter cluster distance observed for between IV and VII (182.08) followed by cluster I and IV (169.94). Suresh *et al.* (2014) analyzed 189 diverse genotypes and grouped into 12 distinct non overlapping clusters. Among the twelve clusters, cluster I was largest with 39 genotypes, followed by cluster IX (33), cluster IV (30) and cluster XII with 28 entries. Cluster IX exhibited very high inter-cluster distances from cluster VIII, VII and VI, while IV showed very high intra-cluster diversity. From cluster mean value of different characters toward genetic divergence, genotypes in cluster IX, VIII, X and II deserve consideration for their direct use as parents in hybridization programs to develop high yielding rice varieties. Devi *et al.* (2015) evaluated 92 rice cultivars using Mahalanobis D² statistic. Based on cluster analysis, the genotypes were grouped into 10 clusters of which clusters VII and IX are the largest clusters consisting of 16 genotypes each while cluster V was the smallest with only a single genotype. The maximum intra cluster distance ($D = 14066.5$) was found in cluster VI consisting of two traditional varieties AS 100 and Chittimutyalu. The most divergent clusters found were Clusters V and VI. Minimum inter cluster distance ($D = 5144.43$) was found between Clusters VIII and IX. Amylase content, gel Consistency, 1000 grain weight and head rice recovery were found to be the most contributing traits towards genetic diversity. Hoque *et al.* (2015) analyzed 60 rice genotypes and grouped them into seven distinct clusters. The highest intra-cluster distance (21.95) was observed in cluster II whereas that was lowest (7.62) for cluster VI. Maximum inter-cluster distance was observed between cluster

III & VII (46.75) followed by cluster II & VII (42.91), cluster V & VII (38.48), and cluster III & VI (30.87). In all cases inter-cluster distance was higher than the intra-cluster distance suggesting wider diversity among the genotypes. Traits such as number of filled grains per panicle, number of unfilled grains per panicle, flag leaf area, plant height and days to maturity contributed highest towards genetic diversity. Mohan *et al.* (2015) evaluated 43 genotypes derived through pedigree method of breeding involving 11 divergent parents using D2 studies. Highest inter cluster distance (8.69) was observed between cluster II & V followed by cluster II & III (7.87) suggesting wide diversity between traits. Among the traits studied, test weight and days to flowering contributed highest. The genotypes grouped in cluster II could be crossed with JGL 21002 and JGL 21005 of cluster III to derive transgressive sergeants for improvement of seed yield, number of grains per panicle and test weight.

2.3 CART Analysis in Agriculture

Zhang *et al.* (2012) observed that to produce sufficient food with limited arable lands has been a challenging issue. Thus, identification of the main factors influencing crop productivity has attracted the attention of many researchers. Fengqiu County of Henan Province, located in North China was chosen as study area; soil property and agronomic practice data of 111 sites were collected during the 2009 growing season. Measurement on soil parameters were made on top-soil (0 to 20 cm) and sub-surface soil (20 to 40 cm) of sampling sites, while agronomic practices data were obtained through survey using questioner. The relative importance of soil parameters and agronomic practices in influencing yield variability was analyzed with step-wise linear regression analysis and classification and regression tree (CART) model.

Zheng *et al.* (2009) observed that drought is the most critical environmental factor limiting the productivity of agricultural crops worldwide. Increased frequency and severity of drought are expected to accompany climate change and will negatively impact global food security. Wide yield variability from field to field, and consequently reduced average yield on a regional scale often occur under drought conditions. The reasons for the yield variability are still poorly understood. In this study, we explored sources of soybean yield variability among fields in a rural village of Northeast China associated with a severe drought growing season in 2007. Soil

parameter measurements were made on fields following three transects with different distances from homestead. Management data were assembled from household interviews. The relative importance of soil parameters and management practices resulting in yield variability among fields was analyzed with general linear model (GLM) and classification and regression trees (CARTs) models.

Tittonell *et al.* (2008) observed that to guide soil fertility investment programmers in sub-Saharan Africa, better understanding is needed of the relative importance of soil and crop management factors in determining smallholder crop yields and yield variability. Spatial variability in crop yields within farms is strongly influenced by variation in both current crop management (e.g. planting dates, fertilizer rates) and soil fertility. Variability in soil fertility is in turn strongly influenced by farmers' past soil and crop management. The aim of this study was to investigate the relative importance of soil fertility and crop management factors in determining yield variability and the gap between farmers' maize yields and potential yields in western Kenya. Soil fertility status was assessed on 522 farmers' fields on 60 farms and paired with data on maize-yield and agronomic management for a sub-sample 159 fields. Soil samples were analyzed by wet chemistry methods (1/3 of the samples) and also by near infrared diffuse reflectance spectroscopy (all samples). Spectral prediction models for different soil indicators were developed to estimate soil properties for the 2/3 of the samples not analyzed by wet chemistry. Because of the complexity of the data set, classification and regression trees (CART) were used to relate crop yields to soil and management factors. CART proved a useful tool for simplifying analysis and providing robust models linking yield to heterogeneous crop management and soil variables.

Barton *et al.* (2010) conducted an experiment for the identification of fossil pollen at the generic rather than species level is hampering progress in understanding the biogeography and dynamics of paleo-vegetation. They used CART analysis to facilitate the differentiation of fossil pollen of *Pinusbanksiana* and *Pinusresinosa*, which are morphologically similar and nearly always combined in paleoecological studies. The CART model, using four of the ten morphological traits measured, exhibited a high level of correct identification for pollen of each of the species and shows promise as a tool for increasing the detail of paleoecological records and inferences.

CHAPTER III

MATERIAL AND METHODS

The present experiment was carried out during kharif, 2018. The experiments were conducted in the Plant Breeding Research Field, Department of Genetics and Plant Breeding, Hajee Mohammad Danesh Science and Technology University, Dinajpur.

3.1 List of the experimental materials

A total of twenty cultivars were collected from different parts of Bangladesh. The materials included twelve land races, one developed (Paijam) and two exotic (Philippine katari and Ranjit) cultivars. The name of the cultivars and places of collection are presented in Table 1.

3.2 List of the experimental materials

A total of twenty cultivars were collected from different parts of Bangladesh. The name of the cultivars and places of collection are presented in Table 1.

Table 1. The sources of the experimental genotype used in are listed below:

Sl. No.	Cultivar name	Place of collection	
		Upazila	District
1	Katharivog	Sadar	Dinajpur
2	Ranjit	Fulbari	Dinajpur
3	Philippine katari	Birol	Dinajpur
4	Kalosoru	Sadar	Dinajpur
5	Paijam	Fulbari	Dinajpur
6	Badshavog	Chiribondar	Dinajpur
7	Shadakatari	Chiribondar	Dinajpur
8	Kalizira	Sadar	Narail
9	Jaistha kathari	Chiribandar	Dinajpur
10	Chinigura	Ulipur	Kurigram
11	Radhunipagol	Birol	Dinajpur
12	Bolder	Sadar	Lalmonirhat
13	Begunbichi	Sadar	Rangpur
14	Salna	Fulbari	Dinajpur
15	BR-34	Birol	Dinajpur
16	Ukhnimadu	Sadar	Gaibandha
17	BR-49	Sadar	Dinajpur
18	Malshira	Fulbari	Sherpur
19	Binnipakri	Birol	Dinajpur
20	Dhanchikon	Sadar	Dinajpur

3.2.1 Location

The experimental field was located at 24.00° N latitude and 90.25°E longitude at an altitude of 34m from the sea level (Fig. 1). The land belonged to the agro-ecological region of the AEZ (Old Himalayan Piedmont Plain).

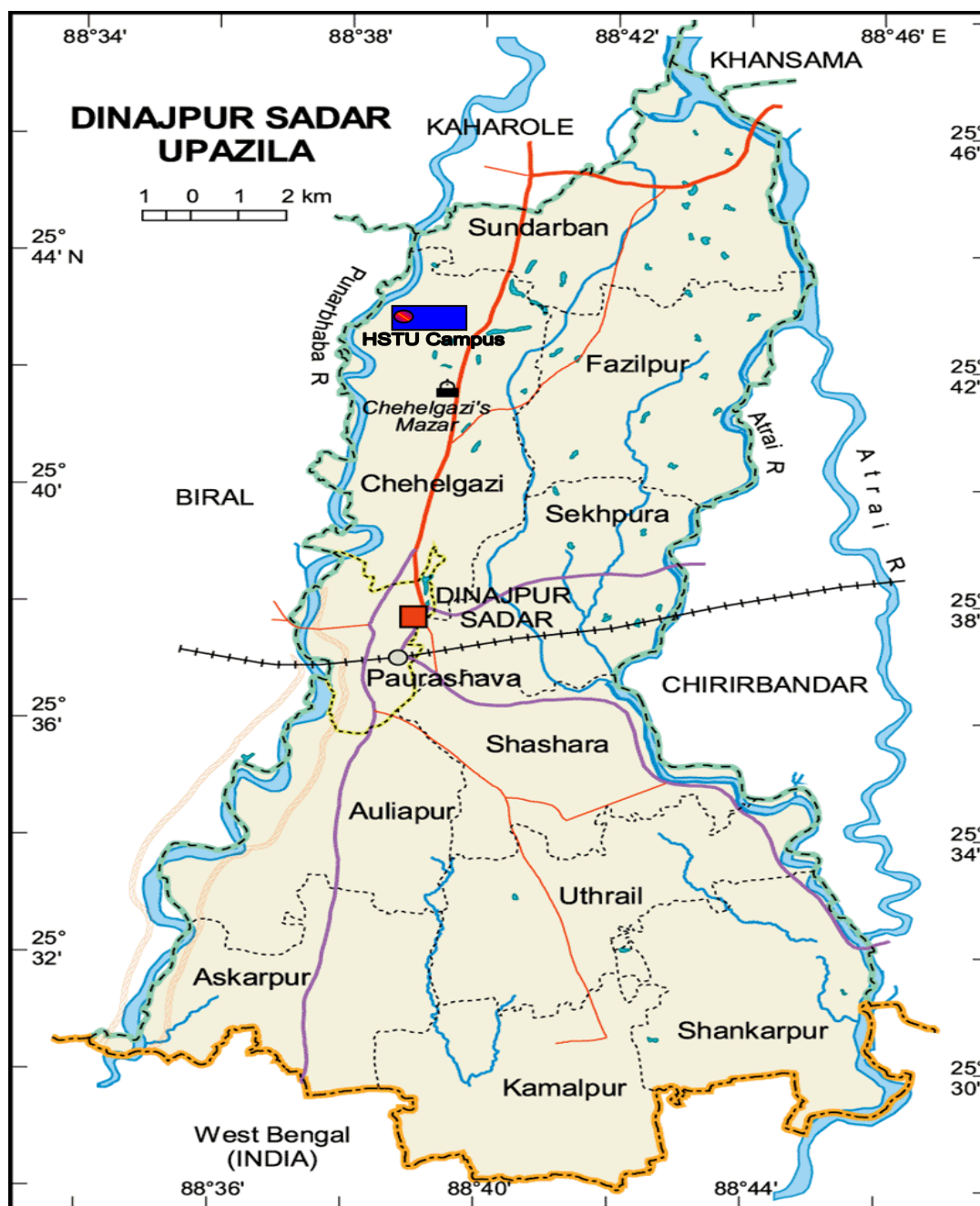


Fig. 1. Map of Dinajpur district showing experimental site

3.2.2 Climate and soil

The experimental site is situated in the tropical climatic zone, characterized by heavy rainfall during the months from May to September and minimum rainfall during winter season. The average yearly temperature (°C) and rainfall (mm) are presented in Appendix 1.

Soil of the experimental field was sandy loam in texture having a pH of around 6.2.

3.3 Experimental design and layout

The experimental plots were laid out in Randomized Complete Block Design with three replications. Each replication contained 19 plots each cultivar having 20cm×20cm spacing. The unit plot size was 3m in length and 2m in breadth. The cultivars were randomly distributed to each of the plots within a block.

3.4 Field and other operations

3.4.1 Land preparation

The land was prepared by two Ploughing and one cross ploughing with a tractor mounted disc plough. Three days later the land was again ploughed and cross ploughed with the country plough followed by laddering to get a good puddle condition. Weeds and stubbles were removed from the field prior to sowing of seeds and transplanting of seedlings. Manures and fertilizers were applied as per the recommended doses and irrigation channels were made around each block.

3.4.2 Seedbed preparation and rising of seedling

Each seedbed was prepared with 2m length and 1m width and recommended doses of manure and fertilizers were applied. A 50cm drainage channel was allowed between two adjacent seedbeds to drain out excess water whenever needed. The grains were soaked in water for 24 hours and then incubated in a moist jute sack for 48 hours with a view of quick germination. The sprouted seeds were sown in the seedbeds on 1 July in every year. The beds were irrigated to a depth of 2-3cm after establishing the roots. Excess water was occasionally drained off to attain water depth of 5cm that partially

controlled weeds, and the remaining weeds were removed to raise healthy and vigorous seedlings.



Fig.2. Field view at tillering stage with border plots

3.4.3 Fertilizer application

The following doses of manure and fertilizers were applied in the fields.

Recommended doses of manure and fertilizers

Types of Fertilizers	Recommended dose (Kg/ha)
Urea	150
TSP	100
MP	70
Gypsum	60
Cow dung	4000

The cow dung was applied at the beginning of land preparation and all the fertilizers except urea were applied as basal dose at the time of final land preparation. Urea (150kg / ha) was applied in equal three splits. The first dose of urea was applied at 21 days after transplanting (DAT), the second dose of urea was added as top dressing at 45 days (active vegetative stage) after transplanting and third dose was applied at 60 days (panicle initiation stage) after transplanting as recommended by BRRI.

3.4.4 Uprooting of seedlings

The seedbeds were made wet by applying water both in the morning and in the evening on the previous day of uprooting the seedlings. Seedlings were uprooted carefully without causing any injury of the roots and were kept in a shade for transplant in the next day.

3.4.5 Transplanting

Twenty five years old seedlings of the aromatic rice cultivars were transplanted with a single seedling/hill on 25 July in 2016.

3.4.6 Intercultural operations

The following necessary intercultural operations were taken during entire cropping period for proper growth and development of the plants and to receive a good harvest

from the research field whereas, the farmer's plot was independently maintained by the farmer.

3.4.6.1 Gap filling

Some gaps were created within in a plot due to establishment failure of some transplanted seedlings. These gaps were filled in after seven days of transplanting by the excess seedlings kept between the plots.

3.4.6.2 Weeding

Weeding was done during first two top dressings of urea to break the soil crust, to keep the plots free from weeds and to incorporate the urea properly into the soil which reduced the loss of urea through gentrification and leaching.

3.4.6.3 Irrigation

Three irrigations were given to maintain 5-7cm water depth at hard drought stage of the field and adequate measures were taken to keep the pest and disease infestation to a minimum level.

3.4.6.4 Harvesting

Maturity of crops was determined when 80% of the seeds became physiologically mature. The harvested crop of each plot was separately bundled, properly tagged and then brought to the threshing floor. The yield of grain was recorded after thoroughly drying in the sun.

3.4.6.5 Processing

After harvest grains were threshed, cleaned and sun dried to record the grain yield / plot. The grain was adjusted to 14% moisture content. Then grain yield was converted to t/ ha.

3.5 Collection of data

3.6 Recording of Observations

Twenty plants of each genotype in each replication selected randomly from central rows, were used to record data on 14 characters. The mean values were considered for statistical analysis.

3.6.1 Plant height (cm)

Plant height from each line of twenty randomly selected plants was measured from the ground level to the tip of the longest panicle.

3.6.2 Panicle length (cm)

Panicle length was recorded from the basal node of the rachis to the apex of each panicle. Average number of panicle length was calculated from the total of ten randomly selected hills for each cultivar.

3.6.3 Non effective grain

It expressed the number of sterile grain out of total grain/ panicle multiplied by 100.

$$\left[\text{Sterility percentage of grain} = \frac{\text{Number of sterile spikelets/ panicle}}{\text{Total number of spikelets/ panicle}} \times 100 \right]$$

3.6.4 100-grain weight (g)

One hundred clean dried grains were counted from the seed stock obtained from ten randomly selected hill of each plot and weighed by using an electrical balance

3.6.5 Grain breadth

The breadth of 20 grains for each cultivar was measured in mm by slide calipers and then averaged and determined in mm.

3.6.7 Grain flatness

The flatness of 20 grains for each cultivar was measured by slide calipers.

3.6.8 Grain color

By visual estimates grain color was determined.

3.6.9 Number of tillers/plant (maximum vegetative stage)

Tillers that had at least one leaf visible area were counted. It was calculated from the tillers of ten randomly selected hills of each genotype at vegetative stage.

3.6.10 Productive tillers/plant

The tillers which had at least one grain / panicle were considered as effective tillers. The total number of ear bearing tillers were counted from each of the sample hills and average were taken.

3.6.11 Sterility percentage

It expressed the number of sterile grain out of total grain/ panicle multiplied by 100.

$$\left[\text{Sterility percentage of grain} = \frac{\text{Number of sterile spikelets/ panicle}}{\text{Total number of spikelets/ panicle}} \times 100 \right]$$

3.6.12 Days to 50% flowering

Number of days required for protrusion of panicles from the boot leaves in 50% of the hills in each replication was counted and their average was taken as the days to 50% flowering.

3.6.13 Days to maturity

It was the average maturity days of each cultivar over the replications. Recorded as days on plot basis when about 80% of the hills were ready for harvesting.

3.6.14 Grain length (mm)

The grain length of a cultivar was obtained by a digital slide calipers. Ten grains were randomly selected from each of the cultivars and after measuring the lengths the average was taken.

3.7 Statistical analysis

The collected data on each line were statistically analyzed for compare the morphological characters of the twelve cultivars of rice. For construction of random decision tree R software 3.5.0 (R Core Team, 2017) was used.

Classification and regression-tree (CART) analysis provides a simple, nonparametric method for recursively classifying levels of a dependent variable using a set of independent variables. CART models recursively partition the data to find increasingly homogeneous subsets based on independent variable splitting criteria using variance minimizing algorithms. The dependent data are partitioned into a series of descending left and right child nodes derived from parent nodes (Breiman *et al.*, 1984). Once the partitioning has ceased, the child nodes are designated as terminal nodes. In this case, the twelve rice cultivars are classified based on morphological traits. In each step of the CART analysis, the splitting criterion that minimizes the probability of miss classification, measured by the Gini index, is chosen. A 10-fold cross-validation estimate of predictive error is computed for each split. The tree is “grown” recursively, adding a new split in each step, until reaching a specified level of complexity, after which the tree is pruned back to the number of splits that minimizes the cross-validation error. Then analysis, therefore, produces a classification or decision tree, much like a standard taxonomic key, allowing robust identification of twelve rice cultivars using a small set of morphological measurements. In order to test the accuracy of the CART tree, we reserved a test set of 20 randomly selected plants for each cultivar. The model was then built and the accuracy of the model was tested on the reserve data set. The R programming environment (R Development Core Team 2017) was used to carry out the CART analysis (Maindonald and Braun, 2003; Therneau *et al.*, 2009).

In order to exclude Kaligira, Kalosuru, Katharivog, Badshavog, Sada Kathari, Fillipine Kathari, Bolder, Ranjit, Chinigura, Paijam, Jaistha Kathari, Radhuni Pagol, we also carried out preliminary analyses of collected data from these twelve cultivars.

CHAPTER - IV

RESULTS AND DISCUSSION

The present study was done with an objective of characterizing the rice varieties in morphological, basis for utilization in improvement programmes. The salient findings of the study are summarized below:

Out of 16 morphological traits observed, plant height, panicle length, number of spikes per plant, panicle weight, number of tillers per plant, hundred grain weight, effective tillers, number of days to 50% flowering, days to maturity, grain length and width, internode distance, lodging, grain flatness, single grain weight showed most variation among the genotypes.

The twenty genotypes characterized were grouped into five clusters based on morphology and grain quality traits.

4.1 Plant Height (cm)

Plant height is a yield contributing trait that related to the food source of rice plant. Semi dwarf plant height in rice is preferred because they suffer from source limitation and a tall type suffers from lodging, operatively tall varieties were cluster III which includes only kalozira. Comparatively dwarf variety br 49 and dhanchikon were cluster ii and shows the shortest plant height dwarf. Sabouri *et al.* (2008) recommended the plant height as an important trait for selection of high yielding rice plants. Akram *et al.* (2007) and Osekita *et al.* (2015) also found the significant result of plant height and the genotypes were obtained moderate plant height.

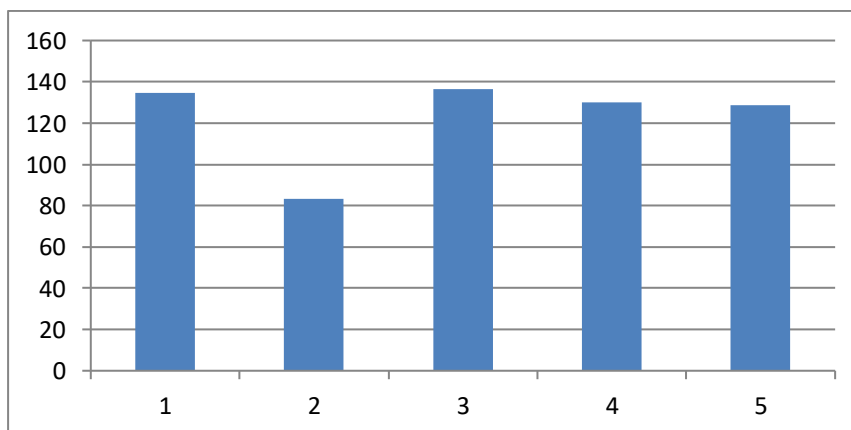


Fig: 3. Showing different of Plant Height (cm) in fine clusters

4.1.1 Panicle length (cm)

Panicle length is an important character of rice cultivars and it influences on grain yield through number of grain per panicle. Long panicle length was found in cluster iv which includes rojit, br-34, radhnipagol, and kathrifog (22.94167) while the cluster ii iii and v were so very close. Short panicle length was found. Patel, (1967) has reported that the yield, in general was associated with panicle length and with grains/panicle (Mathure *et al.* 2011, Sarawgi *et al.* 2012) found a better association among panicle length, number of tillers/plant and 1000-seed weight.

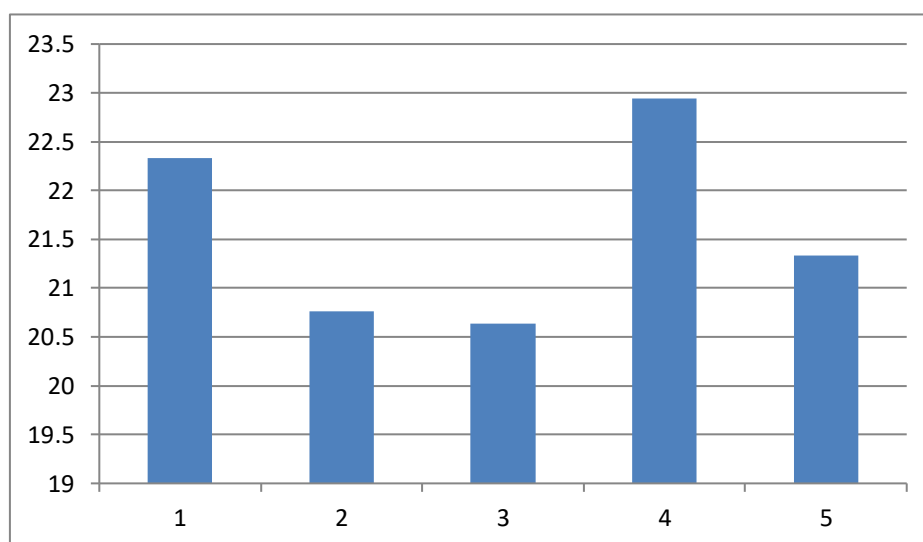


Fig. 4: Showing different of panicle length (cm) in fine clusters

4.2.2 No. of Grains/panicle

Investigation of the number of grain per panicle is important because this directly influence the grain number and grain mass per panicle in rice. In previous research Pachauri *et al.* 26 and Begum *et al.* 9 suggested considering grain per panicle by using their phenotypic and/or genotypic direct effects as economic trait for better varietal development. Cluster iv were the highest number of grains per panicle, (151.2833) these are ronjit, br-34, radgnipagol. Katharivog and chanchikon (0.6). While cluster II, III and V were the lowest number of grains per panicle include.

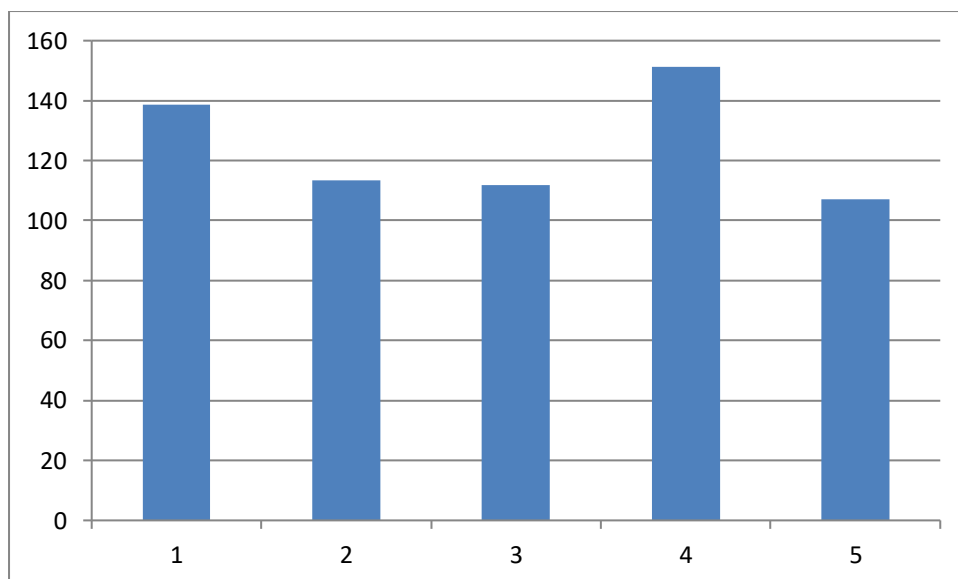


Fig. 5: Showing different number of grain per panicle in fine clusters

4.1.3 Panicle weight

Panicle weight is a key quality attribute and an important component of yield. Although this is genetically controlled, the growing conditions exert considerable influence on its expression. In the present investigation, wide variation between the varieties was observed for seed weight per panicle, where the longest panicle weight found in cluster III which includes only kalozira.

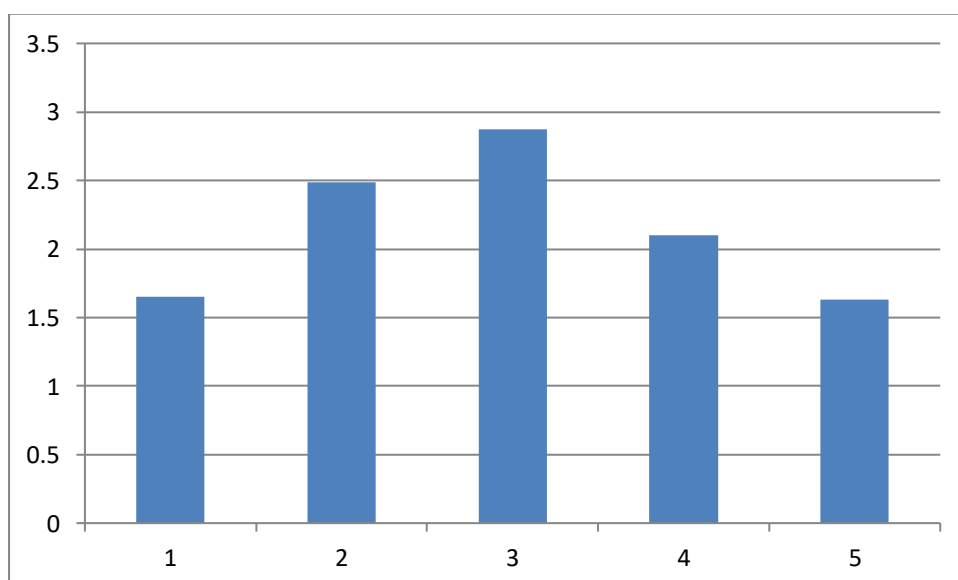


Fig. 6: Showing different panicle weight in fine clusters.

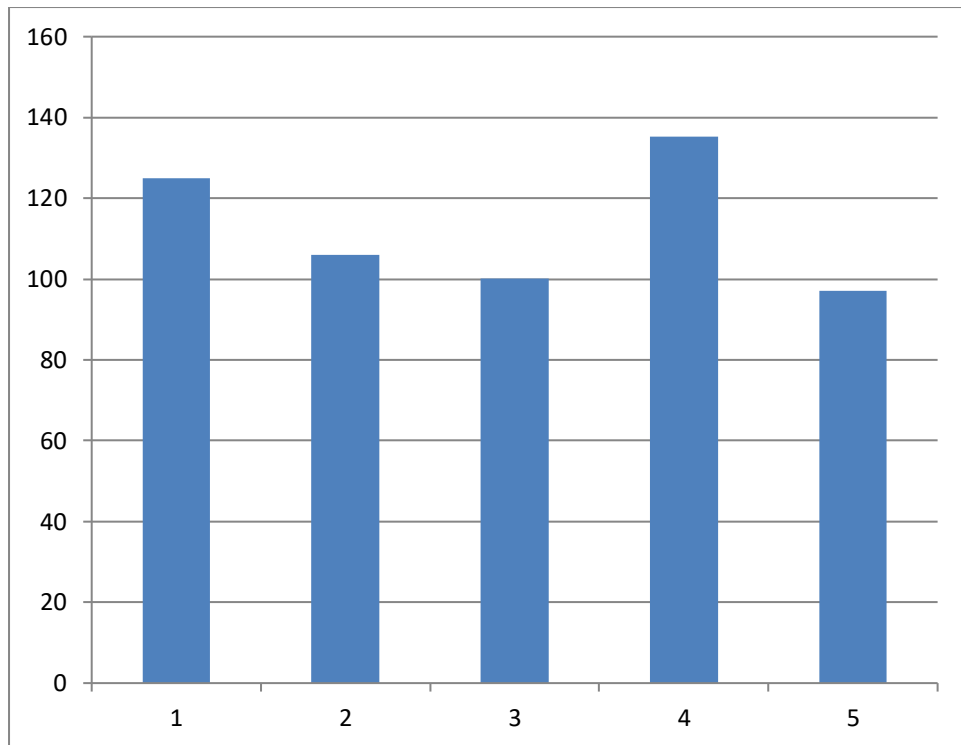


Fig 7: Showing different of effective grain in fine clusters.

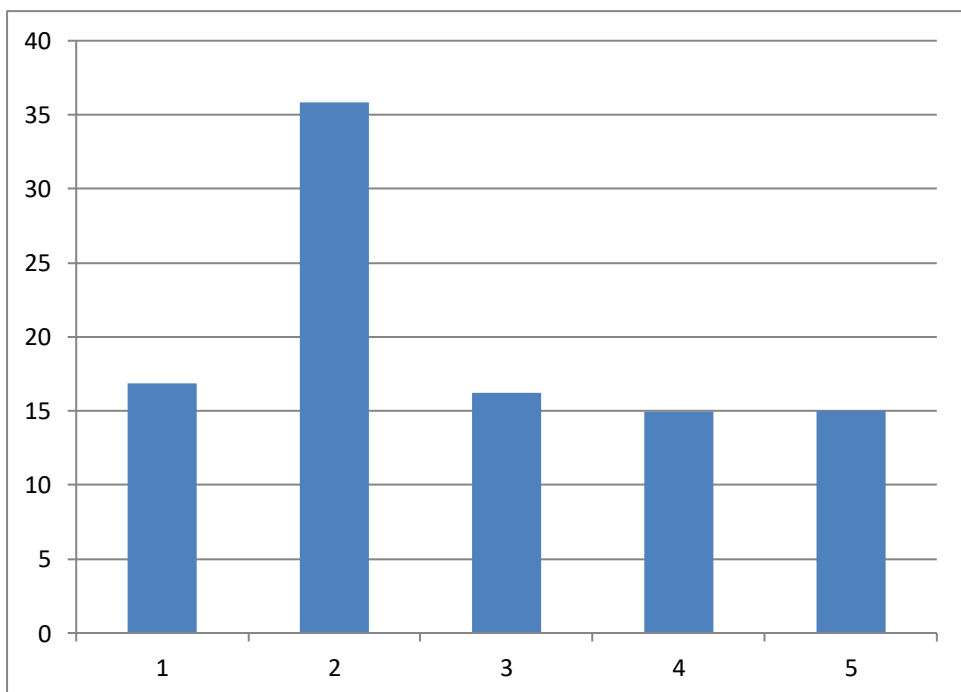


Fig 8: Showing different of non effective grain in fine clusters.

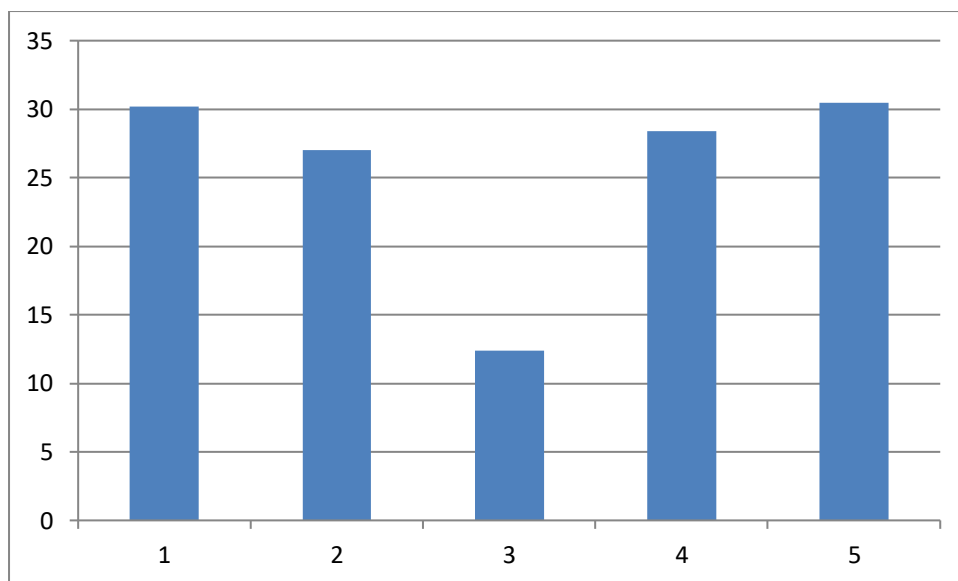


Fig 9: Showing different of internodes distance in fine clusters.

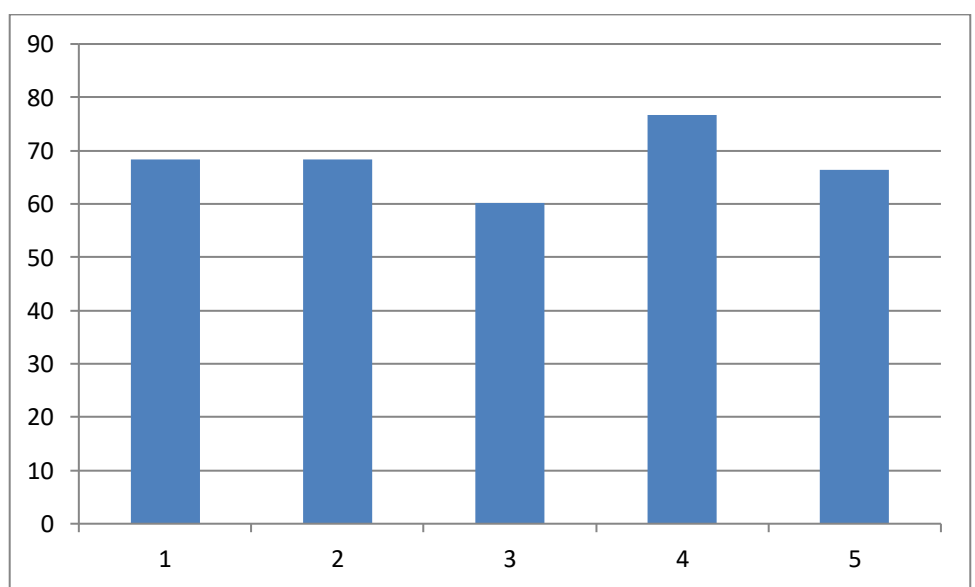


Fig 10: Showing different of days of heading in fine clusters.

4.1.4 100 grain weight

The 100-grain weight (g) is one of the most important characters for choosing the rice cultivars, because it increases seed germination percent, seedling emergence, tillering, panicle density and yield. Generally, as the number of plants increases, the number of panicles per unit area increases as well and the increase in the number of seeds per panicle resulted in a decrease in the weight of individual seeds. A variation was found

among the cultivars and It was ranged from 0.81 to 1.86 (Table 2). The highest thousand grain weight followed by Badshavog, Radhunipagol was recorded in the cluster badhshavog, begunbichi, salna, and chinigura. III which includes only sadakathari, badhshivog, begunbichi, salna, chinigura, piazam.

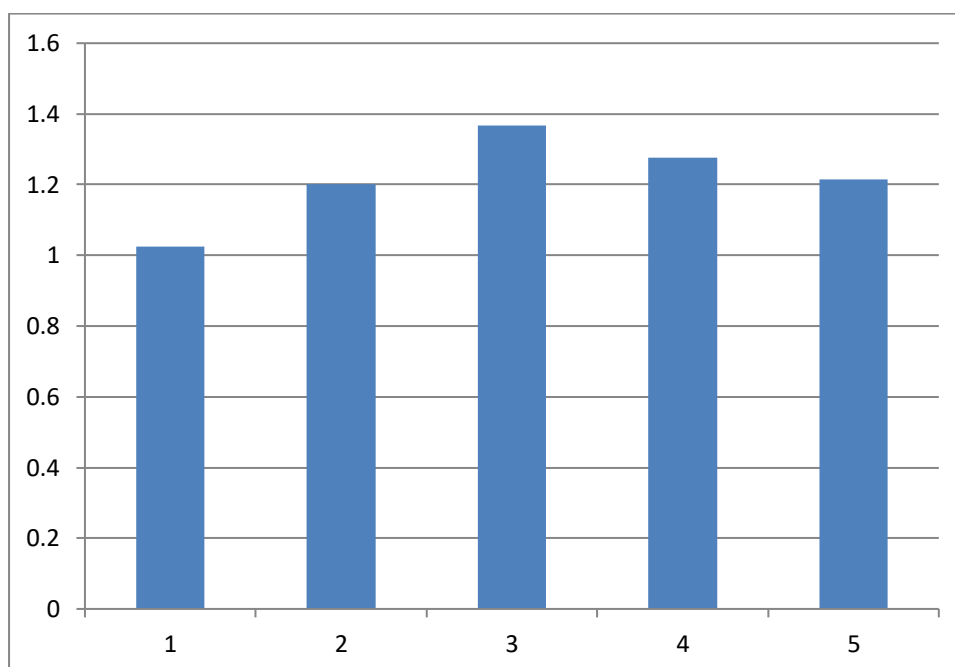


Fig 11: Showing different of hundred grain weight in fine clusters

4.1.5 Grain length (mm)

One of the main components of rice yield is grain size. Because it affects yield and increasing grain size continues to be a major breeding target. A wide variation was found in length of grain among the cultivars. The long grain was found in cluster V, (1.24) this cluster consists of ukhnimadu, kalosharu, malshira and binipakri. While the lowest seed length was cluster III (-1.16).

Mamun *et al.* (2012) and Osekita *et al.* (2015) found to have highest values of positive significant (at 5% level) correlations in grain length and width, this implies that grain length and width ratio can be simultaneously selected for improvement of the studied genotypes and that they can also be used concurrently in improving the genotypes studied.

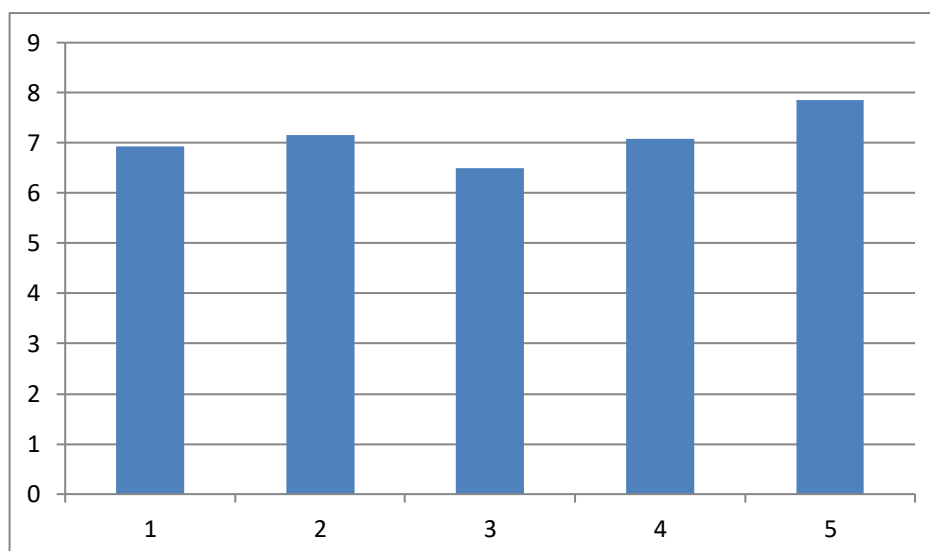


Fig 12: Showing different of grain length (mm) in fine clusters

4.1.6 Grain breadth (mm)

Rice seed length and breadth are two important quantitative traits also closely related to the exterior quality of rice (Shi *et al.*, 2000). The length, breadth and grain flatness is one of the quantitative measures of grain shape. In the present study both grain length and width showed wide variation among varieties (Table 2). The grain breadth among the varieties varied from one to another. Cluster V shows the longest grain breadth and includes only kalozira.

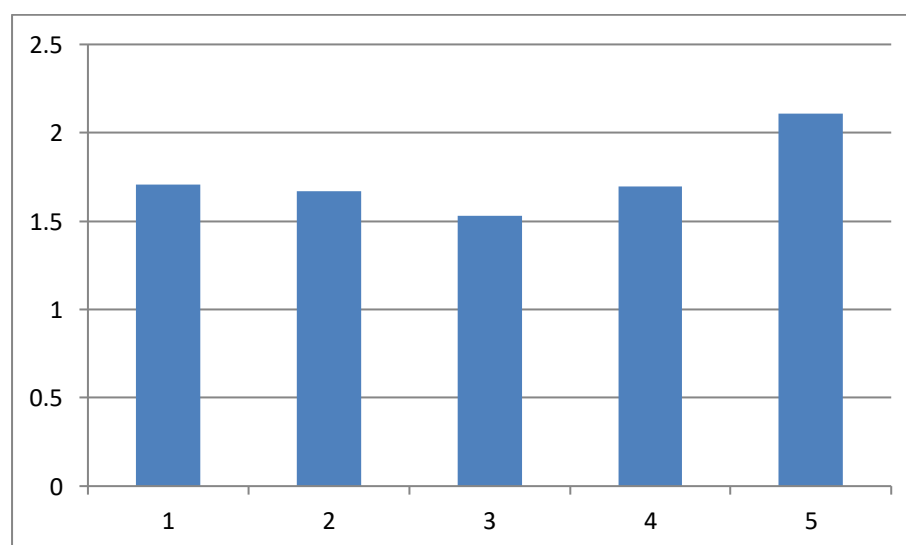


Fig 13: Showing different of grain breadth (mm) in fine clusters

4.1.7 Grain flatness

A wide range of variation was observed for 20 rice cultivars. The Highest seed flatness was observed in cluster II includes br-49 and dhanchikon, while. The lowest were cluster ii and v. Rice seed length and breadth are two important quantitative traits also closely related to the exterior quality of rice. (Shrirame MD and Muley DM, 2003). The length breadth and seed flatness is one of the quantitative measures of grain shape.

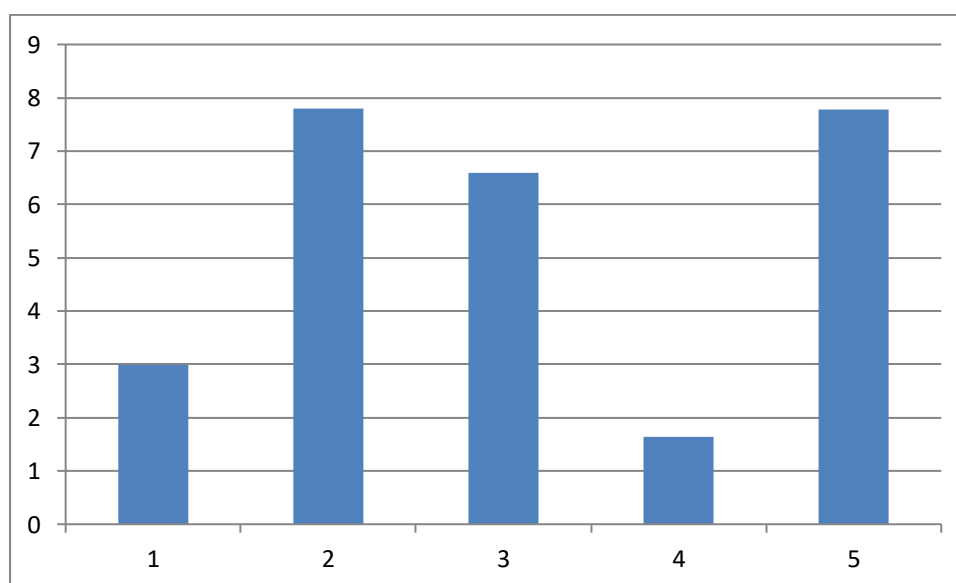


Fig 14: Showing different of grain flatness in fine clusters

Characterization of morphological traits will enable rice breeders to exploit a wide range of genotypic diversities to further crop improvement practices hence increase the rice productivity. In this study, 20 rice genotypes were characterized based on nineteen quantitative traits which were observed in different stages of rice growth. Ligule is a thin, upright, papery membrane that lies at the junction between the sheath and the blade. It can have either a smooth or hairy-like surface (IRRI, 2009).

Panicle exertion is an essential physiological process for obtaining high grain yield in rice and is mainly driven by peduncle (uppermost internode) elongation. When some of the spikelet's at lower down the panicle are trapped inside the flag leaf sheath, it increases the sterility in the lower unasserted spikelet's hence reduce the grain yield (Muthurajan *et al.*, 2010). In present study, panicle exertion of more than half of the genotypes was recorded as well exerted hence they are good for grain yield

improvement. However, the extent of panicle exertion is largely influenced by the agro-climatic condition and cropping seasons (Hoan *et al.*, 1998). Panicle type of rice refers to the mode of branching, the angle of the primary branches and the spikelet density (IRRI, 2009). Flowering duration is an important character that is frequently considered before release of a variety for commercial cultivation (Shahidullah *et al.*, 2009). Number of days to 50% flowering ranged from 65 to 111 that suggested significant variation in days to flowering that could be exploited for cultivar development. Mwangaza was recorded the earliest in flowering (65 days) and Jyambere; Bug 2013A was the latest (111 days).

This type of variation might be due to genetic makeup of genotypes and genotypic environmental interactions. Almost fifty percent of genotypes evaluated showed very early to early days to 50% flowering i.e. <71 days represent very early flowering and 71-90 days represent early flowering. Moreover, days to maturity also exhibited high range of variation (96-142 days). Minimum value for days to maturity represents that the variety has a benefit of early ripening. Early maturity genotypes could be selected for areas with short rain seasons and in areas where farmers grow a second crop to take advantage of residual water after harvesting the early rice crop.

The panicle length and number of panicle per plant directly control the yield of a particular variety (Ashfaq, *et al.*, 2012).

Thirty nine genotypes were observed having long panicle and very long for only one genotype; as length of greater than 25 cm and less than 30 cm represent long panicle and greater than 30 cm is very long. The remaining genotypes were observed to be short and medium. Similar results were obtained by Sarma *et al.* (2004) where they characterized 142 ahu rice genotypes of 50. Assam and found that eight genotypes showed more than 25 cm panicle length and the remaining genotypes were recorded lesser panicle length. Moreover, the panicle number per plant ranged from few (4) to medium (17). Analysis of data revealed that plant height mean value was 95.13, and a wider range of 66.47 cm to 129.02 cm. similar ranges was observed with Zafar *et al.* (2004) and this is typical of landrace genotypes which excel in their capacity to support panicle growth by large stem reserve mobilization. Ali *et al.* (2000) has also observed relatively greater range in plant height than the other characters. In this study, the genotypes were classified as semi dwarf and intermediate as per IRRI

standard evaluation system for rice (1996) with majority of landraces having high heights.

Hirano *et al.* (1992) confirmed the success of Green Revolution to be directly related to intensive use of semi dwarf varieties. Since the semi dwarf plant type was greatly utilized in the improvement of rice cultivars throughout the world, then this was true. However, depending on the part of the world where farmers live and their need for tall rice, there is a rising need to combine desirable characteristics of tall varieties with yielding ability and a new type of architecture: intermediate plant height as explained by Zafar *et al.* (2004). Agbo and Obi (2005) observed that percentage of fertile spikelet's had higher correlation values with yield. With good crop management and growth, high yields are obtained with normal spikelet sterility as much as 10% to 15%. The evaluated genotypes were classified as partly sterile, fertile and highly fertile on percentage spikelet fertility basis.

However, the percentage of spikelet fertility varied from 5169.70% for Kungahara; Bug 2011A to 96.17% for Yunyin suggesting that the genotypes have higher yielding ability. He 1000-grain weight varied from 16.52 g to 38.44 g. Grain weight provides information about the size and density of the grain. IRRI (2009) reported that longer grains are lighter in weight than medium or bold grains but the contrary was observed in this study. For example, CH_50 (Nawa Tule na Bwana), CH_163 (IR 03A262) and CH_166 (Shingo ya Mwali) were recorded as longer grains but had higher weight, while CH_43 (Kihogo) had low weight though it was recorded as medium grain, probably this is due to the reason that most of the varieties used had long grains. 53. Determining the physical dimension of rice varieties is very important, since it is produced and marketed according to grain size and shape. The length and width of rice grain are important attributes that determine the shape of the rice (IRRI, 2009). Based on the brown rice length, the varieties were classified as short, medium, long and extra long using a scale set by IRRI (1996).

Takoradi (2008) reported that long grain rice is highly demanded by the rice consuming populace. Hence the long grains obtained in this study can be used in breeding programmes so as to meet the consumers' need. The ratio of the length and the width is used internationally to describe the shape of the variety. From this study, the varieties were categorized into three groups as bold, medium and slender.

Although the preference for rice grain. Characteristics vary with consumer groups, long and slender grains are generally preferred and are good valuable attributes that could be exploited to improve the grain characteristics.

4.2 Cluster Analysis

The cluster analysis of both quantitative morphological and grain quality traits revealed the grouping of genotypes into five clusters. Minimum number (1) of genotypes was included in cluster 3 and the maximum (9) in cluster 1. Cluster 2, 4, and 5 consisted of 2, 4 and 4 genotypes respectively.

In this study similar name for some genotypes from either same or different collection regions were grouped into same clusters e.g. Zambia and Rumbuka varieties, hence indicating that they seem to be originated from the same genetic materials. Also varieties named Supa Surungai, Supa Kijivu, Supa, Supa India and 54 Supa Katrin all from Tanzania was grouped in the same cluster (cluster 4). Although they have different names in some cases but it shows that they are all Supa variety. This can be due to free exchange of materials and the farmers tend to change/add names of the varieties. However, the similar name genotypes (Kia la ngawa) were grouped into quite different clusters, therefore indicating that they are not duplicates and suggesting that similar names are not always same as a rule of a thumb. The distribution pattern of genotypes in this study into different clusters revealed in few cases no parallelism in morphology, grain quality traits and geographic location as genotypes collected from same geographic region was found in different clusters as well as in same cluster. This indicates that although genetic diversity is generally associated with geographical diversity, but factors other than geographical separation are also responsible for divergence, which might be due to selection, genetic drift and continuous exchange of genetic materials among the countries.

Similar results were also reported by Chandra *et al.*, (2007), Hosan *et al.*, (2010), Sharma and Koutu (2011) and Chakma *et al.*, (2012). Considering this, parents should not be selected on basis of geographic diversity but on genetic diversity. Cluster 1 exhibited highest mean value for seedling height, brown rice length and shape and lowest in leaf width, 50% flowering and days to maturity. This indicated that genotypes in this cluster could be used as parents for grain quality improvement and for developing short duration varieties.

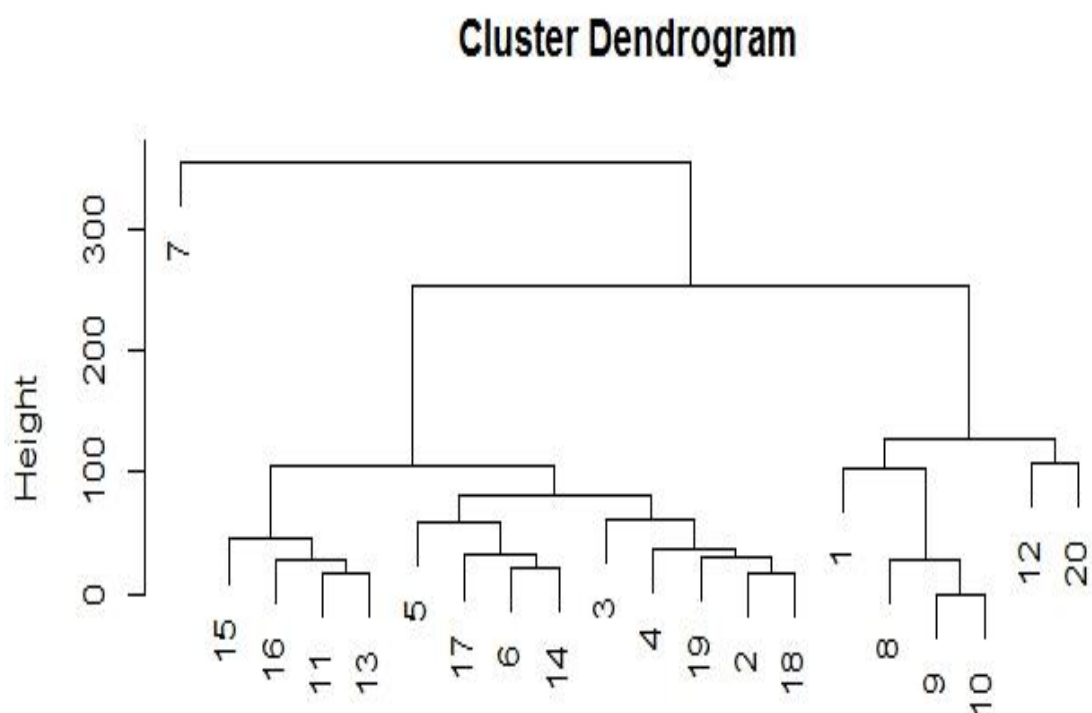


Figure 15: Cluster Dendrogram.

Dendrogram using agglomerative clustering method representing distribution of 20 rice genotypes based on morphological and grain quality trait the highest cluster mean value was observed in cluster 1 for plant height; panicle length in cluster iv, no of grains in cluster v, panicle weight in cluster iv, hundred grain weight in cluster iv, effective grain in cluster v, non effective grain in cluster iv, internode distance in cluster iv, days of heading in cluster I, 100 grain weight in cluster iv, grain length in cluster ii. Grain breadth in cluster iii. Grain flatness in cluster iii. The differences among the studied rice genotypes.

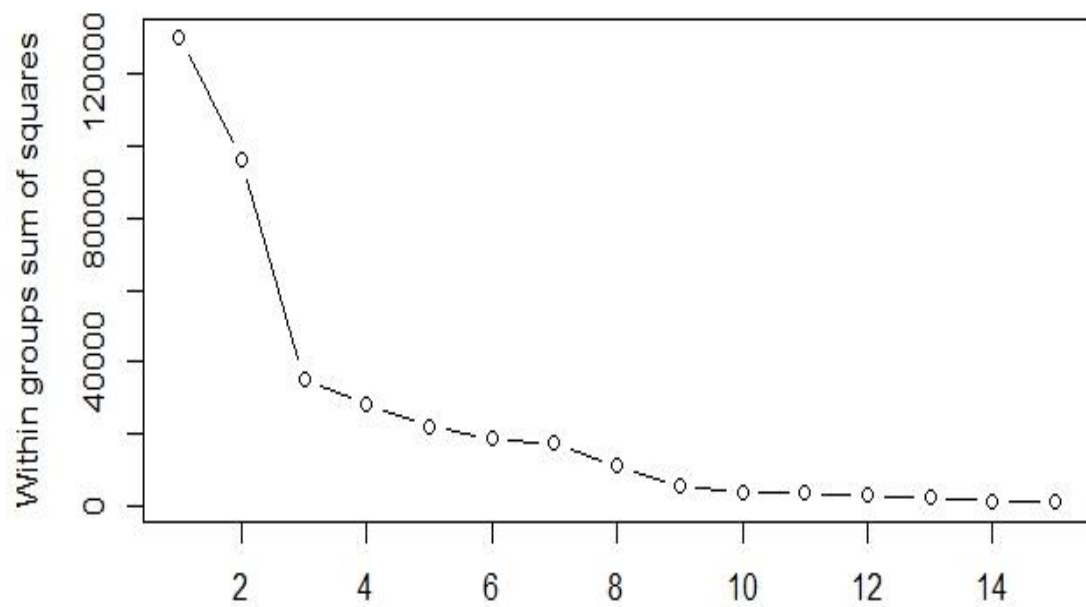
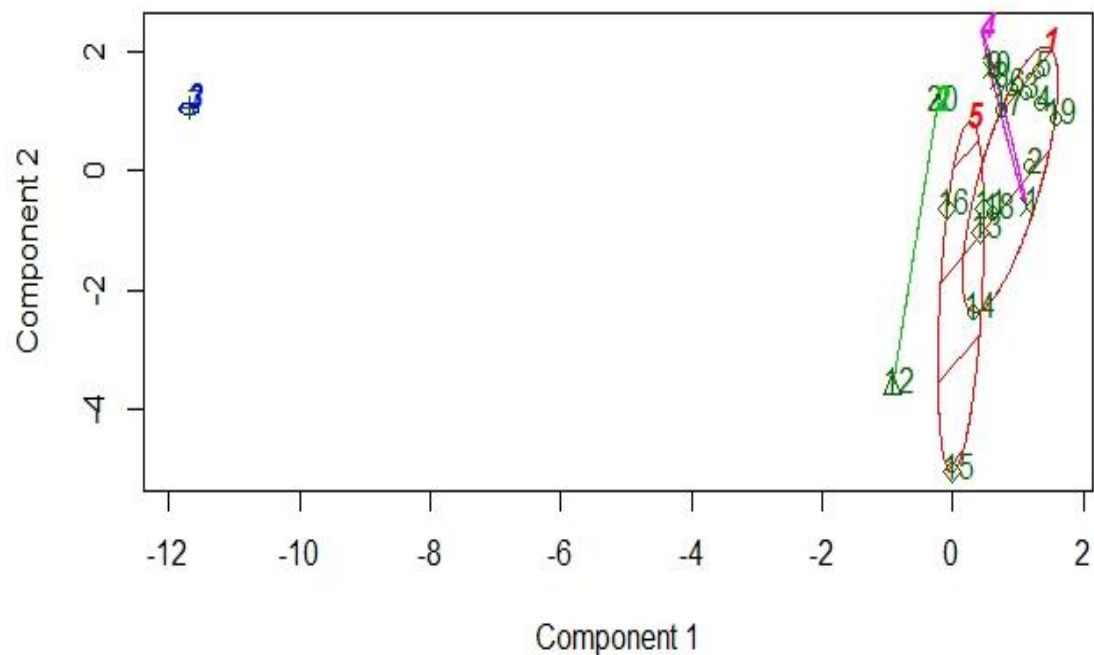


Figure 16: Number of Clusters



These two components explain 64.2 % of the point variability.

Figure 17: 2D representation of the cluster solution

Table of cluster members

Cluster	No of genotypes	Genotypes
I	9	Sadakathari, badhshavog, begunbichi, Salna, Chinigura, Piazam.
		Bolder, Filipinekathari, Jaitakathari.
II	2	br-49 , Dhanchikon.
III	1	kaloziara
IV	4	ronjit, br-34, radhnipagol, katharifog.
v	4	Ukhnimadu, Kalosharu, Malshira, Binipakri.

Mean Performance of the rice Genotypes

The mean performance and variance of the twelve rice cultivars for morphological characters showed significant variation. These are shown in graphs below-

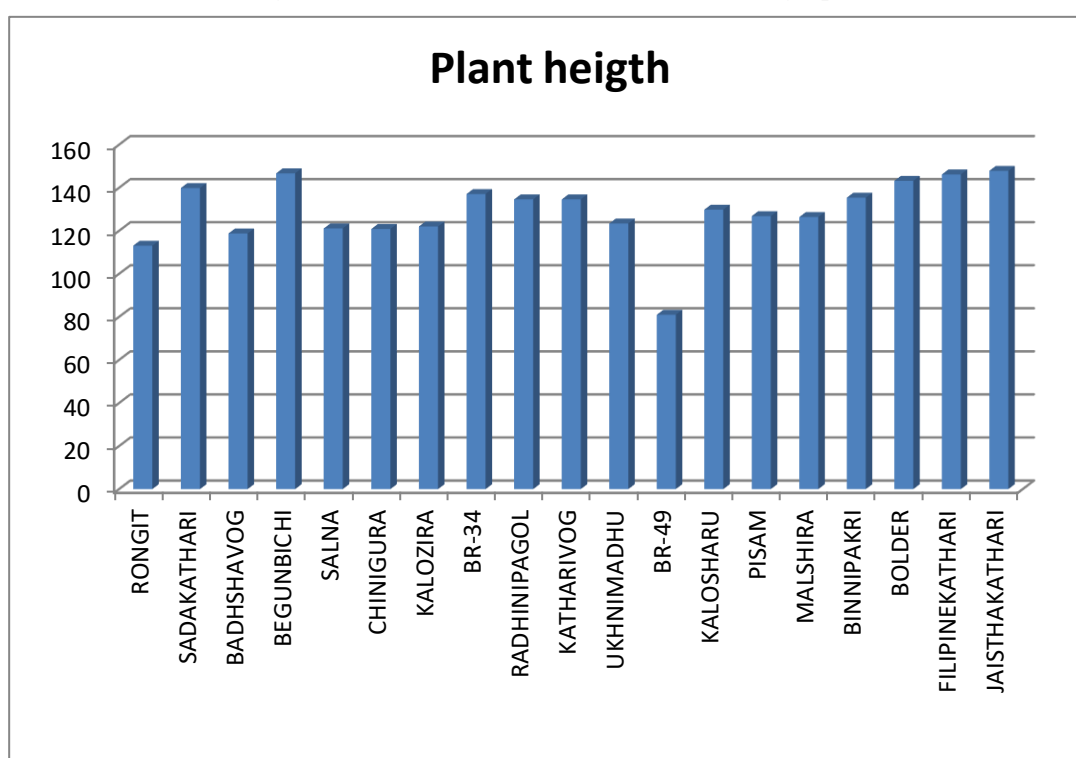


Fig 18: Showing difference of plant height in twenty rice cultivars

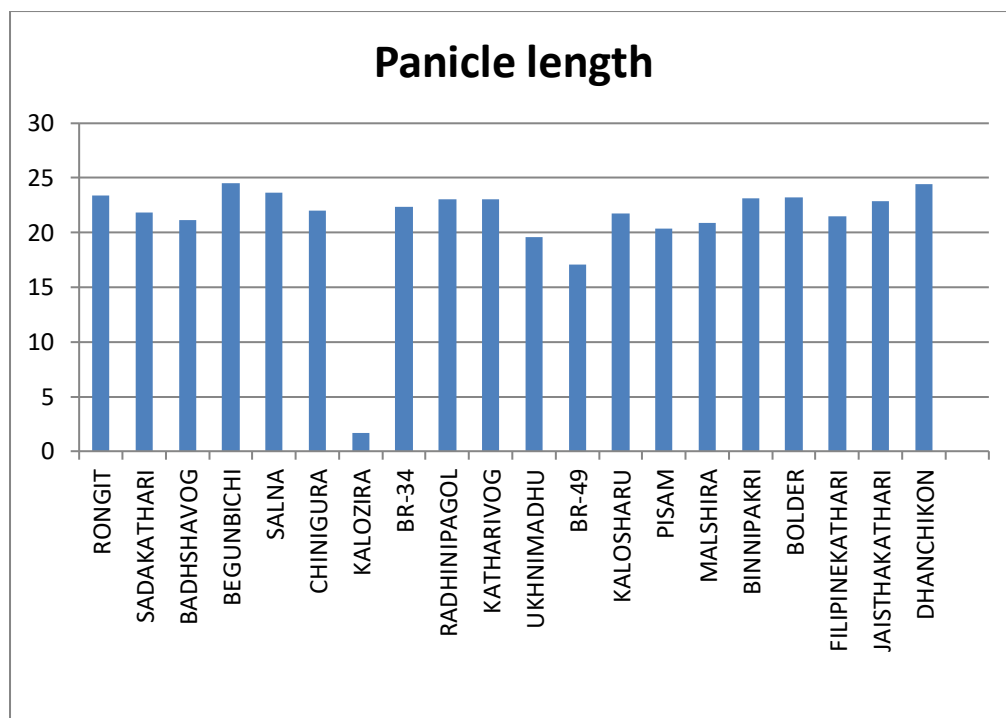


Fig 19: Showing difference of panicle length in twenty rice cultivars

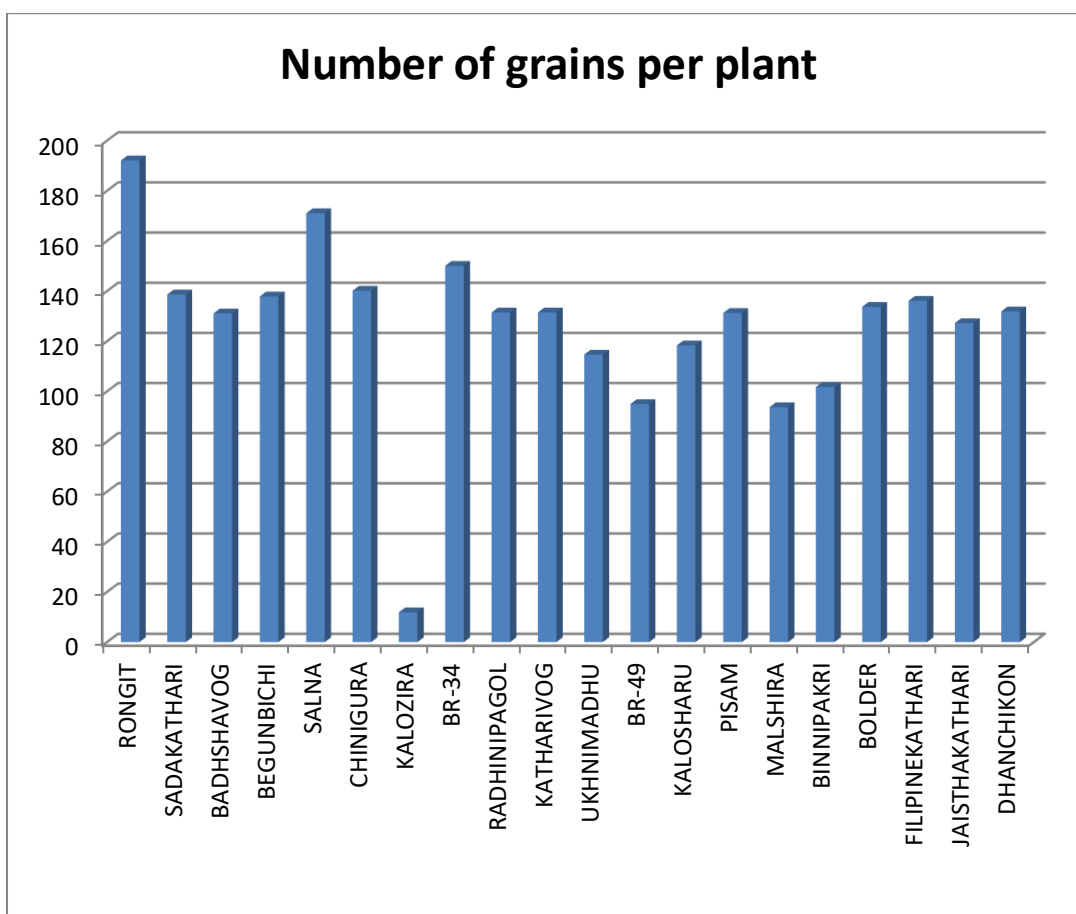


Fig 20: Showing difference of Grains per panicle in twenty rice cultivars

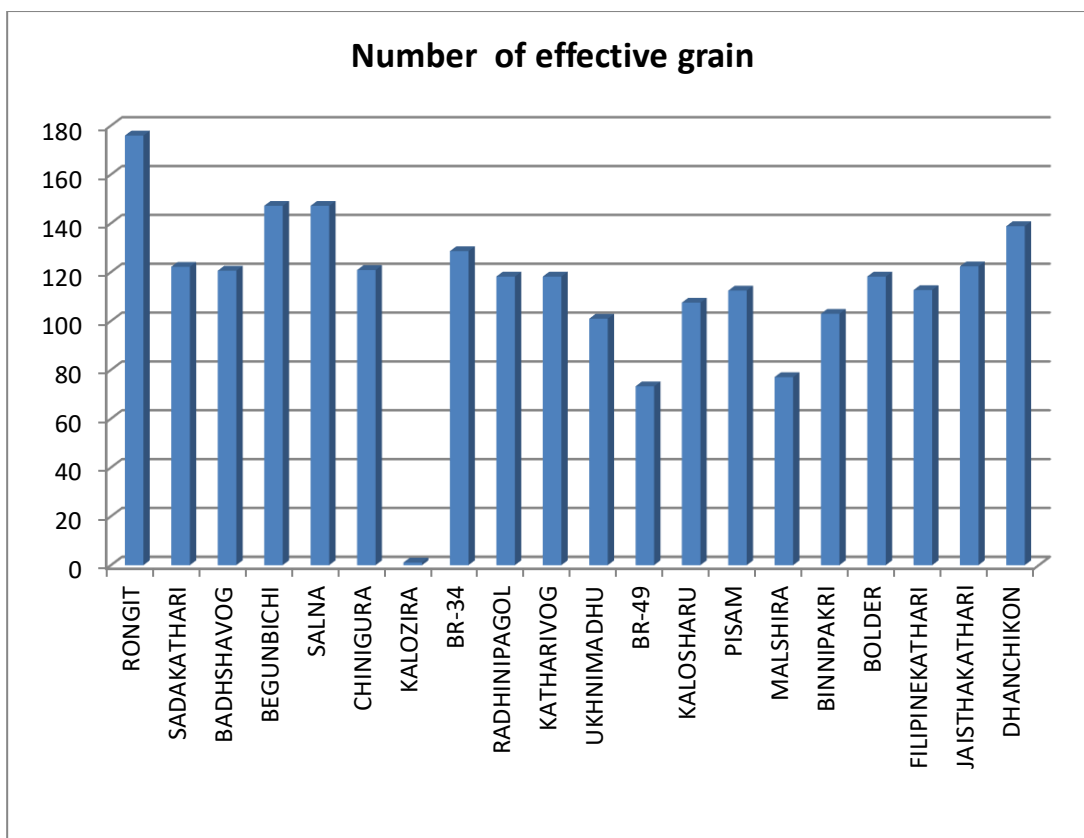


Fig 21: Showing difference of number effective grain in twelve rice cultivars

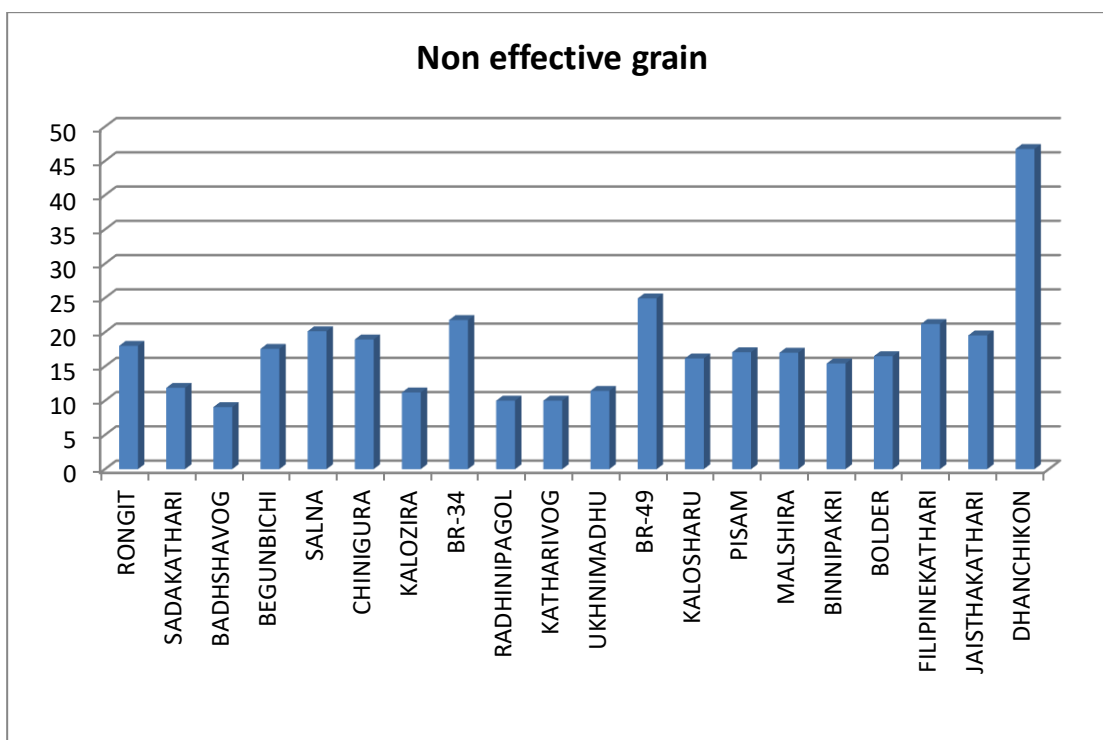


Fig 22: Showing difference of no effective grain in twenty rice cultivars

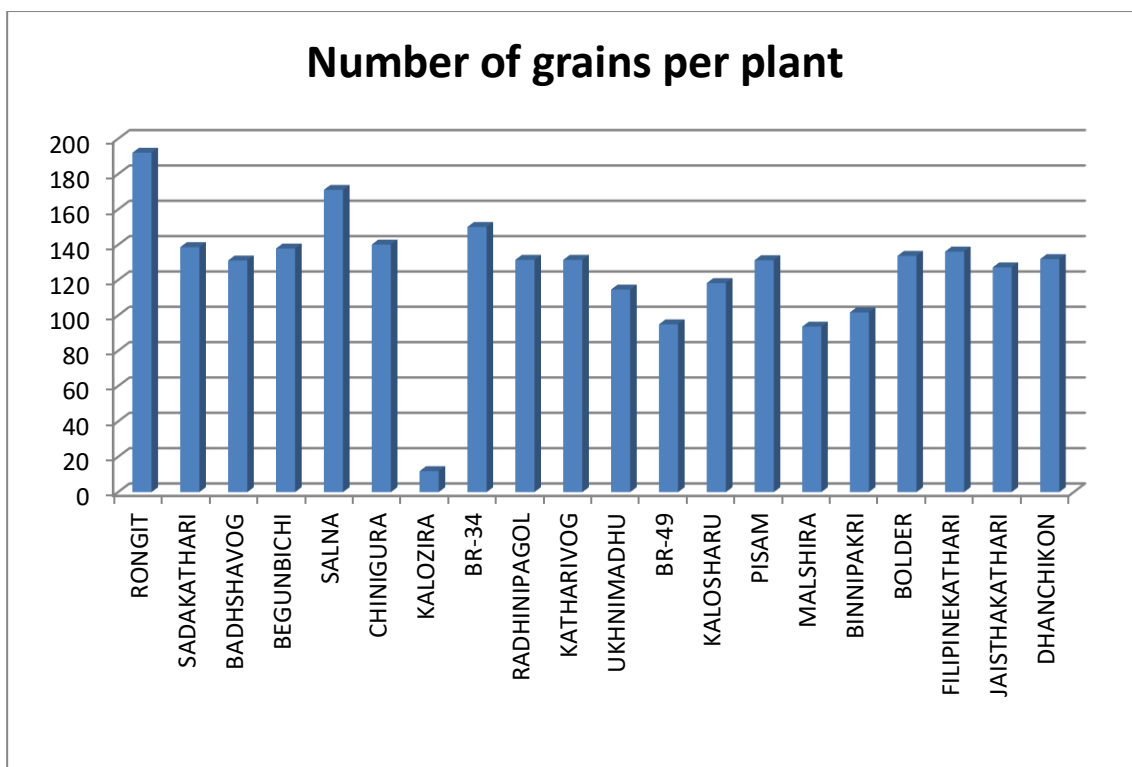


Fig 23: Showing difference of number of grains per plant in twenty rice cultivars

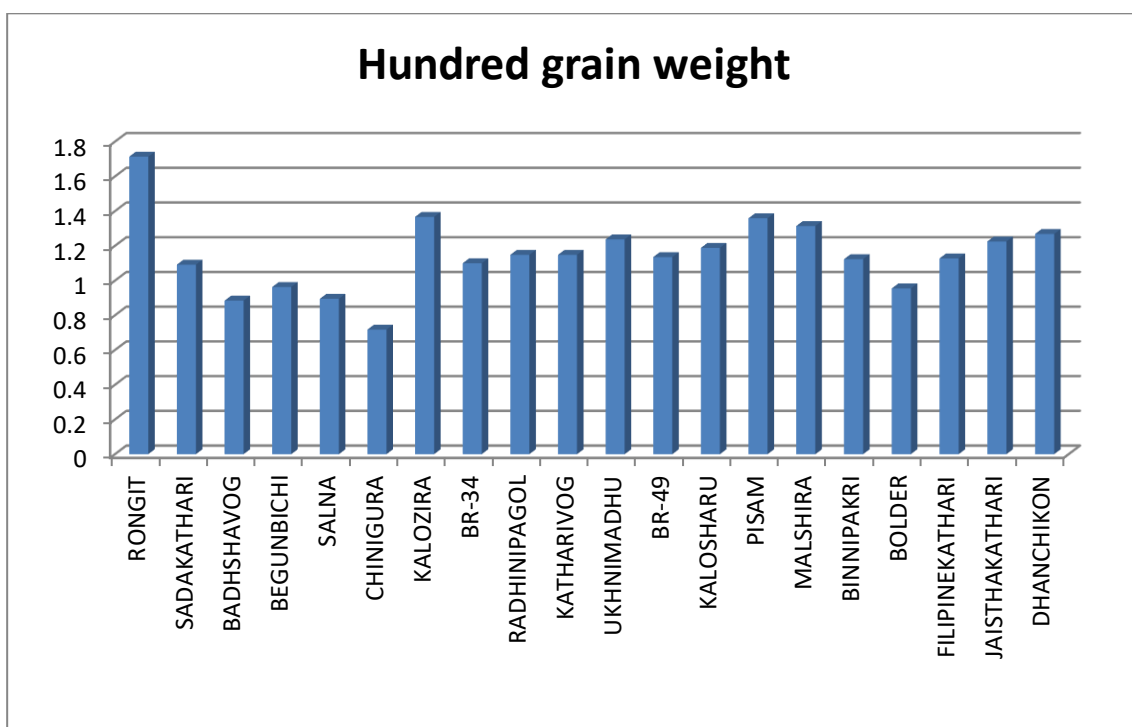


Fig 24: Showing difference of hundred grain weight in twenty rice cultivars

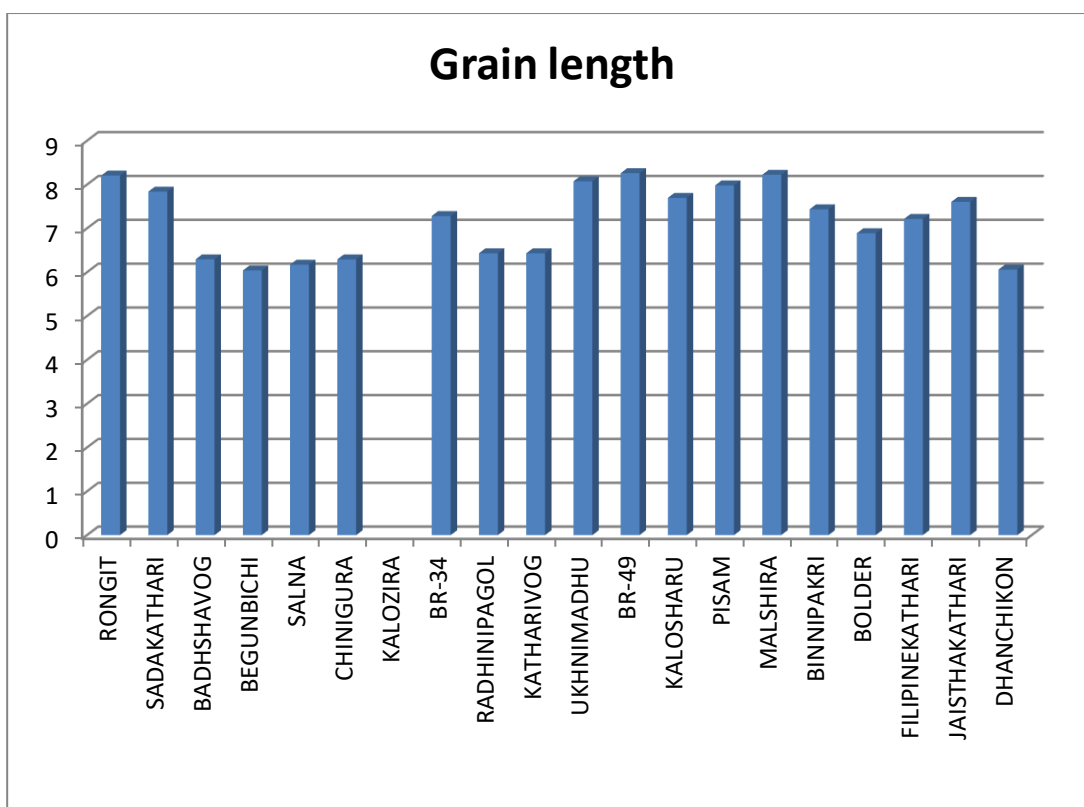


Fig 25: Showing difference of grain length in twenty rice cultivars

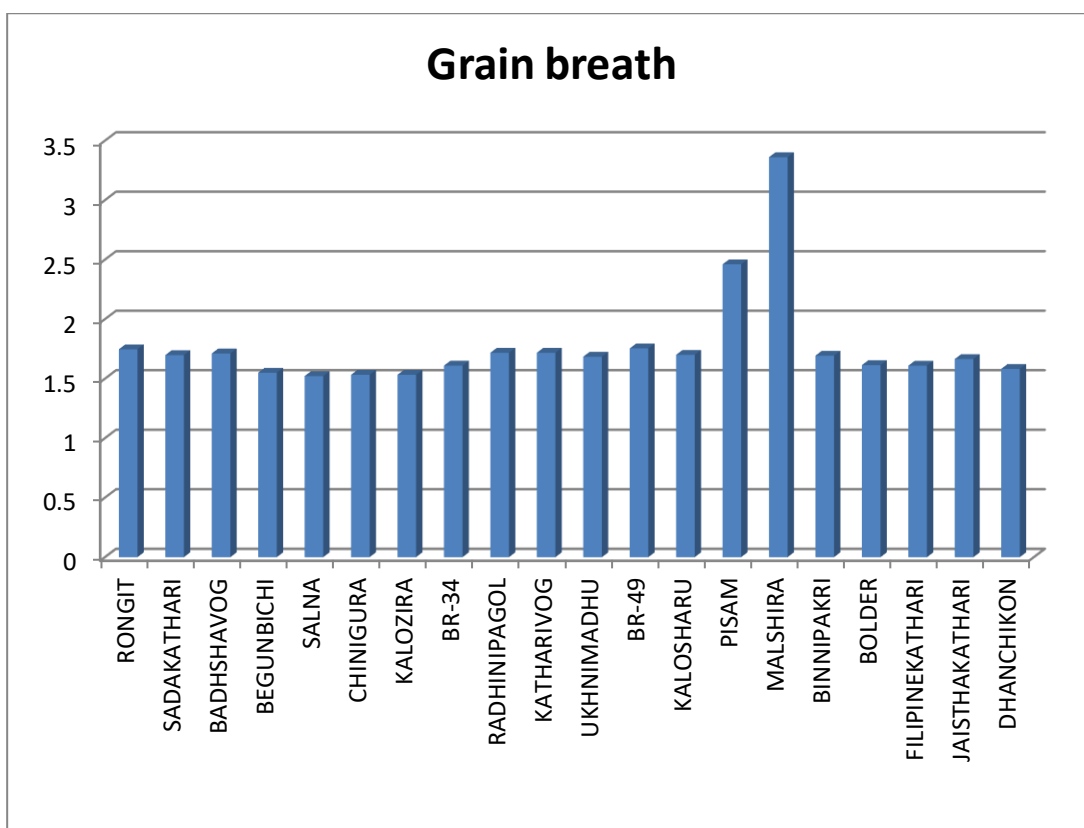


Fig 26: Showing difference of grain breath in twenty rice cultivars

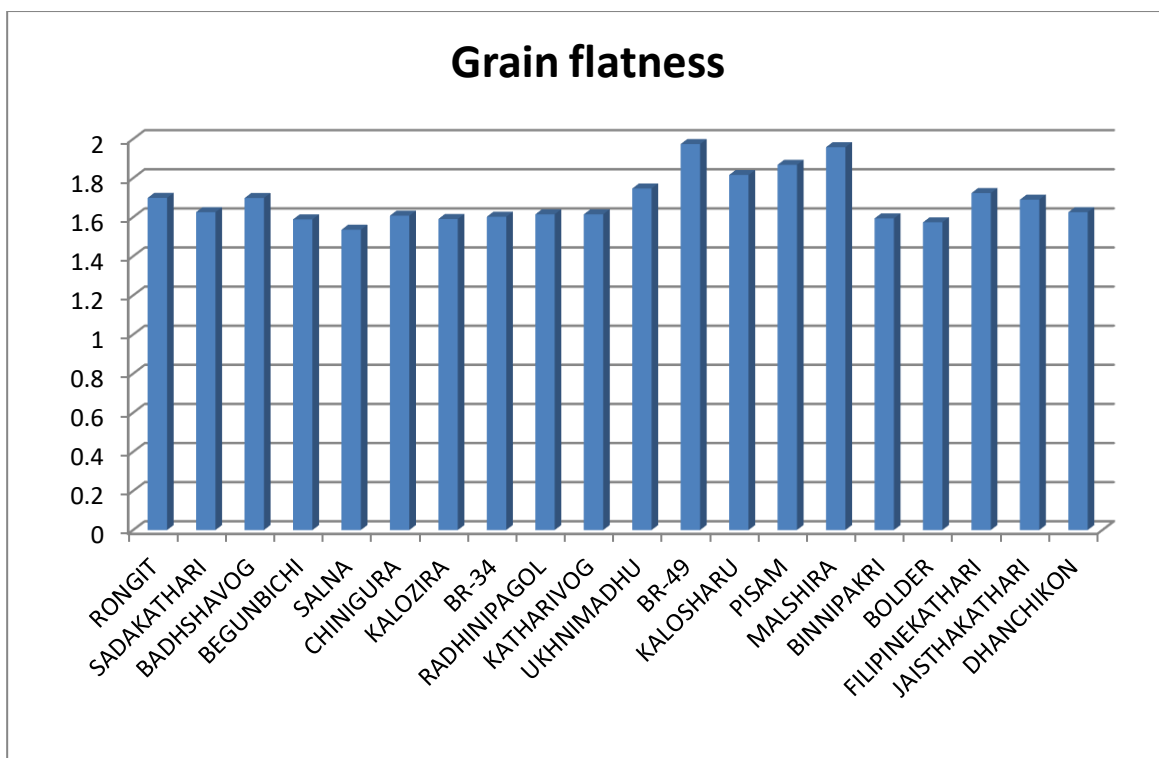


Fig 27: Showing difference of grain flatness in twenty rice cultivars

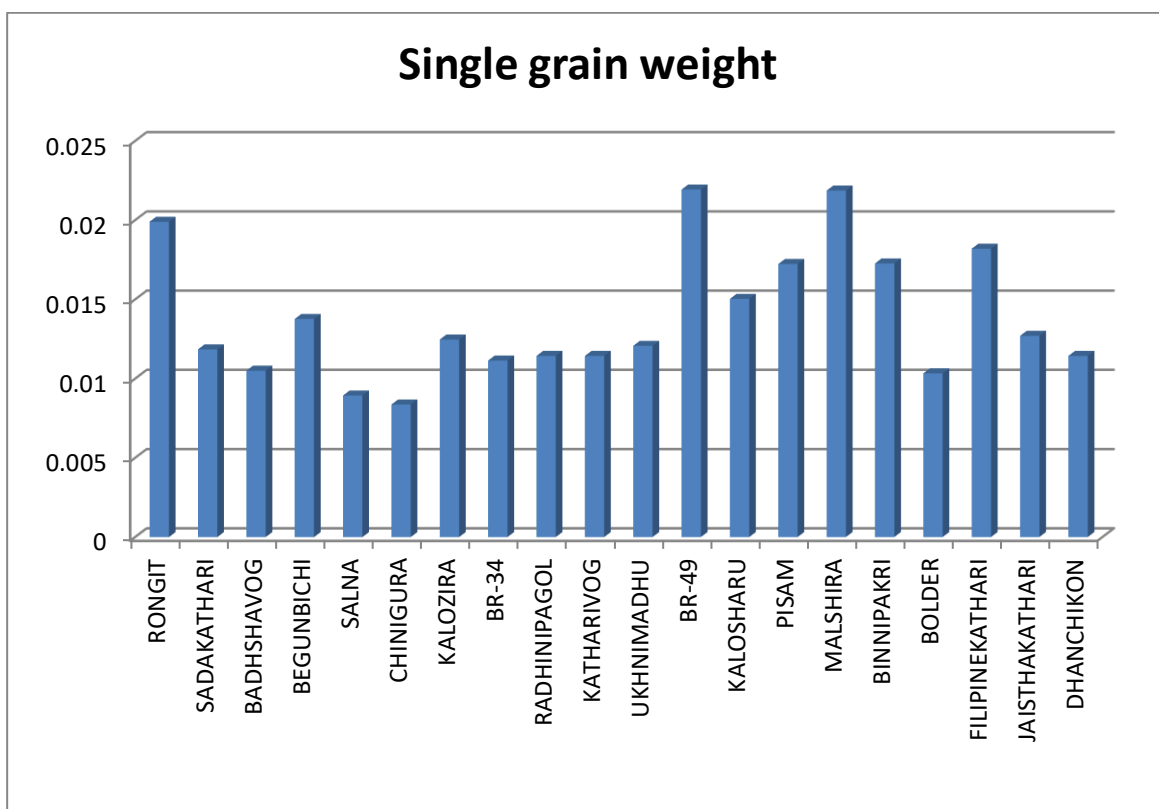


Fig 28: Showing difference of single grain weight in twenty rice cultivars

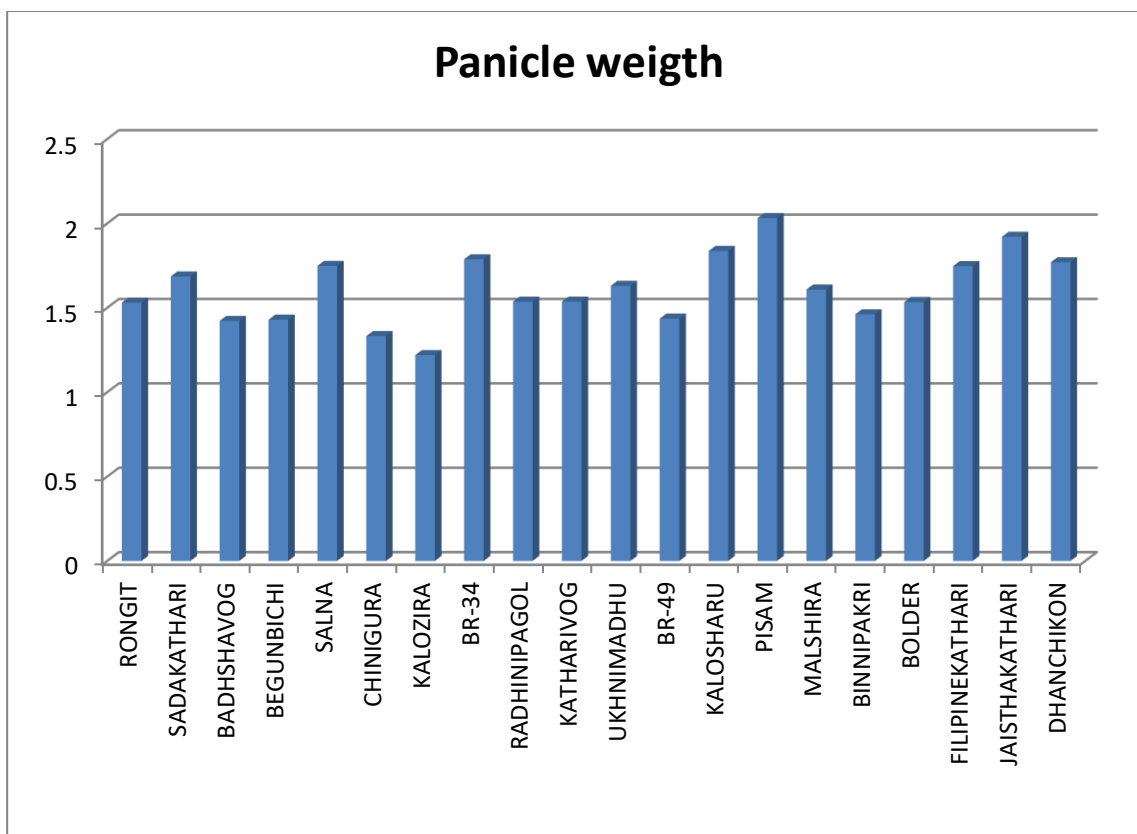


Fig 29: Showing difference of panicle weight in twenty rice cultivars

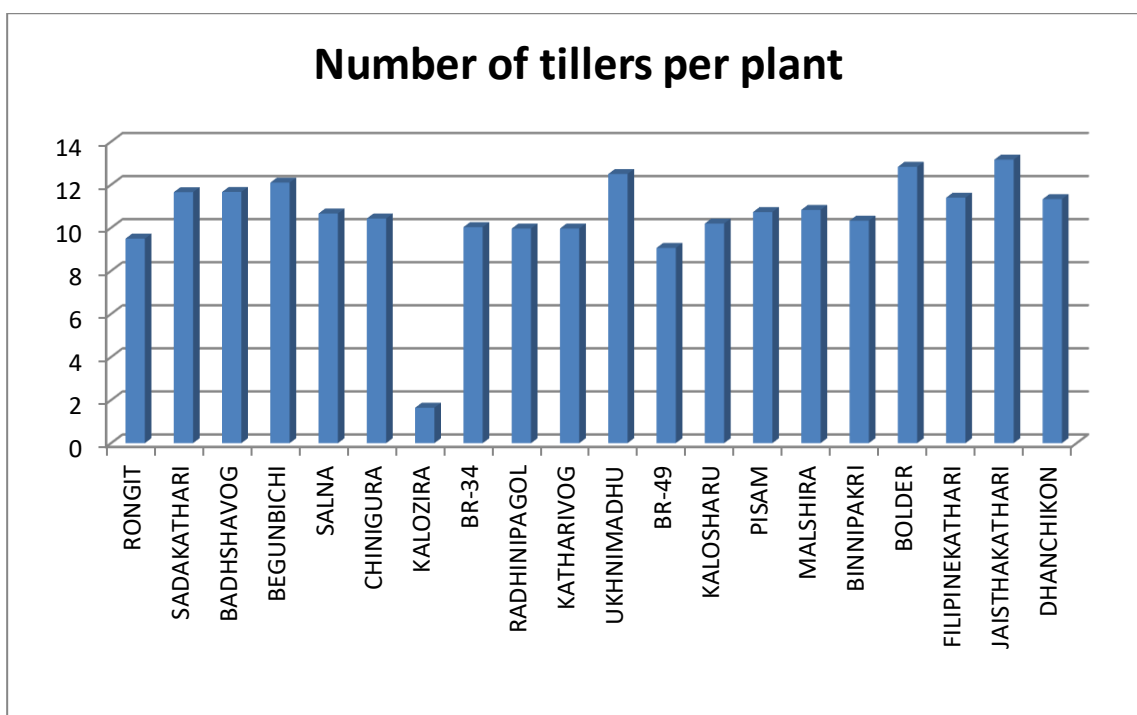


Fig 30: Showing difference of number of tillers per plant in twenty rice cultivars

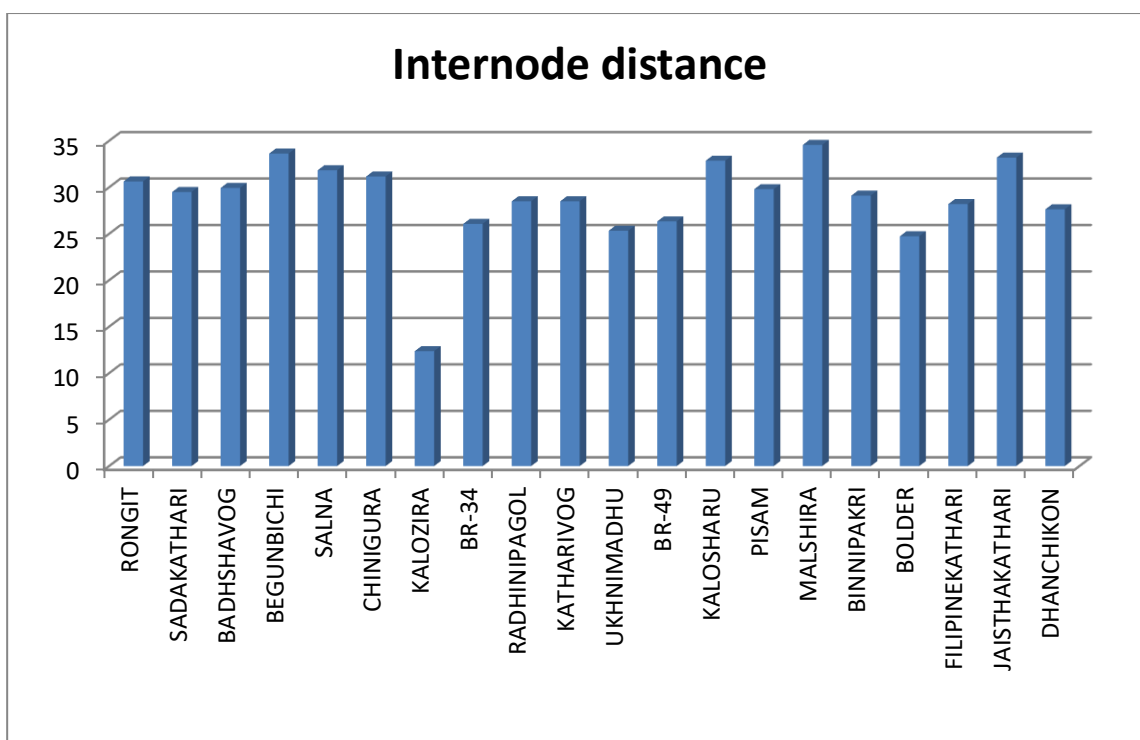


Fig 31: Showing difference internodes distance in twenty rice cultivars

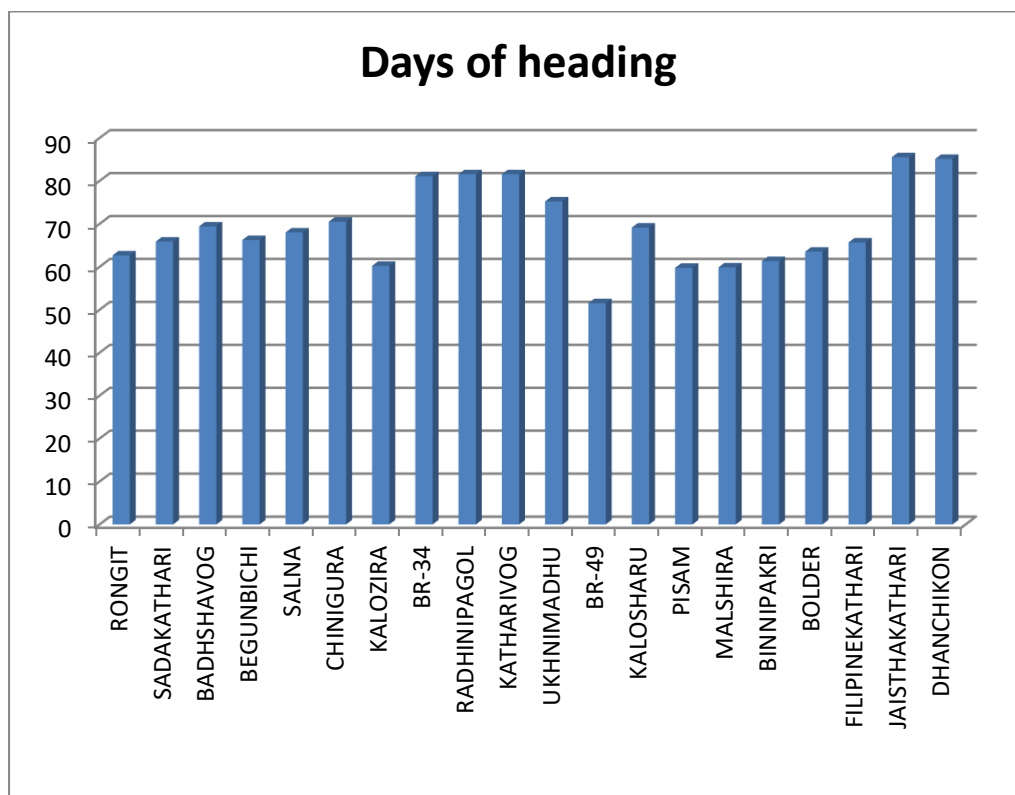


Fig 32: Showing difference days of heading in twenty rice cultivars

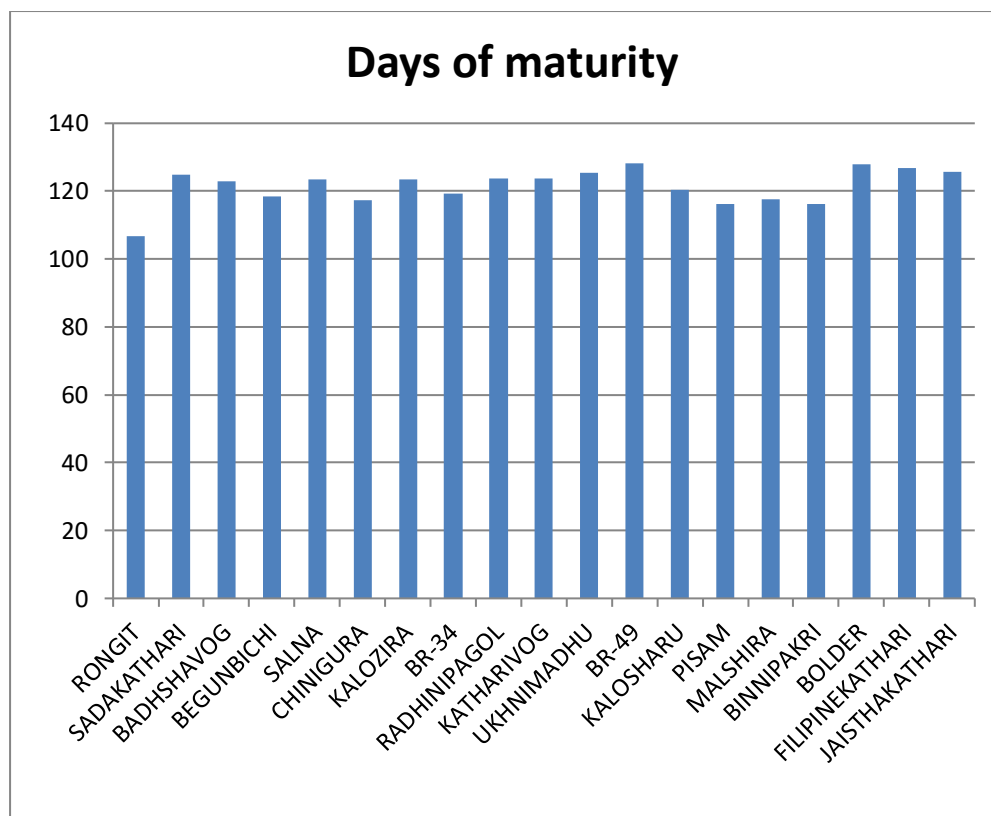


Fig 33: Showing difference days of maturity in twenty rice cultivars

4.3 CART (Classification and Regression Tree) Analysis

The classification tree produced by CART analysis used six morphological variables to distinguish the twenty rice cultivars in figure11. The variables are seed color, seed breadth, seed length, seed weight and seed flatness, grains per panicle and the mean variation of these characters is given in table 2.

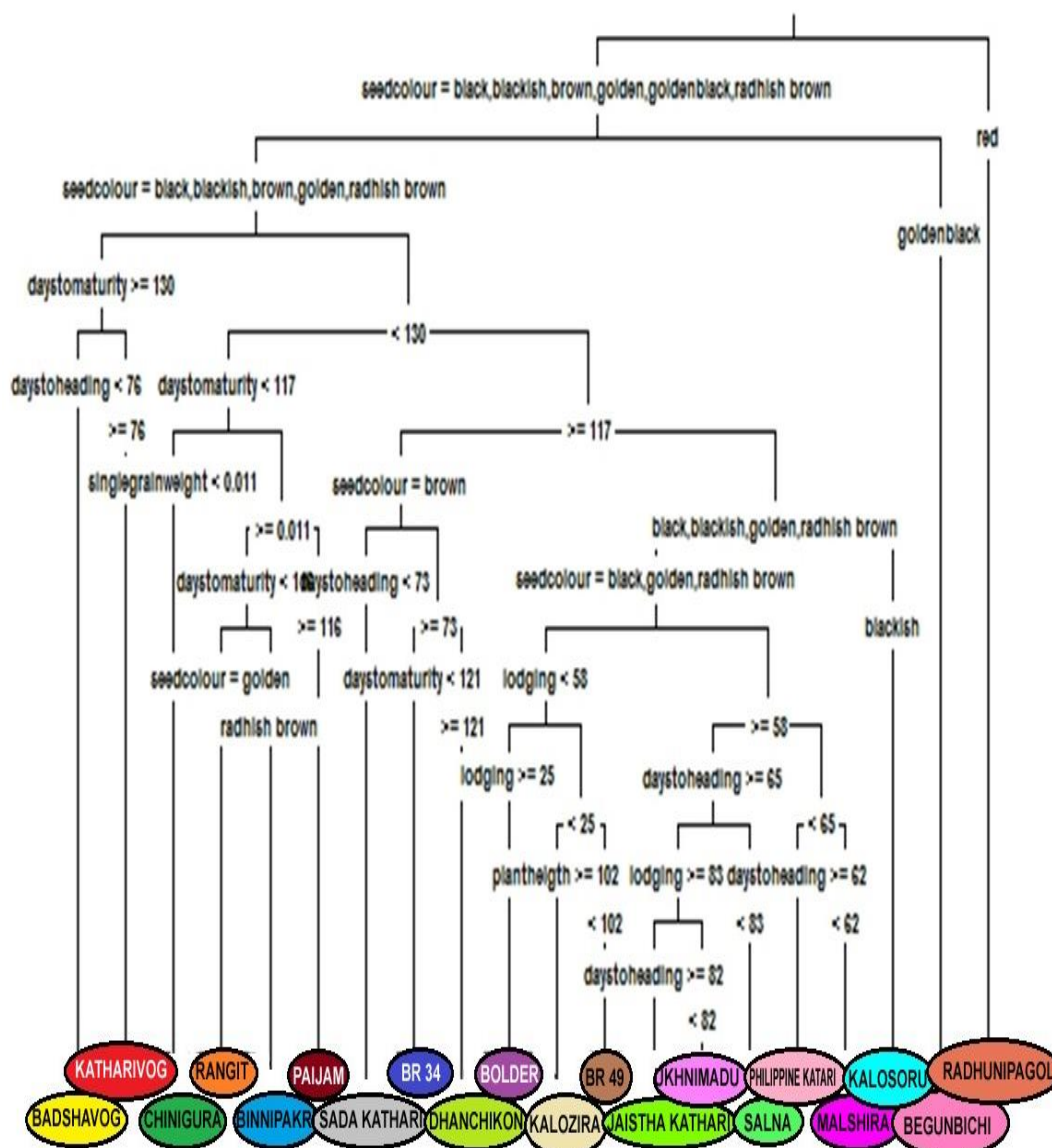


Figure 34: CART (Classification and Regression Tree) Analysis

In this experiment, the morphological variation of different traits among the twelve rice cultivars were studied and indicated that there were large genetic variation. In majority of previous investigation, similar results have been reported for morphological variations in koshta *et al.*, (2013). In this experiment, the

morphological variation of different traits among the twelve rice cultivars were studied and indicated that there were large genetic variation. From the classification and Regression Tree analysis the identification characteristics of selected 20 aromatic fine rice varieties are listed below:

Jaistha Kathari has golden seed color days of maturity < 121 days of heading < 73 and lodging > 25. Sada Kathari is golden color days of maturity < 121 and days of heading > 73, lodging > 25, Seed color of Paijam is golden days of maturity < 100 and days of heading < 73. Seed color of Filipain Kathari is golden in color, days of heading :> 62. Seed color golden in Kathari vog, days of heading <76 days of maturity >130.seed color of Chinigura is golden in color, days of maturity < days of heading >73.Seed color of Bolder is golden plant height > 102 lodging < 53.Seed color of Badshavog is golden in color, days of heading < 76, days of maturity > 130 Seed color of Ranjit is radish brown Seed color of Radhuni Pagol is light brown with golden in color. Buchinbigi is radish brown, days of maturity <121, days of heading >73, lodging >25.salna is golden in color, lodging > 83, days of heading is >62.BR-34 seed color is brown, days of maturity is <121, days of heading is >73, lodging > 25.malshira seed color is radish brown, days of heading is>64.binnipakri is radish brown, days of maturity < 100.dhanchikon seed color is red, days of maturity >117. The above these are the identifying characteristics of aromatic fine rice, which are described by Cart analysis.

CHAPTER-V

SUMMARY AND CONCLUSION

The present study was done with an objective of characterizing the rice varieties in morphological, basis for utilization in improvement programmers. The salient findings of the study. Out of 16 morphological traits observed, plant height, panicle length, number of spikes per plant, panicle weight, no of tillers per plant, hundred grain weight, number of days to 50% flowering, days to maturity, effective grain, and non effective grain, inter node distances grain length, grain breath, grain flatness, single grain weight showed most variation among the genotypes. The 20 genotypes characterized were grouped into five clusters based on morphology characters' traits. The cluster analysis based on similarity index of simple matching grouped the studied rice genotypes into five clusters. The information about the genetic diversity of studied rice varieties will be very useful in identification and selection of suitable parents for use in breeding programmes to develop unique germplasms that complement existing varieties. The cluster analysis of both quantitative morphological and grain quality traits revealed the grouping of genotypes into five clusters. Minimum number (1) of genotypes were included in cluster 3 and the maximum (9) in cluster 1. Cluster 2, 4, and 5 consisted of 2, 4 and 4 genotypes respectively.

Dendrogram using agglomerative clustering method representing distribution of 20 rice genotypes based on morphological and grain quality trait the highest cluster mean value was observed in cluster I for plant height; panicle length in cluster iv, no of grains in cluster v, panicle weight in cluster iv, hundred grain weight in cluster iv, effective grain in cluster v, non effective grain in cluster iv, internode distance in cluster iv, days of heading in cluster I, 100 grain weight in cluster iv, grain length in cluster ii. Grain breath in cluster iii. Grain flatness in cluster iii. The differences among the studied rice genotypes,

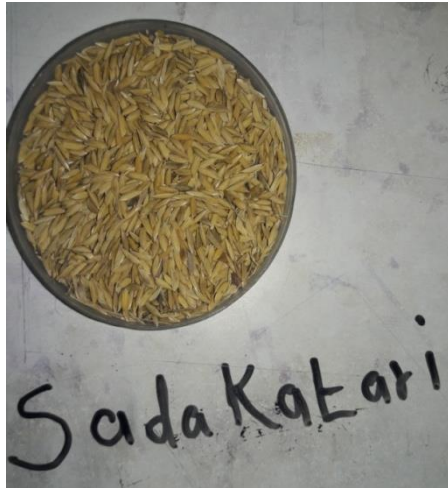
Jaistha Kathari has golden seed color, days of maturity < 121 days of heading < 73 and lodging > 25. Sada Kathari is golden color. Days of maturity < 121 and days of heading > 73, lodging > 25, Seed color of Paijam is golden days of maturity < 100 and days of heading < 73. Seed color of Filipain Kathari is golden in color, days of heading > 62. Seed color golden in Kathari Vog, days of heading < 76 days of maturity > 130. seed color of Chinigura is golden in color, days of maturity < days of

heading >73. Seed color of Bolder is golden plant height > 102 lodging < 53. Seed color of Badshavog is golden in color, days of heading < 76, days of maturity > 130. Seed color of Ranjit is radish brown. Seed color of Radhuni Pagol is light brown with golden in color. Buchinbigi is radish brown, days of maturity < 121, days of heading > 73, lodging > 25. salna is golden in color, lodging > 83, days of heading is > 62. BR-34 seed color is brown, days of maturity is < 121, days of heading is > 73, lodging > 25. malshira seed color is radish brown, days of heading is > 64. binnipakri is radish brown, days of maturity < 100. dhanchikon seed color is red, days of maturity > 117. The above these are the identifying characteristics of aromatic fine rice, which are described by CART analysis.

TWENTY FINE RICE CULTIVERS







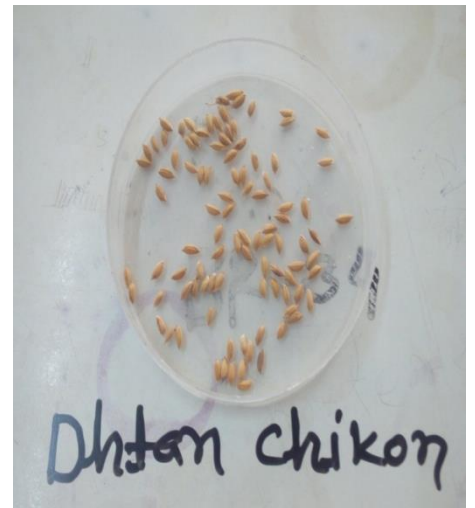
Sada Katari



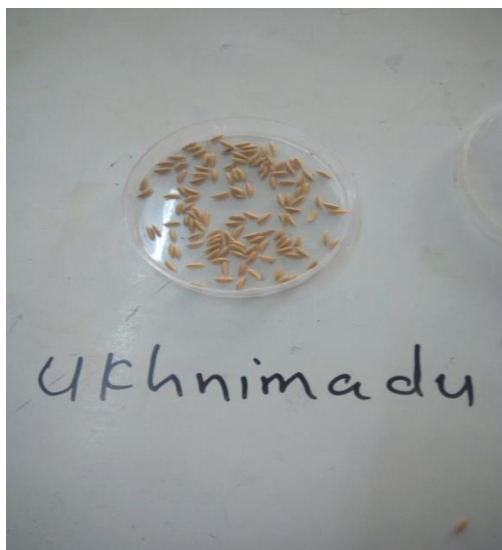
Rongit



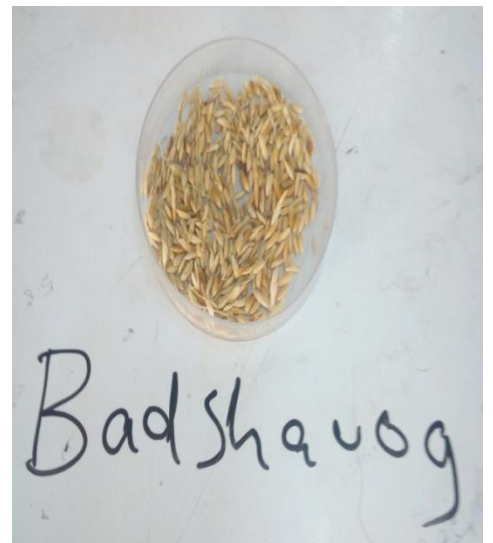
BR-34



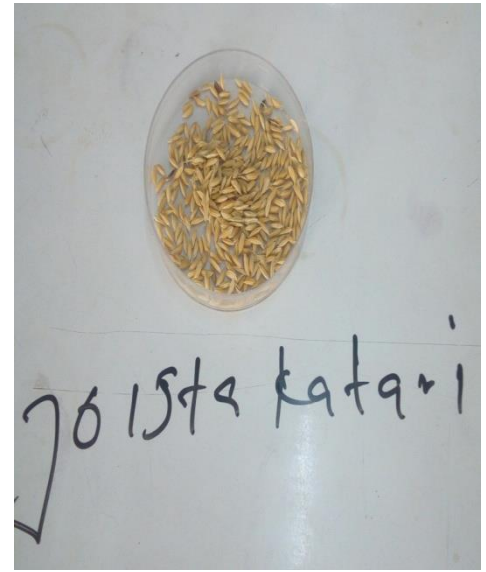
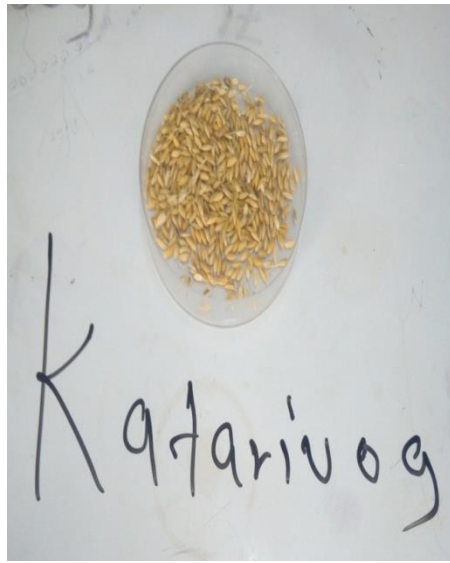
Dhitan chikon



UKhnimadu



Badshavog



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