DEVELOPMENT OF AROMATIC FINE RICE (*Oryza sativa* L.) GENOTYPES FOR BANGLADESH

A PhD DISSERTATION

BY

MD. MOZAFFOR HOSSAIN
Registration No. 0905038

DEPARTMENT OF GENETICS AND PLANT BREEDING
HAJEE MOHAMMAD DANESH SCIENCE AND TECHNOLOGY UNIVERSITY
DINAJPUR-5200

JANUARY, 2022

DEVELOPMENT OF AROMATIC FINE RICE (*Oryza sativa* L.) GENOTYPES FOR BANGLADESH

Dissertation submitted to the
Hajee Mohammad Danesh Science and Technology University, Dinajpur
In partial fulfillment of the requirements for the

Degree of

DOCTOR OF PHILOSOPHY
IN
GENETICS AND PLANT BREEDING
BY

MD. MOZAFFOR HOSSAIN

Registration No. 0905038

DEPARTMENT OF GENETICS AND PLANT BREEDING
HAJEE MOHAMMAD DANESH SCIENCE AND TECHNOLOGY UNIVERSITY
DINAJPUR-5200

JANUARY, 2022

DEVELOPMENT OF AROMATIC FINE RICE (*Oryza sativa* L.) GENOTYPES FOR BANGLADESH

Thesis submitted to the
Hajee Mohammad Danesh Science and Technology University, Dinajpur
in partial fulfillment of the requirements for the

Degree of

DOCTOR OF PHILOSOPHY

IN

GENETICS AND PLANT BREEDING

BY

MD. MOZAFFOR HOSSAIN

Registration No. 0905038

Approved as to style and contents by

(Professor Dr. Bhabendra Kumar Biswas)
Supervisor

(Professor Dr. Md. Hasanuzzaman)
Co-Supervisor

(Professor Dr. Md. Arifuzzaman)
Chairman, Examination Committee

DEPARTMENT OF GENETICS AND PLANT BREEDING
HAJEE MOHAMMAD DANESH SCIENCE AND TECHNOLOGY UNIVERSITY
DINAJPUR-5200

JANUARY, 2022

Dedicated
To my
Beloved wife
Dilwara Most. Samina Aktar and
my two sons Mohtasim Rafid and
Mohtasim Raad

কৌলিতত্ত্ব ও উদ্ভিদ প্রজনন বিভাগ
হাজী মোহাম্মদ দানেশ বিজ্ঞান ও প্রযুক্তি বিশ্ববিদ্যালয়, দিনাজপুর
DEPARTMENT OF GENETICS AND PLANT BREEDING
Hajee Mohammad Danesh Science and TechnologyUniversity, Dinajpur

Ref. ----------------- Date: -----------------

Certification

This is to certify that the thesis entitled “**Development of Aromatic Fine Rice (*Oryza sativa* L.) Genotypes for Bangladesh**” a study on aromatic fine rice, prepared by the examinee, bearing Registration No. 0905038, Session 2015, Department of Genetics and Plant Breeding, Hajee Mohammad Danesh Science and Technology University, Dinajpur, for the award of the degree of Doctor of Philosophy in Genetics and Plant Breeding, is a record of original research work carried out by him under my supervision. The work is an original and unique one and to the best of my knowledge, no part of the thesis has been produced elsewhere for any degree.

(Professor Dr. Bhabendra Kumar Biswas)
Supevisor
Department of Genetics and Plant Breeding
Hajee Mohammad Danesh Science and Technology University, Dinajpur, Bangladesh

Phone: + 880-531-65429 Extension 144, Fax: +880-531-61311,
(Attention: Chairman, Dept. of Genetics and Plant Breeding)

DECLARATION

I do hereby declare that the Dessertation entitled "**Development of Aromatic Fine Rice (*Oryza sativa* L.) Genotypes for Bangladesh**" submitted to the Department of Genetics and Plant Breeding, Hajee Mohammad Danesh Science and Technology University, Dinajpur for the degree of Doctor of Philosophyis a record of my research work, original and unique, and no part of this thesis has been presented elsewhere for obtaining any degree or diploma.

The Author
Department of Genetics and Plant Breeding
Hajee Mohammad Danesh Science and Technology University, Dinajpur, Bangladesh

ACKNOWLEDGEMENT

All praises, gratitude and thanks are due to "Almighty Allah" the great gracious and merciful of the universe, which enabled me to complete the research and write up the thesis for the degree of Doctor of Philosophy in Genetics and Plant Breeding. The author desires to express immense gratitude to his respected father for his constant inspiration and blessing in life.

The author expresses his profound respect and sincere gratitude to his reverend research supervisor Professor Dr. Bhabendra Kumar Biswas, Department of Genetics and Plant Breeding, Hajee Mohammad Danesh Science and Technology University, Dinajpur for his ingenious and scholastic guidance, instructive criticisms and valuable suggestions throughout the study period and preparation of the thesis.

The author also expresses his gratitude and appreciation to his co-supervisor Professor Dr. Md. Hasanuzzaman, Department of Genetics and Plant Breeding, Hajee Mohammad Danesh Science and Technology University, for his encouragement and valuable suggestions during the period of the research work and at the time of preparing of the thesis.

The author humbly desires to acknowledge his heartiest appreciation and cordial thanks to Professor Dr. Md. Abul Kalam Azad, Professor Dr. Md. Arifuzzaman, Mst. Tanjina Shahanaj Turin, Lecturer, Shohana Jui, Lecturer, Department of Genetics and Plant Breeding, Hajee Mohammad Danesh Science and Technology University, Dinajpur for their valuable suggestions and help during the research work, data analysis and preparation of the thesis.

Sincere heartiest appreciation to my beloved wife, Dilwara Most.Samina Aktar and my two sons Mohtasim Rafid and Mohtasim Raad, for their constant encouragement during the whole period of study.

The author acknowledges with great thanks, gratefulness and gratitude for approval of my study in Ph.D program and provided research plot at BADC Seed Multiplication Farms for conducting my experiment.

The author extents his thanks to Md. Tazul Islam, Senior Lab Assistant, Department of Genetics and Plant Breeding, Hajee Mohammad Danesh Science and Technology University, Dinajpur for his continuous assistance both at field and laboratory during the research work.

The Author

Development of Aromatic Fine Rice (*Oryza sativa* L.) Genotypes for Bangladesh

ABSTRACT

At the beginning of the investigation 32 F_4 lines derived from eight crosses including six aromatic fine rice varieties as parents were received from the Department of Genetics and Plant Breeding, HSTU, Dinajpur. The field experiments were conducted at Randomized Complete Block Design (RCBD) with three replications. The unit plot size was 3m x 2m and spacing was 20 cm x 20cm in every experiment. Field data were recorded on plant height (cm), productive tillers/hill, panicle length (cm), fertile grains/panicle, sterile grains/panicle, panicle weight (g), sterility percentage, lodging percentage, 1000-grain weight (g), days to 50% flowering, days to maturity, harvest index and grain yield/hill (g). Broad sense high heritabilities (h^2b) were measured for all the characters except productive tillers/hill and genetic advances of the characters were in general low which suggest both additive and non-additive interactions of genes were envolved upon the expression of the characters. Genotypic and phenotypic associations among the characters were in same direction and panicle weight, 1000-grain weight and harvest index showed positive and significant correlation, whereas plant height, panicle length and sterility percentage were negatively associated with grain yield/hill. Hence, short stature plants to resist lodging with high spikelet fertility must be considered during selection. Thousand grain weight extorted maximum positive direct effect (0.843) followed by fertile grains/panicle (0.361), plant height and sterility percentage exercised maximum negative direct effects (-0.821) and (-0.965), respectively to build up association with grain yield. The negative direct effects of these two characters were not counter balanced by other grain yield enhancing characters. Therfore, panicle weight, 1000-grain weight and harvest index were the important characters for improving yield potential. Upon measuring the response to selection from F_4 to F_5, plant height, sterile grains/panicle, sterility percentage, panicle length and days to maturity exhibited negative direction, but high realized heritabilities were estimated for productive tillers/hill, grain yield/hill and harvest index. So, the latter three characters had high realized heritability might consider during advancing the generation. The thirty-two advanced lines (F_4) were grouped into five clusters following Mahalanobis's D^2 statistics and principal component analysis (PCA). Considering grain yield potential, aroma assessed from green leaves and powder grain and clustering pattern with cluster means, ten lines of F_6 (PL1, PL2, PL12, PL13, PL15, PL16, PL17, PL22, PL24 and PL26) were forwarded to assess performance in three locations. Overall, the Plant Breeding Research Farm, HSTU, Dinajpur projected the highest environmental index (1.397), suggests superior to BADC Seed Multiplication Farms Nilphamari and Faridpur. Applying Eberhart and Russell model along with GGE biplot analysis, the stability and sensitivity of the advanced lines were evaluated over the three locations. The highest grain yield/hill was obtained from PL13 (18.85 gm/hill) followed by PL16 with 18.10 g/hill and Pl1 with 16.12 g/hill and both the lines had regression coefficients (bi) closed to unity and deviation from regression (s^2di) very near to zero, suggest average stable with considerable yield potential across the three locations. The aroma contents in F_5 and F_6 were assessed by the sensory method with the help of a six members panel. The highest aroma contents were assessed in the lines, PL1 (Kalozira x Kataribgog) and PL13 (Kataribhog x Chinigura) from cooked rice. While other cooking qualities were considered, PL13 exhibited the maximum cooked rice expansion (5.87cm) and PL6 had resulted the minimum semi-liquid starch (348ml) during cooking. Therefore, considering all findings the advanced lines PL1 and PL13 appeared outstanding both for grain yield and aroma content, and the line PL16 was stable with average yield potential over three locations. Therefore, the advanced lines PL1, PL13 and PL16 (F_6) might be forwarded for further utilization in aromatic rice breeding in the country.

CONTENTS

CONTENTS (CONTD.)

CONTENTS (CONTD.)

CONTENTS (CONTD.)

CONTENTS (CONTD.)

CONTENTS (CONTD.)

LIST OF TABLES

LIST OF TABLES (CONTD.)

LIST OF TABLES (CONTD.)

LIST OF FIGURES

LIST OF FIGURES (CONTD.)

LIST OF FIGURES (CONTD.)

LIST OF APPENDICES

ACRONYMS AND ABBREVIATION

Acronym & abbreviation	Full meaning
2AP	2-acetyl-1-pyrroline
ANOVA	Analysis of variance
AT	Aroma test
BADC	Bangladesh Agricultural Development Corporation
bi	Regression coefficient
CRL	Cooked rice length(cm)
CRW	Cooked rice weight(g)
CT	Cooking time(min)
CV	Coefficient of variation
DTF	Days to flowering
DTM	Days to maturity
ECR	Expansion of cooked rice (cm)
EMS	Error mena sum of square
FGPP	Fertile grain per panicle
GA	Genetic advance
GCV	Genotypic coefficient of variation
GGE	Genotype and G × E
GMS	Genotypic mean sum of square
GYPH	Grain yield per hill
h^2	Narrow sense heritability
H_2b	Heritability

Acronym & abbreviation	Full meaning
HSTU	Hajee Mohammad Danesh Science and Technology University
LP	Lodging percentage
PCA	Principal combination analysis
PCV	Phenotypic coefficient of variation
PH	Plant height
PL	Panicle length
PTPH	Productive tillers per hill
PW	Panicle weight
R	Selection to response
r_g	Genotypic correlation coefficient
RL	Rice length (cm)
r_p	Phenotypic correlation coefficient
S	Selection differential
S^2di	Deviation from regression
SGPP	Sterile grain per panicle
SLSW	Semi solid starch weight (ml)
SP	Sterility percentage
TGW	1000 grain weight
$Б^2g$	Genotypic variance
$Б^2p$	Phenotypic variance

CHAPTER I

INTRODUCTION

Rice (*Oryza sativa* L.) is the most important staple food crop because more than half of the world's population (>3.5 billion) depends on it for their livelihood. It is cultivated in more than 100 countries worldwide. Global rice production must be doubled by 2050 to cope up with the situation of population growth (Roy and Shil, 2020). Bangladesh is the fourth largest rice producer in the world. It is not only the staple food of the country but also the source of employment for 48% of the rural population, as almost all of the 15 million farms in the country grow rice. Rice fields account for 70% of Bangladesh's cropped area of 1.54 crore hectares. It constitutes 70% of the agricultural GDP and one-sixth of the national income (Light Castle Analytics Wing, 2019). Globally, rice production was 499.31 million tons in 2019-20 and in the year of 2020 it will be 496.08 estimated million tons could represent a decrease of 2.99 million tons or 0.60% in rice production around the globe (USDA, 2019). Although the geographical, climatic and edaphic conditions of Bangladesh are favorable for year-round rice cultivation, the national average of rice yield is rather low, only 3.067 tons per hectare (BBS, 2019). Total cultivated area of rice is nearly 11.52 million hectares with an annual production of 36.39 million tons (BBS, 2020). Bangladesh will stand out by growing at record 8% in 2019 and 2020, making it the fastest growing economy in Asia-Pacific. However, South Asia would buck this trend growing at 6.8% in 2019 and 6.9% in 2020 (Ahmed, 2019).

The country has imported 3.7 million tons and the import might exceed 4.0 million tons by the end of next June year. So far, the public sector has imported over 1.0 million tons, while the private sectors import also increased to a record 2.65 million tons, of which 90% was from India and of which demand for the fine-quality rice now is around 30% of total requirement (Financial Express, 2018). Most of the rice exported in the international market is par-boiled (Atap) and sticky rice, but 95% of rice produced in Bangladesh is hard grained with hardly any demand in the international market. However, Bangladesh exports about 50,000 tons of fragrant rice to the Middle East, the US and Europe every year. The main consumers of this rice are expatriate Bangladeshis (Chowdhury, 2021). Once upon a time Bangladesh was treated as a bottomless basket but today it has emerged as a global model of food security producing sufficient food products (Kabir *et al*., 2015). Aromatic rice is a delicious exportable excellent product of

Bangladesh. It has attractive flavor which creates hunger. Aromatic rice is very suitable for good health. It is rich with natural chemical compounds which give it distinctive scent. The exporters are shipping aromatic rice to the Middle East countries, the USA, the UK, Australia and Canada and other countries including South Africa.

The demand for aromatic rice has been increasing in recent years along with traditional rice culture in our country. Rice breeders have an interest in developing a simple and inexpensive method for distinguishing aromatic from non-aromatic rice. Genetic uniformity could become a problem for the selection in advance generation to develop improved varieties.

The economic value of rice in specific markets is mainly influenced by the textural properties of the cooked rice as it is mainly consumed as a whole grain. Consumers generally favor certain varieties with valued specific appearances, tastes, and texture of cooked rice. As in recent times, there has been a steady increase in new processes for products development involving rice as an ingredient, along with characterization of rice grains, the study of physicochemical, thermal, and rheological aspects of rice flour also holds paramount importance in quality determination of rice cultivars along with their flour-based products (Kaur *et al.* 2016). Rice flours with different physicochemical properties yield products with different textural qualities. Therefore, an appropriate rice variety must be selected as a raw material to produce different rice-based products.

Rice breeders are interested in developing high yielding cultivars with improved yield and other desirable agronomic characters. To achieve this goal, the breeder has the option of selecting desirable genotypes in early generations or delaying intense selection until advanced generations, when progenies are nearly homozygous. In early stages of breeding programs, direct estimation of yield is quite difficult. Plant breeders are commonly selecting for yield components which indirectly increase yield. Yield component breeding to increase grain yield would be most effective, if the components involved are highly heritable and genetically independent or positively correlated. The selection criteria for production may be yield, one or more of the morphological components of yield; number of panicle /unit area, the number of grains /panicle, or grain weight. Woodworth (1931) suggested that yield might be increased in small grains by selecting for the component of yield and that parental varieties should be selected on the basis of component attributes. Whereas, Frankel (1935) and Adams (1967) reported that the components of yield are influenced greatly by environment and that negative correlations among them are common. Thus, selection for one of the components may fail in increasing yield, because of negative associations among the components. Knowledge of genetic parameters like genetic variance, character association, path coefficients, principle component analysis and clustering are the pre-requisites for improvement of any crop including rice for selection of superior genotypes and improvement of any trait (Krishnaveni *et al.,* 2006). Genetic variability is pre-requisite for commencement of any breeding program. It is very difficult to judge whether observed variability is heritable or not. Heritability indicates the extent of transmissibility of a character into future generations. Moreover, knowledge of heritability is also essential for selection of component traits for yield improvement. Genetic advance measures the difference between the mean genotypic values of selected population and the original population from which these were selected. Heritability estimates along with genetic advance is normally more helpful in predicting the genetic gain under selection than heritability estimates alone (Rai *et al.,* 2014 and Rashid *et al.,* 2017).

Measurement of correlation coefficient helps to 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 *et al*., 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 influences of one character upon another (Dewey and Lu, 1959). Considering the above facts, the present study has been undertaken to assess the character association and contribution of characters towards grain yield of selected genotypes, and to find out the direct and indirect effect of component characters on grain yield with the help of correlation coefficient analysis. The genetic diversity of various characters in local cultivars of rice is the greatest in the area extending from Assam in India and Bangladesh to Myanmar and northern Thailand, and to Yunnan Province in China (Oka, 1988). This area is characterized by topographical and hydrological heterogeneity, and is considered as the center of diversity of rice.

The success of any plant breeding program largely depends on the existence of diversity among the genotypes (Allard, 1960). This helps in the choice of parents for hybridization in yield improvement programs. Hence, estimation of genetic diversity for yields and its components among genotypes is important for planning the future crossing program. In the present study an attempt was made to assess the genetic divergence using Mahalanobis D^2 statistics and different clustering procedures, based on yield and its component characters and assessing the relative contribution of different components to total divergence (Rao, 1952). Modern breeding techniques could improve the yield of fine rice to overcome this problem. Successful breeding for crop improvement, however, depends on genetic variability in the parents, such that a lack of genetic variability would have the potential to significantly limit breeding progress and/or yield and quality crop improvements. Increased knowledge into the genetic diversity of any germplasm collection, therefore, enhances the possibility of crop improvement and the development of superior cultivars. Genetic variability is the fundamental requirement of any crop breeding program to develop superior cultivars (Tiwari *et al.,* 2019). Clustering a large number of germplasms represents a simple and effective process for assessing the genetic variability of germplasm, along with other statistical approaches such as population structures, principal component analysis (PCA), principal coordinate analysis (PCoA), and ANOVA are commonly utilized globally for diverse crops, such as rice.

The presence of Genotype (G) × Environment (E) interactions is characterized by the differentiated genotype response to the variations of the environmental conditions, which can cause an alteration in the performance ordering of the genotypes in the environmental gradient (Falconer and Mackay, 1996). The G × E interactions can be expressed in different ways and with different intensities and are of fundamental importance in genetic evaluations (Resende, 2015). According to Robertson (1959), variance component of the G × E interactions can be deployed into a simple part from the interactions, explained by the change in genetic variation (variance heterogeneity) of the genotypes in different environments, and into a complex part from the interactions arising from a lack of genetic correlation between the genotype performance from one environment to another. This is the problematic part of the interactions, meaning that the good genotype in one environment may not be in another. According to Resende (2007), a genotype is considered stable when it presents small variations in its overall behavior under various environmental conditions. Another important concept is the adaptability or responsiveness to environmental improvement. This concept is associated with the plasticity of genotypes. In these terms, an ideal genotype is one that responds predictably or proportionally to environmental stimulus. There are several procedures to evaluate the effects of G × E interactions in plant breeding (Van Eeuwijk *et al.,* 2016). One of the main methods used in cotton is based on simple linear regression analysis, proposed by Eberhart and Russell (1966). This method considers the coefficients of linear regression of the phenotypic values from each genotype concerning the environmental index and the deviations of this regression to select genotypes with stability and adaptability to favorable and unfavorable environments. It is noted that the diversity in the studied materials is an indication of outstanding advanced generations derived with specific adaptability to favorable and unfavorable environments, concluding that the use of more than one evaluation methods allow more reliable recommendations. The consistency of this response pattern can be determined by measuring correlations or distances regarding the performance of pairs of advanced lines in environments; the performance of a line in pairs of environments and the relationship between genotypes and environments (Cruz *et al.,* 2014). Although similarity measures have already been successfully used in clustering methods (Cruz *et al.,* 2011), few studies currently adopt correlation or distance measurements to aid in the classification of genotypes as to adaptability and stability (Silva *et al.,* 2019).

The quality of rice is evaluated in terms of its sensory quality, processing quality, eating quality, and nutritional quality. The assessment indexes of sensory quality of rice are mainly based on the color, appearance, smell, taste and other features which are identified by the examiner's sense organs and practical experience. It is the only cereal crop eaten mainly as whole grains and, therefore, grain quality consideration is much more important than for any other crop. The appearance of milled rice grain is an important quality attribute considered by consumers first (Danbaba *et al.,* 2012). Thus, grain shape and size are the first criteria of rice quality that breeders consider in developing new varieties for release for commercial production. Breeders are currently working to develop new rice varieties with improved agronomic characters to aim at giving higher grain yields. But evaluation early breeding lines for grain quality and more advanced lines for nutritional factors such as cooking and eating qualities of rice are ignored in breeding programs in our country, as a consequence aromatic and non-aromatic varieties are being cultivated without considering moistness, tenderness, gloss and taste. Recently, however, the breeding program has turned its attention to the development of long grain rice varieties, with respect to cooking and eating quality. The complex trait of rice grain quality is the sum of a number of component characters, including appearance, cooking and eating quality, and nutritional quality (Lang *et al.*, 2013). Hera *et al.* (2013) reported that demand by consumers for rice for better quality can also influence its production. Different characteristics of grain quality of rice largely determine the product's market price and acceptability. If the consumesr do not like the flavor, texture, aroma, appearance or ease of cooking and processing in a new variety, whatever other outstanding characters it may possess, loses its value. The quality of rice is closely related to the quality of its milled whole kernels, since all the domestic rice grains are milled to a high degree.

Estimates of realized heritability of the particular character is important in determining its response to yield and its components has been reported by some workers in rice (Kato, 1997; Takeda and Saito, 1983 and Gravois and MCnew, 1993). Selection pressure in rice based on grain yield, total tillers and grains/panicle could be advantageous (Talwar, 1976). Effectiveness of early generation selection could be reduced by genotype and environment interaction (Whan *et al.*, 1981 and Rahman and Bahl, 1986). Direct selection may not be effective in segregating population for improvement of grain yield (Bartley and Weber, 1952; Johnson *et al.*, 1955). Parent offspring correlation and regression between two generations shows lesser influence of environment and its very useful method for selection in segregating population. For rapid and effective genetic improvement for any economic trait, late generation selection would be advantageous because a genotype possessing all the desirable genes either in homozygous or heterozygous condition occurs most often in the early segregating generations (F_4 and F_5). The scientific rationale of late selection has been critically examined by Yonezawa and Yamagata (1981a and 1981b) and they observed some key points such as (i) genetic potentiality of crosses is determined essentially in F_4 and F_5 generations (ii)some morphological-physiological traits are predictive of yielding capacity of plants and lines (iii) with a larger F_4 population, the selection among and within crosses is useful (iv) cross-combinations are therefore assessed by the presence or absence of the promising phenotypes, and (v) F_4 population should be entirely discarded if no promising phenotype is found. These important considerations on late selection (F_4-F_5 generations) may lead to develop of high yielding cultivar.

Rice is the only cereal crop cooked and consumed mainly as whole grain, and quality considerations are much more important than for any other food crop (Hossain *et al.*, 2009). Although production, harvesting and post harvesting operations affect overall quality of milled rice, cultivars remains the most important determinant of market and end use qualities. Desired quality of rice vary from one geographical region to another and consumers demand certain cultivars and favors specific quality traits of milled rice for home cooking (Juliano *et al.* 1964). One of the major concerns in rice production has to do with seed and grain quality (Traore, 2006). While many components contribute to rice quality, the most important are cooking and eating qualities. These parameters primarily involve the physical and chemical characteristics of starch. The constituents that play important roles in cooking and eating quality are amylose content, gelatinization temperature, and gel consistency (Traore, 2006). According to Horna *et al.* (2005) grain quality is one of the key selection criteria highly prioritized by farmers and consumers of rice and therefore, farmer select rice with characters that are desirable for consumption as well as for production and sale. However, defining quality is very difficult since it is defined by the end user and their preferences are highly variable. Keeping eyes on the above facts the present investigation was undertaken with the following objectives-

I. Estimation of genetic parameters for yield and yield contributing characters
II. Selection of yield enhancing characters through correlation and path analysis
III. Assessment of genetic diversity in F_4 advanced lines
IV. Prediction of response to selection in two successive generations (F_4 and F_5)
V. Identification of superior advanced lines for high yield and aroma content in different locations (F_6)

CHAPTER II

REVIEW OF LITERATURE

Sufficient information regarding promising genotypes of fine rice with morphological and physiological properties is presented in world literature. Improvement in grain yield and quality is normally achieved by selecting genotypes with desirable characters' combinations existing in the genotypes or by hybridization between desirable parents. The parents identified on the basis of selection in advanced (F_4 –F_6) generation based on agro-morphological traits would be more effective for improving grain yield. In this chapter an approach has been made to review important available information related to the study. The literatures relevant to this study have been arranged under the following heads:

2.1 Genetic parameters for yield and its related characters

Siddi (2020) investigated variability and trait association studies in 18 rice (*Oryza sativa* L.) genotypes with two replications in a RBD design during kharif, 2017 at Agricultural Research Station, Kunaram. The traits, plant height, number of productive tillers per m^2 and number of grains/panicle showed high heritability coupled with high genetic advance values indicating these traits were predominantly governed by the additive genes. Grain yield had positively correlated with days to 50% flowering, plant height and number of grains /panicle, and negatively correlated with gall midge incidence at both genotypic and phenotypic levels suggesting that genotypes with longer duration, more plant height and good number of grains panicle with relatively very less silver shoots contribute for more grain yield.

Sudeepthi *et al.* (2020) investigated with 107 elite rice genotypes to study the variability, heritability and genetic advance as per cent of mean for yield and yield component traits. In addition, character association between the yield and yield components and their direct and indirect effects on grain yield were also studied. High PCV and GCV were recorded for ear bearing tillers per plant, while high heritability was recorded for all the traits studied. Further, the high genetic advance as percent of mean was recorded for plant height, the number of ear bearing tillers per plant, the total number of grains /panicle, test weight and grain yield per plant. Among these, ear bearing tillers per plant had recorded a high variability, heritability and genetic advance as percent of mean in addition to correlation and direct effects with grain yield per plant indicating its effectiveness as important selection criterion for the yield improvement.

Tiwari *et al.* (2019) studied to estimate the genetic variability and find out the correlation among the different quantitative traits of rainfed early lowland rice. The experiment was conducted consecutively two years during 2015 and 2016 in wet season across the four different locations in Regional Agricultural Research Station, Khajura, National Wheat Research Program, Bhairahawa, National Maize Research Program, Rampur and National Rice Research Program, Hardinath along the Terai region of Nepal representing sub-tropical agro-climate. Seven genotypes including Hardinath-1 as standard check variety were evaluated in the randomized complete block design with three replications. Various quantitative traits were measured to investigate the variability and correlation coefficients. All the genotypes andlocations showed significant variations for all the traits considered. Genotypic coefficient of variation was lower than phenotypic coefficient of variation for all traits studied. The magnitudes of genotypic coefficient of variations were relatively higher for grain yield, 1000-grain weight and days to heading. The highest broad sense heritability of 94% was recorded in days to maturity and the lowest heritability of 16% was observed in plant height.

Saha *et al.* (2019) studied to estimate genetic parameters of thirteen yield and yield attributing traits in 40 landraces of rice with a view to select better yield attributes in rice. The higher value of phenotypic co-efficient of variation (PCV) compared to the corresponding genotypic coefficient of variation (GCV) for all the studied traits, indicated that there was an influence of the environment. Number of unfilled grains /panicle exhibited high estimates of PCV and GCV followed by number of filled grains /panicle, number of grains /panicle, flag leaf area. High heritability coupled with high genetic advance was observed in flag leaf area, pollen fertility, number of grains /panicle and number of filled grains /panicle which reflected that the direct selection of these characters based on phenotypic expression by simple selection method for yield improvement would be more reliable. Grain yield per plant showed significant and positive association with days to 50% flowering, days to maturity, flag leaf area, number of total tillers /hill, number of effective tillers /hill, pollen fertility, number of grains/panicle, number of filled grains /panicle indicating selection of these characters for yield improvement may be rewarding. Both at phenotypic and genotypic level, days to 50% flowering, flag leaf area, number of effective tillers /hill, pollen fertility, panicle length, number of grains /panicle and 100 seed weight had direct positive effect on yield per plant indicating their importance during selection in yield improvement program. Moreover, the information generated from this study, can be exploited in future rice breeding program.

Konate *et al.* (2016) evaluated genetic variability of agro-morphological traits and also determine the correlation between grain yield with its components in rice lines, 17 recombinants inbred lines, their parents and a check variety were grown in research station of Africa rice center in Benin republic during two consecutive years 2013 and 2014. The experiments were laid out in a randomized complete block design with four replications. Phenotypic coefficients of variance were higher than genotypic coefficients of variance in all the characters across the two years. High heritability in broad sense (H^2) estimates were obtained for biomass (68.77%), date of 50% flowering (98.11%), plant height (81.94%), leaf area (82.90%), number of panicles (64.40%), leaf dry weight (72.91%), root weight (67.43%) and yield/plant (62.23%) suggesting that the traits were primarily under genetic control. A joint consideration of broad sense heritability (H^2) and genetic advance as percent mean expected (GAM) revealed that leaves dries weight and roots weight combined high heritability and high GAM. Furthermore, high (H^2) and high GAM recorded in these characters could be explained by additive gene action. However, high estimates (H^2) combined with moderate GAM recorded for biomass, day to 50% flowering, leaf area, number of panicle and yield/plant could be due to non-additive gene effect. This result indicates that selection based on these two characters will be highly effective for yield improvement in rice.

Hossain *et al.* (2015) evaluated thirty-five local aman rice varieties for their variability with regards to yield and yield components. Estimates of heritability and genetic advance in percent of mean were also obtained for the above traits. In addition, studies on character associations and path coefficients were also undertaken. The highest $\sigma2g$ was found for number of root hair (103415.40) and the lowest magnitude of $\sigma2g$ was observed in number of primary branches /panicle (1.97). The highest $\sigma2p$ was found for number of root hair (109410.31) and the lowest magnitude of $\sigma2p$ was observed in number of primary branches /panicle (2.61). High GCV and PCV for number of effective tiller, root weight, number of root hair and grain yield /hill (g) indicated that selection of these traits would be effective. Correlation of Grain yield /hill was found to be highly significant and positive for number of root hair, days to flowering and plant height at both genotypic and phenotypic level and negatively significant for number of secondary branches perpanicle at both level. Significant positive correlation of grain yield /hill with number of root hair, days to flowering and plant height implied that selection for these characters would lead to simultaneous improvement of grain yield in rice. Further, yield was observed to be positively associated with panicle bearing tillers and number of filled grains/panicle and these characters were noticed to exert high direct effects on grain yield per plant. High indirect effects of most of the traits were noticed mostly through panicle bearing tillers /hill indicating importance of the trait as selection criterion in crop yield improvement programs.

Das *et al.* (2014) experimented on forty genotypes comprising nineteen land races, one local check variety (Acharmati) and six high yielding varieties, twelve popular aromatic rice cultivars and two advanced breeding lines were evaluated to determine character association, variability and diversity for grain yield, yield components and aroma level under irrigated and non-irrigated conditions at RRTTS, Bhawanipatna, Odisha. High values of phenotypic coefficient of variance (PCV), genotypic coefficient of variance (GCV), high heritability (H^2) and genetic advance (GA) were recorded for aroma level, grains /panicle and thousand grain weights. Significant positive correlation for panicles per plant ($r = 0.603$) and negative correlation for aroma level ($r = -0.370$) was observed with yield. All the genotypes were grouped into 11 clusters. Most of the indigenous aromatic rice cultivars were found in Cluster I and others distributed in cluster IV, cluster V, cluster VII and cluster XI. Cluster II consisted of basmati types and cluster III comprised HYV. Aromatic Test (sensory test) using 1.7% KOH solution was done for rapid evaluation of aroma level of the genotypes. The present study revealed that the indigenous aromatic rice cultivars like Gangaballi, Khosakani, Neelabati, with high aroma level, Dubraj and Dhanaprasad with faint aroma were superior genotypes of their respective clusters under both irrigated and non-irrigated conditions. Crossing between superior genotypes of diverse cluster pairs may provide desirable transgressive segregants for developing high yielding varieties of aromatic rice and can be used as potential breeding materials for improvement of aromatic land races.

Umadevi *et al.* (2010) conducted a study on 110 rice genotypes to assess the genetic variability, heritability and correlation among the genotypes for sixteen grain quality characters and grain yield. The genotype ASD 06-4 recorded maximum mean value for hulling percent and milling percent. CRMS 32 A recorded intermediate value for gelatinization temperature, gelconsistency, amylose content and superior performance for volume expansion ratio. Higher magnitude of genotypic variability interms of GCV of more than 20 percent was recorded for gel consistency, volume expansion ratio, alkali spreading value, single plant yield, and amylose content. The single plant yield had highly significant and positive association with L/B ratio, water uptake, breadth-wise expansion ratio, gel consistency and amylose content. The traits viz., single plant yield, volume expansion ratio, gel consistency, alkali spreading value and amylose content possessing high GCV, heritability and genetic advance could be effectively used in selection.

Hasan *et al.* (2010) studied on twenty-four hybrid rice varieties of diverse origin for genetic variability, correlation and path analysis under medium high land of Gazipur. The PCV values were greater than GCV, revealing little influence of environment in character expression. High values of heritability along with moderate genetic advance were observed for panicle/m^2, days to 50% flowering and plant height. Grain yield showed positive significant association with number of effective tillers/hill, panicle/m^2, spikelet fertility and thousand grain weight at both genotypic and phenotypic levels. Same traits had highest significant positive effect on yield.

2.2 Genetic diversity in rice

Devi *et al.* (2020) conducted an experiment with 71 rice genotypes to assess the genetic diversity and variability by using Mahalanobis D^2 Statistical and principal component analysis. All genotypes exhibited a wide and significant variation for 21 traits. The cluster analysis indicated that 71 genotypes were grouped into eleven clusters and cluster 1 followed by cluster 11 consisted with 33 and 29 genotypes respectively and rest of the nine clusters contain one genotype each. The maximum inter cluster distance was recorded between clusters VIII (906.17) with cluster V followed by cluster VII (682.74) and cluster I and also between cluster V (657.43) and cluster 11. The lowest inter cluster distance (70.66) was observed between cluster III and cluster IV. The intra cluster D^2 values ranged from zero (cluster XI, X, IX, VIII, VII, VI, V, IV, III) to 128.42 (cluster I).

Cluster VIII recorded highest cluster mean for water uptake, alkali spreading value, while cluster IX showed highest cluster mean for grain yield/plant and effective tillers and second highest for kernel length, days to 50% flowering and panicle density. Milling percent head rice recovery Kernel length, length/breadth ratio, Kernel length after cooking and water uptake. Contribution of days to 50% flowering was highest towards genetic divergence (36.05) by taking 896 times ranked first followed by kernel length after cooking (23.9) by 593 times, water uptake (10.0) and kernel length (8.5). The PCA analysis showed that the first five principal components accounted for about 82.23% of the total variation and exhibited very high correlation among them. Phenotypic coefficient of variation was higher than genotypic coefficient of variation. The traits panicle density, filled seeds/panicle volume expansion ratio and yield per plant exhibited high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV).

Perween *et al.* (2020) evaluated a set of 48 rice genotypes to assess the magnitude of genetic diversity under irrigated (control) and reproductive stage drought stress conditions during *Kharif*, 2018 at Rice Research Farm, Bihar Agricultural University, Sabour (Bhagalpur), India. On the basis of D^2 statistics, all the genotypes were grouped into nineteen clusters in irrigated condition with cluster I consisting of maximum number of genotypes (24) followed by cluster III (7) and rest of the clusters were represented by single genotype in irrigated condition. Under drought stress condition, forty-eight genotypes were grouped into eleven clusters, cluster I consisted of maximum number of genotypes (24) followed by cluster II and III (8 genotypes in each cluster) and rest of the clusters were mono-genotypic. The highest inter-cluster distance was recorded between cluster XVIII and XIX (28.53), followed by cluster X and VIII (24.20), cluster XIII and XVIII (23.98) and cluster VII and XVIII (23.79) in irrigated condition while in drought stress condition the highest inter-cluster distance was observed between cluster IX and X (31.72), followed by cluster V and IX (28.77), cluster VI and VII (25.98) and cluster IV and IX (25.98) indicating wider genetic diversity among the genotypes between these clusters. The hybridization programme involving genotype of cluster XVIII and cluster XIX under irrigated condition and the genotypes of cluster IX and X under drought stress condition could be undertaken to isolate high yielding segregants, since these genotypes have high yielding potential, number of effective tillers /hill, relative water content, leaf area, root biomass, panicle length, biological yield, harvest index, plant height, number of fertile grains /panicle, total number of spikelets /panicle, leaf area and proline content with more genetic distances. The parents for hybridisation could be selected on the basis of their large inter-cluster distance for isolating useful recombinants in the segregating generations. Hence, these genotypes might be used in a multiple crossing programme to recover transgressive segregants. Therefore, it is suggested that if the diverse genotypes from these groups along with the other desirable attributes are used in breeding programmes, it is expected to produce better segregants for high grain yield and yield contributing traits due to non-allelic interaction.

Tiruneh *et al.* (2019) studied to estimate the genetic diversity of 36 upland rice genotypes based on quantitative morphological traits. The field experiment was conducted using 6×6 simple lattice design in to two locations of southwestern Ethiopia (viz., Gojeb and Guraferda) during the 2016 main cropping season. Cluster analysis, distance analysis and principal component analysis were done using the SAS software version 9.3. The analysis of variance over the two locations revealed significant differences ($p<0.05$) among genotypes for plant height, panicle length, culm length, filled grains /panicle, number of primary branches /panicle, days to maturity, days to heading, harvest index and grain yield. Cluster analysis indicated that 36 genotypes were grouped into 6 clusters and divergences between all pairs were significant ($p<0.01$). The inter-cluster distance was maximum between cluster five and six ($D^2 = 997$) followed by cluster four and six ($D^2 = 811$). The first six principal components (PCs) with eigen values greater than one explained 75.2% of the total variation among genotypes. The first and second PCs were responsible for about 19.3 and 14.5% of the total variation, respectively. In the first principal component character such as plant height (16.8%), panicle length (18.6%) and culm length (18.3%) accounted high contribution effect of the total variation. This study confirmed the presence of variability among genotypes for most of the studied traits, which will create an opportunity for breeders to improve the yield of rice and other traits.

Tejaswini *et al.* (2018) experimented on the nature and magnitude of genetic divergence in one hundred and fourteen F_5 families of rice obtained from six different crosses along with their seven parents using Mahalanobis D^2- statistics. ANOVA revealed the presence of considerable amount of variability among the genotypes. Mahalanobis D^2 analysis revealed considerable amount of diversity in the material. The genotypes were grouped into twelve clusters. Cluster IX constituted maximum number of genotypes (26). The genotypes falling in cluster VII had the maximum divergence, which was closely followed by cluster VII and cluster XI. The maximum inter cluster D^2 values was observed between cluster X and XI (931.276) followed by cluster VII and XI (814.784) suggesting that the genotypes constituted in these clusters may be used as parents for future hybridization programme.

Singh *et al.* (2018) studied on morphological characterization of twenty-three rice accessions which includes, four of high Zinc (R-RHZ-7, CGZR-1, IR83294-66-2-2-3-2 and IR83668-35-2- 2-2), fifteen of drought tolerant and four checks (Swarna, MTU-1010, Sahbagi dhan and NDR-97) was done to observe genetic diversity to identify suitable genotypes for future breeding program. Data on fifteen morphological characters were recorded for this study. Analysis of variance (ANOVA) revealed highly significant differences among the accessions for all the characters under study which explains a wide range of morphological diversity among them. These accessions were grouped into five different clusters based on Tocher method of clustering. Cluster I contains 7 out of 23 accessions, cluster II comprises 6 accessions and cluster III having 8 accessions. Clusters IV and V consist of only one accession each, indicating their distinctness among themselves and also from other accessions. The highest intra-cluster distance was observed in the cluster III (754.11) which comprised of 8 accessions. The highest inter-cluster distance (6465.17) was found between cluster II and V followed by cluster I and V (4819.21) and cluster III and V (3431.24). The smallest inter-cluster distance (555.01) was observed between I and II followed by cluster I and III (759.32) and cluster II and III (1428.35). The highest intra-cluster distance was found in cluster III (754.11) and least was found in clusters IV and V due to their monogenotypic nature. The clusters II and V were found to be most diverse and hybridization between the accessions of these clusters may produce desirable segregants.

Babu *et al.* (2017) assessed genetic divergence among fifty genotypes of rice to study the nature and magnitude of genetic divergence using D^2 statistics. Based on the genetic distance the fifty genotypes were grouped into six clusters. Of the six clusters formed, cluster I having maximum number of genotypes (12) followed by cluster II with nine entries. Maximum intra cluster distance (746.9) was observed in cluster VI and minimum in Cluster III (327.8). Days to 50% flowering, gelatinization temperature score and water uptake together contributes around 72% to total divergence. Maximum inter cluster distance was recorded between clusters III and VI (827.45) followed by cluster III and

IV indicating wide genetic diversity and it may be used in rice hybridization programme for improving grain yield.

Sowmiya and Venkatesan (2017) experimented on 48 rice genotypes for nine characters. In D^2 analysis, the 48 genotypes were grouped into nine clusters. The clustering pattern indicated that there was no parallelism between genetic diversity and geographical origin as the genotypes from different origins were included in same clusters and vice versa. The maximum intra cluster distance was registered in cluster VIII (35.87). The maximum inter cluster distance was found between Cluster VI and Cluster VIII (54.23) followed by Cluster VIII and IX (51.01), cluster V and VIII (50.26) and cluster IIIand VIII (45.60). Genetically distant parents from those clusters could be able to produce higher heterosis in progenies on hybridization. Grain yield per plant and thousand grain weight were the major contributors towards the total genetic divergence among the genotypes studied. Selection could be made based on grain yield per plant and thousand grain weight for the progenies identified.

Bhandari *et al.* (2017) studied and showed that plant breeding is facing challenge to feed the ever increasing population with diminishing cultivable land. Modern plant breeding has achieved some success in this regard. However, it has resulted in the genetic vulnerability because of narrow genetic base of cultivated varieties in many crops. Hence, there is a need of paradigm shift in plant breeding focusing on diverse genetic resources. Genetic diversity has now been acknowledged as a specific area that can contribute in food and nutritional security. Better understanding of genetic diversity will help in determining what to conserve as well as where to conserve. Genetic diversity of crop plants is the foundation for the sustainable development of new varieties. So there is a need to characterize the diverse genetic resources using different statistical tools and utilize them in the breeding programme. Morphological data in conjunction with molecular data are used for precise characterization of germplasm resources. With the advent of high through put molecular marker technologies, it is possible to characterize larger number of germplasm with limited time and resources. The analysis is based on statistical tools for better interpretation. The most used statistical tools for morphological data are D^2 statistics and PCA because of their easy interpretation. PCoA is very much in use for molecular diversity analysis. POWERMARKER and GenAlEX are mostly used software because of their high informativeness. The diversity indicated by different analysis can further be utilized in heterosis breeding, transgressive breeding and interogression of alien genes for specific traits.

Tripathi *et al.* (2017) studied on variability and diversity of 32 genotypes of rice (*Oryza sativa* L.) under direct seeded condition revealed significant variability at 5% level among the genotypes for all the characters. High level of broad sense heritability was observed for days to 50% flowering (0.986) followed by filled grains (0.8216) and 1000-grain weight (0.7306). Expected genetic advance was highest for yield per hectare (39.639) and filled grains /panicle (51.39). Genetic divergence analysis using Mahalanobis's D^2 statistic grouped the genotypes into 7 clusters. Cluster II had maximum number (16) of genotypes. Maximum inter cluster distance was found between cluster IV and VII (984.82). However, intra cluster distance was maximum in cluster III (363.58). Genotypes from diverse clusters viz.NR 89, PAU 3284, ARIZE SWIFT, RY 248, Varadhan, RYC489, MTU 1010 and RYC 674 could be recommended for inclusion in hybridization programme for breeding under aerobic rice condition.

Ahmed *et al.* (2016) studied thirty-one duplicate and similar named rice germplasms of Bangladesh to assess the genetic variation for the agro-morphological and physico-chemical traits and simple sequence repeat banding patterns during 2009–2012 at Bangladesh Rice Research Institute. The range of variations within the cultivar groups showed higher degree. The principal component analysis showed that the first five components with vector values > 1 contributed 82.90% of the total variations. The cluster analysis grouped the genotypes into four clusters, where no duplicate germplasm was found. The highest number (11) of genotypes was constellated in cluster I and the lowest (3) in cluster II. The intra- and inter-cluster distances were maximum in cluster I (0.93) and between clusters I and IV (24.61), respectively, and the minimum in cluster IV (0.62) and between clusters I and III (5.07), respectively. The cluster meanrevealed that the crosses between the genotypes of cluster I with those of clusters II and IV would exhibit high heterosis for maximum good characters. A total of 350 alleles varied from 3 (RM277) to 14 (RM21) with an average of 7.8 per locus were detected at 45 microsatellite loci across the 31 rice accessions. The gene diversity ranged from 0.48 to 0.90 with an average of 0.77, and the polymorphism information content values from 0.44 (RM133) to 0.89 (RM206) with an average of 0.74. RM206, RM21, RM55, RM258 and RM433 were considered as the best markers on the basis of their higher polymorphism information content values. The dendrogram from unweighted pair-group method with arithmetic average clustering also classified the genotypes into four groups, where group IV comprised of 20 genotypes and group III of one genotype, but no duplicate was found. Finally, similar and duplicate named rice germplasms need to be conserved in gene bank as are distinct from each other.

Devi (2016) studied with 64 exotic rice germplasm to investigate the nature and magnitude of genetic divergence during Kharif 2011. The analysis of variance showed significant differences for all the characters studied among the genotypes. Based on the analysis, the genotypes were grouped into 9 clusters. Maximum numbers of 27, 17, 10 and 5 genotypes were grouped under cluster III, I, II and IV respectively, while clusters V, VI, VII, VIII, and IX had only one genotype each. Maximum inter cluster distance was observed between cluster IV and IX (2091.48) followed by cluster VII and IX (1893.05) indicates wider the genetic diversity between genotypes. Cluster VI showed highest mean for seed yield per plant (25.67 g) followed by cluster IX, cluster VII and cluster III. The maximum inter cluster distance exhibited by cluster IV – IX and cluster IV also identified for selecting parents for incorporating the two traits viz., short plant structure and harvest index whereas cluster IX also identified for selecting parents for incorporating the three traits viz., early number of panicles per plant, flag leaf length and seed yield per plant. The genotypes in the above cluster may be involved in a multiple crossing programme to recover transgressive segregants with high genetic yield potential. Among the traits studied, number of spikelets /panicle had maximum contribution towards the genetic divergence followed by plant height, panicle length and harvest index whereas number of panicle /hill and panicle length had no contribution towards the genetic divergence.

Johnson *et al.* (2015) studied the nature and magnitude of genetic divergence of 112 genotypes (85 Germplasm accession, 12 improved varieties and 15 advance breeding lines) of chickpea carried out using Mahalanobis's D^2 statistics, correlation using Miller and path analysis by Dewey and Lu. 112 genotypes of chickpea were grouped in eight cluster. The highest inter cluster distance was observed clusters IV and VII (6.296) followed by I and VII (5.867), IV and V (5.681), I and IV (5.658). The highest intra-cluster distance was observed for cluster V (2.328). Hence, genotypes belonging to this cluster viz. ICC 251834, ICC 275466, ICC 269530, Indira Chana-1, ICC 269563, RG

2011-01, RG 2011-03, and JG 11 can be utilized as parents in future maize improvement programmes. Correlation coefficient analysis revealed that biological yield and harvest index exhibited the positive correlation with seed yield per plant. path coefficients for seed yield per plant recorded the highest positive direct effect contributing to seed yield plant-1 is harvest index, biological yield and pods plant^{-1}.

Kumar (2015) investigated to assess the nature and magnitude of genetic diversity was in 57 genotypes of rice using Mahalanobis D^2 statistics. They were evaluated for thirteen yield and yield attributing characters and based on D^2 analysis, 57 genotypes were grouped into 13 clusters. Clusters II and IV was the largest cluster containing 14 genotypes each followed by cluster III with 11 genotypes. The pattern of distribution of genotypes within different clusters was random and independent of geographical origin or region of adaptation. The characters like days to maturity (34.21%), days to flowering (27.44), grain length (19.55%) and grain width (12.16%) contributing maximum towards diversity. Hence these characters can be given consideration for selection of genotypes for future breeding programmes. The effective tillers (0.474), spikelet fertility (0.323), biological yield (0.723) and harvest index (0.744) in land races, plant height (0.542), panicle length (0.356), effective tillers (0.436), spikelet fertility (0.317), biological yield (0.766) and harvest index (0.744) in new plant types and panicle length (0.386), spikelet’s and grains /panicle (0.459, 0.498), biological yield (0.627) and harvest index (0.627) in japonicas were positively associated with grain yield indicating that these are the important characters and can be strategically used to improve the yield of rice.

Ovung *et al.* (2012) estimated the nature and magnitude of genetic divergence in 70 rice genotypes using Mahalanobis D^2 – statistics by considering 13 quantitative characters. ANOVA revealed the presence of considerable amount of variability among the genotypes. High estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for grain yield /hill followed by tillers /hill and harvest index. High heritability coupled with high genetic advance was recorded for spikelets /panicle. Mahalanobis D^2 analysis revealed considerable amount of diversity in the material. The genotypes were grouped into nine clusters. Cluster I and cluster III constituted maximum number of genotypes (12 each). The genotypes falling in cluster VII (2907) had the maximum divergence, which was closely followed by cluster V (2027) and cluster I (1762). The inter cluster distance was maximum between cluster VI and VII (18054) followed by cluster III and IX (12520), suggesting that the genotypes constituted in these clusters may be used as parents for future hybridization programme. Traits like spikelets /panicle; plant height and biological yield were the major contributors to genetic divergence.

Garg *et al.* (2011) experimented on the forty-eight genotypes of rice to study the nature and magnitude of genetic divergence using D^2 statistics. Seventeen yield and quality traits were recorded on the genotypes raised in the α-Design with three replications. The forty-eight genotypes were grouped into five clusters based on Euclidean cluster analysis with cluster I containing the maximum of 18 genotypes. Maximum intra-cluster distance was observed in cluster I indicating greater genetic divergence between the genotypes belonging to this cluster. Days to maturity, gel consistency and days to 50 per cent flowering contributed 74.55 percent of total divergence. Maximum inter-cluster distance was recorded between clusters II and III followed by clusters III and IV indicating wide genetic diversity and it may be used in rice hybridization programme for improving grain yield.

Baradhan and Thangavel (2011) worked on Mahalanobis D^2 statistics to study the nature and magnitude of genetic diversity among 45 genotypes of rice. The genotypes were grouped into six clusters. Cluster III, had the highest genotypes (13) followed by cluster I (9). The genotypes falling in cluster I (8.04) had the maximum divergence which was closely followed by cluster II (8.03) and cluster V (8.02). The inter cluster distance ranged from 7.58 to 13.20 as exhibited between cluster III and V and cluster II and VI, respectively. In the present study, parental lines selected from cluster VI for grain yield, number of productive tillers /hill, panicle length and plant height and cluster I for number of grains /panicle exhibited high mean values. It is suggested that varietal improvement through hybridization, should be done among the genotypes more of divergent clusters.

Vennila *et al.* (2011) investigated on 41 rice genotypes to identify diverse genotypes. They were evaluated for nine yield and yield attributing characters using Mahalanobis D^2 statistics. 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 under thirteen 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. 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 /panicle, plant height, grain length and grain breadth contributed maximum towards genetic diversity. Hence these characters could be given due importance for selection of genotypes for further crop improvement programme.

Palaniraja and Anbuselvam (2010) studied genetic divergence for different yield and its component traits for 51 rice genotypes collected from different eco-geographical regions of India. The analysis of variance revealed significant differences among the genotypes for all the characters studied. Based on genetic distance all the 51 genotypes were grouped under fifteen 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. The characters like plant height, panicle length and grain yield per plant contributed maximum towards genetic diversity. The maximum inter-cluster distance was recorded between cluster I and XV. Selection of genotypes in these clusters which may serve as potential donors for future hybridization programmes to develop potential recombinants with high yield coupled with desirable traits.

Biswas *et al.* (2008) integrated a set of thirty genotypes of fine rice collected from different parts of Bangladesh in the investigation to assess variability and diversity pertained among them. The experiment was conducted in the experimental field, Hajee Mohammad Danesh Science and Technology University, Dinajpur, Bangladesh and laid out at RCBD with three replications during July to December, 2006. Analysis of variance revealed significant variation for each of the characters that instigated to study variability and diversity present in the materials. High heritability was estimated for panicle length followed by spikelets/panicle, yield /ha and tillers/plant but high heritability coupled with high genetic advance was estimated for panicle length and spikelets/panicle. The genotypes fell into 7 different clusters based on D^2 statistics. Cluster I contained the highest number of genotypes viz. Katari, Zira, Badshabhong, Zethakatari, Philippinekatari, Neniya, Chinigura, Shadakatari, Dudshar and Bolder. The popular known primitive cultivar, Kalazira was included in cluster II along with Shilkamal and Shitabhog. The only variety, BRRI 34 had fallen under cluster VI containing Darkashail too. Moulata alone was included alone in cluster V. The genotypes under cluster I produced the highest yield (3.307 t/ha). The contribution of spikelets/panicle alone exerted maximum load (19.58%) to evolve genetic diversity and the ultimate end product yield/ha contributed only 5.38% to the genetic diversity.

2.3 Correlation and path analysis on yield and other related characters

Siddi (2020) investigated variability and trait association studies in 18 rice (*Oryza sativa* L.) genotypes with two replications in a RBD design during kharif, 2017 at Agricultural Research Station, Kunaram. The traits viz, plant height, number of productive tillers per m^2 and number of grains /panicle showed high heritability coupled with high genetic advance values indicating that these traits were predominantly governed by the additive genes. Grain yield was positively correlated with days to 50% flowering, plant height and number of grains /panicle, and negatively correlated with gall midge incidence at both genotypic and phenotypic levels suggesting that genotypes with longer duration, more plant height and good number of grains panicle with relatively very less silver shoots contributed for more grain yield.

Sudeepthi *et al.* (2020) investigated with 107 elite rice genotypes to study the variability, heritability and genetic advance as per cent of mean for yield and yield component traits. In addition, character association between the yield and yield components and their direct and indirect effects on grain yield were also studied. High PCV and GCV were recorded for ear bearing tillers per plant, while high heritability was recorded for all the traits studied. Further, the high genetic advance as per cent of mean was recorded for plant height, the number of ear bearing tillers per plant, the total number of grains /panicle, test weight and grain yield per plant. Among these, ear bearing tillers per plant had recorded a high variability, heritability and genetic advance as per cent of mean in addition to correlation and direct effects with grain yield per plant indicating its effectiveness as important selection criterion for the yield improvement.

Nikhil *et al.* (2019) experimented to study the correlation and path analysis in 40 rice (*Oryza sativa* L.) genotypes during Kharif, 2011 at the Department of Genetics and Plant Breeding, SHIATS, Allahabad in Randomized Block Design with three replications to analyze correlation and path Analysis. Character association of the yield attributing traits revealed significantly positive association of grain yield /hill with biological yield /hill and number of panicles /hill. Hence, selection for these traits can improve yield. Path coefficient analysis revealed that biological yield /hill and harvest index exhibited positive direct effect on yield. Among these characters, biological yield /hill possessed both positive association and high direct effects. Hence, selection for this character could bring improvement in yield and yield components in rice.

Tiwari *et al.* (2019) studied to estimate the genetic variability and find out the correlation among the different quantitative traits of rainfed early lowland rice. The experiment was conducted consecutively for two years during 2015 and 2016 in wet season across the four different locations in Regional Agricultural Research Station, Khajura, National Wheat Research Program, Bhairahawa, National Maize Research Program, Rampur and National Rice Research Program, Hardinath along the Terai region of Nepal representing sub-tropical agro-climate. Seven genotypes including Hardinath-1 as standard check variety were evaluated in the randomized complete block design with three replications. Various quantitative traits were measured to investigate the variability and correlation coefficients. Positive and highly significant correlations were found both in genotypic and phenotypic levels between days to heading and days to maturity (rg=0.9999**, rp=0.997**), days to heading and grain yield (rg =0.9999**, rp= 0.9276**), days to maturity and grain yield (rg =0.9796**, rp=0.9174**). However, negative and highly significant genetic correlation was observed between plant height and 1000 grain weight (rg = -0.9999**). Thus results indicated that days to heading, days to maturity, grain yield, 1000 grain weight demonstrated higher heritability and remarkable genetic advance could be considered for the most appropriate traits for improvement and selection of trait to achieve stable and high yielding early rice genotypes under rainfed environments.

Tiwari and Priya (2018) studied the character association and path analysis in twenty-three recombinant inbred lines (RILs) of Sabita/Sambamahsuri derivatives and four check varieties of rice (*Oryza sativa* L.). Character association of the yield attributing traits revealed significantly positive association of grain yield per plant with number of panicles per plant (genotypic), panicle weight, panicle length, number of florets /panicle, number of grains /panicle, kernel breadth and harvest index. Hence, selection for these traits can improve yield. Path coefficient analysis revealed that ten characters viz. days to maturity, panicle length, number of primary branches /panicle, number of florets

/panicle, number of grains /panicle, fertility percentage, grain length, kernel breadth, kernel Length/Breadth (L/B) ratio and harvest index had positive direct effect on yield.

Kumar *et al.* (2018) experimented and showed that, biological yield per plant, harvest index, spikelet fertility, 1000-grain weight, L/B ratio, plant height and panicle length showed positive and significant correlation with grain yield per plant to emerge as most important associates of grain yield in rice. Path analysis identified biological yield per plant followed by harvest-index as most important direct yield contributing traits and biological yield per plant followed by 1000-grain weight and panicle length exhibited high order of positive indirect effect as most important indirect components which merit due consideration at time of devising selection strategy aimed at developing high yielding varieties in rice. Out of 82 entries tested under natural condition, none were found to be immune or resistant. However, 30 genotypes were found moderately resistant, 47 genotypes moderately susceptible, while 3 genotypes susceptible and rest two genotypes were highly susceptible.

Singh *et al.* (2018) investigated to study the correlation and path analysis in eighty-four (including Check) rice (*Oryza sativa* L.) varieties. Biological yield per plant, harvest index, 1000-grain weight, panicle bearing tillers/plant and panicle length showed positive and significant correlation with grain yield per plant to emerge as most important associates of grain yield in rice. Path analysis identified biological yield per plant followed by harvest index as the most important direct as well as indirect yield. Contributing traits or components which merit due to consideration at time of devising selection strategy aimed at developing high yielding varieties in rice. On the contrary, most of the previous reports in rice, comparatively small proportion of direct and indirect effects of different characters attained high order value in the present study. This may be attributing to presence of very high genetic variability and diversity in the fairly large number of germplasm lines.

Bagudam *et al.* (2018) examined correlation and path analysis in 46 rice genotypes including tropical japonica accessions, indica land races and elite indica cultivars as new plant type (NPT) core set al.ong with checks during kharif 2017. The data was recorded on twelve quantitative traits viz., days to 50% flowering, plant height, number of tillers, number of panicles, panicle length, panicle weight, grain number, test weight, single plant yield, plot yield, biomass and harvest index. Correlation studies revealed highly significant and positive association of single plant yield with days to 50% flowering, tillers per plant, productive tillers per plant and biomass, indicating that these characters are very important for yield improvement and concurrent selection will directly lead to high yield. Path coefficient analysis showed that productive tillers per plant exerted highest positive direct effect followed by panicle length, number of grains /panicle, test weight, panicle weight, harvest index and biomass on single plant yield, indicating that selection for these characters is likely to bring about an overall improvement in grain yield per plant directly. In view of the results obtained, it may be concluded that characters like productive tillers per plant and biomass could be used as a direct selection criteria for higher grain yield.

Chuchert *et al.* (2018) evaluated on twenty-two upland rice genotypes and the genotypes indicated significant variations in nine traits. High phenotypic and genetic coefficients of variation were observed for yield per plant, number of panicles per plant, and number of spikelets /panicle. High broad-sense heritability and genetic advance were found for yield per plant. Positive significant correlations were recorded between flag leaf length, number of panicles per plant, and number of spikelets /panicle. The highest direct effects on yield were attributed to the number of spikelets /panicle and the number of panicles per plant. Cluster analysis grouped the 22 genotypes into groups I, II, and III, and the out groups consisting of nine, five, six, and two genotypes. These results may facilitate upland rice breeding programs to improve yield.

Rashid *et al.* (2017) conducted studies on character association and path-coefficient analysis in ten rice genotypes including seven landraces and three released varieties for their yield and yield contributing traits. Character association of the yield attributing traits revealed significantly positive association of yield panicle^{-1} with days to 50% flowering, days to maturity, plant height and number of filled grains panicle^{-1}. Hence, selection for these traits can improve yield. Path coefficient analysis revealed that days to maturity, number of filled grains panicle^{-1}, number of unfilled grains panicle$_{-1}$ and 1000 grains weight exhibited direct positive effect on yield panicle^{-1} at genotypic level and days to 50% flowering, plant height, panicle length, number of effective tillers plant^{-1}, percent fertility exhibited direct positive effect on yield panicle^{-1} at phenotypic level. Hence, selection for this character could bring improvement in yield and yield components. This study revealed that genetic improvement of yield in rice was admissible by selecting characters having high positive correlation and positive direct effect on grain yield.

Devi *et al.* (2017) studied variability, correlation and path analysis for yield and quality traits on 27 rice genotypes. The higher estimates of PCV and GCV were observed for yield per plant (42.04) and filled seeds /panicle (33.9) indicate possibility of genetic improvement through direct selection. High heritability in broad sense coupled with high genetic advance as percent of mean exhibited by effective tillers, plant height, flag leaf length, filled grains /panicle, test weight, yield per plant, head rice recovery and length/breadth ratio indicated preponderance of additive gene action which provided good scope for further improvement by selection. Grain yield per plant had highest significant positive association with filled seeds /panicle, plant height, flag leaf length, effective tillers, flag leaf width and panicle length indicating importance of these characters for yield improvement, while head rice recovery was found to be significantly and positively correlated with milling percent and hulling percent. Path analysis reveals that test weight (3.48), effective tillers (1.57), and filled grains /panicle (1.41) had positive direct effect on grain yield per plant. Among the quality traits kernel length followed by milling percent and kernel elongation ratio had direct effect on head rice recovery.

Kalyan *et al.* (2017) evaluated seventy genotypes of rice (*Oryza sativa* L.) during Kharif 2014 to study the nature and extent of correlation among yield and yield attributing characters viz; number of tillers per plant, number of effective tillers per plant, plant height, panicle length, number of filled grains /panicle, 1000-grain weight, days to 50 percent flowering, days to maturity, grain yield per plant. Character association studies revealed that grain yield per plant showed significant positive association with plant height, number of tillers per plant, number of productive tillers per plant, number of filled grains /panicle and 1000 grain weight. This indicated that simultaneous selection of all these characters was important for yield improvement.

Kar *et al.* (2016) investigated to establish the nature of relation between grain yield and yield components by partitioning the correlation coefficients between grain yield and its components into direct and indirect effects by using simple correlation and path analysis. By the help of correlation coefficients selection indeices were constructed to increase the selection efficiency. The results indicated that grain yield was positively correlated with days to flowering, plant height, fertile grain number and fertility percentage indicating the importance of such traits for realization of high yield in rice. The traits like days to 50% flowering exhibited maximum positive direct effect on grain yield followed by plant height, grain yield per plant, fertility percentage and 100-grain weight, thus, indicating the importance of such traits as criteria for selection for realization of higher productivity. Using grain yield as economic criterion, ten selection indices were constructed. On the basis of selection criteria, the promising genotypes selected were IR 85086-SUB 33-3-2-1, IR 88760-SUB 93-3-3-3, Upahar, IR 88250-20-1-1-3, Jagabandhu, IR 88230-60-1-2-2, Savitri-Sub 1, IR 87092-26-3-1-3, Savitri, IR 87098-55-2-1, Mahanadi, PSBRc 68, Swarna, Swarna-Sub 1, PSBRc 70.

Kohnaki *et al.* (2016) studied the relationship between morphological characters in rice lines derived from two populations at F_3 generation grown in research field of Agricultural Sciences and Natural Resource University, Sari, Iran, during 2012. Statistical analysis on important agronomic traits showed that maximum standard deviation belonged to total grain number followed by filled grains /panicle and grain yield. Result of correlation analysis revealed positive and significant relation of grain yield per plant with panicle length, panicle per plant, total grain number and filled grains /panicle. Path coefficient analysis indicated that filled grains /panicle had highest direct effect on yield followed by panicle length, plant height, and panicle per plant. Panicle per plant had highest indirect effect on grain yield. This study revealed that selection based on filled grains /panicle, panicle length and panicle per plant will be highly effective for yield improvement in rice breeding programs.

Lakshmi *et al.* (2014) evaluated seventy genotypes of rice (*Oryza sativa* L.) during Kharif 2012 to study the nature and extent of correlation among yield and yield attributing characters viz; days to 50 percent flowering, days to maturity, number of effective tillers per plant, plant height, panicle length, number of grains /panicle, 1000-grain weight, grain yield per plant, kernel length, kernel breadth and L/B ratio. The results revealed that grain yield per plant was positively and significantly associated with days to maturity, number of productive tillers per plant, plant height and kernel length indicating importance of these traits as selection criteria in yield improvement programmes.

Ranawake and Amarasinghe (2014) examined to understand the relationship between individual trait and yield of one hundred rice cultivars according to Pearson's correlation coefficient. Completely randomized block design with four replicates. Twenty plants were evaluated in each replicate and eighty plants were evaluated in each cultivar in four replicates. Faculty of Agriculture, University of Ruhuna, Sri Lanka in 2011-2013. Data were collected in 80 plants of four replicates on: plant height (cm), number of tillers per plant, number of fertile tillers per plant, panicle length (cm), panicle weight (g), number of spikelets /panicle, number of fertile spikelets /panicle, 100 grain weight (g), days to maturity and yield per plant (g). Pearson's correlation coefficients were calculated using SPSS. According to statistical analysis grain yield was significantly and highly correlated with number of fertile spikelets/panicle (r = 0.765), panicle weight (r = 0.727), number of spikelets/panicle (r = 0.638), filled grain percentage (r = 0.620), number of fertile tillers/plant (r = 0.611), number of tillers/plant (r = 0.575), hundred grain weight (r = 0.336) and plant height (r = 0.278) were also correlated with at 1% significant level. None of the studied trait was negatively correlated with the yield. Fertile spikelets /panicle, panicle weight, number of spikelet /panicle were the most important characters.

Basavaraja *et al.* (2011) investigated 100 local rice cultivars to understand the association among yield components and their direct and indirect influence on the grain yield. The correlation analysis indicated that grain yield was significantly associated with panicle length, test weight, number of tiller per plant, number of productive tiller per plant, number of spikelet /panicle, per cent spikelet fertility and amylase percent. Path coefficient analysis revealed those days to 50 % flowering, plant height, panicle length, panicle number, number of productive tiller per plant, percent spikelet fertility and amylase percent had positive direct effect on grain yield. Hence, selection based on these traits could help to bring simultaneous improvement of yield and yield attributes.

Bagheri *et al.* (2011) studied to determine the relationship between grain yield and yield component in rice (*Oryza sativa* L.). Twenty-six rice genotypes were used in this research. A field experiment was conducted in a randomized complete block design with three replications at the Sari Agricultural Sciences and Natural Resources University. The traits, panicle length (r = 0.818), the total number of spikelet /panicle (r = 0.617), the number of filled grains /panicle (r = 0.790), and the panicle number per plant (r = 0.498) correlated significantly with grain yield. Path coefficient analysis revealed that panicle length had the highest positive direct effect (0.510) on grain yield. Grain yield linearly correlated with panicle length, the number of panicle per plant, and the number of filled grains /panicle. Therefore, these traits may be used in the selection for grain yield in rice.

Golam *et al.* (2011) evaluated a total of 53 rice genotypes including 12 globally popular aromatic rice cultivars and 39 advanced breeding lines for yield and yield contributing characters in Malaysian tropical environment. Two local varieties MRQ 50 and MRQ 72 were used as check varieties. Correlation analysis revealed that the number of fertile tillers (r = 0.69), grains/panicle (r = 0.86) and fertile grains/panicle (r = 0.65) had the positive contribution to grain yield. Highest grain yield was observed in E36, followed by Khau Dau Mali, E26 and E13. E36 appeared with lowest plant height and it also produced highest number of fertile tillers. After evaluation of yield components four genotypes namely E36, Khau Dau Mali, E26 and E13 were selected as outstanding genotypes, which could be used as potential breeding materials for Malaysian tropical environment.

Ekka *et al.* (2011) stated that grain yield per plant had positive significant correlation with leaf width, days to 50% flowering, plant height, panicle length, number of filled grains /panicle, 100 seed weight and paddy (grain) length. A positive and significant correlation of head rice recovery percentage was also observed with leaf length, leaf width, days to 50% flowering, number of filled grains /panicle, spikelet sterility (%) and milling (%). Path coefficient analysis revealed that direct selection for days to 50% flowering, 100 seed weight, panicle length, leaf length and milling percentage would likely be effective for increasing grain yield. Direct selection for days to 50% flowering and number of filled grains /panicle would increase head rice recovery percentage. This study indicated that there is no common causal factor that directly influence grain yield per plant and head rice recovery percentage. Although, days to 50% flowering and leaf length could be used as selection criteria for the simultaneous improvement of both the traits.

Hairmansis *et al.* (2013) investigated the relationship between agronomic characters and grain yield of rice as a basis for selection of high yielding rice varieties for tidal swamp areas. Agronomic characters and grain yield of nine advanced rice breeding lines and two rice varieties were evaluated in a series of experiments in tidal swamp areas, Karang Agung Ulu Village, Banyuasin, South Sumatra, for four cropping seasons in dry season

(DS) 2005, wet season (WS) 2005/2006, DS 2006, and DS 2007. Result from path analysis revealed that the following characters had positive direct effect on grain yield, i.e. number of productive tillers /hill (p = 0.356), number of filled grains /panicle (p = 0.544), and spikelet fertility (p = 0.215). Plant height had negative direct effect (p = -0.332) on grain yield, while maturity, number of spikelets /panicle, and 1000-grain weight showed negligible effect on rice grain yield. Present study suggested that indirect selection of high yielding tidal swamp rice could be done by selecting breeding lines which had many productive tillers, dense filled grains, and high spikelet fertility

2.4 Realized heritability

Govintharaj *et al.* (2017) was experimented the effectiveness of early generation selection in bacterial blight resistance genes, introgressed F_2 and $F_{2:3}$ population of the cross CB 174 R × IRBB 60 in rice. F_2 Selection has been proved to be robust and effective tool in crop improvement program. Selection differential was positive for all the studied traits. Selection response was high for number of grains, thus indicating the effectiveness of selection for this character. Realized heritability was found high for number of grains and thousand grain weights, suggesting that direct selection was effective. Expected selection response and predicted genetic gain was high for number of grains. Parent-offspring correlation showed low but significance association for number of productive tillers ($r=0.47^{**}$, $P<0.01$), single plant yield ($r=0.35^{**}$, $P<0.01$) and ($r=0.30^{*}$, $P<0.05$) panicle length in F_2 and $F_{2:3}$ generation indicating that selection was fruitful in early generation. Statistically regression coefficient was not significant linear dependence of the mean of F_2 and $F_{2:3}$ generations.

Kumar *et al.* (2009) estimated effectiveness of plants selected in early segregating F_2 and F_3 populations in their corresponding F_3 and F_4 generation of two rice crosses, Jhona 349 × IET-12944 and Narendra 80 × Lalmati. Both the F_2 and F_3 selected plants showed consistency in increment of response to selection and realized heritability in their corresponding F_3 and F_4 generation for grain yield/plant and 100-grain weight, whereas these estimates were inconsistent for spikelets/main panicle and in undesirable direction for panicle/plant. Among intergeneration correlations, the F_2 selected plants showed inconsistent significant correlation with their F_3 progenies over crosses for all the characters, while F_3 selected plants had significant correlations with their F_4 progenies for 100-grain weight and grain yield/plant in both the crosses. The higher estimates of selection parameters like response to selection and realized heritability as well as significant correlation for grain yield/plant and 100-grain weight in F_4 generation suggested that selection for these two polygenic traits should preferably be started from F_3 generation.

Venuprasad *et al.* (2008) experimented on realized heritability and stated that lack of effective selection criteria was a major limitation hampering progress in breeding for drought tolerance. In an earlier report, authors showed in two populations that one cycle of direct selection was effective in increasing grain yield under stress. In the present study, we retested the efficiency of direct selection for grain yield under drought stress in rice using four populations derived from crossing upland-adapted, drought-tolerant varieties (Apo, Vandana) to high-yielding, lowland-adapted, drought-susceptible varieties (IR64, IR72). Each population was subjected to two cycles of divergent selection either under drought stress in upland or under nonstress conditions in lowland conditions. Following selection, approximately 40 high-yielding lines selected under each protocol from each population, along with a set of unselected lines, were evaluated in a series of selection response trials over a range of moisture levels. Significant response to direct selection under stress was realized in 9 out of 15 combinations of populations and stress environments, and in 6 of the 7 severe stress trials. Averaging over all the populations and stress environments, the stress-selected lines had a yield advantage of 25 and 37% over nonstress-selected and random lines, respectively. In contrast to this, under nonstress, the nonstress-selected lines had an average yield advantage of only 7 and 13% over stress-selected and random lines, respectively. Direct selection in managed stress trials during dry seasons gave significant response (25% on average relative to indirect selection in nonstress conditions) under naturally occurring wet season stress. In addition, direct selection under stress in upland gave an average gain of 16 and 45% over nonstress-selected and random lines, respectively, under stress in lowland. The yield advantage of the stress-selected lines appeared to result mainly from maintenance of higher harvest index. These results showed that direct selection for grain yield under stress is effective and does not reduce yield potential. Overall, this is the first report in rice demonstrating that (a) selection under managed drought stress in the dry season can result in yield gains under natural stress in the wet season, and (b) that selection under upland drought stress can, at least under the conditions of the present study, result in gains under lowland drought conditions.

2.5 Response and stability over the locations

Silva *et al.* (2020) studied to evaluate the similarity network graphic methodology for the classification of flood-irrigated rice (*Orzya sativa*) genotypes regarding their adaptability and stability. Two statistical measures were used to represent the proximity of the behavior (based on Pearson's correlation) or values (based on Gower's distance) between pairs of genotypes or between genotype and environment. Productivity data of 18 genotypes were evaluated in three locations in the state of Minas Gerais, Brazil, in the harvests of 2012/2013, 2013/2014, 2014/2015, and 2015/2016, in a randomized complete block design. The genotypes were previously assessed for adaptability and stability by the Eberhart and Russell and centroid methods. The graphical representations provided by the similarity networks allowed bettering identifying the pattern of the genotype x environment interaction, overcoming the interpretation difficulties due to the disagreements between the results obtained by the Eberhart and Russell and centroid methods. The similarity networks improve genotype x environment interaction studies.

Dessie *et al.* (2020) conducted an experiment in Fogera and Shire-Maitsebri from 2016-2018 main cropping seasons with the major objectives of high yielding, cold tolerant, disease resistant and early maturing GSR rice varieties for the high altitude of lowland production system. A total of 15 GSR genotypes including two checks were used in the study. The trial was laid out in randomized complete block design with three replications with plot size of 7.5 m^2. The combined analysis of variance revealed significant difference on grain yield, days to maturity, days to heading, panicle length, filled grain /panicle, plant height and thousand grains weight ($P \leq 0.01$). Three genotypes (G2, G6 and G4) showed significant difference than the standard checks on grain yield and gave grain yield advantage of 32.6 %, 27.9 % and 22.3 %, respectively. The genotype main effect plus genotype x environment interaction (GE) biplots were used to analyse and visualize pattern of the interaction component. The first two principal components (PC1 and PC2) of the GGE explained 79.34 % with PC1= 54.09 % and PC2=25.25 % of GGE sum of squares, respectively. Genotypes, G2 (Yungeng 31) and G6 (KB-2) combined both high stability performance and high mean grain yield across the test environments and characterized as an ideal genotypes and proposed for national variety release.

Al-kordy *et al.* (2019) studied on genetic stability which is considered as one of the most important genetic tests used to ascertain the extent of genetic stability reached in plants; consequently, the goal of this research is to detect the degree of genetic stability of a group of a superior rice lines under different climatic environments. The seven entries of rice exhibited highly genetic stability depending on the results obtained from genetic stability analysis where they were recorded as high yielding; in addition, positive data for the remaining traits studied under the 12 environmental conditions were tested. Line numbers 1, 3, 4, and 5 were in the first rank for high genetic stability and high stable yielding under all experiments, while line numbers 2, 6, and 7 were recorded in the second rank. The values of broad sense heritability were very high in some traits (plant height, heading date, number of filled grains/panicle, grain yield/plant, and flag leaf area) which indicated that the genetic variance played an important role for controlling and inheriting these traits. A total of 101 fragments were generated using six primers of ISSR through comparison among the seven rice lines, where 34 of them were monomorphic and 67 bands were polymorphic with 66.33% polymorphism. From the previous results, it could be concluded that the seven promising lines showed high genetic stability and recorded highly stable yield under various environments which confirmed their importance in rice breeding programs for enhancing salinity tolerance, resistance to many diseases, and other stresses under Egyptian conditions.

Rahman and Shah (2019) studied to assess genotype by environment interaction (GEI) for yield and yield related traits in rice. The genetic material comprised 87 rice $F_{5:7}$ recombinant inbred lines (RILs) along with three check cultivars namely Pakhal, Kashmir Basmati and Fakhr-e-Malakand. The genetic material was planted in alpha lattice design using three replications across different locations namely Peshawar, Swat, Manshera and Charsadda of the Khyber Pakhtunkhwa province of Pakistan during 2017. Pooled analysis of variance indicated significant ($p \leq 0.01$) differences among the environments, genotypes and GEI for spikelets panicle^{-1}, grains panicle^{-1}, 1000-grain weight and grain yield. Across four locations, AUP-30 showed the highest number of spikelets panicle^{-1} (242.5), grains panicle^{-1} (228.6) and maximum 1000-grain weight (29.0 g). Rice RILs AUP-3, AUP-30 and AUP-29 manifested the higher grain yield of 4.3, 4.2 and 4.1 tonnes ha^{-1} across locations, respectively. On the basis of individual locations, rice RILs AUP-3, AUP-29, AUP-30 and AUP-40 displayed the highest grain yield of 4.8, 4.6, 5.4 and 3.9 tonnes ha^{-1} at Peshawar, Swat, Mansehra and Charsadda, respectively. Grain yield displayed significantly positive correlation with spikelets panicle^{-1}, grains panicle^{-1} and 1000-grain weight. The study indicated differential behavior of the rice RILs for different traits across different environments. Rice RILs AUP-3, AUP-30 and AUP-29 excelled in performance for yield and yield attributes across locations while AUP-3, AUP-29, AUP-30 and AUP-29 displayed adaptation to specific environments of Peshawar, Swat, Mansehra and Charsadda, respectively.

Jadhav *et al.* (2019) experimented to obtain consistent yield across diverse environments. A variety should have adaptability and stability to fit into various growing conditions. G×E interaction and stability performance of 59 rice lines of different maturity durations were investigated for grain yield-related traits in three environments. This study was carried out to identify stable lines for varietal development as well as to identify parental lines with stable contributing traits for further breeding programs. AMMI and GGE analysis showed significant genotype, environment, and G×E interaction indicating the presence of variability among the genotypes and environments. The G×E interaction effect showed that the genotypes responded differently to the variation in environmental conditions or seasonal fluctuations and explained that most of the traits were contributed mainly by genotype, followed by environment and their interaction. As per AMMI biplot analysis, environment1 was identified as the best suited for potential expression of grain yield and related traits. Results of stability analysis revealed that early and mid-early genotypes NH776, NH4371, 27K, NH686, 258S, NH219, and Tellahamsa were identified as the best stable genotypes across all the three seasons for single plant grain yield and hence suitable for wider environments. These selected genotypes can be suggested for hybridization in further breeding programs to develop early genotypes with high yield. The stable early and mid-early lines with high yield potential will be tested in multi-location trials for commercial cultivation.

Girma (2018) evaluated eleven rice genotypes in 6 environments in Western Ethiopia during 2015 and 2016 main cropping season. The objective of the study was to determine the magnitude of genotype x environment interaction and performance stability in the rice genotypes. The study was conducted using a randomized complete design with 3 replications. Genotype x environment interaction and yield stability were estimated using the additive main effects and multiplicative interaction and site regression genotype plus genotype × environment interaction bi plot pooled analysis of variance for grain yield showed significant ($P<0.01$) to significant ($P<0.05$) differences among genotypes, environment, genotype x environment interaction effects. This indicates that genotypes differentially respond to the change in test environments or the test environments differentially discriminated the genotypes or both. Environment accounted for 69.39%, of the total yield variation, genotype for 8.50% and genotype x environment for 3.90%, indicating the need for spatial and temporal replication of the trials. Regression and AMMI analysis were employed in order to determine the stability of genotypes. The two models regression analysis and AMMI revealed similar result in that Adet and Hidassie were stable and widely adapted genotypes. Adet and Hidassie varieties were the most stable and high yielding genotype and therefore recommended for commercial production in the western Ethiopia upland rice growing areas.

Laxami *et al.* (2017) studied the nature and magnitude of genotype x environment interaction (GEI) among 12 Basmati rice genotypes across four environments viz., normal transplanting, late transplanting, system of rice intensification (SRI) and direct seeded rice (DSR) during Kharif 2016 using GGE biplot analysis. Genotype x management interaction followed by environment was found to be the major source of variation and the first two principal components (PCs) of GGE biplot accounted for more than 70% of variation for yield. As per AMMI analysis, discriminating ability of E2 and E3 was found to be closest to the ideal environment and G5 and G10 are top performing in E2 and E3 and G6 and G8 are better performing in E4 and E1 respectively while, stability mean of genotypes revealed that G4 is most stable cultivar and G8, G9 and G6 are the most unstable cultivars. "Which-won-where" analysis revealed two mega environments (ME) among the test locations, with ME1 represented by 2 locations E2 and E3 with G10 as winning genotype and ME2 with 2 locations E1 and E4 with G8 as another winning genotype.

Lakew *et al.* (2017) conducted an experiment on multi-environment rice evaluation trials in eight environments across Northwest Ethiopia to select promising varieties that could be cultivated by farmers. Sixteen upland rice genotypes were planted in a randomized complete block design of three replications in each location. Data were analyzed using combined analysis of variance, Additive Main Effects and Multiplicative Interaction (AMMI) and GGE bi-plot analysis. The MMI analysis of variance for grain yield (kg ha^{-1}) of 16 upland rice genotypes revealed that the main effects of genotypes (G) and environments (E) accounted for 53.8% and 26.8 % of the treatment SS, respectively. The

G × E interaction also accounted for 19.4% of the treatment SS. The mean grain yield value of genotypes averaged over environments indicated that WAB450-1-B-P-462-HB (G11) had the highest (4085.8 kgha-1), followed by ARCCU3Fa11-L1P1-B-B-1 (G4) and ARCCU2Fa11-L2P1-B-B-1(G9) with grain yield of 3975.8 and 3853.3 kg ha^{-1}, respectively. As revealed by AMMI and GGE bi-plots, the genotype G11 was identified as specifically adapted to Fogera (Woreta areas). Following evaluation of candidate genotypes (G11, G4 and G9) and collecting farmer's feedback, the National Variety Release Committee also recommended G11 as the variety for cultivation in Fogera and other areas of similar cultivation conditions.

Kulsum *et al.* (2013) investigated genotype-environment interaction and stability performance on amylase, protein and grain yield with 13 hybrid rice promising combinations in five environments. The combined ANOVA showed that the mean sum of square due to genotype (G), environment (E) and G × E interaction were significant for amylose content, protein content and grain yield. This suggested a number of variabilities among the genotypes and environments and the indicated genotypes interacted significantly with environments. The additive Main Effects and Multiplicative interaction (aMMi) biplot for yield clearly indicated that the hybrids BR10a/BR12R, ii32a/BR15R, ii32a/BR16R, ii32a/BR10R, BR9a/BR15R, BRRI hybrid dhan2 and BRRI hybrid dhan3 were high yielding, stable and had general adaptability at all locations. The aMMi estimation had a profound effect in producing sharp and stratified ranking patterns and on this basis BRRI hybrid dhan2 would be considered more adapted to a wide range of environments than the rest of the genotypes. The biplot technique was used to identify appropriate genotype to special locations. This consideration was on the basis of average yield for specific genotype to the specific location. The hybrid combination ii32a/BR12R was more suitable for Gazipur location and the hybrid combination BR10a/BR13R was considered for Comilla region. Barisal was more stable site than other locations for grain yield due to iPCa score being near zero which had no interaction effect.

2.6 Assessment of aroma and cooking qualities of fine rice

Srivastava *et al.* (2019) experimented on Kalanamak which is an important aromatic rice variety in India. Tall stature of Kalanamak causes lodging due to which its yield and other characters severely decline. Introgression of the semi-dwarfing gene (sd1) from CSR10 was performed with the help of marker assisted breeding. Backcross-derived plants were characterized for semi-dwarf nature. Improved Kalanamak lines were analyzed for the sd1 gene and to check the presence of aroma, sensory analysis test and amplification with betaine aldehyde dehydrogenase 2 (badh 2) derived primer was performed. Improved versions of Kalanamak rice lines were either on par or superior in terms of yield, grain type and cooking quality with reduced height implicating the potentiality of marker-assisted backcross breeding for improvement of this rice variety.

Megha *et al.* (2019) studied to analyze ten Indian rice varieties of common use for their physico-chemical characteristics and cooking quality using standard methods. For cooking quality, both pressure and microwave cooking were used. For physico-chemical parameters, the range of values obtained for different rice varieties were as follows: length/width ratio, 1.16-3.25mm; bulk density, 0.401-0.461g/ml; density, 0.786-1.33g/ml; and porosity, 41.36-58.32%. The initial gel consistency was in the range of 28.0–69.5 and after 60 min of setting increased to 33.0-74.5. The maximum equilibrium moisture content for soaked rice at the end of 24 hours ranged between 16.04-19.96%. Amylose content of rice also showed variations ranging from 16% in Ponni boiled rice to 23.2% in Mallige idli rice. The cooking quality of rice samples revealed highest elongation ratio for microwave cooked Mallige idli rice (2.06) and lowest for pressure cooked Basmati rice and Sonamasoori high polish rice (1.06). Most of the rice samples were graded either as ‘good’ or ‘satisfactory’ for cooked volume except Gandasala rice which was graded as poor because of low volume. In general, microwave cooking required more water and longer cooking time with lesser cooked volume. In conclusion, the selected rice varieties differed in their physico-chemical characteristics as well as in cooking quality, and hence, can influence the consumer’s preferences.

Mo *et al.* (2018) proved that aromatic rice (*Oryza sativa* L. subsp. japonica Kato) is globally popular due to its pleasant aroma and enchanting flavor. 2-Acetyl-1-pyrroline (2-AP) is recognized as the only major flavoring compound in aromatic rice. Plant nutrition affects the production and accumulation of 2-AP in rice, but the effect of time-specific nutrient application during the developmental phases of rice on 2-AP has not yet been reported. Three N levels (N0: 0 kg ha^{-1}, N1: 30 kg ha^{-1}, and N2: 60 kg ha^{-1}) at the booting stage were applied to a popular aromatic rice cv. Yungengyou 14, to assess the accumulation pattern of 2-AP, proline, and N as well as relationships among the investigated indices regarding 2-AP accumulation. Amongall other plant parts, the highest 2AP contents were found in ear axes and flag leaves, i.e. 17.04%-18.26% and 14.37%- 15.05% at 17 as well as 18.41%-22.74% and 14.38%-15.75% at 30 DAF under all N-levels. Interestingly, N application at the booting stage also maintained higher proline and 2-AP contents in different plant tissues during the early grain filling stage. Hence additional N dose at booting stage could improve the grain aroma contents of aroma rice while considering the amount of N fertilizer added.

Yanjie *et al.* (2018) compared the sensory quality and physicochemical properties of three japonica rice varieties harvested in two different growing locations (Xiangshui and Hangzhou in China) to determine the most important factors affecting the sensory quality. All the three varieties had higher scores for overall sensory quality in Xiangshui than in Hangzhou, indicating that the growing location is a key factor in determining the sensory quality of cooked japonica rice. In addition to growing location, variety (genotype) also had an important effect. Longdao 18 scored the highest for overall sensory quality in the two locations, whereas Longdao 30 had the lowest score in Xiangshui, and both Longdao 20 and Longdao 30 had the lowest scores in Hangzhou. Many physicochemical properties, such as apparent amylose content, protein content, thermal properties and free amino acid contents, showed significant differences between the two locations. Correlation analysis showed that apparent amylose content and protein content had contrasting effects on all the sensory attributes. The overall sensory quality was negatively correlated with protein content ($r = -0.89$, $P < 0.01$) and positively correlated with gel hardness ($r = 0.91$, $P < 0.01$), indicating that the protein content and hardness are important physicochemical properties for predicting the sensory quality of japonica rice. These findings will provide guidance for selection from the diverse genotypes available to develop new varieties with the desired eating and cooking quality.

Zhou *et al.* (2018) investigated the four main aspects of rice-grain quality, namely, milling (brown-rice, milled-rice, and head-rice percentage), appearance (length/width ratio, chalky-kernel percentage, and chalkiness), nutrition (protein content), and cooking and eating quality (apparent amylose content, gel consistency, and pasting viscosities) of two rice cultivars (Shendao 47 and Jingyou 586) under four N rates (0, 140, 180, and 220 kg/ha), and three planting densities (25 * 104, 16.7 * 104, and 12.5 * 104 hills/ ha) in a field trial from 2015 to 2016. The four main aspects of rice-grain quality were significantly influenced by cultivar. Several aspects were affected by the interactions of

N rate and cultivar. No significant interaction between N rate and plating density was detected for all grain-quality parameters. A higher N rate increased the percentages of brown rice and head rice, chalky-kernel percentage, and setback and peak time values, but reduced the length/width ratio, chalkiness, apparent amylose content, gel consistency and peak, trough and final-viscosity values. These results indicate that the N rate has a beneficial effect on milling and nutritional quality, but a detrimental effect on appearance and cooking and eating quality. Jingyou 586 and Shendao 47 had different responses to planting density in terms of grain quality. Our study indicates that low planting density for Jingyou 586, but a medium one for Shendao 47, is favorable for grain quality.

Nadvornikova *et al.* (2018) evaluated eight staple rice cultivars consumed in Kyrgyzstan for physical properties in this study. The dimensions of investigated grains correspond to 5.29– 6.99 mm for length, 2.52–3.10 mm for width, and 1.88–2.13 for thickness. Equivalent diameter was in range of 3.14 – 3.47 mm, surface area took 25.35–31.90 mm^2. The sphericity analysis values varied from 0.480 to 0.559, aspect ratio from 0.39 to 0.55, volume of the grain was measured in range from 16.25 to 22.02 mm3, bulk density values were 0.77–0.87 g/cm3, and solid density from 1.17 to 1.41 g/cm3. The porosity of grain was equal to 28.27–39.83%, thousand kernel weight correspond to 19.67 to 27.15 g, rupture force of grain was measured in range of 63.47–155.50 N, color characteristic varied in parameters L*, a* and b*, 37.58–72.19, –0.22–10.17, and 9.65–21.12, respectively. Optimum cooking time ranged from 19.33 to 33.00 min. The water uptake ratios for 30 min of soaking were 1.21–1.28, 1.18–1.45, and 1.14–1.57 for 30, 45, and 60°C, respectively. While the water uptake ratios for 60 min of soaking were 1.22–1.42, 1.19–1.54, and 1.25–1.75 for 30, 45, and 60°C, respectively. Optimal cooking time showed that imported varieties needed lower interval for full grain cooking compared to the local Kyrgyz varieties. It was found that Kyrgyz rice varieties staying more firms after cooking as compared to imported varieties and therefore more suitable for the local traditional dish such as plov.

Haripriya *et al.* (2017) investigated the milling characteristics, physical characteristics, nutrient composition, physico chemical and cooking properties of the traditional organic rice variety Kouni nel. The organically grown traditional Kouni nel paddy was obtained from Centre for Indian Knowledge Systems, Chennai, India. The milling characteristics, physical characteristics, nutrient composition, physico chemical and cooking properties of Kouni nel were analyzed using standard procedures. The study infers Kouni nel to be a long bold grain. On parboiling, Kouni nel exhibited better milling characteristics. The Kouni nel rice is non-aromatic variety with normal taste and acceptable cooking and textural characteristics. It is ideal to parboil and use it.

Simonelli *et al.* (2017) carried out an experiment on the characterization of ten Italian rice varieties by chemical analysis which requires the use of more or less sophisticated equipment and of technicians trained to the application of analytical methods. Beside this type of analysis, defined as “traditional”, it was carried out a descriptive evaluation of the samples from a sensory point of view. Descriptive analysis was a new experience in the evaluation of Italian rice that allows describing and quantifying the sensory properties of the different varieties. As with traditional analysis the calibration of instruments is fundamental and the choice of the adequate analytical method, so the equipment for sensory analysis was the basic choice of assessors who will be part of the panel and their training. Ten heterogeneous varieties of Italian rice had been characterized both from a traditional point of view, namely, chemical, physical and textural (length and width, gel-time, resistance to extrusion, stickiness, amylose content), and sensory, involving a panel of selected, chosen and trained tasters. The analytical data will then be compared in order to bring out similarities and differences. It appeared that there is agreement between the sensory analysis and the chemical physical and textural characterization of milled rice. The sensory characterization undoubtedly provides a more complete and accurate information than the instrumental one.

Ren *et al.* (2017) experimented and showed that aromatic rice has a high market value due to its special fragrance and the most important compound in the grains of aromatic rice is 2-acetyl-1-pyrroline (2-AP). In an effort to improve the 2-AP content and the yield of aromatic rice, two known rice cultivars, Yungao and Yundi, were cultivated across two seasons, and two irrigation and nitrogen management practices were investigated. The results showed that the treatment management practice (TNW) treatment improved panicle number /hill, seed setting rate, and 1000 grain weight and grain yield for both cultivars in early and late season. Significant improvement in grain yield was only observed in Yundi in both seasons. Moreover, the 2-AP content in grains was increased for both cultivars in both seasons during grain filling period. Significant increase in 2-AP in grains was observed for Yungao at maturity in both seasons, at 7 d AH in early season and at 14 d AH in late season whilst for Yundi at 7 d AH, 14 d AH and 21 d AH in early season, and at 14 d AH in late season. Furthermore, 2-AP content in leaves and grains was decrease during grain filling period while proline content in grains was enhanced during grain filling period. Significant relationships were also observed between 2-AP and proline contents in the leaves/grains of both rice cultivars.

Ohtsubo and Nakamura (2017) stated that quality evaluations of rice in Japan were performed by sensory testing and physicochemical measurements. The former was a basic method that required large amounts of samples and several panelists. The latter was an indirect method that estimated the eating quality based on the chemical composition, cooking quality, gelatinization properties, and physical properties of cooked rice. Satake Co Ltd. developed a taste analyzer in the 1980s equipped with a palatability estimation formula that was based on the combination of near-infrared spectroscopy (NIR) and physicochemical measurements related with sensory test. A novel method to evaluate the quality of the cooked rice was necessary to breed high-quality rice cultivars and to select the suitable rice for each consumer and each purpose. They tried to develop the novel method to evaluate the rice quality using various kinds of apparatus, such as Tens presser, RVA, NIR, and spectrophotometer. Simple, rapid, and accurate method to evaluate the quality of rice grains is very valuable. They evaluated 16 Japanese and Chinese rice cultivars in terms of their physicochemical properties. Based on these quality evaluations, they concluded that Chinese rice cultivars are characterized by a high protein and that the grain texture after cooking has higher hardness and lower stickiness than Japanese ones reflecting the difference in consumers' preference. The relationship between the palatability of rice and agronomical condition to preserve the bio-diversity for Crested Ibis was investigated. Furthermore, the quality of rice grown in Sado Island, Japan, was assayed using rice grains grown in mountainous areas and in the field areas as samples.

Shamim *et al.* (2017) studied on the cooking quality and physico-chemical characteristics of 14 newly developed lines and two check varieties which were widely grown grown in Punjab, Pakistan. Significant variation ($P<0.05$) was detected among the 15 rice varieties for all the traits evaluated. The results predicted that two newly developed rice Lines showed higest cooked grain length (CGL) during cooking. The grains of PK9533-9-6-1-1 had the highest elongation ratio of 1.900. "PK 9966-10-1 had the best physical appearance in terms of length but easily dissolved in water during cooking. Most of the physicochemical characteristic such as amylose, protein and gelatinization temperature were significantly correlated (positively or negatively) with some of the cooking quality traits i.e., elongation ratio, CGL indicating that efforts aimed at selecting rice varieties with improved cooking quality traits would warrant a consideration of the physico-chemical attributes of the rice grain. The overall cooking quality and physico-chemical attributes of some of new lines were even relatively better than the Check (Super Basmati). Farmers should, therefore, be critical in accepting new varieties that may not be comparably outstanding in yield but also in cooking quality and physico-chemical characteristics, in order to preserve the integrity of new rice varieties.

Okpala *et al.* (2017) investigated the cooking and eating qualities of Basmati 385 and Hua Jing Xian 74. Both are rice cultivars with different phenotypic traits. The results showed that Basmati 385 increased by an average of 102.14% after cooking while Hua Jing Xian 74 increased by an average of 69.91% after cooking. Basmati 385 had a pasting temperature of 78°C, while Hua Jing Xian 74 had a pasting temperature of 84°C. However, Hua Jing Xian 74 had a final viscosity of 4,686 cP while Basmati 385 had a final viscosity of 3,514 cP. The amylose contents of the two cultivars were also different; Hua Jing Xian 74 had an amylose content of 19.4%, while that of Basmati 385 was 18%. They also discovered that the starch granule morphology of the two cultivars were remarkably different. The lower pasting temperature of Basmati 385 positively correlated with good cooking qualities of rice. However, Hua Jing Xian 74 appeared to have relatively better eating qualities due to its higher viscosity and higher amylose content. It would be pertinent to do more research about hybrid lines resulting from a cross of Hua Jing Xian 74 and Basmati 385, to see if they possess the good cooking qualities of Basmati 385 and the good eating qualities of Hua Jing Xian 74.

Tamu *et al.* (2017) evaluated grain appearance, cooking and eating qualities of 87 rice varieties. The varieties differed significantly at $P > 0.001$ for Grain length; volume expansion ratio, water uptake, length of blue Gel, Gel consistency, elongation ratio, alkaline spread value, gelatinization temperature and aroma. The gelatinization temperature (GT) was determined based on alkaline spreading score, and 64% of the rice varieties showed intermediate GT (70-74 ºC), 20% exhibited low GT (55-69 ºC), and only 16% of the rice varieties showed high GT above 74ºC. Hard gel consistency was observed in 71% of rice varieties evaluated, 22% recorded medium gel consistency, and only 7% of the rice varieties recorded soft gel consistency. Of the 87 test varieties, 34% were aromatic while 66% were not. Alkaline spread value had significant and positive correlation with water uptake, but gel consistency had negative correlation with volume expansion ratio. Based on the L/W ratio, 33 of the rice varieties had long slender grain type, 45 recorded medium slender grain and only 9 varieties recorded short bold grain. The characteristics of the various grain types make them suitable for different food preparations and meet the preferences of majority of consumers.

Simonelli *et al.* (2016) evaluated the physicochemical, cooking and eating properties of eleven rice cultivars grown in Italy. Variations existed in grain dimensions, and the rice grains were classified (according to Italian legislation) as round, medium, long A, long B. The chemical analysis was done to determine the proximate composition as main determinants of cooking quality. The proximate composition results indicated that protein and lipid contents ranged from 6.08 to 9.68 and 0.21 to 0.40 respectively (for milled rice). The gel-time of milled rice from different cultivars varied from 17’15’’ (Carnise) to 24’56” (Ronaldo). CRLB1, Fragrance and Tigre varieties had the highest amylose content, while Cerere and Ronaldo presented the lowest amylose content. The content of amylose is correlated to texture properties, in particular with hardness and stickiness: stickiness is negatively correlated with amylose content with a R2 of 0.93, however hardness is positively correlated with R2 of 0.94. The differences in the physicochemical properties could be used to determine the end use of these rice cultivars.

Khammari *et al.* (2016) experimented on rice and stated that as a major cereal crop, rice (*Oryza sativa L.*) is crucial to food security for at least half the world population. After yield, quality is one of the most important aspects of rice breeding. Preference for rice quality varies among cultures and regions; therefore, rice breeders have to tailor the quality according to the preferences of local consumers. Rice quality assessment requires routine chemical analysis procedures. Eating and cooking qualities (ECQs) are important determinants of cooked rice grain quality. ECQs comprise three physical and chemical characteristics of starch in the endosperm: amylose content (AC), gel consistency (GC) and gelatinization temperature (GT). Grain quality is a general concept which covers many characteristics ranging from physical to biochemical and physiological properties.

The advancement of molecular marker technology has revolutionized the strategy in breeding programs. The availability of rice genome sequences and the use of forward and reverse genetics approaches facilitate gene discovery and the deciphering of gene functions. A well-characterized gene is the basis for the development of functional markers, which play an important role in plant genotyping and, in particular, marker-assisted breeding. In addition, functional markers offer advantages that counteract the limitations of random DNA markers.

Ritika *et al.* (2016) studied physicochemical, cooking, pasting and textural properties of some Indian rice varieties of basmati (PB-1, PB-1401, P-2511, and PP-1509) and non-basmati (HKR-47, HKR-127). L/B ratio for the grains of all the studied varieties was more than 3.0 and the L/B ratio of basmati varieties grains was significantly higher than non-basmati grains ($p \leq 0.05$). The hardness of rice kernels varied from 64.6 to 213.7 N with P-2511 showing the highest hardness among all the varieties. PP-1509 and P-2511, PB-1 and PB-1401 cultivars had intermediate amylose content and HKR-47 and HKR-127 were grouped as low amylose containing cultivars. P-2511 exhibited the highest value of gelatinization temperature (70°C). The water absorption index and water solubility index varied from 4.50 to 7.26 g/g and 2.00 to 7.66 % respectively. Rice flours from different cultivars showed different behavior in regard to their pasting characteristics including peak, hot paste and cold paste viscosities. PV and HPV of different flour samples varied from 620 to 2588 cP and 549 to 1853 cP respectively. The cooking time of different cultivars varied from 17 to 25 min with PB-1401 showed the highest water uptake ratio. Hardness value of the cooked rice cultivars varied from 1419.76 to 3417.56 g with maximum hardness observed in case of PB-1. Significant varietal differences were observed in the physicochemical, pasting, cooking and textural properties of studied rice cultivars.

Subedi *et al.* (2016) studied five rice varieties newly adopted in Nepal for their varietal differences in relation to quality characteristics such as physicochemical and cooking qualities. In physical analysis bulk density, density, thousand kernel weight and length to breadth ratio were recorded as highest in ‘Lumle-2’ (0.60gm/ml), ‘UPLRI-5’ (1.40gm/ml) ‘Lumle-2’ (27.28gm), and ‘IET- 16775’ (4.73) varieties respectively. The milling and head rice recovery were recorded maximum in ‘Lumle-2’ (78.76%) and ‘UPLRI-5’ (78.27%) respectively, protein, fat, amylose, crude-fiber and total-ash were ranged from 8.28-12.85%, 1.14-1.86%, 24.57-27.48%, 0.70-1% and 0.79-1.39% respectively. Iron, phosphorous and calcium content were estimated in the range 1.08-2.47mg/100g, 203.28-337.05mg/100g and 16.17-28.77mg/100g respectively. From organoleptic test, ‘IET-16775’variety was scored as having strongest aroma. ‘Lumle-2’, ‘Chhomrong’, ‘Machapuchhre-3’ varieties were shown as having intermediate gelatinization-temperature and ‘UPLRI-5’ and ‘IET-16775’ varieties recorded with high gelatinization-temperature. Water uptake ratio, cooking time, elongation ratio and gruel loss were found in the range 1.72-2.67, 18-25minutes, 1.29- 1.63, and 2.50-6.12% respectively.

Ekka *et al.* (2016) evaluated the cooking quality for four selected varieties of rice (Swarna, Vishnubhog, HMT and Basmati) used in Chhattisgarh state of India. Quality parameters used for this study measured were Optimum cooking time, Water uptake ratio, Grain elongation, Swelling index and Residual solid loss. The results showed that among different varieties of rice, optimum cooking time was maximum for Swarna rice on 300 watts (26.15 min.) and minimum for Vishnubhog rice on 2100 watt (13.43 min.). Water uptake ratio was maximum for Basmati rice on 300 watts (4.27%) and minimum for Vishnubhog rice on 2100 watt (2.84%). Cooking coefficient was maximum for Swarna rice on 1800 watt (7.37) and minimum for Vishnubhog rice on 2100 watt (1.85). Grain elongation was maximum for Basmati rice on 800 watts (0.475) and minimum for Swarna rice on 1600 watt (0.215). Residual solid loss was maximum for Swarna rice on 300 watts (3.2%) and minimum for Vishnubhog rice on 300 watts (1.1%). Swelling index was maximum for Basmati rice on 2100 watt (0.446) and minimum for Vishnubhog rice on 1800 watt (0.3).

Chukwuemeka *et al.* (2015) analyzed four local rice varieties grown and processed in Ohaukwu and One foreign rice varieties (caprice gold) for their cooking, chemical and physical properties. Cooking time differed with variety ($p<0.05$) and the ranged between 17-23 minutes. Volume expansion ratio varied from 1.67-3.67cm^3. Caprice, Faro44 and Faro 15 had higher volume expansion ratio than the other varieties ($P<0.05$). Gelatinization time varied with variety and the range between 4-11 minutes. Caprice took a longer time to gelatinize and Faro 14 and IRR8 the shortest time. The other varieties differ ($p<0.05$) in their gelatinization time. Grain elongation during cooking, amount of water evaporating during cooking and solid in cooking water ranged between

0.180.38m, 19-42%, 0.02-0.64(g). The values for the amylose ranged between 7.6-37.2% and amylopectin ranged between 69.8-79.8%. The range of physical properties from all the varieties were, length 0.595 to 0.753m, width 0.217 to 0.287m, length/ width ration 2.188 to 3.470mm.

Faruq *et al.* (2015) stated that ageing can improve cooking quality of rice by influencing major cooking quality parameters i.e., kernel expansion, water absorption, alkali digestion value, and gelatinization temperature along with changes in internal structure of rice grains. In this research, the effects of natural and artificial ageing on the selected cooking quality parameters of two Malaysian rice cultivars, named Mahsuri and Puteri, were studied. A relation was observed between water absorption and elongation ratio in both varieties under different aging conditions. Alkali digestion value and gelatinization temperature were also influenced by varieties and ageing conditions. This study revealed the potentiality of ageing for the improvement of rice cooking quality.

Singh and Sengar (2015) studied and showed that Rice (*Oryza sativa* L.) is the staple food of more than half of the world’s population. Grain quality in rice plays an important role in consumer acceptability. The quality in rice is considered based on milling quality, grain size, shape, appearance, aroma and other cooking characteristics. Most of the scented rice varieties in India are of traditional type, photoperiod sensitive, and cultivated during the Aman/kharif season. Majority of these indigenous aromatic rice cultivars are low yielding but its higher price and lowcost of cultivation generate higher profit margins compared to other varieties. Aroma development in rice grain is influenced by both genetic and environmental factors. The biochemical basis of aroma was identified as 2-acetyl-1-pyrroline. Most of the rice varieties have been developed traditionally by selection, hybridization and back crossing with locally adapted high-yielding lines. The conventional methods of plant selection for aroma are not easy because of the large effects of the environment and the low narrow sense heritability of aroma. More recently molecular markers, such as SNPs and simple sequence repeats (SSRs), which are genetically linked to fragrance and have the advantage of being inexpensive, simple, and rapid and only requiring small amounts of tissue, have been developed for the selection of fragrant rice.

Ahmad *et al.* (2015) reported that the demand for aromatic rice is increasing in Afghanistan and the surrounding countries. Aromatic rice due to its good taste, aroma and soft texture after cooking is favorable to consumers. In the present study, some important morphological and agronomic characters such as panicles number per plant, grains number /panicle, 1,000-grain weight, grain length and grain width, for eleven native Afghan rice cultivars and three foreign cultivars as check, were analyzed. In this research, the grains number /panicle was ranged between 69 ± 10.8 (mean ± standard deviation) in Luke Qasan and 175 ± 59.4 in Izayoi (check). Also 1,000-grain weight was ranged between 20 ± 0.7 in Torishi and 32 ± 3.5 in Pashadi Konar. Aroma was also estimated by tasting individual grains, cooking test, 1.7% KOH sensory test, gas chromatography-mass spectrometry-selected ion monitoring (GC-MS-SIM) and polymerase chain reaction (PCR) analysis. Mean comparison by Duncan's method in 5% confidence level was used. Finally cluster analysis for assessment of aroma were performed by Ward's method and cultivars divided to three clusters included: 1) Lawangi and Sarda Bala, 2) Torishi, Sela Takhar and Sela Doshi, 3) Surkha-Bala, Germa Bala, Surkhamabain, Surkha-Daraz-Baghlan, Pashadi Konar, Koshihekari (Check), Izayoi (Check), Fajer (Check) and Luke Qasan. This study showed that Afghan native ricecultivars such as Surkha-Bala, Surkhamabain, Sela Takhar, Sela Doshi and Pashadi Konar with the desirable agronomiccharacters such as thin and slender grains, and favorable aroma can be used for further improvement of aromatic rice in breeding.

Roy *et al.* (2015) worked on aromatic rice and showed that the North-eastern (NE) India, comprising of Arunachal Pradesh, Assam, Manipur, Meghalaya, Mizoram, Nagaland, Sikkim and Tripura, possessed diverse array of locally adapted non-Basmati aromatic germplasm. The germplasm collections from this region could serve as valuable resources in breeding for abiotic stress tolerance, grain yield and cooking/eating quality. To utilize such collections, however, breeders need information about the extent and distribution of genetic diversity present within collections. In this study, authors report the result of population genetic analysis of 107 aromatic and quality rice accessions collected from different parts of NE India, as well as classified these accessions in the context of a set of structured global rice cultivars. A total of 322 alleles were amplified by 40 simple sequence repeat (SSR) markers with an average of 8.03 alleles per locus. Average gene diversity was 0.67. Population structure analysis revealed that NE Indian aromatic rice can be subdivided into three genetically distinct population clusters: P1, joha rice accessions from Assam, tai rice from Mizoram and those from Sikkim; P2, chakhao rice germplasm from Manipur; and P3, aromatic rice accessions from Nagaland.

Pair-wise FST between three groups varied from 0.223 (P1 vs P2) to 0.453 (P2 vs P3). With reference to the global classification of rice cultivars, two major groups (Indica and Japonica) were identified in NE Indian germplasm. The aromatic accessions from Assam, Manipur and Sikkim were assigned to the Indica group, while the accessions from Nagaland exhibited close association with Japonica. The Tai accessions of Mizoram along with few chakhao accessions collected from the hill districts of Manipur were identified as admixed. The results highlight the importance of regional genetic studies for understanding diversification of aromatic rice in India. The data also suggest that there is scope for exploiting the genetic diversity of aromatic and quality rice germplasm of NE India for rice improvement.

Nadaf *et al.* (2014) reported 2-acetyl-1-pyrroline as the major compound responsible for pleasant aroma in basmati and other scented rice varieties. The biosynthesis of this molecule is due to deletion in the betaine aldehyde dehydrogenase2 gene. This deletion leads in the accumulation of Δ1-pyrroline which reacts non-enzymatically with methylglyoxal to form 2-acetyl-1-pyrroline. Due to non-functionality of this gene that regulates the synthesis of Gamma-amino butyric acid, the plant species synthesizing 2-acetyl-1-pyrroline suffers for the yield losses, sterility and susceptibility to biotic and abiotic stresses. Thus the non-functionality of betaine aldehyde dehydrogenase2 gene coupled with 2-acetyl-1-pyrroline synthesis serves as a metabolic disease. In this review these aspects are discussed in detail.

Ahmad *et al.* (2014) studied and showed that aromatic rice has become popular owing to its aroma. Growing demand for aromatic rice has spurred interest in the development of domestic cultivars that offer similar combinations of grain attributes such as texture, cooking characteristics, aroma, and taste. In this study, the most important agronomic attributes and aroma of 26 cultivars from Afghanistan, Iran, and Uzbekistan, and controls from Japan, Thailand, and India were characterized. Also F_2 populations derived from the cross between (Jasmine 85 aromatic x Nipponbare non-aromatic) and (Jasmine 85 x Basmati 370 aromatic) were obtained. Tasting individual grains, cooking test, 1.7% KOH sensory test, and molecular marker analysis have been applied to distinguish between aromatic and non-aromatic rice. Diversity for some traits of agronomic importance, such as plant height was detected among countries, e.g. Afghan cultivars classified as tall, and Iranian and Uzbek intermediate and short, respectively.

Differentiations of panicle, grain, leaf, basal internode, and culm dimension among rice cultivars, indicating the source of rice diversity in Central Asia. According to the results, 6 of 10, 2 of 7, and 0 of 6 of Afghan, Iranian, and Uzbek rice cultivars were scored as aromatic, respectively. Therefore, Afghan cultivars are a good source of aromatic rice germplasm for Central Asia. The expression between aromatic and non-aromatic, and aromatic and aromatic combinations has been evaluated. The observed segregation ratio of these crosses in the F_2 populations was tested by D^2 analysis against the expected ratio for a single gene. A segregation ratio of 3:1 between non-aromatic and aromatic combination has been detected, while segregation has not been detected between the aromatic and aromatic combinations. Also, parallel results were obtained from the tested aromatic rice cultivars. Thus, our results suggest that a single recessive gene controls aroma in all aromatic rice cultivars.

Correia *et al.* (2013) conducted an experiment and stated that rice is consumed mainly as whole grain, and quality considerations are much more important than for any other food crop. Rice grain quality preference varies from country to country and among regions. Nowadays, aromatic rice varieties are playing a vital role in global rice trading, and also in Portugal. The economic value of rice depends on its cooking and processing quality, such as water uptake ratio, cooking time and texture properties. Three types of aromatic rice were collected and analyzed for biometry characteristics, cooking time, water absorption, and texture properties. The rice grains were collected from the Portuguese trade market. Biometric characteristics of all rice grains were evaluated by S21 (LKL) and C-300 (Kett) colorimeter. The rice flour gels texture was performed by a TPA (texture profile analysis), giving information about adhesiveness, chewiness, gumminess, hardness, resilience and cohesiveness. The extrusion force was also determined according to ISO 11747:2012. Rice samples are commercially classified as long grains B type, because they presented a length higher than 6 mm and the ratio length/ width higher than 3. The samples presented a high degree of whiteness, with a strictly relationship between the total and vitrea whiteness (r2 = 0.95). The cooking time varied from 12 to 17 minutes and these properties was strongly related with water uptake (from 155.7-209.1 g). Generally, aromatic rice cultivars presented different textural properties. Aromatic rice samples are different for hardness, adhesiveness, gumminess, resilience, and extrusion force. From the results obtained it was concluded that the studied aromatic rice cultivars presented different physical properties, mainly the cooking time, water uptake and texture. These differences could be a commercial advantage considering the consumer point of view, because the enterprise could provide specific aromatic rice in order to attend different consumer targets.

Oko *et al.* (2012) assessed the cooking quality and physico-chemical characteristics of 15 selected indigenous and five newly introduced hybrid rice varieties grown in Ebonyi State, Nigeria. Significant variation ($P<0.05$) was detected among the 20 rice varieties for all the traits evaluated. The results showed that all the five newly introduced hybrid rice varieties do not swell appreciably during cooking. The grains of Cv "China" had the highest elongation values of 3.2 ± 0.00 mm. "E4197" has the best physical appearance but easily dissolves in water during cooking. Most of the physico-chemical characteristic such as amylose, amylopectin, gel consistency and gelatinization temperature were significantly correlated (positively or negatively) with some of the cooking quality traits (elongation during cooking, solids in cooking water and optimum cooking time), indicating that efforts aimed at selecting rice varieties with improved cooking quality traits would warrant a consideration of the physico-chemical attributes of the rice grain. The overall cooking quality and physico-chemical attributes of some of the indigenous rice varieties were even relatively better than the newly introduced hybrid varieties. Farmers should, therefore, be critical in accepting new varieties that may not be comparably outstanding in cooking quality and physico-chemical characteristics, in order to pre-serve the integrity of the all-cherished indigenous rice varieties of Ebonyi State, Nigeria.

Danbaba *et al.* (2011) conducted a study to evaluate the cooking and eating quality of Ofada rice. Quality parameters measured were; volume increase, grain elongation (GE), water uptake (WU), cooking time (CT), solids in cooking gruel (SCW), gelatinization temperature (GT) and amylose content (AC). The result showed that Ofada rice had high cooked rice volume with length and breadth increase of 152.54% and 87.85% respectively. GE ratio ranged from 1.24-1.75 with Ofada 10 having the lowest value and Ofada 11 having the highest value. The highest length/breadth ratio of cooked rice (3.68) was recorded by Ofada 8, while Ofada 3 had the lowest (2.49). GE index ranged from 0.99-1.44 with Ofada 10 having the lowest value and Ofadas 4 and 11 having the highest value. WU ratio, CT, SCW and AC of Ofada rice samples ranged from 174.0-211.0, 17-24 min, 0.8-2.1%, and 19.77-24.13% respectively. The GT were low to intermediate.

There was significant positive correlation between AC and WU ratio, while significant positive association was observed between length/breadth ratio and AC. Based on the result of the study, Ofada rice have good cooking and eating quality, hence selection for improvement based on this parameter will be a right step in the right direction.

Lestari *et al.* (2011) conducted a research to study the grain quality and aroma of aromatic new plant type (NPT) promising rice lines. Thirty-five lines as well as Ciherang and Sintanur varieties were planted at Bogor and Pusakanagara, West Java in the dry season (DS) 2009 and wet season (WS) 2009. Three methods, i.e. leaf aroma tested with KOH, rice aroma tested in the test tube, and cooked rice aroma test, were used to evaluate the aroma of the lines. The results showed that line B11742-RS*2-3-MR-34-1-2-1 was aromatic identified using different methods. The line had long, slender, and small chalkiness grains, high percentage of head rice, high amylose, and hard texture. Lines IPB 140-F-6, B11249-9C-PN-3-3-2- 2-MR-1, and B11955-MR-84-1-4 also had a high aroma score and grain yield. Testing leaf aroma with KOH can be used as early selection method in breeding program for aromatic lines. Lines derived from aromatic parents from highlands of South Sulawesi did not show consistent aroma under three testing methods. Those tested lines had good grain quality, both physical and cooked rice quality.

Garcia *et al.* (2011) evaluated rice cooking quality by texture and stickiness characteristics using many different methods. Gelatinization temperature, amylose content, viscosity (Brookfield viscometer and Rapid Visco Analyzer), and sensory analysis were performed to characterize culinary quality of rice grains produced under two cropping systems and submitted to different technologies. All samples from the upland cropping system and two from the irrigated cropping system presented intermediate amylose content. Regarding stickiness, BRS Primavera, BRS Sertaneja, and BRS Tropical showed loose cooked grains. Irrigated cultivars presented less viscosity and were softer than upland cultivars. Upland grain samples had similar profile on the viscoamylografic curve, but the highest viscosity peaks were observed for BRS Alvorada, IRGA 417, and SCS BRS Piracema among the irrigated cropping system samples. In general, distinct grain characteristics were observed between upland and irrigated samples by cluster analysis. The majority of the upland cultivars showed soft and loose grains with adequate cooking quality confirmed by sensory tests. Most of the irrigated cultivars, however, presented soft and sticky grains. Different methodologies allowed to improve the construction of the culinary profile of the varieties studied.

Rosniyana *et al.* (2010) studied the physical properties, physico-chemical properties, cooking characteristics and nutritional content of freshly harvested Maswangi rice. Organic and inorganic paddy was obtained from Kg. Ewa, Langkawi, Kedah and Kubang Kerian, Kelantan respectively. These samples were evaluated in the form of paddy, milled rice and brown rice. The physico-chemical properties determined were amylose content, gelatinization temperature and gel consistency. The samples analyzed had high gelatinization temperature while the mean amylose content was 24.4. Hard gel was detected in the rice samples. Variations in cooking time, elongation ratio, and volume of expansion, water uptake ratio and solid loss were observed. The rice had elongation ratio of less than 2 which indicated that fresh rice samples did not elongate during cooking. Cooking properties showed that brown rice took a longer time to cook and had lower values in water uptake and volume expansion. Organic Maswangi milled rice contained 8.57% protein and 0.94% fat with 14.9% moisture content. Inorganic Maswangi had 8.16% protein and 2.56% fat. Brown rice of both organic and inorganic had higher nutritional quality than milled rice particularly with respect to fat, protein, mineral, thiamin, and riboflavin and niacin contents.

Faruq *et al.* (2010) studied and showed that aroma and cooked kernel elongation are the most important quality traits of aromatic rice, which differentiate the highly valued aromatic rice from the other rice types. Previous studies on genetic analysis have shown that genes/ QTLs for these two traits are linked. In the present study, it tried to evaluate the expression of aroma, kernel elongation and their association in 55 fine rice genotypes in the tropical environment of Malaysia. Highest percentage of elongation ratio was observed in Genotype E2 followed by E11, Gharib, E6, E26, E34, E35, E36, E19, E20 and E27. Aroma was observed in 34 rice genotypes and 10 were identified as superior. They are E11, Sadri, Gharib, E7, Kasturi, Rambir Basmati, E21, E13, E24, and Rato Basmati. Positive correlation ($r = 0.59$, $p \leq 0.05$)) was observed between aroma and kernel elongation in these selected 10 genotypes. Three of them had strong aroma (score 4) and three genotypes were E11, Sadri and Garib. We observed that the outstanding 10 genotypes for aroma and highest kernel elongation ratio are not the same except for two of the genotypes (Garib and E11). Aroma concentration was significantly different in highest kernel elongation ratio performance of 10 genotypes. Similar results were also observed in top 10 aroma performing genotypes and their kernel elongation ratio also varied among each other. In addition, out of 55 aromatic genotypes 17 did not have any aroma; comparatively low kernel elongation ratio was also observed in many of the genotypes. This investigation indicated that association of aroma and kernel elongation ratio can be highly influenced by tropical environment. However, since two genotypes (Garib and E11) exhibited high aroma and Kernel elongation ratio and aromatic expression were even in tropical Malaysian Environment, it can be concluded that this expression might be as a result of the influence of dominant nature of some associated genes.

CHAPTER III

MATERIALS AND METHODS

A total of thirty-two advanced generation (F_4) of fine rice were received from the Department of Genetics and Plant Breeding, Hajee Mohammad Danesh Science and Technology University, before commencing of Transplant aman season of 2015. In general, the land races are low yielding but having high aroma emitted from all parts of the cultivars except roots. The northern part of Bangladesh is famous for the production of different types of fine rice cultivars. From 32 advanced (F_4) fine rice lines 10 lines, such as PL1, PL2, PL12, PL13, PL15, PL16, PL17, PL22, PL24, PL26 were advanced upto F_6 generation were used as parental materials to develop high yielding as well as high aroma content fine rice genotypes. The experiments were conducted at the Plant Breeding Research Field (PBRF), Hajee Mohammad Danesh Science and Technology University, Dinajpur as well as another two locations of the country, *viz* BADC Seed Multiplication Farm (SMF), Nilphamari and BADC Seed Multiplication Farm (SMF), Faridpur. The experiments were sequentially completed according to the frame work of the study.

The outline for the development of 32 F_4 lines are produced by previous researcher presented below

Table 3.1.The process of development of eight experimental hybrids

	FR1	**FR2**	**FR3**	**FR4**	**FR5**	**FR6**
FR1	××	FR1×FR2 (Success)	FR1×FR3 (Success)	FR1×FR4 (Success)	FR1×FR5 (Failed)	FR1×FR6 (Failed)
FR2		××	FR2×FR3 (Success)	FR2×FR4 (Success)	FR2×FR5 (Success)	FR2×FR6 (Failed)
FR3			××	FR3×FR4 (Success)	FR3×FR5 (Failed)	FR3×FR6 (Failed)
FR4				××	FR4×FR5 (Success)	FR4×FR6 (Failed)
FR5					××	FR5×FR6 (Failed)

FR1= Kataribhog, FR2= Kalozira, FR3= Chinigura, FR4= Badshabhog, FR5= Begunbichi and FR6= BRRI Dhan 34

3.1 List of the experiments

Experiment I. Evaluation of F_4 generation for yield and yield contributing characters

Experiment II. Assessment of selection response and realized heritability from F_4 to F_5 generation

Experiment III. Assessment of aroma in F_5 generation

Experiment IV. Stability analysis of F_6 generation over the locations

Experiment V. Estimation of cooking quality in F_6 generation

These experiments were conducted during the period from July 2015 to January 2018

Table 3.2. Presentation of experiment wise duration and location

	Experiment	**Duration**	**Location**
01.	Experiment I	July-December/2015	HSTU, Dinajpur
02.	Experiment II	July-December/2016	HSTU, Dinajpur
03.	Experiment III	July-December/2016	HSTU, Dinajpur
04.	Experiment IV	July-December/2017	HSTU, Dinajpur; BADC Farm, Nilphamari; BADC Farm, Faridpur.
05.	Experiment V	January/2018	HSTU, Dinajpur

3.2 General experimental features of the experimental sites

3.2.1 Plant Breeding Research Field (PBRF), HSTU, Dinajpur

3.2.2 BADC Seed Multiplication Farm (SMF), Nilphamari

3.2.3 BADC Seed Multiplication Farm (SMF), Faridpur

Table 3.3. Agro-ecological characters of experimental sites:

Field Experimental Site	Soil type	Soil pH and Fertility	Name of the AEZs	Location
HSTU	Medium high with sandy clay loam texture	5.5 to 6.00 with medium fertility level and low organic matter content	Old Himalayn Piedmont Plain (AEZ1)	Located at 25°13´ N latitude and 88°23´E longitude and it is situated at elevation 42 meters above sea level.
Nilphamari	Medium high with sandy clay loam texture	6.00 to 6.5 medium fertility level and low organic matter content	Active Tista Flood Plain (AEZ2)	25'48' N latitudes and 88'44' E longitude and it is situated at elevation 40 meters above sea level.
Faridpur	Medium high with clay loam texture	6.5 to 7.0 medium fertility level and low organic matter content	Active Ganges Floodplain (AEZ10)	Located at 23.5958°N latitudes 89.84°E longitudes it is situated at elevation 15 meters above sea level.

3.2.4 Land preparation: The experimental plot was at a lower elevation with high water holding capacity. The land was prepared thoroughly with 4 ploughing and cross ploughing followed by harrowing and laddering.

3.2.5 Fertilizer application: The crop was fertilized with recommended doses of cowdung (5t/ha) and fertilizers such as 100kg/ha Urea, 25kg/ha TSP and 45kg/ha MOP respectively. The whole amount of TSP, MOP and half of the amount of urea were applied at final land preparation. The remaining half urea was applied in two equal installments after two weeks and six weeks of transplanting.

3.2.6 Irrigation and drainage: After transplanting of seedling, the field was irrigated properly and, necessary soil moisture maintained throughout the crop period. A good drainage system was also ensured for immediate release of excess rainwater from the experimental field during the crop growing period.

3.2.7 Intercultural operations: Necessary intercultural operations were performed for proper growth and development of the plants. Weeding was done simultaneously at the time of two top dressings with nitrogen. These practices were helpful to break the soil crust, to maintain uniform growth of plant population and to incorporate the nitrogen fertilizer (urea) into the soil, thus reducing the loss through denitrification. Proper control measures were taken against blast, nematode and stem borer of rice.

3.2.8 Crop harvesting: The sample plants from individual plots were harvested at physiological maturity stage when around 80% grains became mature. The other details of materials and methods are described in the relevant of the specific experiments.

3.3 Experiment I: Evaluation of F_4 generation for yield and yield enhancing characters

3.3.1 Materials and Methods

Thirty-two F_4 generations derived from eight experimental hybrids were evaluated at Plant Breeding Research Field (PBRF), HSTU, Dinajpur. The genetically pure and healthy seeds of these genotypes were obtained from the HSTU Breeding Laboratory.

The experiment was conducted during the period from July to December' 2015. The seeds of the experimental materials were sown in well-prepared seed beds and 25 days old seedlings were transplanted in the plots in Randomized Complete Block Design with three replications.The plot size was 3m x 2m. The seedlings of each genotype were transplanted according to design with one seeding per hill. Therefore, total number of seeding per plot was 150. The rows were 20 cm apart with planting space also 20 cm. The replications (blocks) were inter-spaced at 60 cm. The genotypes were assigned randomly to each plot within each block. The agronomic practice with fertilizer application was carried out in accordance with normal recommendations.

Table 3.4. List of the 32 pure lines (PL) at F_4 generation (received).

Experimental Hybrids	Selected F_4 (PL) Lines
FR1×FR2	PL1, PL2, PL3 and PL4
FR1×FR3	PL5, PL6, PL7 and PL8
FR1×FR4	PL9, PL10, PL11 and PL12
FR2×FR3	PL13, PL14, PL15 and PL16
FR2×FR4	PL17, PL18, PL19 and PL20
FR2×FR5	PL21, PL22, PL23 and PL24
FR3×FR4	PL25, PL26, PL27 and PL28
FR4×FR5	PL29, PL30, PL31 and PL32

Rice is a self-pollinated crop, therefore, after hybridization, the hetezygous allelic pairs were rapidly fixed to attain homozygocity with advancing generations.

3.3.2 Data recording

1. **Plant height (cm):** Plant height from ten randomly selected plants was measured from the ground level to the tip of the longest panicle. It was measured in centimeter (cm).

2**. Number of productive tillers/hill**: The tillers which had fertile grains considered as productive tillers. The total number of productive tillers was counted from each of the sample hills and average was taken.

3. **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 line.

4. **Number of fertile grains/panicle**: Spikelets containing food material or not were counted as total fertile grains /panicle. It was calculated from the panicle of ten randomly selected hill of each line.

5. **Number of sterile grains/panicle**: Spikelets containing food material or not were counted as total sterile grains / panicle. It was calculated from the panicle of ten randomly selected hill of each line.

6. **Panicle weight (g)**: Ten panicles obtained from each line were sun dried and weighed carefully. The dry weights of panicles of three samples/lines were recorded to obtain the final panicle weight/line.

7. **Sterility percentage**: It expressed the number of sterile spikelets out of total spikelets / panicle multiplied by 100.

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

8. **Lodging percentage**: It expressed the number of lodged hills / plot out of total number of hills / plot.

$$\left[\text{Lodging percentage} = \frac{\text{Number of lodged hills/plot}}{\text{Number of hills/plot}} \times 100\right]$$

9. **1000-grain weight (g):** One thousand clean dried grains were counted from the seed stock obtained from ten randomly selected plants of each plot and weighted by using an electrical balance in gram (g).

10. **Days to 50% flowering**: Days to 50% flowering was determined by counting the number of days from transplanting of seedling up to appearing of 50% plants bearing flowers in the plot.

11. **Days to maturity**: It was the average maturity days of each advance line over the replications. Recorded a days on plot basis when about 80% of the hills were ready for harvesting.

12**. Harvest index (%)**: It is expressed by the following formula-

$$\left[\text{Harvest index} = \frac{\text{Biological yield/plot}}{\text{Grain yield/plot}} \times 100\right]$$

Biological yield= Straw yield+ Grain yield

13. **Grain yield/hill (g):** The grains obtained from each unit plot were sun dried and weighed carefully. The dry weight of grains of three samples/plots was recorded to obtain the final grain yield/ plot (kg).

3.3.3 Statistical analysis of data

Different statistical analyses were done using computer based software. Mean data of the characters were subjected to both univariate and multivariate analyses. Univariate analysis of the individual characters (analysis of variance) was done using STAR software. Mean, range and coefficient of variance (CV) were also estimated using STAR software. Multivariate analysis viz. Principal component analysis, Principal co-ordinate analysis, Cluster analysis and Canonical vector analysis were done as suggested by Anderson (1987) using Genstat 5.13 software.

3.3.4 Estimation of phenotypic and genotypic variances

Genotypic and phenotypic variances were estimated by Johnson *et al.* (1955). Genotypic variance ($\delta^2{}_g$) was obtained by subtracting error mean sum of square from the genotype mean sum of square and dividing by the number of replications as shown below:

$$\delta^2_g = \frac{\text{GMS - EMS}}{r}$$

Where,

GMS = Genotypic mean sum of square

EMS = Error mean sum of square

r = Number of replication

The phenotypic variances (δ^2_p) were derived by adding genotypic variances (δ^2_g) as given by the following formula:

$$\delta^2_p = \delta^2_g + \delta^2_e$$

3.3.5 Estimation of coefficient of range

Coefficient of range was calculated using following formula:

$$\text{Coefficient of range} = \frac{(H - L)}{(H + L)}$$

Where,

H = highest value in a set of observation

L = lowest value in a set of observation

3.3.6 Estimation of genotypic and phenotypic coefficient of variation

Genotypic and Phenotypic Coefficient of Variations were estimated according to the formula given by Johnson *et al.* (1955).

$$\text{Genotypic Coefficient of Variation}\,(\text{GCV}) = \frac{\delta_g}{X} \times 100$$

Where,

δ_g= Genotypic standard deviation

X = Grand mean

$$\text{Phenotypic Coefficient of Variation}\,(\text{PCV}) = \frac{\delta_p}{X} \times 100$$

Where,

δ_p= Phenotypic standard deviation

X = Grand mean

3.3.7 Estimation of heritability

Broad sense heritability was estimated by the formula suggested by Jhonson *et al.* (1955).

$$\% \, h^2_b = \frac{\delta^2_g}{\delta^2_p} \times 100$$

Where,

h^2_b = Heritability in broad sense

δ^2_g = Genotypic variance

δ^2_p = Phenotypic variance

3.3.8 Estimation of genetic advance

The expected genetic advance for different characters under selection was estimated using the formula suggested by Johnson *et al.* (1955).

$$\text{Genetic Advance}\left(\text{GA}\right) = \frac{\delta^2_g}{\delta^2_p} \times K \times \delta_p$$

Where,

K = Selection intensity, the value of which is 2.06 at 5% selection intensity

δ_p = Phenotypic standard deviation

δ^2_g = Genotypic variance

δ^2_p= Phenotypic variance

3.3.9 Estimation of genetic advance in percentage of mean

Genetic advance in percentage of mean was calculated from the formula given by Comstock and Robinson (1952).

$$\text{Genetic advance in percentage of mean} = \frac{\text{Genetic advance}}{\text{Grand mean}} \times 100$$

3.3.10 Genetic divergence based on yield and its related characters

At first the data were subjected to principal component analysis (Rao, 1964) to group the lines into different clusters using non-hierarchical classification based on maximum variance and succeeded components with latent roots greater than unity (Jeger *et al.,* 1983). Genetic divergence based on thirteen characters was computed using GENSTAT 5.5 software program and the lines were clustered by using on hierarchical classification through covariance matrix. The intra and inter-cluster distances were measured following the D^2 statistics proposed by Mahalanobis (1936).

$$P^{D^2} = Wij(\overline{x}^1 i - \overline{x}^2 i)(\overline{x}^1 j - \overline{x}^2 j)$$

P^{D^2} = Genetic divergence between two advance line.

Wij = The inverse of estimated variance and covariance matrix.

x_i and x_j = The multiple measurements available for each of the lines.

3.3.11 Definition of Mahalanobis distance

The probability contours used to define the Mahalanobis distance are stated below-

- It accounts for the fact that the variances in each direction are different.
- It accounts for the covariance between variables.
- It reduces to the familiar Euclidean distance for uncorrelated variables with unit variance.

For uni-variate normal data, the uni-variate z-score was standardized for the distribution (so that it has mean and unit variance) and given a dimensionless quantity that specified the distance from an observation to the mean in terms of the scale of the data. For multivariate normal data with mean μ and covariance matrix Σ, de-correlated the variables and standardized the distribution by applying the Cholesky transformation $z = L^{-1}(x - \mu)$, where L is the Cholesky factor of Σ, $\Sigma = LL^T$.

After transforming the data, standard Euclidian distance from the point z to the origin was calculated. In order to get rid of square roots, computed the square of the Euclidean distance, which was $\text{dist}^2 (z, 0) = z^T z$ was measured to estimate how far from the origin a point was, and the multivariate generalization of a z-score.

Then rewrited $z^T z$ in terms of the original correlated variables. The squared distance $\text{Mahal}^2(x, \mu)$ is $= z^T z$

$$= (L^{-1}(x - \mu))^T \ (L^{-1}(x - \mu))$$
$$= (x - \mu)^T (LL^T)^{-1} (x - \mu)$$
$$= (x - \mu)^T \Sigma^{-1} (x - \mu)$$

The last formula was the definition of the squared Mahalanobis distance. The derivation used several matrix identities such as $(AB)^T = B^T A^T$, $(AB)^{-1} = B^{-1} A^{-1}$, and $(A^{-1})^T = (A^T)^{-1}$. Notice that if Σ was the identity matrix, then the Mahalanobis distance reduced to the standard Euclidean distance between *x* and μ.

The Mahalanobis distance accounted for the variance of each variable and the covariance between variables. Geometrically, it had this by transforming the data into standardized uncorrelated data and computing the ordinary Euclidean distance for the transformed data. In this way, the Mahalanobis distance was like a uni-variate z-score: it provided a way to measure distances that takes into account the scale of the data.

3.3.12 Genotypic and phenotypic correlation coefficients

The genotypic and phenotypic correlation coefficients of yield and its different contributing characters were estimated by the following formulae given by Johnson *et al.* (1955) and Singh and Chaudhary (2010).

Genotypic correlation coefficient:

$$r_{g1.2} = \frac{\text{Cov.}_{g1.2}}{\sqrt{\sigma^2 g_1 \times \sigma^2 g_2}}$$

Where

$\text{Cov.}g_{1.2}$ = genotypic covariance between the variables x_1 and x_2.

$\sigma^2 g_1$ = genotypic variance of the variable x_1

$\sigma^2 g_2$ = genotypic variance of the variable x_2

Similarly,

Phenotypic correlation of coefficient:

$$r_{p1.2} = \frac{\text{Cov.}_{ph1.2}}{\sqrt{\sigma^2 ph_1 \times \sigma^2 ph_2}}$$

Where

Cov.$ph_{1.2}$ = phenotypic covariance between the variable x_1 and x_2

$\sigma^2 ph_1$ = phenotypic variance of the variable x_1

$\sigma^2 ph_2$ = phenotypic variance of the variable x_2

3.3.13 Path co-efficient analysis

The cause and effect relationship between yields and its components characters, were studied through path coefficient analysis. Path coefficient analysis was done according to the procedure stated by Singh and Choudhury (2010).

Assuming twelve independent (x_1, x_2……….x_{10}) and one dependent variable x_y. Path coefficient analysis was performed.

The relationship between them can be represented as follows:

$r_1y = r_{1.1}p_1y + r_{1.2}p_2y + r_{1.3}p_3y + r_{1.4}p_4y + r_{1.5}p_5y + r_{1.6}p_6y + r_{1.7}p_7y + r_{1.8}p_8y + r_{1.9}p_9y + r_{1.10}p_{10}y + r_{1.11}p_{11}y + r_{1.12}p_{12}y$

$r_2y = r_{2.1}p_1y + r_{22}p_2y + r_{23}p_3y + r_{24}p_4y + r_{25}p_5y + r_{26}p_6y + r_{27}p_7y + r_{28}p_8y + r_{29}p_9y + r_{210}p_{10}y + r_{2.11}p_{11}y + r_{2.12}p_{12}y$

$r_3y = r_{3.1}p_1y + r_{3.2}p_2y + r_{3.3}p_3y + r_{3.4}p_4y + r_{3.5}p_5y + r_{3.6}p_6y + r_{3.7}p_7y + r_{3.8}p_8y + r_{3.9}p_9y + r_{3.10}p_{10}y + r_{3.11}p_{11}y + r_{3.12}p_{12}y$

....

....

$r_{11}y = r_{11.1}p_1y + r_{11.2}p_2y + r_{11.3}p_3y + r_{11.4}p_4y + r_{11.5}p_5y + r_{11.6}p_6y + r_{11.7}p_7y + r_{11.8}p_8y + r_{11.9}p_9y + r_{11.10}p_{10}y + r_{11.11}p_{11}y + r_{11.12}p_{12}y$

Where,

p_1y, p_2y…. $p_{12}y$ = Path coefficient of the variable x_1, x_2……x_{12} on variable x_y respectively

r_1y, r_2y……. $r_{12}y$ = Correlation coefficient of the variable x_1, x_2……x_{12} on variable x_y respectively.

The indirect effect of a particular character through other character worked out by multiplying direct paths and particular correlation coefficient between those characters, respectively.

Residual effect was estimated as follows:

Residual effect (R) = $[1-(r_1yp_1y + r_2yp_2y + \ldots. r_{12}yp_{12}y)^{1/2}$

3.3.14 Principal component analysis (PCA)

The technique was used to examine the interrelationships among five quantitative characters. The principal components were computed from the correlation matrix obtained from sum of squares products matrix of the characters, and genotype score obtained from the first component and the succeeding component with latent roots greater than unity. The latent roots are called 'Eigen values'. The component has the property of accounting for maximum variances. The PCA displays most of the original variability in a smaller number of dimensions, since it finds linear combinations of a set of variates that maximize the variation contained within them. Contributions of the different characters towards divergence are discussed from the latent vectors of the first two principle components.

3.3.15 Cluster analysis

Cluster analysis was performed by D^2 analysis (originally proposed outlined by Mahalanobis, 1928 and 1936, and extended by Rao, 1952), which divides the genotypes based on the data set into more or less homogeneous groups. D^2 is the sum of squares of differences between any two populations for each of the uncorrelated variables, obtained by transforming correlated variables through pivotal condensation method.

3.3.16 Computation of average intra-cluster distances

The average intra-cluster distance for each cluster was calculated by taking possible D^2 values within the members of a cluster obtained from the Principal Coordinate Analysis (PCO) after the cluster were formed. The formula used to measure the inter-cluster distance $=\sum D^2/n$, where $\sum D^2$ is the sum of distances between all possible combinations (n) of the genotypes included in a cluster. The square root of the average D^2 values represents the distance (D) within cluster.

3.3.17 Computation of average inter-cluster distances

The procedure of calculating inter-cluster distance was first to measure the distance between cluster I and II, between I and III, between I and IV, between II and III, between II and IV and so on. The clusters were taken one by one and their distances from other clusters were calculated.

The inter cluster distance were calculated by the formulae described by Singh and Chaudhary (1985).

$$\text{Square of inter cluster distance} = \frac{\sum Di^2}{n_i n_j}$$

Where,

$\sum Di^2$ is the sum of distances between all possible combinations (ninj) of the entries included in the cluster study.

n_i = Number of entries in cluster i

n_j = Number of entries in cluster j

3.3.18 Cluster diagram

Cluster diagram was drawn using D^2 values between and within clusters i.e. the intra-and inter-cluster distances. It gives a brief idea of the pattern of diversity among the genotypes and relationships between different genotypes included in a cluster.

3.4 Experiment II: Assessment of selection response and realized heritability from F_4 to F_5 generation

3.4.1 Experimental Design: RCBD with three replications.

3.4.2 Period: Transplant Aman season (July-December/2016)

3.4.3 Materials and methods

Thirty-two F_5 generations derived from F_4 generation.

3.4.4 Data recording

Thirteen characters were considered in the study viz. plant height (cm), number of productive tillers/hill, panicle length (cm), number of fertile grains/panicle, number of sterile grains/panicle, panicle weight (g), sterility percentage, lodging percentage, 1000-grain weight (g), grain yield/hill (g), days to 50% flowering, days to maturity and harvest index.

3.4.5 Estimation of selection response and realized heritability on the above characters

Selection can act on any phenotypic variation and may cause evolutionary change if the variation is due to genetic region. Population biologists often use an index called realized heritability (h^2), to quantify the degree to which a trait in a population can be pushed by selection. To calculate this index, initial response to selection was calculated by subtracting the average of the second generation from that of the entire first generation. The selection differential was also estimated by subtracting the average of the selected parents from that of the entire first generation. Realized heritability was the response divided by the differential**.** Thus realized heritability values were calculated by the formulae described by Lstiburek *et al.* (2018) as follows :

$$\text{Realized heritability} = \frac{\text{Response to selection}\left(\text{R}\right)}{\text{Selection differential}\left(\text{S}\right)} \times 100$$

Where, R =Mean of offspring – Mean of starting population

=Field mean of F_5 generation – Field mean of F_4 generation

S =Mean of the parents – Mean of the starting population

=10% selection mean of F_4 generation - Field mean of F_4 generation

$$\text{Realized heritability} = \frac{\text{Avg } 1^{\text{st}} \text{ gen} - \text{Avg } 2^{\text{nd}} \text{ gen}}{\text{Avg } 1^{\text{st}} \text{ gen} - \text{Avg selected parents}} \times 100$$

A low h^2 (less than 0.01) occurs when the offspring of the selected parents differ little from the original population, in spite of a big difference between the population as a whole and the selected parents. A high h^2 (greater than 0.6) occurs when the offspring of the selected parents differ from the original population almost as much as the selected parents did were considered.

3.5 Experiment III: Assessment of aroma in F_5 generation

3.5.1 Location: Plant Breeding Research Field and Laboratory, HSTU, Dinajpur

3.5.2 Experimental Method: Sensory method constituted by a six member panel.

3.5.3 Period: Transplant Aman season (July-December/2016)

3.5.4 Materials

Green leaves and gain powder of F_5 generations were assessed by sensory method constituted by a six member's panel for estimation of aroma contents.

3.5.5 Aroma assessment and data recording

Aromatic characteristics of the rice (F_5 generations) were identified by tasting individual plant leaves and grain powder. For the test, 1.7% KOH solution was applied to the tissue (Sood and Siddiq, 1978). One gram of the first green leaf blade at heading stage was cut into small pieces and put into Petri dishes with 5 mL of 1.7% KOH solution at room temperature. Similarly, 100g of crushed grain was taken into Petri dishes with 5 ml of 1.7% KOH solution. After 30 minutes, the dishes were opened and immediately smelled. The presence or absence of aroma was scored. Each individual sample was evaluated by panel of six persons.

3.5.6 Working procedure

- A sensory panel was formed by six members having knowledge about aroma content of fine rice.

- Green young leaves were collected from the field and the grains from the store. The leaves were cut into small pieces and the grains were crushed and kept in a small container.

- The small pieces of leaves and the crushed grains were dipped into 1.7% KOH for 10 minutes in test tubes.

Aroma was assessed by a six member's panel keeping the following grades under consideration.

Table 3.5. Aroma score and category

Score	Category
9	High aroma
7	Medium aroma
5	Low aroma
3	Very low aroma
1	No aroma

Source: Hien *et al.* (2006)

3.6 Experiment IV: Stability Analysis of F_6 Generation over the Locations

3.6.1 Experimental materials: Ten F_6 generations derived from F_5 generation.

3.6.2 Location: 1. Genetics and Plant Breeding Research Field, HSTU, Dinajpur 2. BADC Seed Multiplication Farm, Faridpur. 3. BADC Seed Multiplication Farm, Nilphamari.

3.6.3 Experimental Design: RCBD with three replications.

3.6.4 Period: Transplant Aman season (July-December/2017)

3.6.5 Materials and procedure

Ten advanced lines (F_6) generation derived from F_5 were evaluated over three locations. The research was carried out at the sites: 1. Plant Breeding Research Field, HSTU, Dinajpur; 2. BADC Seed Multiplication Farm, Nilphamari and 3. BADC Seed Multiplication Farm, Faridpur.

3.6.6 Observations and data recording

Recorded data were similar as experiment I.

3.6.7 Stability analysis

The stability of yield performance for each advanced line was calculated by regressing the mean yield of individual lines on environmental index and calculating the deviations from regressing the mean yield of individual lines on environmental index as suggested by Eberhart and Russell (1966). Regression coefficient (bi) was considered as an indication of the stability and deviation from regression coefficient (s^2d) as response of the lines to varying environment, while the environment and genotype × environment interactions were partitioned into three components viz., environment (linear), genotype x environment (linear) and deviation from regression (pooled deviation over the genotypes). As described by Eberhart and Russell (1966), the behavior of the lines was assessed by the model $Y_{ij} = m + b_i I_j + d_{ij} + \overline{\varepsilon_{ij}}$,

Where,

Y_{ij} = observation of the i-th (i = 1, 2,…, g) advance line in the j-th (j = 1, 2, ...n)

environment,

m = general mean,

b_i = regression coefficient,

I_j = environmental index obtained by the difference among mean of each environment and the general mean $(\sum_{j=1}^{n} I_j = 0), \delta_{ij}$ = the regression deviation of the i-th advance line in the j-th environment and e_{ij} = effect of the mean experimental error.

3.7 Biplot analysis

Biplot analysis is the most powerful interpretive tool of AMMI models. Biplots aregraphs where aspects of both genotypes and environments were plotted on the same axis so the inter-relationships were effectively visualised. There are two basic AMMI biplots, the AMMI1 biplot where the main effects (genotype mean and environments) were plotted against each other and the AMMI2 biplot where scores for PCA1, PCA2 and PCA3 were considered.

3.8 Experiment V: Estimation of cooking quality of F_6 generation lines

3.8.1 Experimental materials: Rice kernels from selected advance lines of F_6 generation

3.8.2 Location: Plant Breeding Research Laboratory, HSTU, Dinajpur.

3.8.3 Period: January/2018

3.8.4 Data recording

Table 3.6: Data on estimation of cooking qualities of fine rice

No.	Name of the characters recorded	Abbreviated forms used
1	Rice length(cm)	RL
2	Cooked rice length(cm)	CRL
3	Cooked rice weight(g)	CRW
4	Aroma test	AT
5	Expansion of cooked rice(cm)	ECR
6	Semi solid starch volume(ml)	SLSL
7	Cooking time(min)	CT

3.8.5 Working procedure

1. Different cooking qualities were accomplished by cooking 200 g of whole rice kernels from each treatment in 500 ml distilled water for a minimum cooking time in a boiling rice cooker and draining the superficial water from the cooked rice.

2. The cooked samples were then weighed accurately and the water uptake ratio was calculated as the ratio of final cooked weight to uncooked weight.

3. Cooking times for samples were determined as described by Mohapatra and Bal (2006). A mass of 200 g rice grain from each sample was cooked in boiling distilled water (500 ml) at required time in a rice cooker.

4. Measurements were taken after 10 min of cooking and every minute thereafter. The measurements involved collection of 10 grains from the cooking vessel and pressing between two glass slides.

3.8.6 Procedure of recording data on estimation of cooking qualities

Different cooking qualities were measured by repeating end item three times in the laboratory. Ten parental lines were selected for cooking qualities. PL1, PL2, PL12, PL13, PL15, PL16, PL17, PL22, PL24, PL26 were selected for estimating cooking qualities.

3.8.6.1 Rice length (cm)

After selecting the fine rice samples, the length of rice was measured by slide calipers and scale in the laboratory.

3.8.6.2 Cooked rice length (cm)

The length of the cooked rice was measured by slide calipers and scale. After cooking, the data was taken.

3.8.6.3 Weight of cooked rice (g)

The weight of cooked rice was measured by a weight balance in the laboratory. After cooking the fine rice, the data was measured**.**

3.8.6.4 Aroma test

Five-gram rice samples were taken in a test tube; 15 ml of water added and soaked for 10 minutes. Rice samples were cooked in water bath for 15 minutes and transferred in to a Petri disc and scored as per panel test performance (Anonymous, 2004). After required time, the aroma was serially tested one by one by from the panel members and the data were recorded as scale of 1-9. The meaning of the scale was as follow-

Score	**Category**
9	High aroma
7	Medium aroma
5	Low aroma
3	Very low aroma
1	No aroma

Source: Hien *et al.* (2006)

After completing the work, the average value was calculated against each of the advanced lines. Thus the aroma content was estimated in the advanced line.

3.8.6.5 Expansion of cooked rice (cm)

The length of cooking rice was measured and expressed as the ratio of cooked grain versus uncooked grain (Sidhu *et al.,* 1975). Cooked rice where: volume of 200g of cooked grain was unmeasured in a measuring cylinder and cooking quality graded poor (350-375 ml), satisfactory (375-400 ml) and very good (425-450 ml) (Sowbhagya *et al.,* 1987).

3.8.6.6 Volume of semi liquid starch (ml)

A 200g sample of rice was taken and cooked with 500ml of water in a rice cooker. It was allowed to cool and the weight of semi liquid starch was determined by draining the unabsorbed water. It was expressed as ml (Sidhu *et al.,* 1975).

3.8.6.7 Cooking time (min)

All advanced lines of fine rice were cooked by a rice cooker with 200g if raw rice per sample the cooking time and semi liquid starch weight for individual rice were standardized. The soaking and cooking were done in glass distilled water. The complete soften of rice samples were tasted by tactile tenderness method where one cooked rice was pressed by keeping between two fingers.

3.9 Statistical analysis

The data obtained for different characters were recorded first on MS excel sheet. Afterwards, the data were analyzed using the software package R of version 3.4.2 (R Core Team, 2017) and Statistical Tool for Agricultural Research (STAR) Version: 2.0.1 (STAR 2014).

CHAPTER IV

RESULTS AND DISCUSSION

Though aromatic rice contributes to a small share in the world market, but is valued at the highest price among all types of rice. The demand for aromatic rice is expected to increase because of increasing preference of the by consumers due to specific taste. Nevertheless, traditional aromatic rice varieties are low yield potential compared to other coarse grain rice varieties. The breeding for new aromatic rice is going to be increasingly more competitive as primitive aromatic rice advance line of our country are popular to the growers, traders and cosumers. Besides, the scientists in Bangladesh are continuously working in developing coarse grain high yielding or in imroproving specific shortcoming like Zn deficit fulfilment, saline tolerance or resistance to particular disease or insect resistance varieties; their innovation to increase yield are compromised with quality, as a threat from losing their competitive advantage in aromatic rice production has been realized. Unless new aromatic rice varieties with high quality are available for commercial cultivation, it is a challenge to maintain reputation of local cultivars without evolving new varieties Therefore, the experiments were undertaken to improving the aromatic rice cultivation scenario and the results are discussed below-

4.1 Experiment I: Evaluation of F_4 line for yield and yield controbuting characters.

4.1.1 Description of means of different characteristics of F_4 line of fine rice

The mean performance of 13 characteristics in 32 define the generation of the advanced population of rice were separated by DMRT test at 5% level of probability and have been presented in **Table 4.1**. The characteristics evaluated were plant height (cm), productive tillers /hill, panicle length (cm), fertile grains /panicle, sterile grains /panicle, panicle weight (g), sterility percentage, lodging percentage, 1000-grain weight (g), grain yield /hill, days to 50% flowering, days to maturity and harvest index.

4.1.1.1 Plant height (cm)

Plant height of the advanced lines (F_4) was measured at maturity stage. It was evident from the **Table 4.1** that the height of the plants differed among the advanced lines. The tallest plant (159.93 cm) was found in PL13 and the shortest (123.66 cm) plant was in

PL6. The grand mean value for this trait was 137.33 cm. Dwivedi (1985) reported that plant height might not have role in the expression of vigor of hybrid rice. At maturity, the height of plants among the varieties tested revealed highly significant differences. The significant variation in plant height could be attributed to genetic diversity among the advanced lines. The group of genotypes that showed higher plant height were constituted by PL13 (159.93 cm), PL17 (150.06 cm) and PL19 (144.23 cm). The group of genotypes that showed lower plant height were constituted by PL6 (123.66 cm), PL31 (125.70 cm) and PL24 (126.13 cm), respectively (**Table 4.1**). These findings are with an agreement of Ganapati *et al.* (2020) for the range of plant heights in fine rice. Development of short stature plant in fine rice is indispensable to resist lodging before maturity.

4.1.1.2 Productive tillers /hill

Productive tillers are an important yield component in rice. The trait, number of productive tillers /hill is believed to be highly effective to increase high grain yield /hill. So, the advanced lines with more number of panicle bearing tillers/hill should be identified. The advanced lines with low tillering capacity are not desirable in transplanted rice culture. The highest effective tillers/hill (8.90) was found in PL2 and (8.50) in PL8 and the lowest (4.90) was in PL13. The grand mean value for this trait was 6.73. The group of genotypes that showed higher number effective tillers /hill were constituted by PL2 (8.90), PL8 (8.50), PL9 (8.10), PL3 (7.80) and PL6 (7.70) respectively. The group of genotypes which showed the least number of effective tillers /hill was constituted by PL13 (4.90) and PL19 (4.90) respectively (**Table 4.1**). The significant differences could be attributed to the fact that high yielding varieties (HYV's) have relatively high tillering capacity (De Datta, 1981).

4.1.1.3 Panicle length (cm)

The panicle length varied due to variety shown in **Table 4.1**. Advanced lines are generally characterized by having longer panicles indicating their efficiency in partitioning of assimilates to reproductive parts. This is one of the attributes of higher yields in advanced lines. According to Zhende (1988) hybrid rice have bigger panicles and more spikelets /panicle and thus in the study, PL23 (30.46 cm) and PL26 (29.86 cm) had significantly produced the longest panicle among the advanced lines used as seen in **Table 4.1**. The shortest panicle was registered by PL25 (22.80 cm) which is significantly different from the other advanced lines. The grand mean value for this trait was 26.56 cm. The significant differences in panicle length among the advanced lines of rice could be attributed to their genetic make-up.

4.1.1.4 Fertile grains /panicle

The number of fertile grains/panicle is another important as well as main yield contributing character in the rice. It directly contributes to the seed yield and maximum mean value was highly desirable for this trait. The thirty-two genotypes evaluated here significantly differed in terms of the produced number of fertile grains /panicle. PL6 (198.30) and PL31 (186.50) produced maximum fertile grains/panicle, which are significantly different from the number produced by the rest of the lines. PL27 produced the lowest number that was 126.70 (**Table 4.1).** The grand mean value for this trait was 157.42. Fernandez (2002) supported that hybrid rice produces long roots and broad leaves that enable them to take up more nutrients and produce more grains.

4.1.1.5 Sterile grains /panicle

Results showed that lines had effect in respect of the number of sterile grains/panicle. PL27 produced minimum numbers (8.60) of sterile grains/panicle and PL1 produced maximum number (26.10) of sterile grains/panicle (**Table 4.1**). The grand mean value for this trait was 15.10. This variation might be due to genetic characteristics. BINA (1993) and Chowdhury *et al.* (1993) also reported differences in number of unfilled grains panicle-1 due to varietal differences.

4.1.1.6 Panicle weight (g)

Panicle weight is another important yield contributing character of rice. It directly contributes to the seed yield and maximum mean value was highly desirable for this trait. Among all the genotypes PL6 showed highest panicle weight (4.87 g) and PL27 showed lowest weight (1.92 g), with a grand mean of 3.03g. The highly performing group was constituted by the genotypes PL6 (4.87 g), PL31 (4.15 g) and PL7 (3.76 g), respectively. The group which showed lowest panicle weight was PL27 (1.92 g), PL25 (2.08 g), PL32 (2.16 g), and PL18 (2.15) respectively (**Table 4.1**).

Table 4.1. Mean values of different characters in F_4 generation of fine rice

Genotype	PH	PTPH	PL	FGPP	SGPP	PW	SP
PL1	137.93 jk	7.50 b-e	28.28 b	177.20 c	26.10 a	3.17 j	14.48 a
PL2	135.66 lm	8.90 a	26.51 e-h	140.50 m	14.80 e-g	2.22 r	11.88 f
PL3	140.83 f-h	7.80 a-d	26.26 f-i	128.40 pq	14.20 e-g	2.60 o	12.12 e
PL4	135.66 lm	7.10 c-g	26.85 d-f	177.10 c	22.80 b	3.09 k	13.07 c
PL5	136.63 kl	6.70 d-i	27.28 c-e	185.90 b	22.90 b	3.74 c	12.45 d
PL6	123.66 q	7.70 a-d	27.31 c-e	198.30 a	24.90 a	4.87 a	12.54 d
PL7	134.36 m	7.20 c-g	28.10 bc	165.20 e	21.70 b	3.76 c	13.40 b
PL8	142.03 ef	8.50 ab	26.01 g-l	158.50 g	14.30 e-g	3.09 k	10.30 mn
PL9	135.60 lm	8.10 a-c	26.80 d-g	153.70 h	12.10 ij	3.10 k	9.54 pq
PL10	144.53 c	7.30 b-f	25.43 j-l	171.30 d	14.90 e-g	3.61 e	9.88 o
PL11	139.90 g-i	7.40 b-f	24.43 n	180.20 c	15.20 d-f	3.27 i	9.36 qr
PL12	138.96 h-j	5.80 h-m	26.66 d-h	184.30 b	15.30 d-f	3.04 lm	9.89 o
PL13	159.93 a	4.90 m	24.40 n	131.70 op	14.00 f-h	2.18 rs	11.65 g
PL14	135.56 lm	6.40 e-k	24.03 n	159.10 g	9.20 k-m	2.45 p	7.77 u
PL15	143.33 c-e	6.90 d-h	28.61 b	183.60 b	17.70 c	3.58 ef	10.57 kl
PL16	135.26 lm	7.20 c-g	25.26 lm	160.40 fg	18.20 c	3.67 d	12.05 ef
PL17	150.06 b	6.80 d-h	26.33 f-i	147.50 j-l	16.90 cd	2.85 n	12.58 d

Table 4.1. Mean values of different characters in F_4 generation of fine rice (Contd.)

Genotype	PH	PTPH	PL	FGPP	SGPP	PW	SP
PL18	141.53 e-g	6.90 d-h	26.11 f-k	152.50 hi	12.40 h-j	2.15 st	9.7 op
PL19	144.23 cd	4.90 m	24.41 n	148.70 j-l	10.70 j-l	3.27 i	9.20 r
PL20	129.20 o	5.20 k-m	27.43 cd	163.40 ef	14.50 e-g	3.54 f	10.21 n
PL21	143.10 c-e	5.60 i-m	24.53 mn	137.90 mn	9.00 lm	3.37 h	8.66 s
PL22	134.56 m	6.90 d-h	26.85 d-f	147.80 j-l	13.10 g-i	3.55 f	10.47 lm
PL23	129.63 o	6.00 g-m	30.46 a	149.40 i-k	14.80 e-g	3.48 g	11.07 i
PL24	126.13 p	6.20 f-l	25.51 i-l	160.80 fg	14.70 e-g	2.58 o	10.19 n
PL25	128.83 o	5.00 lm	22.80 o	135.70 n	10.70 j-l	2.08 u	9.78 o
PL26	132.16 n	6.80 d-i	29.86 a	146.90 kl	14.50 e-g	2.99 m	10.90 ij
PL27	139.13 h-j	5.40 j-m	25.30 k-m	126.70 q	8.60 m	1.92 v	8.05 t
PL28	142.40 def	7.40 b-e	28.53 b	134.60 no	13.60 f-i	2.12 tu	11.33 h
PL29	134.63 m	6.20 f-l	25.95 h-l	146.50 kl	15.80 de	3.07 kl	11.46 gh
PL30	138.40 i-k	6.70 d-i	28.86 b	150.60 h-j	10.90 jk	2.3 q	8.77 s
PL31	125.70 p	6.60 d-j	28.53 b	186.50 b	9.80 k-m	4.15 b	6.96 v
PL32	135.23 lm	7.30 b-f	26.25 f-j	145.40 l	14.10 e-h	2.16 st	10.71 jk
Grand mean	137.34	6.73	26.56	157.39	15.08	3.03	10.66
CV%	12.28	15.96	7.28	14.86	17.60	13.57	18.31
LSD	1.957	1.236	0.832	3.386	1.810	0.044	0.191

Table 4.1. Mean values of different characters in F_4 generation of fine rice (Contd.)

Genotype	LP	TGW	DTF	DTM	HI	GYPH
PL1	15.00 h-j	15.62 jk	89.67 a-c	113.00 b-d	26.71 k	15.05 f
PL2	19.33 e	12.68 o	79.00 fg	114.00 bc	28.68 i	12.07 j
PL3	26.33 b	16.71 hi	79.00 fg	111.66 b-e	30.78 g	11.90 k
PL4	25.33 bc	14.90 kl	78.00 f-h	101.67 jk	31.84 ef	11.81 k
PL5	15.33 hi	16.17 ij	76.33 f-h	99.00 k	34.88 a	15.35 e
PL6	7.00 l	20.72 a	77.00 f-h	101.00 jk	33.51 b	18.81 a
PL7	11.33 k	19.35 cd	89.00 bc	109.00 e-g	33.83 b	17.85 bc
PL8	11.33 k	16.58 i	84.00 e	106.00 g-i	32.13 c-e	16.17 d
PL9	15.33 hi	17.38 gh	84.67 de	112.00 b-e	34.69 a	15.81 ef
PL10	17.66 e-g	17.78 fg	88.00 b-d	111.00 c-e	33.42 b	13.76 h
PL11	17.33 fg	14.71 l	87.00 b-e	113.00 b-d	33.71 b	14.37 g
PL12	26.33 b	13.94 m	84.00 e	112.00 b-e	31.84 ef	10.10 l
PL13	30.33 a	13.65 mn	84.00 e	110.00 d-f	29.72 h	18.06 ab
PL14	25.66 b	12.47 o	86.00 c-e	109.00 e-g	32.10 c-e	10.32 l
PL15	14.67 h-j	15.75 j	88.00 b-d	109.00 e-g	33.85 b	14.65 g
PL16	11.33 k	19.85 bc	89.00 bc	112.00 b-e	31.74 ef	17.59 c
PL17	19.33 e	16.62 i	89.67 a-c	114.00 bc	29.93 h	12.04 j

Table 4.1. Mean values of different characters in F_4 generation of fine rice (Contd.)

Genotype	LP	TGW	DTF	DTM	HI	GYPH
PL18	26.33 b	12.89 o	93.00 a	115.00 b	29.50 h	10.56 l
PL19	22.67 d	19.53 cd	90.00 ab	112.00 b-e	31.26 fg	10.83 l
PL20	18.33 ef	18.54 ef	90.00 ab	112.00 b-e	29.92 h	11.81 k
PL21	19.33 e	19.62 c	87.00 b-e	109.00 e-g	31.70 ef	12.37 j
PL22	11.33 k	20.48 ab	84.00 e	104.00 h-j	33.56 b	16.79 d
PL23	13.33 j	19.68 c	90.00 ab	113.00 b-d	32.48 cd	13.04 i
PL24	23.33 d	12.92 no	79.00 fg	129.00 a	32.69 c	10.09 l
PL25	26.33 b	12.60 o	79.00 fg	102.00 jk	27.87 j	10.56 l
PL26	14.33 ij	17.91 fg	84.00 e	107.00 f-h	31.99 de	12.06 j
PL27	30.33 a	13.16 no	74.67 h	101.00 jk	30.97 g	9.06 m
PL28	16.33 gh	12.61 o	80.00 f	107.00 f-h	31.66 ef	10.85 l
PL29	14.66 h-j	17.47 g	76.00 gh	130.00 a	31.27 fg	12.05 j
PL30	23.67 cd	9.68 q	79.00 fg	103.33 ij	31.67 ef	10.06 l
PL31	11.33 k	18.83 de	84.00 e	107.00 f-h	31.97 de	18.05 b
PL32	13.66 ij	11.68 p	88.00 b-d	112.00 b-e	29.93 h	10.59 l
Grand Mean	18.57	16.02	84.06	110.02	31.62	13.60
CV%	18.34	5.00	12.37	14.69	19.73	20.08
LSD	1.861	0.756	3.670	3.450	0.607	0.416

Here, PH=Plant height, PTPH=Productive tillers/hill, PL=Panicle length, FGPP=Fertile grains/panicle, SGPP=Sterile grains/panicle, PW=Panicle weight, SP=Sterility percentage, LP=Lodging percentage, TGW=Thousand grain weight,DTF=Days to 50% flowering, DTM=Days to maturity and HI=Harvest index, GYPH=Grain yield /hill.

The mean values bearing same letter(s) did not differ significantly at 5% level of probability.

4.1.1.7 Sterility percentage

Among all the genotypes PL1 showed the highest sterility percentage (14.48%) and PL31 showed the lowest percentage (6.96%), with a grand mean of 10.66%. The highly performing group was constituted by the genotypes PL 31 (6.96%), PL14 (7.77%) and PL27 (8.05%), respectively. The lines which showed the lowest performance of this trait were PL1 (14.48%), PL7 (13.40%) and PL4 (13.07 %), respectively (**Table 4.1**).

4.1.1.8 Lodging percentage

Among all the genotypes PL13 and PL27 showed the highest lodging percentage (30.33%) and PL6 showed the lowest percentage (7.00%), with a grand mean of 18.57%. The highly performing group was constituted by the genotypes PL6 (7.00%), PL7 (11.33%), PL8 (11.33%), PL16 (11.33%), PL22 (11.33%) and PL31 (11.33%) respectively. The lines which showed lowest performance of this trait were PL13 (30.33%), PL27 (30.33%), PL3, PL4, PL12, PL14, PL18 and PL25 (26.330%) respectively (**Table 4.1**).

4.1.1.9 1000 grain weight (g)

Among all the genotypes PL6 showed the highest 1000-grain weight (20.72 g) and PL30 showed the lowest weight (9.68 g), with a grand mean of 16.02 g. The highly performing group was constituted by the genotypes PL6 (20.72 g), PL22 (20.48 g) and PL23 (19.68 g), respectively. The group which showed the lowest 1000-grain weight was PL30 (9.68 g), PL32 (11.68 g) and PL14 (12.47 g), respectively (**Table 4.1**). These findings are with an agreement of Ganapati *et al.* (2020) for the maximum and minimum thousand grain weight in fine rice.

4.1.1.10 Days to 50% flowering

The days to 50% flowering in the advanced lines were measured from the number of days required after transplanting. Among all the advanced lines PL27 showed the earliest flowering range 74.67 days and PL18 showed latest flowering (93.00 days), respectively. The grand mean for days to 50% flower of all genotypes was 83.92 days. The group of genotypes that showed maximum days to flowering was constituted by PL18 (93.00 days), PL19 (90.00 days), PL20 (90.00 days), PL23 (90.00 days) and PL1 (89.67 days), respectively. The group of genotypes that took minimum days to flowering was constituted by PL27 (74.67), PL29 (76.00 days) and PL5 (76.33 days), respectively (**Table 4.1**). Considering all the genotypes PL27 (74.67 days) is superior to others and

PL18 (93.00 days) is inferior to others genotypes. Ajmer *et al.* (1979) and Roy *et al.* (1995) suggested that days to 50% flowering were positively correlated with grain yield.

4.1.1.11 Days to maturity

Early maturing advanced lines are desirable as they produce more yields per day and fit well in multiple cropping systems. Highly significant differences were noted among the advance line on the number of days from sowing to maturity. The range for days to maturity among all the genotypes varied from 99.00 days (PL5) to 130.00 days (PL29). The grand mean for days to maturity of all the genotypes was 110.02 days. The group of genotypes that showed maximum days to maturity was constituted by PL29 (130.00 days) and PL24 (129.00 days), respectively. The group of genotypes which showed the least number of days to maturity was constituted by PL5 (99.00 days) and PL27 (121.00 days), respectively (**Table 4.1**). The earlier ripening of some varieties tested was attributed to their varietal differences; others have shorter life span and attained physiological maturity stage earlier than the other varieties. Hence, these results suggest that the different varieties differ in their performance and adaptability to a certain environment (Bhuiyan *et al.,* 2014).

4.1.1.12 Harvest index

The mean harvest index of the advanced lines was recorded 31.62 percent and range varied from 26.71 percent (PL1) to 34.88 percent (PL5). The highly performing group included PL5 (34.88%), PL9 (34.69%) and PL15 (33.85%), respectively. Moreover, the group with least performance for this character was constituted by the genotypes PL1 (26.71%), PL25 (27.87%) and PL2 (28.68%), respectively (**Table 4.1**). In the present study, the advanced line PL5 (34.88%) is superior to all compared 32 lines for yield components. The yield increase of dwarf over tall lines mainly resulted from higher harvest index, while the yield increase of rice lines over the dwarf ones was mainly from higher biomass production (Jiang *et al.,* 2015). Yield differences among cultivars were due to HI. The superiority of rice genotypes for biomass over conventional varieties was reported widely (Kiniry *et al.,* 2001). And 10-20% superiority of hybrids for total biological yield and grain yield was reported by Blanco *et al.* (1990).

4.1.1.13 Grain yield /hill

Grain yield is a function of interplay of various yield components such as number of productive tillers, grains/panicle. The highest grain yield/hill (18.81 g/hill) was found in

PL6 and the lowest yield (9.06 g/hill) was recorded in PL27 (**Table 4.1**). These findings are with an agreement of Ganapati *et al.* (2020) for yield. Grain yield is the function of number of panicles/hill, number of fertile grains/panicle and 1000-grain weight. Sinha and Bhattaacharya (1980) observed that the genetic advance expressed as a percentage of the mean was highest for yield per plant.

4.1.2 Analysis of variance

The analysis of variance (ANOVA) for 13 quantitative characters viz plant height, productive tillers/hill, panicle length, fertile grains/panicle, sterile grains/panicle, panicle weight, sterility percentage, lodging percentage, 1000-grain weight, grain yield /hill, days to 50% flowering, days to maturity and harvest index were accomplished to assess the variability pertained for a particular character among the thirty-two rice genotypes. The sources of variation included genotype, replication and error presented in **Table 4.2**. It is observed that mean sum of squares of the varieties for all the characters were significant indicating significant variation present in all the genotypes. There was a little significant variation found among the three replications in all the characters. Similar results were reported by Bekele *et al.* (2013), Kumar *et al.* (2006), Salgotra *et al.* (2009) and Dhanwani *et al.* (2013). The mean squares for the advance line exhibited strong and significant differences in each of the selected characters and therefore, breeders could drive the breeding methods either selection or hybridization for the improvement of present yield status of the fine rice advance line. Development of high yielding varieties in almost every year by the rice breeders and by different commercial agencies are being culminated with exploring variability in the popular fine rice land races, that leads to erosion of these valuable rice germplasm.

4.1.3 Genetic Variability on the selected characters in fine rice

Different parameters studied such as genotypic variance (σ^2g), phenotypic variance (σ^2p), genotypic coefficient of variation (GCV %), phenotypic coefficient of variation the character's plant height (PH) 5.31 and 5.31; days to maturity (DTM) 6.19 and 6.12 respectively. The phenotypic coefficients of variation (PCV) were ranged from 5.31 for plant height (PH) to 33.85 for lodging percentage (LP), whereas genotypic coefficients of variation (GCV) were ranged from 5.31 for plant height (PH) to 33.70 for lodging

Table 4.2. Analysis of variance (Mean Squares) for yield and yield contributing characters in 32 lines of F_4 generation of fine rice

Sources of variation	df	PH	PTPH	PL	FGPP	SGPP	PW	SP	LP	TGW	DTF	DTM	HI	GYPH
Replication	2	13.158	0.723	0.141	175.877	0.095	0.0005	0.019	1.760	1.1103	0.166	0.791	0.249	1.079
Genotype	31	159.656**	3.130**	9.300**	1088.25**	60.635**	1.428**	8.817**	117.854**	27.0287 **	80.43**	137.095**	10.886**	153.146**
Error	62	0.365	0.145	0.066	1.094	0.312	0.0002	0.003	0.330	0.0546	1.284	1.135	0.035	0.016
CV(%)		7.35	10.84	8.12	11.87	11.23	6.46	14.72	15.31	5.24	8.09	7.85	10.05	17.78

Here,

1. PH=Plant height, 2.PTPH=Productive tillers/hill, 3.PL=Panicle length, 4.FGPP=Fertile grains/panicle, 5. SGPP=Sterile grains/panicle, 6.PW=Panicle weight, 7.SP=Sterility percentage, 8.LP=Lodging percentage, 9.TGW=Thousand grain weight, 10.DTF=Days to 50% flowering, 11.DTM=Days to maturity and 12.HI=Harvest index 13. GYPH=Grain yield /hill

*and **indicates significant at 5% (0.05) and 1% (0.01) level of probability percentage (LP), According to Subramanian and Menon (1973) PCV and GCV values more than 20% are regarded as high, whereas values less than 10% are considered to be low and values between 10% and 20% to be moderate. Based on this delineation, PCV and GCV values were high for for 1000 grain weight.

The current study suggests that phenotypic variance (δ^2p) and phenotypic coefficient variation (PCV) were higher than theirs corresponding genotypic variance (δ^2g) and genotypic coefficient of variation (GCV) respectively for all the characters studied, indicate that the expression of these characters was influenced by environment. Similar results were reported by Ogunbayo *et al.* (2014), Singh *et al.* (2014); Khatun *et al.* (2015); Rashid *et al.* (2017) in rice.

The estimates of heritability act as predictive instrument in expressing the reliability of phenotypic value. Therefore, high heritability helps in effective selection for a particular trait. Heritability was classified as low (below 30%), medium (30-60%) and high (above 60%) as suggested by Johnson *et al.* (1955). The traits studied in the present investigation expressed moderate to high heritability estimates ranging from 53.02% to 89.95%. Among the traits, high heritability was observed for plant height, fertile grains/panicle, panicle weight, sterility percentage, lodging percentage, 1000-grain weight, grain yield /hill. Similar results were earlier reported by Karthikeyan *et al.* (2009) for 1000-grain weight. The grain yield /hill was observed to possess the lowest heritability (53.02%). High heritability values indicate that the traits under study are less influenced by environment in their expression. The plant breeder, therefore, may make his selection safely on the basis of phenotypic expression of these traits in the individual plant by adopting simple selection methods.

The genetic advance is a useful indicator of the progress that can be expected as result of exercising selection on the pertinent population. Heritability in conjunction with genetic advance would give a more reliable index of selection value (Johnson *et al.,* 1955). The high value of GA was recorded with fertile grains/panicle followed by plant height, grain yield /hill, days to 50% flowering, days to maturity. Sabesan *et al.* (2009) proved the same results for plant height, grain yield /hill, days to 50% flowering, days to maturity. Genetic advance as percent mean expected (GAM) had a general range between 10.94 % for plant height and 69.14% for lodging percentage. Among the characters high values of GAM (>20%) were recorded for productive tillers/hill, fertile grains/panicle, sterile grains/panicle, panicle weight, sterility percentage, lodging percentage, thousand grain weight, grain yield /hill. It was moderate (10% to 20%) for plant height, panicle length, days to 50% flowering, days to maturity (**Table 4.3**).

The present study revealed high heritability accompanied with high genetic advance as percent of the mean for productive tillers /hill, fertile grains/panicle, sterile grains/panicle, panicle weight, and sterility percentage, lodging percentage, 1000-grain weight, grain yield /hill and moderate genetic advance as plant height, days to 50% flowering, days to maturity, harvest index. These results could be explained by additive gene action and their selection may be done in early generations. Similar findings on productive tillers /hill, fertile grains/panicle, sterile grains/panicle, panicle weight, and sterility percentage, lodging percentage, 1000-grain weight, grain yield /hill have been reported by Wolie *et al.* (2013) and Ogunbayo *et al.* (2014). The moderate heritability was being exhibited due to high environmental effects. Therefore, selection for this character might be effective in simple selection.

4.1.4 Estimation of correlation coefficients among all possible paired combinations

The genotypic and phenotypic correlations for yield and yield components are presented in **Table 4.4 and 4.5**. The genetic and phenotypic correlation coefficients among of rice yield and yield contributing traits of F_4 lines showed that most of the traits have higher phenotypic correlation coefficients than corresponding genotypic correlation coefficients (**Table 4.4 and 4.5**). A perusal of these results revealed phenotypic and genotypic correlations to be of similar direction and significance. However, phenotypic correlations had recorded a higher magnitude compared to genotypic correlations indicate the predominant effect of environment. Besides, Ganapati *et al.* (2014) reported that in character association analysis among grain yield and yield contributing characters in most of the cases, the genotypic correlation coefficient was higher than the respective phenotypic correlation coefficients. This indicates the suppressive effect of the environment modifying the phenotypic expression of these characters by reducing phenotypic correlation values. Similar results on productive tillers /hill, fertile grains/panicle, sterile grains/panicle, panicle weight, and sterility percentage, lodging percentage, 1000-grain weight, grain yield /hill were reported by Madhavilatha *et al.* (2005). Since the phenotypic relationship was affected by environment at phenotypic level, it resulted the low phenotypic correlation coefficients (Chaubey and Singh, 1994 and oojo *et al.*, 2006).

Table 4.3. Genetic parameters of different characters in F_4 generation of fine rice

Parameters	Mean range		MSg	Mse	бg	бp	GCV	PCV	GCV%	PCV%	H_2b	GA	GA%
	Min	Max											
PH	123.67	159.93	159.66	0.04	7.3	7.3	0.14	0.15	5.31	5.31	89.95	15.02	10.94
PTPH	4.90	8.97	3.14	0.15	1.0	1.07	0.15	0.16	14.76	15.80	77.21	1.91	28.39
PL	22.80	30.47	9.30	0.07	1.76	1.77	0.07	0.09	6.61	6.68	87.89	3.57	13.46
FGPP	126.73	198.37	108.26	1.1	19.04	19.07	0.10	0.12	12.09	12.11	89.61	39.15	24.88
SGPP	8.63	26.13	60.64	0.31	4.49	4.52	0.30	0.32	29.68	29.91	88.46	9.16	60.66
PW	1.92	4.87	1.43	0.00	0.69	0.69	0.20	0.23	22.69	22.7	89.95	1.42	46.74
SP	6.96	14.48	8.82	0.00	1.71	1.72	0.16	0.17	16.08	16.09	89.88	3.52	33.10
LP	7.00	30.33	117.86	0.33	6.26	6.29	0.34	0.35	33.71	33.85	89.16	12.83	69.14
TGW	9.68	20.73	27.03	0.06	3.0	3.01	0.17	0.19	18.71	18.77	89.39	6.15	38.44
DTF	74.67	93.00	80.43	1.29	5.14	5.26	0.06	0.07	6.12	6.27	85.35	10.33	12.31
DTM	99.00	130.00	137.1	1.14	6.73	6.82	0.05	0.06	6.12	6.20	87.55	13.69	12.45
HI	26.71	34.88	10.89	0.37	1.87	1.97	0.06	0.06	5.92	6.22	80.55	3.67	11.60
GYPH	8.06	18.81	153.15	0.02	7.14	7.15	0.33	0.34	32.53	32.54	53.02	14.71	67.00

Here,

PH=Plant height, PTPH=Productive tillers/hill, PL=Panicle length, FGPP=Fertile grains/panicle, SGPP=Sterile grains/panicle, PW=Panicle weight, SP=Sterility percentage, LP=Lodging percentage, TGW=Thousand grain weight, GYPH=Grain yield /hill, DTF=Days to 50% flowering, DTM=Days to maturity and HI=Harvest index σ_g= genotypic variance, σ_p= phenotypic variance, GCV= genotypic coefficient of variation, GCV%= genotypic coefficient of variation, PCV= phenotypic coefficient of variation, PCV%= phenotypic coefficient of variation GA= geneticadvance, GA%=genetic advance as percent of mean, h_2b=heritability(%), MSg= Mean standard genotype , MSe= Mean standard error

Plant height revealed significant positive association with lodging percentage (rg=0.398**, rp=0.325**) and revealed significant negative association with panicle weight (rg=-0.327**, rp=-0.539**) and grain yield /hill (rg=-0.514**, rp=-0.540**). Productive tillers /hill revealed significant positive association with grain yield /hill (rg=0.518**, rp=0.532**) and revealed significant negative association with lodging percentage (rg=-0.465**, rp=-0.543**). Panicle length revealed significant negative association with lodging percentage (rg=-0.479**, rp=-634**). Fertile grains/panicle revealed significant positive association with sterile grains/panicle (rg=0.683**, rp=0.698**), panicle weight (rg=0.750**, rp=0.762**), grain yield /hill (rg=0.631**, rp=753**) and harvest index (rg=0.411**, rp=0.402**) and revealed significant negative association with lodging percentage (rg=-0.427**, rp=-0.430**). Sterile grains/panicle revealed significant positive association with sterility percentage (rg=0.757**, rp=0.681**), and revealed significant negative association with lodging percentage (rg=-0.423**, rp=-0.431**). Panicle weight revealed significant positive association with 1000-grain weight (rg=0.795**, rp=615**), grain yield /hill (rg=0.863**, rp=0.864**) and revealed significant negative association with lodging percentage (rg=-0.613**, rp=-.0.618**). Lodging percentage revealed significant negative association with 1000-grain weight (rg=-0.609**, rp=-0.596**), grain yield /hill (rg=-0.860** rp=-0.724**) and harvest index (rg=-0.381** rp=-0.396**). 1000-grain weight significant positive association with grain yield /hill (rg=0.670**, rp=0.597**), harvest index (rg=0.211** rp=0.359**). Days to 50% flowering revealed significant positive association with harvest index (rg= 0.111**, rp=0.161**) both at genotypic and phenotypic levels.

The findings suggest that grain yield can be improved in these rice genotypes by using these traits as selection criteria in succeeding generations. The results got conformity with the findings of Nguyen *et al.* (2020) and Phukon *et al.* (2019) who showed positive correlations with these traits. Sterile grains / plant and lodging percentage were found negatively and significantly correlated with grain yield. Negative correlation coefficient of these two characteristics with grain yield indicates that low translocation of photosynthetic from vegetative parts to spikelets at the time of fertilization and tallness in rice reduced the grain yield due to less grain filling and seed formation which ultimately resulted lodging susceptibility (Zahid *et al.*, 2006). Therefore, priority should be given to these traits, while making selection for yield improvement. The findings are in agreement with the reports of Manikyaminnie *et al.* (2013) for productive tillers /hill

Table 4.4. Genotypic correlation coefficients (r_g) for all possible paired combinations in F_4 generation of fine rice

	PH	PTPH	PL	FGPP	SGPP	PW	SP	LP	TGW	DTF	DTM	HI	GYPH
PH		-0.049	-0.216	-0.228	-0.229	-0.327**	0.066	0.398**	-0.211	0.231	0.012	-0.15	-0.514**
PTPH			0.381	0.26	0.377	0.137	0.289	-0.465**	-0.012	-0.027	-0.017	0.121	0.518**
PL				0.254	0.236	0.335	0.253	-0.479**	0.192	0.049	-0.118	0.206*	0.371
FGPP					0.683**	0.750**	0.128	-0.427**	0.243	0.061	-0.119	0.411**	0.631**
SGPP						0.477**	0.757**	-0.423**	0.244	-0.03	-0.064	0.088	0.251
PW							0.126	-0.613**	0.795**	0.168	-0.182	0.541**	0.863**
SP								-0.255	0.166	-0.013	0.056	-0.147	-0.306
LP									-0.609**	-0.219	0.052	-0.381**	-0.860**
TGW										0.294	-0.023	0.211**	0.670**
DTF											0.302	0.111**	0.081
DTM												-0.201	-0.141
HI													0.498*

Here, PH=Plant height, PTPH=Productive tillers/hill, PL=Panicle length, FGPP=Fertile grains/panicle, SGPP=Sterile grains/panicle, PW=Panicle weight, SP=Sterility percentage, LP=Lodging percentage, TGW=Thousand grain weight, DTF=Days to 50% flowering, DTM=Days to maturity and HI=Harvest index, and GYPH=Grain yield /hill. * = 5% level of significance ** = 1% level of significance

Table 4.5. Phenotypic correlation coefficients (r_p) for all possible paired combinations in F_4 lines of fine rice

	PH	PTPH	PL	FGPP	SGPP	PW	SP	LP	TGW	DTF	DTM	HI	GYPH
PH		-0.287	-0.278	-0.393	-0.103	-0. 539**	0. 706	0.325**	-0.266	0. 321	0.022	-0.136	-0. 540**
PTPH			0.218	0.172	0. 439	0.104	0.344	-0.543**	0.022	-0.068	-0. 301	0. 519	0.532**
PL				0. 506	0. 432	0.328	0.167	-0.634**	0. 519*	0.106	-0.161	0.263	0.345
FGPP					0.698*	0.762**	0. 423	-0.430**	0.251	0. 406	-0. 215	0.402**	0. 753**
SGPP						0.649**	0. 681**	-0.431**	0.253	-0.017	-0.048	0.091	-0.562
PW							0.169	-0.618**	0.615**	0.172	-0.143	0.516*	0.864**
SP								-0.266	0.137	-0.013	0.058	-0.148	0.336
LP									-0.596**	-0.217	0.023	-0.396**	-0. 724**
TGW										0.321	-0.021	0.359**	0.597**
DTF											0.262	-0.161**	0.083
DTM												-0. 510	0.134
HI													0.623**

Here, PH=Plant height, PTPH=Productive tillers/hill, PL=Panicle length, FGPP=Fertile grains/panicle, SGPP=Sterile grains/panicle, PW=Panicle weight, SP=Sterility percentage, LP=Lodging percentage, TGW=Thousand grain weight, DTF=Days to 50% flowering, DTM=Days to maturity and HI=Harvest index and GYPH=Grain yield /hill, * = 5% level of significance ** = 1% level of significance and Sudharani *et al.* (2013) for number of fertile grains /panicle. The findings are in consonance with the reports of Yadav *et al.* (2010). In the present study, days to 50% flowering exhibited a positive but non-significant association with panicle length (Yolanda and Das, 1995) and days to maturity (Debchoudhary and Das, 1998), negative non- significant association was estimated for productive tillers /hill, which was opposite interpretation shown by Sawant *et al.* (1995). The results indicates a scope for simultaneous improvement of the traits. Similar results were reported by Sankar *et al.* (2006) and Singh *et al.* (2006).

The degree of correlation among the characters is an important factor especially in economic and complex character like yield. Steel and Torrie, (1984) stated that correlations are measures of the intensity of association between traits. The selection for one trait results in progress for all characters that are positively correlated and retrogress for traits that are negatively correlated. Plant breeders usually select for yield component traits which indirectly increase yield. The relationship between rice yield and its contributing characters has been studied widely at phenotypic level (Akinwale *et al.,* 2011; Hairmansis *et al.,* 2013; Sadeghi SM. 2011 and Ullah *et al.*, 2011). The grain yield is a complex trait, quantitative in nature and a combined function of a number of constituent traits. So, the selection for yield may not be much satisfying unless other yield component traits are taken into consideration (Ramya *et al*., 2012). Understanding of correlation between yield and yield components are basic and foremost effort to find out strategies for trait selection. Correlation between yield and its component traits has effectively been used in identifying useful traits as selection criteria to improve grain yield in rice (Saleh *et al.,* 2020; Hasan *et al.,* 2013; Akinwale *et al.,* 2011; Kole *et al.,* 2008; Mustafa and Elsheikh, 2007).

4.1.5 Path coefficient analysis on yield and other related characters in F_4 generation of fine rice

Path coefficient analysis permitted a thorough of understanding about the contribution of different characters by partitioning the correlation coefficients into components of direct and indirect effects (Laxuman *et al.,* 2011). Therefore, the contribution of correlated characters was partitioned into direct and indirect effects by path analysis **(Table 4.6).**

Rao *et al.* (1997) estimated cause and effect relations of yield and yield components in rice. Since genotypic correlation coefficients have more significant in developing the relationship than phenotypic correlation coefficients and phenotypic correlation coefficients was blended by environmental effects, only genotypic correlation coefficients were partitioned by path analysis to determine the direct and indirect effects of the contributing characters towards grain yield. Harvest index was excluded in path analysis because it has no effect on yield potential and it was calculated after harvesting the lines. From the path analysis **(Table 4.6)** it was revealed that 1000 grain weight exhibited the highest positive direct effect (0.843) to develop strong genotypic correlation coefficients with grain yield /hill. On the contrary, the highest negative direct effect on the development of a genotypic correlation with yield was resulted by sterility percentsge (-0.965) followed by lodging percentage (-0.821) and days to 50% flowering (-0.646). Path analysis revealed that plant height had negative direct effect (-0.319) on grain yield/hill (**Table 4.6**). It showed negligible negative indirect effect through days to maturity, sterility percentage. This finding was in agreement for plant height, productive tillers/hill, panicle length, fertile grains/panicle, sterile grains/panicle, panicle weight, sterility percentage, lodging percentage, thousand grain weight, grain yield /hill, days to 50% flowering, days to maturity and harvest index with the findings of Nguyen *et al.* (2020) and Phukon *et al.* (2019).

Productive tillers /hill had positive direct effect (0.303) on grain yield/hill (**Table 4.6**). It showed negligible positive indirect effect through sterile grains/panicle and showed negligible negetive indirect effect through panicle length. Panicle length had positive direct effect (0.151) on grain yield/hill (**Table 4.6**). It showed negligible positive indirect effect through productive tillers/hill and fertile grains/panicle and showed negligible negeitive indirect effect through sterility percentage. This finding was in agreement with the findings of Nguyen *et al.* (2020) and Phukon *et al.* (2019). Fertile grains/panicle had positive direct effect (0.381) on grain yield/hill (**Table 4.6**). It showed negligible positive indirect effect through plant height and showed negligible negetive indirect effect through days to maturity. This finding was in agreement with the findings of Nguyen *et al.* (2020) and Phukon *et al.* (2019). Sterile grains /panicle had negative direct effect (-0.112) on grain yield/hill (**Table 4.6**). It showed negligible negative indirect effect through panicle length, fertile grains/panicle and showed negligible positive indirect effect through days to maturity, sterility percentage. This finding was in agreement with the findings of Nguyen *et al.* (2020) and Phukon *et al.* (2019). Panicle weight had positive direct effect (0.313) on grain yield/hill (**Table 4.6**). Sterility percentage had negative direct effect (-0.965) on grain yield/hill (**Table 4.6**). Lodging percentage had negative direct effect (-0.821) on grain yield/hill (**Table 4.6**). It showed negligible positive indirect effect through 1000-grain weight, fertile grains/panicle, days to maturity and showed negligible negetive indirect effect through panicale weight. Thousand grain weight had positive direct effect (0.843) on grain yield/hill (**Table 4.6**). It showed negligible negative indirect effect through lodging percentage and showed negligible positive indirect effect through sterility percentage. This finding was in agreement with the findings of Nguyen *et al.* (2020) and Phukon *et al.* (2019). Days to 50% flowering had negative direct effect (-0.646) on grain yield/hill (**Table 4.6**). It showed negligible positive indirect effect through sterility percentage and showed negligible negetive indirect effect through productive tillers/hill. This finding was in agreement with the findings of Nguyen *et al.* (2020) and Phukon *et al.* (2019). Days to maturity had positive direct effect (0.148) on grain yield/hill (**Table 4.6**). It showed negligible negative indirect effect through plant height, panicle length, panicle weight and showed negligible positive indirect effect through lodding percentage. This finding was in agreement with the findings of Nguyen *et al.* (2020) and Phukon *et al.* (2019).

The residual effect, 0.1596 was converted as percentage and then the contribution of twelve component characters on grain yield was estimated by subtracting the residual effect from 100% as 83.97% (Singh and Chaudhary, 2010). Therefore, those characters having 15.96% effect were not included in this studied. However, the direct effects along with correlations of the characters and residual effect are diagrammatically presented for visual confirmation (**Figure 4.1).** Therefore, genotypic correlation of yield components with yield and path analysis of the components was considered to select the characters for the improvement of yield. Mustafa and Elsheikh (2007) made a study on path analysis for twelve characters and revealed that grains/panicle and panicle/m^2 were the important characters for selection in rice. Both genotypic and phenotypic correlation coefficients were initially estimated but path analysis was performed based on genotypic correlation coefficients where panicles/plant, test weight, straw weight and plant height were identified as vital characters to initiate any breeding exercise in rice (Kole *et al.,* 2008). Similarly, Sarawgi *et al.* (1997) studied ten characters in rice and found that grains/panicle, tillers/plant, panicles/plant, spikelet's fertility and panicle size were the desirable characters. Akhond *et al.* (1998) suggested that selection could be made mainly on panicles/hill and grains/panicle but a joint venture of correlation coefficients and path analysis on spikelets/panicle, days to 50% flowering and effective tillers/hill must be considered to develop a discriminant function for the improvement of yield potential in rice. Therefore, the simultaneous consideration of genotypic correlation coefficients of yield contributing characters and cause and effect analysis (path analysis) revealed that panicle length, fertile grains/panicle and 1000 grain weight might be considered to produce all possible selection indices for the improvement of grain yield in fine rice.

4.1.6 Analysis of genetic divergence based on yield and yield contributing characteristics

The analysis of variance revealed significant differences among the genotypes for all the characters (**Table 4.2**). Based on D^2 values, all the genotypes were grouped into five clusters using non-hierarchical Euclidean cluster analysis (**Table 4.7**). The use of Mahalanobis D^2 statistics for estimating genetic divergence has been emphasized by many workers (Roy and Ponwar, 1993; Ramya and Senthil Kumar, 2008). Hence, based on relative magnitude of D^2 statistics, the 32 F_4 genotypes of rice were grouped into five clusters as shown in **Table 4.7**. Maximum number of genotypes (twelve) were included in cluster III followed by cluster II with nine genotypes, cluster IV and V comprised with five and two genotypes respectively, cluster I included four genotypes. Sabesan *et al.,* (2009) and Banumathy *et al.,* (2010) reported that the advanced lines (F_4) from the same cross combination were distributed in different clusters which may be due to differential adaptation of parental lines in different agro-ecosystems.

Based on the values of principal component score 1 and 2 obtained from the PCA, a two-dimensional scatter diagram (Z1-Z2) using component score 1 as X-axis and component score 2 as Y-axis was constructed (**Figure 4.2).** The position of the genotypes in the scatter diagram was apparently distributed into five groups indicating the existence of considerable diversity among the genotypes. The clustering pattern confirmed the results obtained by divergence analysis in rice (Ahmed *et al.,* 2015).

Table 4.6. Genotypic path coefficient analysis of twelve characters on yield in fine rice advance line

Characters	PH	PTPH	PL	FGPP	SGPP	PW	SP	LP	TGW	DTF	DTM	GYPH
PH	**-0.319**	0.066	0.019	0.051	-0.012	0.004	-0.289	0.131	-0.103	0.025	-0.113	-0. 540**
PTPH	-0.209	**0.303**	-0.038	-0.312	0.181	0.391	0.277	-0.407	0.383	-0.025	-0.012	0.532**
PL	0.108	0.111	**0.151**	0.156	-0.019	0.335	-0.249	0.241	-0.292	-0.168	-0.029	0.345
FGPP	0.061	0.422	0.281	**0.381**	-0.021	-0.002	-0.501	0.349	-0.327	0.195	-0.085	0. 753**
SGPP	-0.042	-0.067	-0.027	-0.048	**-0.112**	-0.001	0.681	-0.326	0.527	-0.381	0.358	0.562**
PW	-0.039	-0.011	-0.031	0.116	0.004	**0.313**	0.131	-0.069	0.172	0.305	-0.027	0.864**
SP	0.172	-0.071	0.263	-0.157	0.634	0.503	**-0.965**	-0.725	0.07	0.154	0.458	0.336
LP	-0.031	-0.061	-0.027	-0.155	0.033	-0.002	0.511	**-0.821**	0.117	-0.323	0.035	-0. 724**
TGW	-0.023	-0.032	0.067	0.161	0.072	-0.003	0.521	-0.644	**0.843**	-0.392	0.027	0.597**
DTF	-0.044	-0.014	0.051	-0.079	0.054	0.051	0.571	-0.466	0.537	**-0.646**	0.068	0.083
DTM	-0.292	0.002	-0.034	-0.212	0.033	0.171	0.115	-0.189	0.346	-0.222	**0.148**	-0.134
Residual effect	0.1596											

Here, PH=Plant height, PTPH=Productive tillers/hill, PL=Panicle length, FGPP=Fertile grains/panicle, SGPP=Sterile grains/panicle, PW=Panicle weight, SP=Sterility percentage, LP=Lodging percentage, TGW=Thousand grain weight, DTF=Days to 50% flowering, DTM=Days to maturity and HI=Harvest index and GYPH=Grain yield /hill.

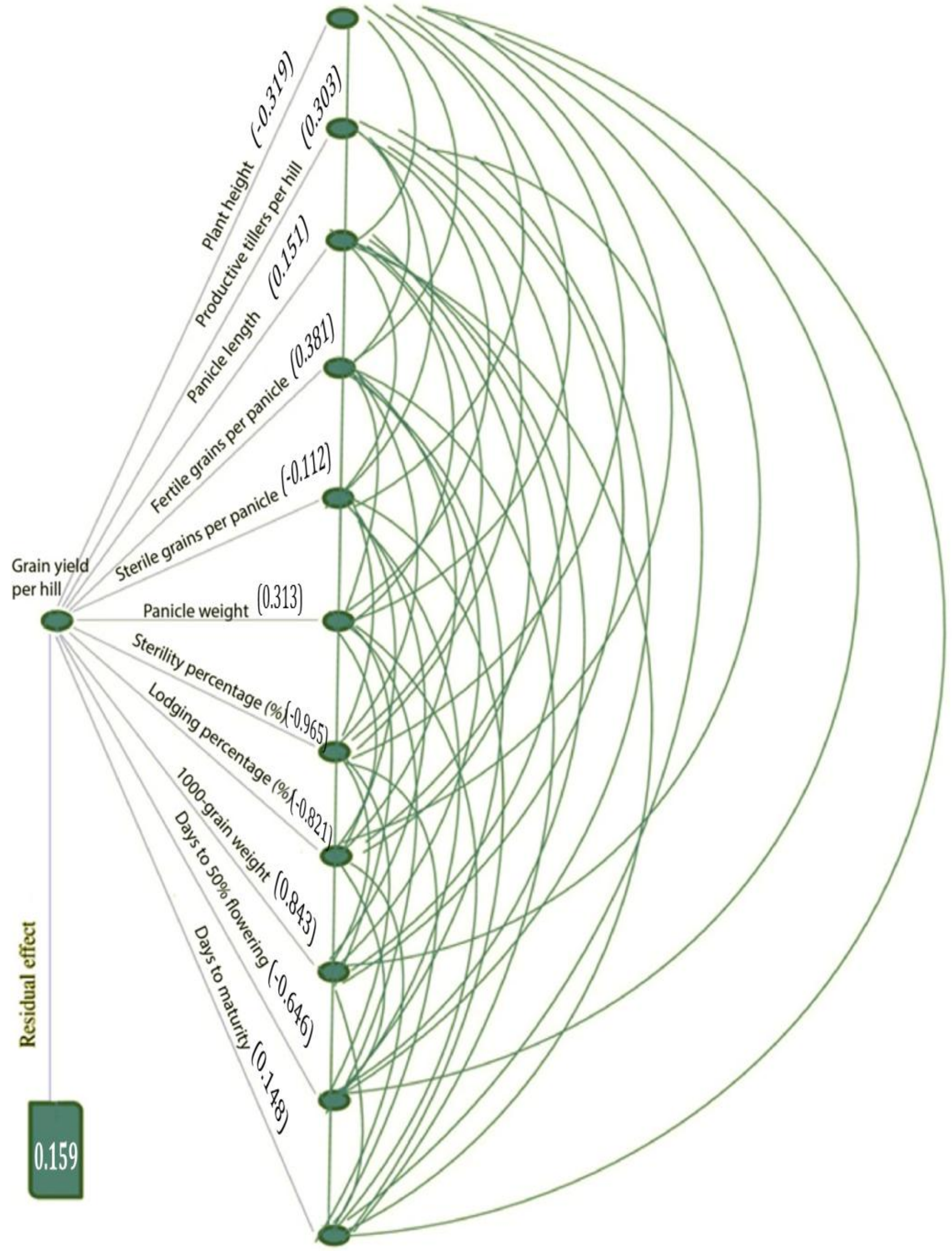


Figure 4.1. Genotypic path diagram for different characters on grain yield/hill

Table 4.7. Number of genotypes under different clusters

Clusters	No. of advanced lines	Name of the advanced lines
I	4	PL1, PL4, PL5, PL6
II	9	PL2, PL3, PL12, PL14, PL17, PL18, PL28, PL30, PL32
III	12	PL7 , PL8, PL9, PL10, PL11, PL15, PL16, PL20, PL22, PL23, PL26, PL31
IV	5	PL13, PL19, PL21, PL25, PL27
V	2	PL24, PL29

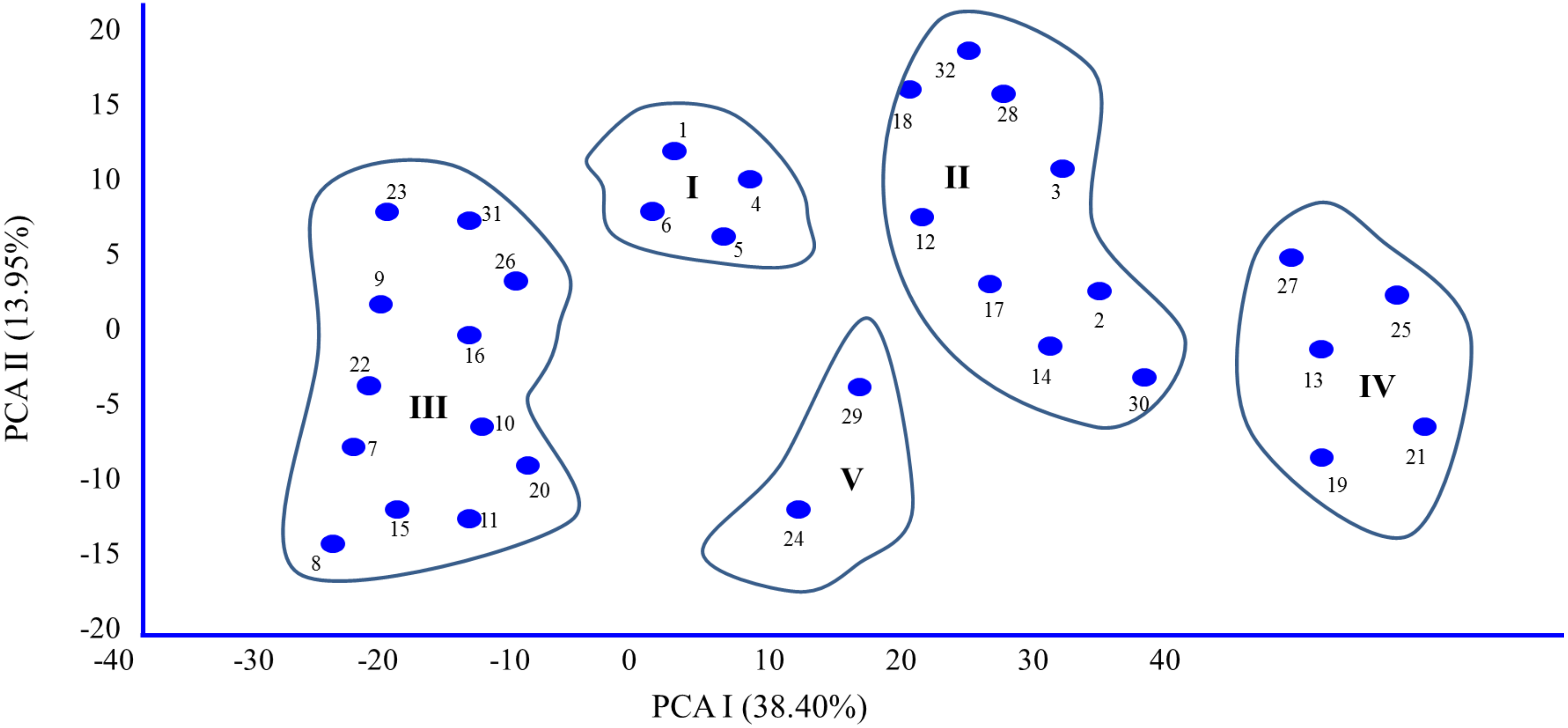


Figure 4.2. Cluster diagram of 32 lines of fine rice developed from D^2 statistics and PCA I and PCA II values

Table 4.8. Inter and intra cluster distances (D^2 values) of different characters in F_4 lines of fine rice

	I	II	III	IV	V
I	**1. 298**				
II	8. 785	**0. 678**			
III	2. 3 07	6. 480	**0. 811**		
IV	10.408	2. 258	6.201	**1. 219**	
V	13.534	11.853	10.071	12.045	**1. 322**

The bold figures along the diagonal are intracluster distances and other values are intercluster distances

The intra and inter cluster average distances among five clusters were variable as indicated in **Table 4.8**. The highest intra-cluster distance was recorded for cluster IV (1.219) followed by cluster V (1.322) and cluster I (1.298) indicated genetic diversity among the genotypes belonging to these clusters. The genotypes belonging to the highest intra-cluster distance in the parenthesis (cluster IV) might develop good segregants by crossing the genotypes of the cluster. Kishore *et al.* (2007) and Chandra *et al.* (2007) reported that the clusters having low intra-cluster distances may not evolve good segregants upon hybridization.

The highest inter-cluster distance was observed between clusters I and V (13.534) suggested wide diversity between these clusters followed by cluster IV and V (12.045), cluster II and V (11.853) and cluster I and IV (10.408). Therefore, advanced lines belonging to these clusters may be further used in hybridization program for the improvement of rice. Crosses involving parents belonging to the most divergent clusters would be expected to manifest maximum heterosis and wide variability of genetic architecture (Souroush *et al.,* 2004). The least inter- cluster distance was observed between clusters II and IV (2.258) followed by clusters I and III (2.307) indicated close relationship between the genotypes of these clusters and hence, may not be emphasized upon to be used in hybridization programs.

The contribution of individual trait to the divergence among genotypes is presented in **Table 4.9**. Fertile grains/panicle contributed maximum towards genetic divergence (16.378%) followed by sterile grains/panicle (15.691%), panicle length (11.034%) and 1000 grain weight (10.694%). Remaining traits had little contribution towards genetic divergence and hence, they were of less importance. Since the advanced lines with narrow genetic base are increasingly vulnerable to diseases and adverse climatic changes, availability of the genetically diverse genotypes for hybridization programs become more important. Since fertile grains/panicle, sterile grains/panicle, panicle length, 1000 grain weight contributed maximum towards the genetic divergence, we may initiate direct selection based on correlation with grain yield of these two characteristics for diversity purpose.

Table 4.9. Contributions of different characters for genetic diversity in F_4 lines of fine rice

Character	Contribution (%) in genetic diversity
PH	1.945
PTPH	9.088
PL	11.034
FGPP	16.378
SGPP	15.691
PW	0.628
SP	3.075
LP	3.982
TGW	10.694
DTF	7.988
DTM	4.214
HI	8.789
GYPH	6.494

Here,

PH=Plant height, PTPH=Productive tillers/hill, PL=Panicle length, FGPP=Fertile grains/panicle, SGPP=Sterile grains/panicle, PW=Panicle weight, SP=Sterility percentage, LP=Lodging percentage, TGW=Thousand grain weight, DTF=Days to 50% flowering, DTM=Days to maturity, HI=Harvest index and GYPH=Grain yield /hill

4.1.7 Principal Component Analysis (PCA)

The result of the principal component analysis (PCA) explained relative contribution of traits to the genetic diversity of the rice collection **(Table 4.10)**. The cumulative variance of 78.94% by the first six axes with Eigen value of > 1.0 indicates that the identified traits within the axes exhibited great influence on the phenotype of germplasm lines. In this study, it is better to choose the criteria used by Clifford and Stephenson (1975), Guei *et al.* (2005) suggested that the first three principal components were often the most important in reflecting the variation patterns among the accessions, and the characters associated with these are more useful in differentiating accessions. According to the criteria, the first three components accounted for more than 63.45 % of total variation giving a clear idea of the structure underlying the variables analyzed. However, the criterion chosen by Raji (2002) to determine the cut off limit for the coefficients of the proper vectors was treated as coefficient greater than 0.3 as having a large effect to be considered important, while traits having a coefficient less than 0.3 were considered not to have important effects on the overall variation observed in the present study.

The distribution of advanced lines based on first and second principal component exhibits the phenotypic variation among the population and explains how they widely dispersed along both the axes. PCA of quantitative traits found that, the first principal component accounted for 38.40 % to the total variability, where by some traits were contributed positively and some traits were contributed negatively and the traits with coefficients greater than 0.3 were panicle weight (0.4017), lodging percentage (-0.3836) and grain yield /hill (0.4252). The second principal component accounted for 13.95 % to the total variability. The variables contributing most positively were fertile grains/panicle (0.4680), 1000 grain weight (0.6174) and the variables contributing most negatively were plant height (-0.3538). The third component accounted for 11.10% to the variance, in which the variable days to 50% flowering (-0.6935), days to maturity (-0.4174) contributed negatively. Fourth principal component accounted for 8.12% of variance in the total variability by productive tillers/hill (0.3452), panicle length (0.3049), days to maturity (0.5346) as positively. The fifth principal component accounted for 7.37% of the total variation. Plant height (-0.4946) contributed the highest negative loadings but productive tillers/hill (0.5482), days to maturity (0.3488) contributed positively in the variation.

Table 4.10. Principle component analysis for different characters of advanced lines

Characters	PC1	PC2	PC3	PC4	PC5
PH	-0.1921	-0.3538	-0.3143	-0.4801	-0.4946
PTPH	0.2022	0.3082	0.1470	0.3452	0.5482
PL	0.2297	0.1284	0.1218	0.3049	0.1831
FGPP	0.3175	0.4680	0.1377	0.1906	0.2034
SGPP	0.3011	-0.0491	-0.0400	-0.2543	-0.2297
PW	0.4017	-0.2212	-0.0982	-0.1966	0.1457
SP	0.1835	-0.2432	-0.0930	-0.1687	-0.1319
LP	-0.3836	0.0408	0.1084	-0.2664	-0.1557
TGW	0.3065	0.6174	0.3500	0.1415	0.0935
DTF	0.0529	-0.0594	-0.6935	0.0209	-0.2199
DTM	-0.0574	0.1021	-0.4174	0.5346	0.3488
HI	0.2347	0.1839	0.1910	0.1064	0.2843
GYPH	0.3065	0.0565	0.0012	0.0254	0.0682
Eigen Values	4.9916	1.8132	1.4434	1.0553	0.9586
Standard deviation	2.2342	1.3466	1.2014	1.0273	0.9791
Proportion of Variance	0.3840	0.1395	0.1110	0.0812	0.0737
Cumulative Proportion	0.3840	0.5234	0.6345	0.7157	0.7894

Here,

PH=Plant height, PTPH=Productive tillers/hill, PL=Panicle length, FGPP=Fertile grains/panicle, SGPP=Sterile grains/panicle, PW=Panicle weight, SP=Sterility percentage, LP=Lodging percentage, TGW=Thousand grain weight, DTF=Days to 50% flowering, DTM=Days to maturity, HI=Harvest index and GYPH=Grain yield /hill, Thus, the prominent characters coming together in different principal components and contributing towards explaining the variability have the tendency to remain together. This may be kept into consideration during utilization of these characters in breeding program. The phenotypic value of each trait measures the importance and contribution of each component to total variance, whereas each coefficient of proper vectors indicates the degree of contribution of every original variable with which each principal component is associated. Characters with high variability are expected to provide high level of gene transfer during breeding programs (Devi *et al.*, 2020; Varthini, 2014; Gana *et al.,* 2013; Gana, 2006).

The diversity was also supported by the appreciable amount of variation among the cluster means for different characters (**Table 4.11**). Cluster IV showed maximum cluster means for plant height (143.05) and lodging percentage (25.80). Cluster I showed maximum cluster means for productive tillers /hill (7.29), panicle length (27.43), fertile grains /panicle (184.66), sterile grains/panicle (24.20), panicle weight (3.72), sterility percentage (13.14) and grain yield /hill (29.18). Cluster III showed maximum cluster means for 1000-grain weight (18.07), days to 50% flowering (86.81) and harvest index (32.78). Cluster V showed maximum cluster means for days to maturity (129.50). Amegan *et al*. (2020) and Anjali *et al.* (2014) opined that ellite genotypes hold great promise as lines for obtaining elite lines through hybridization and to create further variability for these characters.

Table 4.11. Cluster Means of different characters in F_4 generation of fine rice

Characters	I	II	III	IV	V
PH	133.47	139.85	135.53	143.05	130.38
PTPH	7.29	7.15	7.04	5.17	6.20
PL	27.43	26.62	27.32	24.29	25.73
FGPP	184.66	149.25	163.93	136.18	153.70
SGPP	13.52	24.20	15.11	10.65	15.32
PW	3.72	2.45	3.49	2.57	2.83
SP	10.54	13.14	10.40	9.47	10.83
LP	15.67	21.89	13.97	25.80	19.00
TGW	16.86	13.26	18.07	15.72	15.20
DTF	80.25	83.67	86.81	82.93	77.50
DTM	103.67	110.89	109.58	106.80	129.50
HI	31.74	30.68	32.78	30.31	31.98
GYPH	29.86	17.39	26.61	13.98	20.07

Here,

PH=Plant height, PTPH=Productive tillers/hill, PL=Panicle length, FGPP=Fertile grains/panicle, SGPP=Sterile grains/panicle, PW=Panicle weight, SP=Sterility percentage, LP=Lodging percentage, TGW=Thousand grain weight, DTF=Days to 50% flowering, DTM=Days to maturity, HI=Harvest index and GYPH=Grain yield /hill

Figure 4.3. Raising seedling of the 32 advanced lines at F_4 generation in ideal seed bed at Plant breeding research field, HSTU, Dinajpur with my Supervisor.

Figure 4.4. Vegetative phage of the 32 advanced lines at F_4 generation at Plant breeding research field, HSTU, Dinajpur.

4.2 Experiment II: Assessment of selection response and realized heritability from F_4 to F_5 generation

Narrow sense heritability (h^2) is a key concept in quantitative genetics which heritability is technically defined as the ratio of additive genetic variance (the variance of breeding values) to the total phenotypic variance ($h^2 = \sigma^2 a / \sigma^2 p$) and represents the fraction of the phenotypic variation of a quantitative trait that is transmissible from one generation to the next; h^2 determines the degree of resemblance between relatives and the rate of response to artificial and natural selection; therefore, estimating h^2 is often the first step in applied plant breeding programs as well as evolutionary genetics studies. h^2 is also the upper limit for the accuracy of predicting phenotypes from molecular marker data (genomic prediction), and hence is required knowledge for common diseases in organisms in the context of precision medicine (Yang *et al.*, 2010). However, based on univariate and multivariate analyses thirteen characters were included in the study.

Based on individual performances, advanced lines for plant height, productive tillers /hill, panicle length, fertile grains /panicle, sterile grains /panicle, panicle weight, sterility percentage, lodging percentage, 1000-grain weight, days to 50% flowering, days to maturity and harvest index were the component of yield performance of 32 F_4 plants, selected and evaluated in $F_{4:5}$ generations. Heritability was mainly studied to determine how much variation in the phenotype in a population was due to genetic variation between individuals in that population. To develop superior genotype, there should be high mean values with adequate genetic variability, could be achieved in segregating populations like F_4 and F_5.

The highest realized heritability was found in grain yield /hill (93.58) with selection differential (1.87) and response to selection (1.75) followed by productive tillers /hill (91.45) with selection differential (1.04) and response to selection (0.95) and days to maturity (90) with selection differential (-0.1) and response to selection (-0.09) (**Table 4.12**). These values raveled that the offspring of the selected parents differ widely from the original population. On the contrary, the lowest heritability was found in days to flowering (58.33) with selection differential (0.12) and response to selection (0.07) followed by plant height (62.56) with selection differential (-2.03) and response to selection (-1.27) (**Table 4.12**).

Table 4.12. Selection response and realized heritability in advanced generation (F_5) of fine rice

Characters	10% selection mean (F_4)	Field Mean (F_4)	Field Mean (F_5)	Selection differential (S)	Response to selection (R)	R÷S	h^2 =(R÷S)×100
PH	135.31	137.34	136.07	-2.03	-1.27	0.63	62.56
PTPH	7.8	6.70	7.70	1.04	0.95	0.91	91.35
PL	28.47	26.57	27.95	1.9	1.38	0.73	72.63
FGPP	159.40	157.40	158.90	2.04	1.52	0.75	74.51
SGPP	12.90	15.10	13.40	-2.14	-1.64	0.77	76.64
PW	4.11	3.04	3.87	1.07	0.83	0.78	77.57
SP	8.88	10.66	9.25	-1.78	-1.41	0.79	79.21
LP	16.74	18.57	17.15	-1.83	-1.42	0.78	77.60
TGW	17.38	16.02	16.99	1.36	0.97	0.71	71.32
DTF	84.40	83.90	84.00	0.12	0.07	0.58	58.33
DTM	109.90	110.00	109.90	-0.10	-0.09	0.90	90
HI	33.28	31.62	33.15	1.66	1.53	0.93	92.17
GYPH	17.83	15.96	17.71	1.87	1.75	0.94	93.58

Here, PH=Plant height, PTPH=Productive tillers/hill, PL=Panicle length, FGPP=Fertile grains/panicle, SGPP=Sterile grains/panicle, PW=Panicle weight, SP=Sterility percentage, LP=Lodging percentage, TGW=Thousand grain weight, DTF=Days to 50% flowering, DTM=Days to maturity, HI=Harvest index, and GYPH=Grain yield /hill,. R= Response to selection, S= Selection differential, 10% selection mean (F_4) =Mean of the parents, Field Mean (F_4) =Mean of the starting population and Field Mean (F_5) =Mean of the offspring.

These values revealed that the offspring of the selected parents differed not so widely from the original population. Panicle length, fertile grains/panicle, sterile grains/panicle, panicle weight, sterility percentage, lodging percentage and 1000-grain weight showed the realized heritability of 72.63, 74.51, 76.64, 77.57, 79.21, 77.59 and 71.32 with selection differential 1.9, 2.04, -2.14, 1.07, -1.78, -1.83 and 1.36 and response to selection 1.38, 1.52, -1.64, 0.83, -1.41, -1.42 and 0.97, respectively (**Table 4.12**). The findings reported by Sun (1979); Subrahmanyam *et al.* (1986); Surek and Beser (2005); Kumar *et al.* (2009) revealed that selection for heritable characters like 1000-grain weight was effective in early generation in rice because most of the studied characters in F_4 generation showed negative direction in selection response and realized heritability. Although, observed realized responses for the trait might be explained by genotypic differences between the parents and were utilized in breeding programme. Similar results were previously reported by Mishra *et al.* (1993). The present study showed that selection differential had positive value for the studied traits except for 1000-grain weight in F_5. This finding concluded that genetic drift and inbreeding was low (Falconer and Mackay, 1996). The highest and positive realized heritability was reported between F_2 generations for number of grains (Kato, 1997). An extension of the classical methods to use restricted maximum likelihood approach (Patterson and Thompson, 1971) for variance decomposition, both in synthetic and wild populations, provided variance-covariance of phenotypic records is specified by use of a relationship matrix (i.e., complete pedigree linking respective records to the base population) and assumptions of the infinitesimal model hold for the assessment of realized heritability (Sorensen and Kennedy, 1984).

4.3 Experiment III: Assessment of aroma in F_5 generation of fine rice

4.3.1 Assessment of aroma in fine rice

Aromatic rice is known for its better quality flavor and taste, which is caused by the chemical compound 2AP (2-acetyl-1-pyrroline) and proline is the precursor of this aromatic compound. Aroma was assessed from both leaves and grain powder (**Figure 4.5**). A number of oxidation products have been tagged as likely causing stale flavor. However, the amounts of oxidation products, singly or collectively, that need to be present for rice to have stale or rancid flavor have not been established. Only one compound, 2-acetyl-1-pyrroline (2AP; popcorn aroma) has been confirmed to contribute a characteristic aroma. Furthermore, 2AP is the only volatile compound in which the relationship between its concentration in rice and sensory intensity has been established. The challenges of measuring aroma and flavor instrumentally and by human sensory panels and reviewed research examining the effects of genetics, preharvest and postharvest factors on volatile compound profiles and the aroma and flavor of cooked rice.

While the texture of the rice grain may not be directly linked to flavor, it is one of the most important eating quality characteristics of rice. In addition, cooking temperature is known to affect the flavor of many foods, and so the flavor compound profile of cooked rice would be altered by reducing the cooking temperature. The texture and cooking temperature of rice are directly influenced by the properties of rice starch. Fine rice starch has a semi-crystalline structure which is disrupted by cooking, transforming the starch into a softer edible gel like material. Because it is associated with the cooking time and texture of cooked rice, the temperature at which rice starch gelatinizes is an important component of rice eating quality.

The advance line, PL16 scored the highest rank (8.75) in fresh leaf and 8.83 in grain powder followed by PL12 (7.94), PL13 (7.94) and PL18 (7.94) in grain powder and PL14 (7.75) and PL13 (7.63) in fresh leaf and the lowest rank (3.39) scored by PL6 in grain powder and 2.52 by PL5 in fresh leaf followed by PL5 (3.94) in grain powder and PL6 (3.30), PL10 (3.52) and PL31 (3.75) in fresh leaf. The highest yield /hill 18.35 was scored by PL29, followed by PL23 (18.13), PL11 (18.11) and PL31 (18.07) where the lowest yield /hill in PL18 (13.26) followed by PL13 (13.46) PL32 (14.24) (**Table 4.13**). These findings were in agreement with the findings of Setyaningsih *et al.* (2019) and Golam *et al.* (2011).

Table 4.13. Assessment of aroma in F_5 generation of fine rice

Genotype	Aroma in fresh leaf	Aroma in grain powder	Yield /hill (g)
PL1	7.16 ab	6.39 c	14.96 cd
PL2	6.86 c	6.95 bc	14.94 cd
PL3	6.08 c	6.94 bc	15.85 bc
PL4	5.85 d	7.05 b	16.03 b
PL5	2.52 g	3.94 e	16.23 b
PL6	3.30 f	3.39 f	15.81 bc
PL7	5.19 d	6.5 c	14.83 d
PL8	4.64 e	4.83 e	15.08 c
PL9	5.53 d	5.72 d	16.13 b
PL10	3.52 e	4.94 de	15.15 c
PL11	4.53 d	5.28 d	18.12 a
PL12	7.19 ab	7.94 ab	16.03 b
PL13	7.63 ab	7.94 ab	13.46 e
PL14	7.75 ab	7.72 b	14.69 d
PL15	7.19 ab	7.06 b	16.47 b
PL16	8.75 a	8.83 a	15.41 c
PL17	7.41 ab	7.39 b	15.41 c
PL18	6.97 bc	7.94 ab	13.26 e
PL19	6.08 c	6.39 c	15.97 bc
PL20	5.41 d	6.61 c	15.22 c
PL21	5.86 d	6.61 c	16.93 b
PL22	6.97 bc	7.5 b	15.42 c
PL23	6.3 c	7.61 b	18.13 a
PL24	7.19 ab	7.17 b	15.15 c
PL25	6.75 c	7.17 b	15.75 c
PL26	7.53 ab	7.28 b	15.07 c
PL27	6.86 c	7.17 b	15.08 c
PL28	6.08 c	6.39 c	15.87 bc
PL29	6.19 c	7.28 b	18.35 a
PL30	6.74 c	7.61 b	15.63 c
PL31	3.75 e	4.61 e	18.07 a
PL32	5.63 d	7.17 b	14.24 d

The mean values having same letter(s) did not differ significantly at 5% level of probability

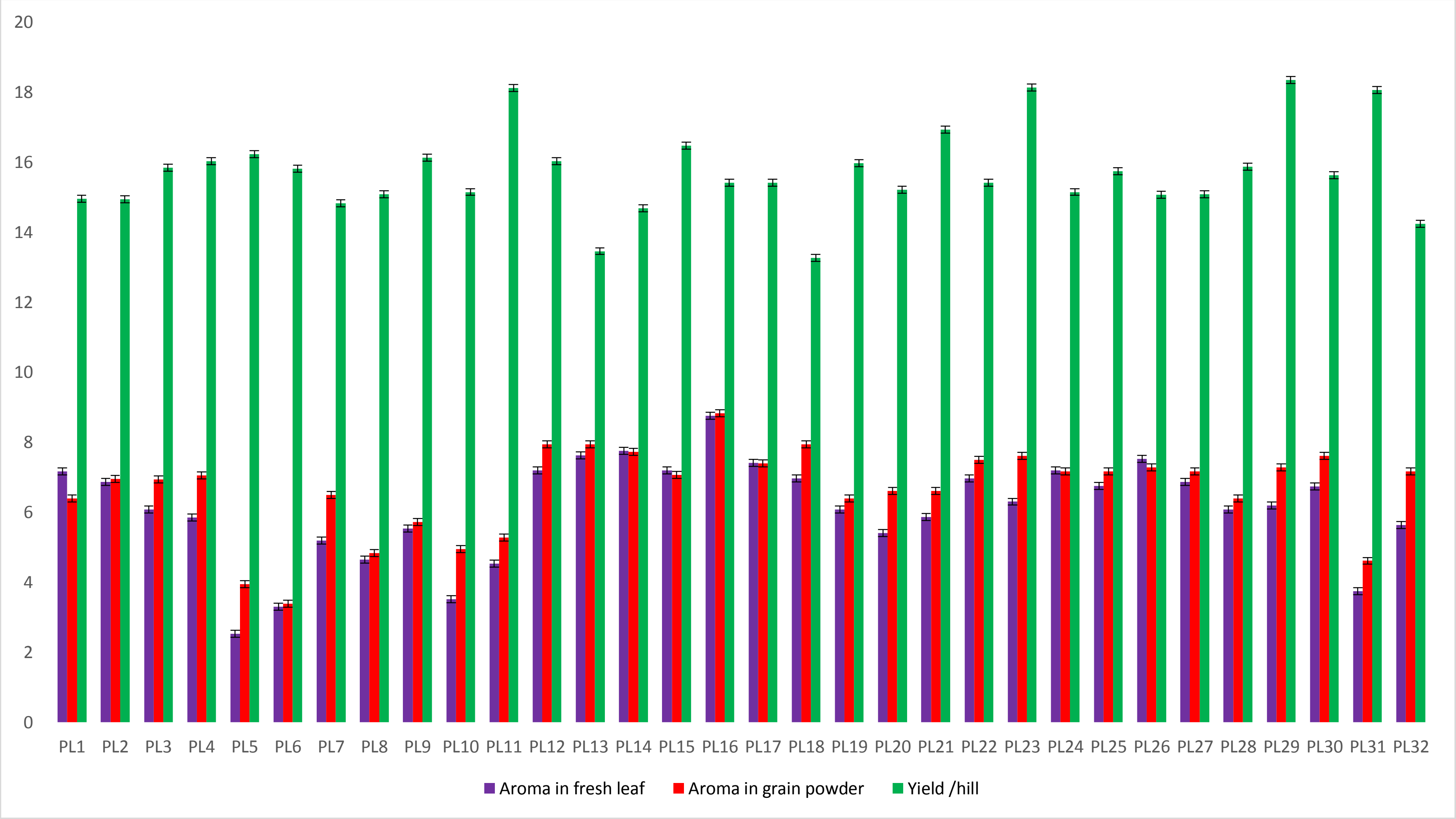


Figure 4.5: Relationship between aroma content and yield /hill.

Figure 4.6. Young green leaves and crashed grains of F_5 generation assessed aroma by sensory method constituted by a six member's panel.

Figure 4.7. I with my co-supervisor in laboratory assessed and observed aroma in young green leaves and crashed grains of F_5 generation by sensory method.

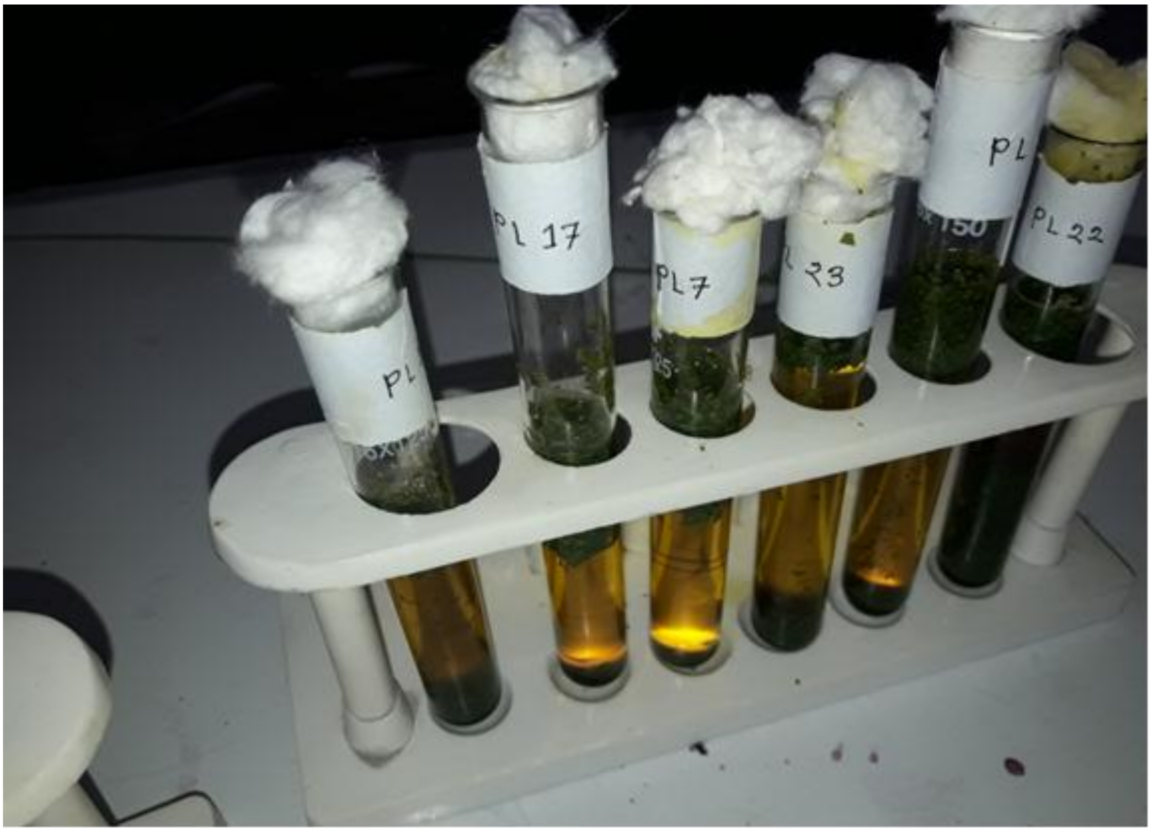


Figure 4.8. Green leaves and crashed grains of the 32 pure lines (PL) at of F_5 generation assessed aroma by sensory method constituted by a six member's panel.

4.3.2 Comparison of variabilty in F_4 and F_5 generations

The variability for four different characters selected based on significant correlation coefficients was compared between F_4 and F_5 generations. The table 4.14 revealed that variabilities of different characters a little bit of increased in F_5 generation compared to F_4. However characterwise variabilities stated below-

Productive tillers/hill

The range of the character has been slightly increase (5.00- 9.02) in F_5 generation. Both GCV and PCV values were not remarkably changed in advancing the generation but heritability has remarkably increased in F_5 with 82.36, suggests next generation developed fron selected population would offer significant gain for the character.

Fertile grains/panicle

The character, fertile grains per panicle did not improve apparently with advancing the generation. The GCV and PCV values appeared very close to each other in F_4 and F_5 generations, suggests less effect of environment upon expression of the character.

Table 4.14. Comparison of variability for important characters of F_4 and F_5 generations

	Mean				GCV		PCV		H^2b	
	F_4		F_5		F_4	F_5	F_4	F_5	F_4	F_5
	Min	Max	Min	Max						
PTPH	4.90	8.97	5.00	9.02	0.053	0.051	0.054	0.052	77.21	82.36
FGPP	126.73	198.37	126.90	200.15	0.121	0.120	0.123	0.121	89.61	90.27
PW	1.92	4.87	1.98	5.21	0.227	0.224	0.229	0.225	89.95	91.84
TGW	9.68	20.37	10.07	19.59	0.187	0.182	0.189	0.187	89.39	92.48

Heritability values were higher both in F_4 and F_5 generatins, indicates rapid fixation of alleles responsible for the expression of the character.

Panicle weight (g)

The degree of increase of the character after advancing from F_4 to F_5 was not apparently noticiable, inaddition, GCV and PCV were almost similar trend in both the generations. The important parameter of variabilty is the broad sense heritability which very slowly increased in F_5 genetation (91.84%). If the breeders choose the character, the resultant product, grain yield might improve in next generation of selection.

Thousand grain weight(g)

In general, 1000-grain weight was low as compared to coarse grain rice, the range of the character was estimated from 10.07-19.59g in F_5 that was 9.68 -20.37g in F_4.Both GCV and PCV values decreased in F_5 compared to F_4, suggests less effect of environment upon expression of the character. The heritability vulue remarkably increased in F_5 (92.48%) that was 89.39% in F_4, indicates rapid fixation of heterozygous allelic pairs with progressing the generation.

4.4 Experiment IV: Stability analysis of F_6 generation over the locations

4.4.1 Pooled analysis

Considering mean performances, significant and positive genotypic correlation coefficient with grain yield and direct effects of the characters 10 advance line (F_6) were selected from 32 (F_4) line for G x E interaction. A total of ten fine rice selected from 32 advanced lines through application of different statistical tools were employed to study G x E interaction following by the model proposed by Eberhart and Russel (1966 in three locations, viz., Dinajpur, Faridpur and Nilphamari. The advanced lines (F_6) differently responded to changing of growing conditions as projected by significant mean square values for each of the selected characters. Significant differences among the lines were observed for fertile grains/panicle and yield/hill (g) when environment was considered linear, indicate significant variation among the lines for these two characters. Environment + advance line × environment (linear) was significant for all the characters except for 1000-grain weight. Testing by pooled error, it was observed that the lines were differentially responsive for all the characters studied. Among the lines, PL12 had shown significant interaction effect against the thirteen characters, suggesting that the line was locally adapted and highly receptive in performance with changing the growing conditions (**Table 4.15**).

All sources of variations were quantified against the pooled error **(Table 4.15)**. Accordingly, highly significant differences among the lines were observed for all the characters except 1000-grain weight and environment had predominantly influenced all the characters also except 1000-grain weight. Therefore, 1000-grain weight was stable over the environmental modifications for the selected lines. Also there was highly significant difference between advanced lines × environment interaction for all the characters excluding sterility percentage and panicle weight. Moreover, heterogeneity between regressions for mean squares was highly significant for plant height and yield/hill. The significant mean squares both for heterogeneity between regression and reminder against yield/hill also indicated strong influence on growing conditions on yield potential of the advanced lines. It was evident that the model of analysis proclaimed significant genetic basis of response and stability for the evaluated lines. Besides, significant differential changes were displayed by the lines due to environmental variation in three locations. In breeders' eyes in three locations the performance of ten fine rice advanced lines on the selected quantitative thirteen characters was better in

Plant Breeding Research Field, HSTU, Dinajpur followed by Nilphamari and Faridpur. The inputs like fertilizer, irrigation and pesticide application and other management practices were utmost appropriate and judicious in three locations plots. However, Eberhart and Russell (1966) defined a stable genotype as the one which showed high mean yield, regression co-efficient (bi) around unity and deviation from regression (s^2di) near to zero. Accordingly, the mean along with corresponding regression coefficient was considered for evaluating the line stability and deviation from regression of each line was for response. Considering response and stability of the lines based on Ebarhart and Russel (1966), the line, PL13 produced the highest yield/hill (18.85 g) and regression coefficient was around unity (1.11) with deviation from regression of 0.46, indicate that PL13 was the most stable among the advanced lines (**Table 4.16**). The developed line, PL16 produced a reasonable yield (18.10 g) and its regression coefficient was close to unity (bi=0.32) and deviation from regression was very nearer to zero (s^2di=0.12), hence the line was also stable irrespective of growing conditions and was suitable for general adaptation. Another advanced line, PL12 produced intermediate yield (11.93 g) and both bi and s^2di were in acceptable boundaries, therefore, this line could be promoted well for cultivation by the farmers (**Table 4.16).** The yield of PL1 was average but its deviation from regression was far away from zero, hence, the line intended to respond favorably to better environment like Plant Breeding Research Field, Dinajpur and would be produced poor yield in unfavorable growing condition and in a comparative view, PL15 was better than PL1. The lower average yield over the locations was obtained from PL24 (11.80 g) and it had average stability (bi=0.74) but far distance calculated from s^2di=1.55, indicate highly responsive and instability of the PL24 line. As the line had high aroma and acceptable cooking quality, this fragrance rice may be incorporated in the future breeding programs for the improvement of fine rice. The line, PL26 produced average high yield (13.21 g) but its regression coefficient was higher than unity (bi=1.41) and deviation from regression (s^2di) was 0.69, so, the advanced lines responded well under a favorable environment.

At the end of this investigation, it may be concluded that among the fine rice advanced lines, PL2, PL12, PL15 and PL26 may effectively be integrated in fine rice breeding exercises for their improvement as all as these lines may be forwarded to cultivate by the farmers. Besides, the advanced lines PL13 and PL17 may be incorporated in breeding programs due to their attractive grain and flavor qualities.

Table 4.15. Pooled analysis of variance for 13 characters of fine rice advanced lines (Eberhart and Russell model)

Sources of variation	df	Plant height (cm)	Productive tillers/hill	Panicle length (cm)	Fertile grains/ panicle	Sterile grains/ panicle	Panicle weight (g)	Sterility percentage (%)	Lodging percentage (%)	1000-grain weight (g)	Days to 50% flowering	Days to maturity	Harvest index (%)	Grain yield/hill (g)
Advance line	9	11.33**	41.55*	283.02**	970.25**	240.27**	213.02**	150.45**	65.15**	35.40**	730.05**	1125.10**	70.25**	79.65**
Env.+C×Env. (linear)	20	9.71*	35.69*	90.82	1070.10**	90.12**	78.82	76.52*	80.60**	36.61	675.55**	881.33**	52.10**	48.30**
Env.(Linear)	1	22.52*	29.81	102.31	345.89*	107.19	92.31	111.75	104.75**	91.34	100.10	180.20	95.89*	99.11**
C×Env. (linear)	9	7.30	9.26	27.61	68.65	38.65	21.61	43.27	44.79	27.17	153.00	65.50	58.65	53.91**
Pooled deviation	20	3.51	12.12	32.31	46.58*	16.54	25.39	21.88	17.25	21.83	85.20	70.85	16.58	11.80
PL 1	2	3.44	11.50**	18.69*	38.25*	12.26*	10.69*	37.08*	112.90**	13.75*	55.11*	98.91**	48.25**	50.20**
PL 2	2	7.07**	9.45*	21.81*	41.10*	21.17*	19.81*	30.55*	91.85*	9.25	64.65**	65.29**	41.10*	41.61*
PL 12	2	10.61**	7.53*	26.27**	25.10*	15.13*	16.27**	54.25**	180.45**	18.65*	40.05**	39.14*	35.10*	37.05*
PL 13	2	4.78*	3.31	31.15**	39.63*	22.63*	24.15**	40.75*	40.55	12.50	70.30**	41.41*	49.63*	43.80**
PL 15	2	3.79*	8.06*	18.90*	18.09	11.12	12.90*	28.64*	25.20	15.85*	45.60*	35.00	28.09	23.55
PL 16	2	8.05**	5.43	15.59*	15.72	9.02	11.59*	19.23	18.35	16.05*	51.92*	42.14*	25.72	30.25*
PL 17	2	7.19**	4.65	9.23	19.58*	5.52	9.03	32.11*	10.11	8.35	45.90*	27.54	49.58*	50.15**
PL 22	2	2.12	2.90	18.65*	35.45*	12.45*	13.65*	50.96*	9.95	11.45	59.20*	25.60	45.45*	45.60**
PL 24	2	1.96	1.09	25.03**	30.90*	17.40*	21.03**	30.51*	19.30	19.50*	61.65**	39.11*	40.90*	26.10**
PL 26	2	5.88**	4.51	21.07*	24.46*	14.06*	13.07*	28.27	12.61	8.33	30.12	21.66	34.46*	35.05**
Pooled error	72	1.05	2.11	4.85	5.12	1.52	2.25	8.77	18.60	3.25	12.20	11.95	7.12	8.50

Table 4.16. Stability parameters for thirteen characters of fine rice advanced lines

Advance lines	Item	Plant height (cm)	Productive tillers/hill	Panicle length (cm)	Fertile grains/ panicle	Sterile grains/ panicle	Panicle weight (g)	Sterility percentage (%)	Lodging percentage (%)	1000-grain weight (g)	Days to 50% flowering	Days to maturity	Harvest index (%)	Grain yield/hill (g)
PL 1	Mean	142.25	11.67	27.78	157.75	22.71	3.78	14.46	19.67	10.87	114.22	144.75	27.43	16.12
	bi	0.29	0.84	0.43	-1.09	0.13	0.23	0.66	0.38	0.02	0.85	0.93	0.17	0.87
	s^2di	4.88	0.90	3.12	0.40	0.72	0.12	-14.11	0.72	0.87	1.32	3.86	1.53	1.03
PL 2	Mean	139.0	13.45	25.97	165.30	22.07	3.97	18.65	8.90	10.90	112.98	144.18	29.19	13.10
	bi	0.10	0.88	0.23	0.65	0.13	0.43	0.43	0.53	0.52	0.62	0.88	0.92	0.92
	s^2di	0.65	0.07	0.09	0.29	0.79	0.19	0.63	0.22	0.41	0.32	0.86	0.16	0.16
PL 12	Mean	136.80	10.36	29.75	167.70	22.05	4.75	9.15	7.03	13.90	115.55	143.40	32.16	11.93
	bi	0.75	0.23	0.28	0.08	0.24	0.18	0.52	0.75	0.63	0.14	0.85	0.70	0.70
	s^2di	0.62	0.02	0.38	0.60	0.31	0.68	0.13	1.07	0.27	0.92	0.10	0.33	0.13
PL 13	Mean	142.25	10.61	27.80	153.40	20.82	3.22	8.90	3.96	14.80	109.42	141.67	30.85	18.85
	bi	0.58	0.92	0.58	0.75	0.28	0.58	0.59	0.73	0.38	0.68	0.61	1.01	1.11
	s^2di	0.39	0.13	0.25	0.15	0.24	0.15	0.14	0.35	0.34	0.26	0.39	0.41	0.46
PL 15	Mean	136.20	12.33	27.20	145.54	23.22	3.20	13.65	8.90	10.12	119.80	145.94	34.92	15.88
	bi	0.90	0.52	0.15	0.74	0.35	0.05	0.84	0.20	0.31	0.82	0.57	0.28	0.28
	s^2di	0.10	0.39	0.35	0.32	0.38	0.15	0.29	0.45	0.75	0.65	0.33	0.45	0.65

Table 4.16. Stability parameters for thirteen characters of fine rice (cont'd.)

Advance line (Place of collection)	Item	Plant height (cm)	Productive tillers/hill	Panicle length (cm)	Fertile grains/ panicle	Sterile grains/ panicle	Panicle weight (g)	Sterility percentage (%)	Lodging percentage (%)	1000-grain weight (g)	Days to 50% flowering	Days to maturity	Harvest index (%)	Grain yield/hill (g)
PL 16	Mean	138.11	13.06	24.86	154.12	19.86	3.16	16.15	10.25	12.65	114.40	140.70	32.34	18.10
	bi	0.45	0.09	0.85	0.34	0.85	0.35	0.76	0.15	0.80	0.42	0.27	0.32	0.59
	s^2di	0.13	0.17	0.94	0.36	0.64	0.54	2.55	0.65	0.61	0.60	0.42	0.12	0.08
PL 17	Mean	145.31	10.90	27.84	161.23	17.84	3.84	11.21	11.75	10.94	114.12	146.95	30.54	13.69
	bi	0.22	0.28	0.91	0.62	0.91	0.81	0.72	0.52	0.85	0.59	0.74	1.08	1.38
	s^2di	0.25	-0.25	0.76	0.74	0.73	0.66	-8.34	0.66	0.46	0.24	2.97	0.43	0.40
PL 22	Mean	133.80	14.60	26.91	180.54	27.11	4.21	9.56	13.87	14.12	117.60	144.71	34.68	17.19
	bi	0.41	4.12	1.28	0.60	0.68	1.73	0.52	0.39	0.83	0.37	0.73	0.24	0.90
	s^2di	0.90	-2.51	0.44	0.45	0.44	0.72	4.76	0.51	0.58	0.76	0.40	0.85	5.25
PL 24	Mean	140.20	10.83	25.64	157.05	25.11	3.69	8.70	11.25	11.70	112.54	143.40	32.80	11.80
	bi	0.65	1.50	1.13	0.37	0.43	0.93	0.85	0.25	0.30	0.41	0.14	0.54	0.74
	s^2di	3.51	0.03	1.11	0.76	0.19	0.98	0.32	0.30	0.21	0.85	2.62	0.95	1.55
PL 26	Mean	150.65	12.51	25.50	161.45	26.20	4.52	8.62	13.04	14.26	117.70	148.20	32.29	13.21
	bi	0.62	0.64	0.33	0.77	0.62	0.71	0.51	0.92	0.33	0.16	0.36	0.91	1.41
	s^2di	0.24	0.73	0.43	0.52	0.51	0.27	0.63	0.33	0.20	0.50	0.54	0.89	0.69

4.4.2 Environmental and phenotypic indices assessment

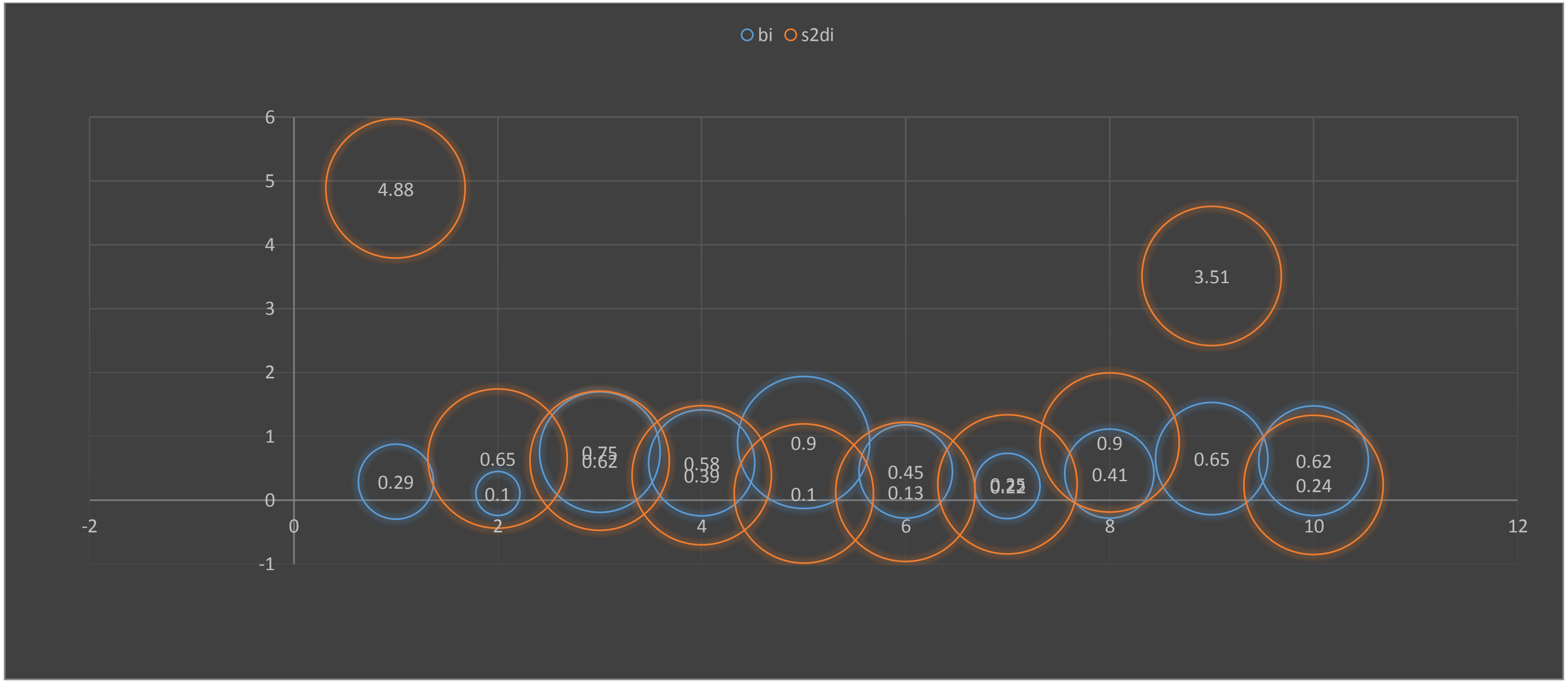
Plant height, productive tillers/hill, panicle length, fertile grains/panicle, sterile grains/panicle, panicle weight, sterility percentage, lodging percentage, 1000-grain weight, grain yield /hill, days to 50% flowering, days to maturity and harvest index of PL1, PL2, PL12, PL13, PL15, PL16, PL17, PL22, PL24 and PL26 lines were estimated in three locations at the same time to assessed the genotype × environment interaction over each of the location and compared the interaction among the locations.

4.4.2.1 Plant height

The mean of plant height of each of the three locations were 142.869 (Dinajpur), 139.812 (Nilphamari) and 138.69 (Faridpur). And the mean of each line over these three locations were PL1 (142.25), PL2 (139.0), PL12 (136.80), PL13 (142.25), PL15 (136.20), PL16 (138.11), PL17 (145.31), PL22 (133.80), PL24 (140.20), PL26 (150.65) **(Table 4.17)**. In case of environmental index, the highest positive value was found 2.412 in Dinajpur and the lowest negative value -1.767 in Faridpur where -0.645 in Nilphamari was moderate but negative. That means Dinajpur was the most suitable environment, Faridpur was the worst and Nilphamari was the moderate but bad environment for the corresponding genotypes in case of plant height **(Table 4.17)**. Also considerable differences were found in the values of phenotypic index for each of the lines over the three locations. The highest positive value was found in PL22 (6.657) followed by PL15 (4.257), PL12 (3.657), PL16 (2.347), PL2 (1.457) and PL24 (0.257) that means these lines were more stable and less sensitive for the three environments and the lowest negative value was found in PL26 (-10.193) followed by PL17 (-4.853), PL1 (-1.793) and PL13 (-1.793) that mean these lines were less stable and more sensitive for the three environments **(Table 4.17)**. According to Eberhart and Russell model (1966), when a variety with unit regression coefficient (bi=1) and deviation not significantly different from zero (s^2di=0) is said to be the stable one. So PL2, PL13, PL16 and PL26 were comparatively stable than others **(Figure 4.9).**

Table 4.17. Environmental and phenotypic indices assessment for plant height

Advanced lines	Dinajpur	Nilfhamari	Faridpur	Total	Mean	Phenotypic index (Grand mean - mean)
PL 1	144.35	142.15	140.25	426.75	142.25	-1.793
PL 2	142.62	138.71	135.67	417.00	139.00	1.457
PL 12	138.41	135.37	136.62	410.40	136.80	3.657
PL 13	144.53	142.89	139.33	426.75	142.25	-1.793
PL 15	139.08	135.66	133.86	408.60	136.20	4.257
PL 16	140.75	137.88	135.70	414.33	138.11	2.347
PL 17	148.06	144.29	143.58	435.93	145.31	-4.853
PL 22	135.06	132.18	134.16	401.40	133.80	6.657
PL 24	143.09	139.68	137.83	420.60	140.20	0.257
PL 26	152.74	149.31	149.90	451.95	150.65	-10.193
Mean	142.869 (X_D)	139.812 (X_N)	138.69 (X_F)	421.371	140.457 (Grand mean)	
Environmental index (X_D/ X_N/ X_F – Grand mean)	2.412	-0.645	-1.767			

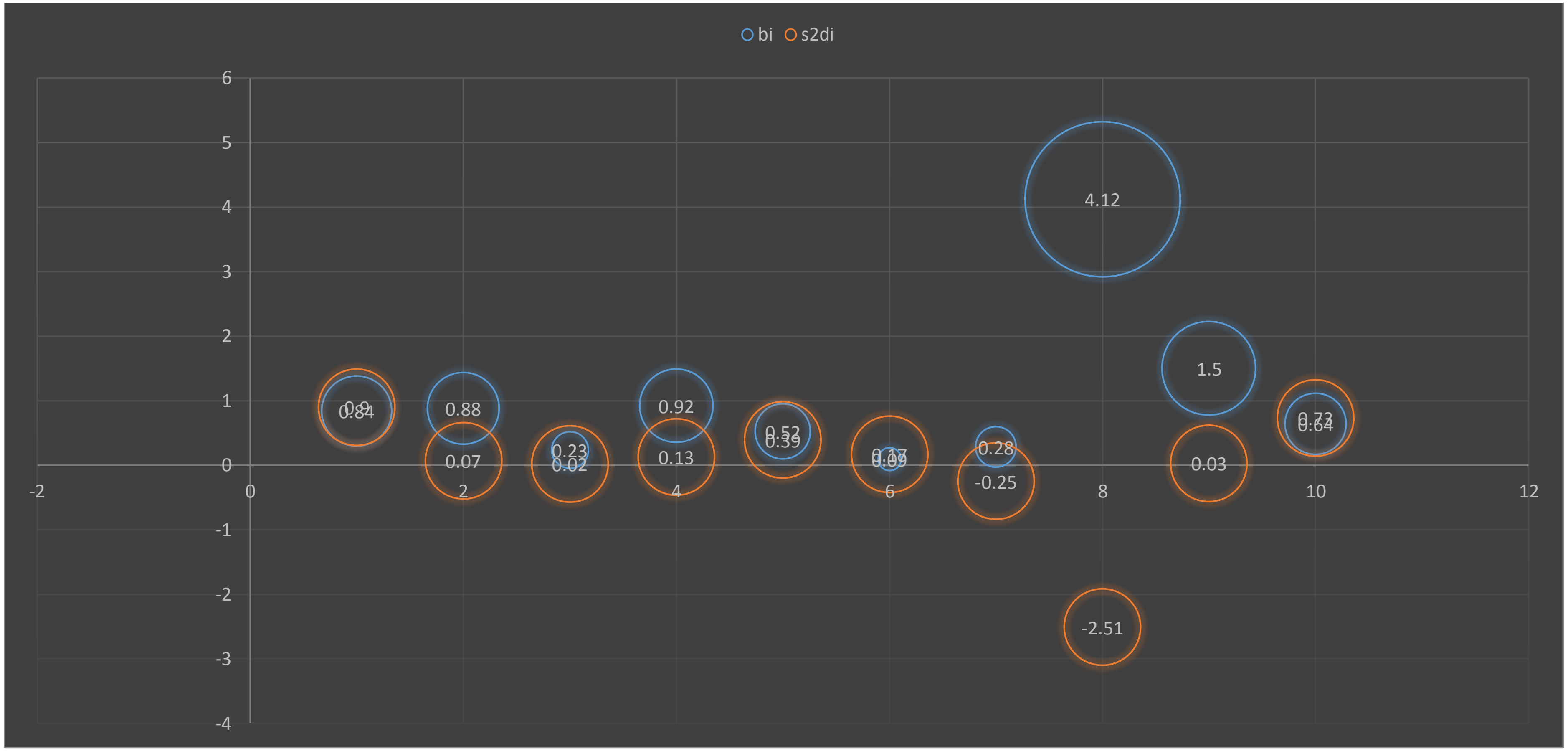


Here, in X-axis 1=PL1, 2=PL2, 3=PL12, 3=PL13, 4=PL15, 5=PL16, 7=PL17, 8=PL22, 9=PL24 and 10=PL26

Figure 4.9. Graphical representation of regression coefficient (bi) and deviation from regression (s^2di) of 10 genotypes in plant height.

Table 4.18. Environmental and phenotypic indices assessment for productive tillers/hill

Advanced lines	Dinajpur	Nilphamari	Faridpur	Total	Mean	Phenotypic index (Grand mean – mean)
PL 1	13.40	11.12	10.49	35.01	11.67	0.362
PL 2	16.55	12.04	11.76	40.35	13.45	-1.418
PL 12	12.71	10.05	8.32	31.08	10.36	1.672
PL 13	13.28	10.00	8.55	31.83	10.61	1.422
PL 15	13.91	12.05	11.03	36.99	12.33	-0.298
PL 16	15.65	12.87	10.66	39.18	13.06	-1.028
PL 17	13.04	9.88	9.78	32.70	10.90	1.132
PL 22	16.65	14.90	12.25	43.80	14.60	-2.568
PL 24	13.42	10.54	8.53	32.49	10.83	1.202
PL 26	14.44	12.12	10.97	37.53	12.51	-0.478
Mean	14.305 (X_D)	11.557 (X_N)	10.234 (X_F)	36.096	12.032 (Grand mean)	
Environmental index (X_D/ X_N/ X_F – Grand mean)	2.273	-0.475	-1.798			



Here, in X-axis 1=PL1, 2=PL2, 3=PL12, 3=PL13, 4=PL15, 5=PL16, 7=PL17, 8=PL22, 9=PL24 and 10=PL26

Figure 4.10. Graphical representation of regression coefficient (bi) and deviation from regression (s^2di) of 10 genotypes in productive tillers/hill.

4.4.2.2 Productive tillers/hill

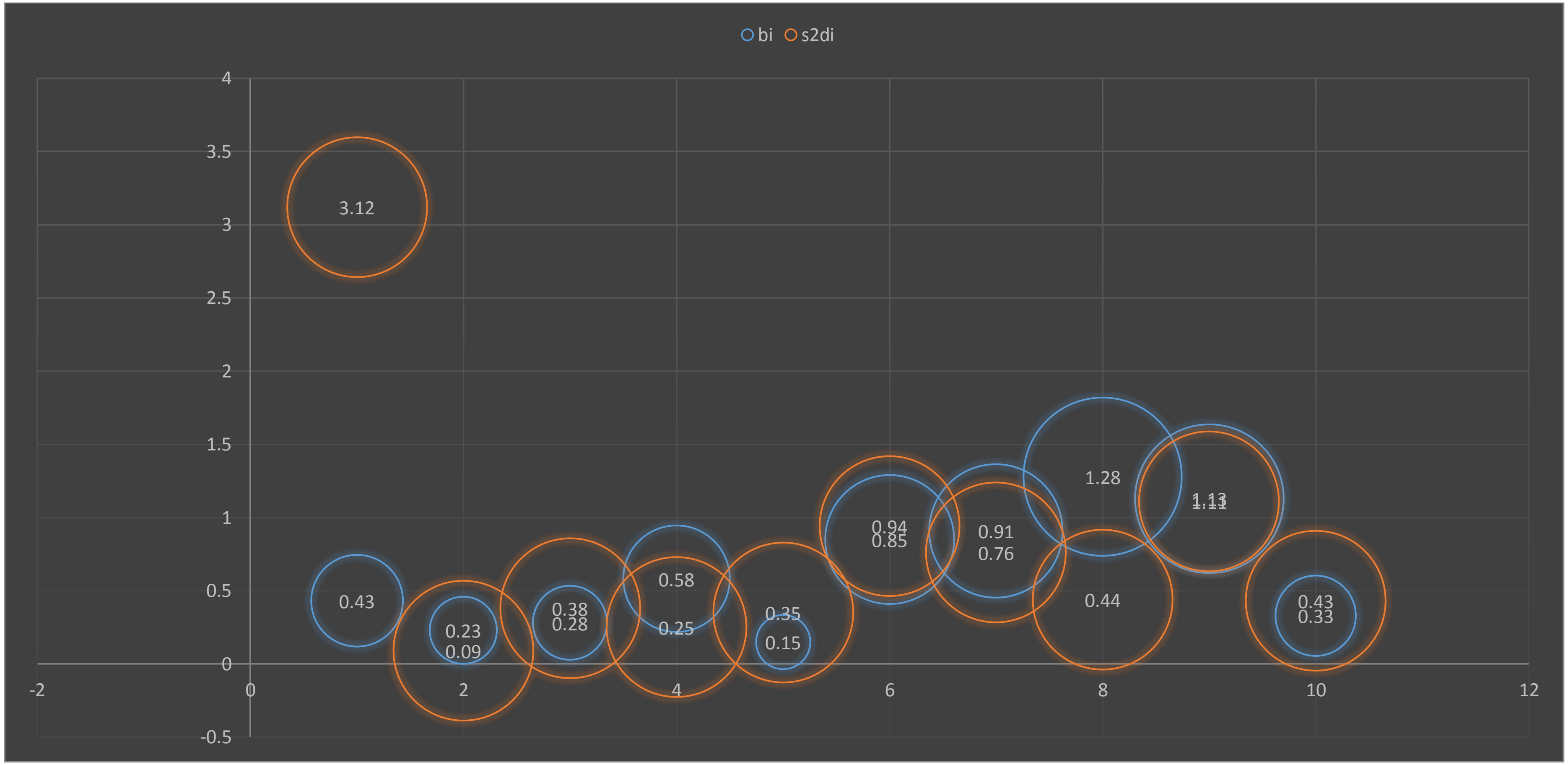
The mean of productive tillers/hill of each of the three locations were 14.305 (Dinajpur), 11.557 (Nilphamari) and 10.234 (Faridpur). And the mean of each line over these three locations were PL1 (11.67), PL2 (13.45), PL12 (10.36), PL13 (10.61), PL15 (12.33), PL16 (13.06), PL17 (10.90), PL22 (14.60), PL24 (10.83), PL26 (12.51) **(Table 4.18)**. In case of environmental index, the highest positive value was found 2.273 in Dinajpur and the lowest negative value -1.798 in Faridpur where -0.475 in Nilphamari was moderate but negative. That means Dinajpur was the most suitable environment, Faridpur was the worst and Nilphamari was the moderate but bad environment for the corresponding genotypes in case of productive tillers/hill **(Table 4.18)**. Also considerable differences were found in the values of phenotypic index for each of the line over the three locations. The highest positive value was found in PL12 (1.672) followed by PL15 (1.422), PL24 (1.202), PL17 (1.132) and PL24 (0.362) that means these lines were more stable and less sensitive for the three environments and the lowest negative value was found in PL22 (-2.568) followed by PL2 (-1.418), PL16 (-1.028), PL26 (-0.478) and PL15 (-0.298) that means these lines were less stable and more sensitive for the three environments in case of productive tillers/hill **(Table 4.18)**. According to Eberhart and Russell model (1966), when a variety with unit regression coefficient (bi=1) and deviation not significantly different from zero (s^2di=0) is said to be the stable one. So PL12, PL15 and PL26 were comparatively stable than others **(Figure 4.10).**

4.4.2.3 Panicle length

The mean of panicle length of each of the three locations were 29.655 (Dinajpur), 26.937 (Nilphamari) and 24.183 (Faridpur). And the mean of each advance line over these three locations were PL1 (27.78), PL2 (25.97), PL12 (29.75), PL13 (27.80), PL15 (27.20), PL16 (24.86), PL17 (27.84), PL22 (26.91), PL24 (25.64), PL26 (25.50) **(Table 4.19)**. In case of environmental index, the highest positive value was found 2.73 in Dinajpur and the lowest negative value -2.742 in Faridpur where 0.012 in Nilphamari was moderate. That means Dinajpur was the most suitable environment, Faridpur was the worst and Nilphamari was the moderately suitable for the corresponding genotypes in case of panicle length **(Table 4.19)**. Also considerable differences were found in the values of phenotypic index for each of the advance line over the three locations. The highest positive value was found in PL16 (2.065) followed by PL26 (1.425), PL24 (1.285), PL2 (0.955)

Table 4.19. Environmental and phenotypic indices assessment for panicle length

Advanced lines	**Dinajpur**	**Nilphamari**	**Faridpur**	**Total**	**Mean**	**Phenotypic index (Grand mean – mean)**
PL 1	30.05	27.00	26.29	83.34	27.78	-0.855
PL 2	28.16	25.88	23.87	77.91	25.97	0.955
PL 12	33.06	30.12	26.07	89.25	29.75	-2.825
PL 13	31.54	26.76	25.10	83.40	27.80	-0.875
PL 15	30.00	28.04	23.56	81.60	27.20	-0.275
PL 16	27.92	25.75	20.91	74.58	24.86	2.065
PL 17	30.11	27.72	25.69	83.52	27.84	-0.915
PL 22	28.95	27.73	24.05	80.73	26.91	0.015
PL 24	28.46	25.79	22.67	76.92	25.64	1.285
PL 26	28.30	24.58	23.62	76.50	25.50	1.425
Mean	29.655 (X_D)	26.937 (X_N)	24.183 (X_F)	80.775	26.925 (Grand mean)	
Environmental index (X_D/ X_N/ X_F – Grand mean)	2.73	0.012	-2.742			

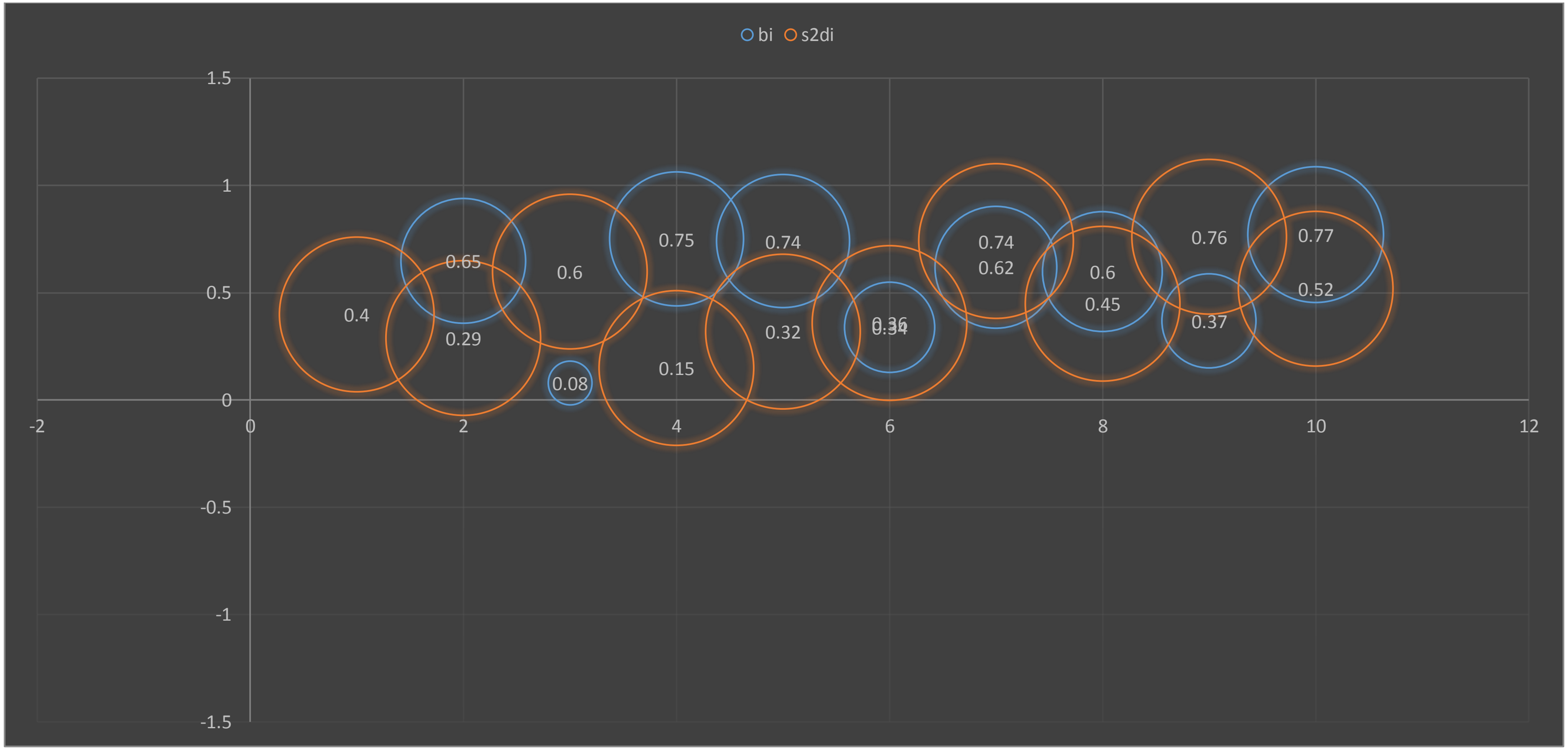


Here, in X-axis 1=PL1, 2=PL2, 3=PL12, 3=PL13, 4=PL15, 5=PL16, 7=PL17, 8=PL22, 9=PL24 and 10=PL26

Figure 4.11. Graphical representation of regression coefficient (bi) and deviation from regression (s^2di) of 10 genotypes in panicle length.

Table 4.20. Environmental and phenotypic indices assessment for fertile grains/panicle

Advanced lines	Dinajpur	Nilphamari	Faridpur	Total	Mean	Phenotypic index (Grand mean – mean)
PL 1	160.5	157.26	155.49	473.25	157.75	2.658
PL 2	167.13	165.2	163.57	495.9	165.3	-4.892
PL 12	170.72	166.45	165.93	503.1	167.7	-7.292
PL 13	155.3	153.5	151.4	460.2	153.4	7.008
PL 15	147.89	145.15	143.58	436.62	145.54	14.868
PL 16	156.6	155.24	150.52	462.36	154.12	6.288
PL 17	165.82	160.43	157.44	483.69	161.23	-0.822
PL 22	182.65	180.14	178.83	541.62	180.54	-20.132
PL 24	159.88	157.4	153.87	471.15	157.05	3.358
PL 26	164.45	160.66	159.24	484.35	161.45	-1.042
Mean	163.094 (X_D)	160.143 (X_N)	157.987 (X_F)	481.224	160.408 (Grand mean)	
Environmental index (X_D/ X_N/ X_F – Grand mean)	2.686	-0.265	-2.421			



Here, in X-axis 1=PL1, 2=PL2, 3=PL12, 3=PL13, 4=PL15, 5=PL16, 7=PL17, 8=PL22, 9=PL24 and 10=PL26

Figure 4.12. Graphical representation of regression coefficient (bi) and deviation from regression (s^2di) of 10 genotypes in fertile grains/panicle

and PL22 (0.015) that means these advanced lines were more stable and less sensitive for the three environments and the lowest negative value was found in PL12 (-2.825) followed by PL17 (-0.915), PL13 (-0.875), PL1 (-0.855) PL13 (-0.875) and PL15 (-0.275) that means these lines were less stable and more sensitive for the three environments in case of panicle length **(Table 4.19)**. According to Eberhart and Russell model (1966), when a variety with unit regression coefficient (bi=1) and deviation not significantly different from zero (s^2di=0) is said to be the stable one. So PL2, PL12, PL15 and PL26 were comparatively stable than others **(Figure 4.11).**

4.4.2.4 Fertile grains/panicle

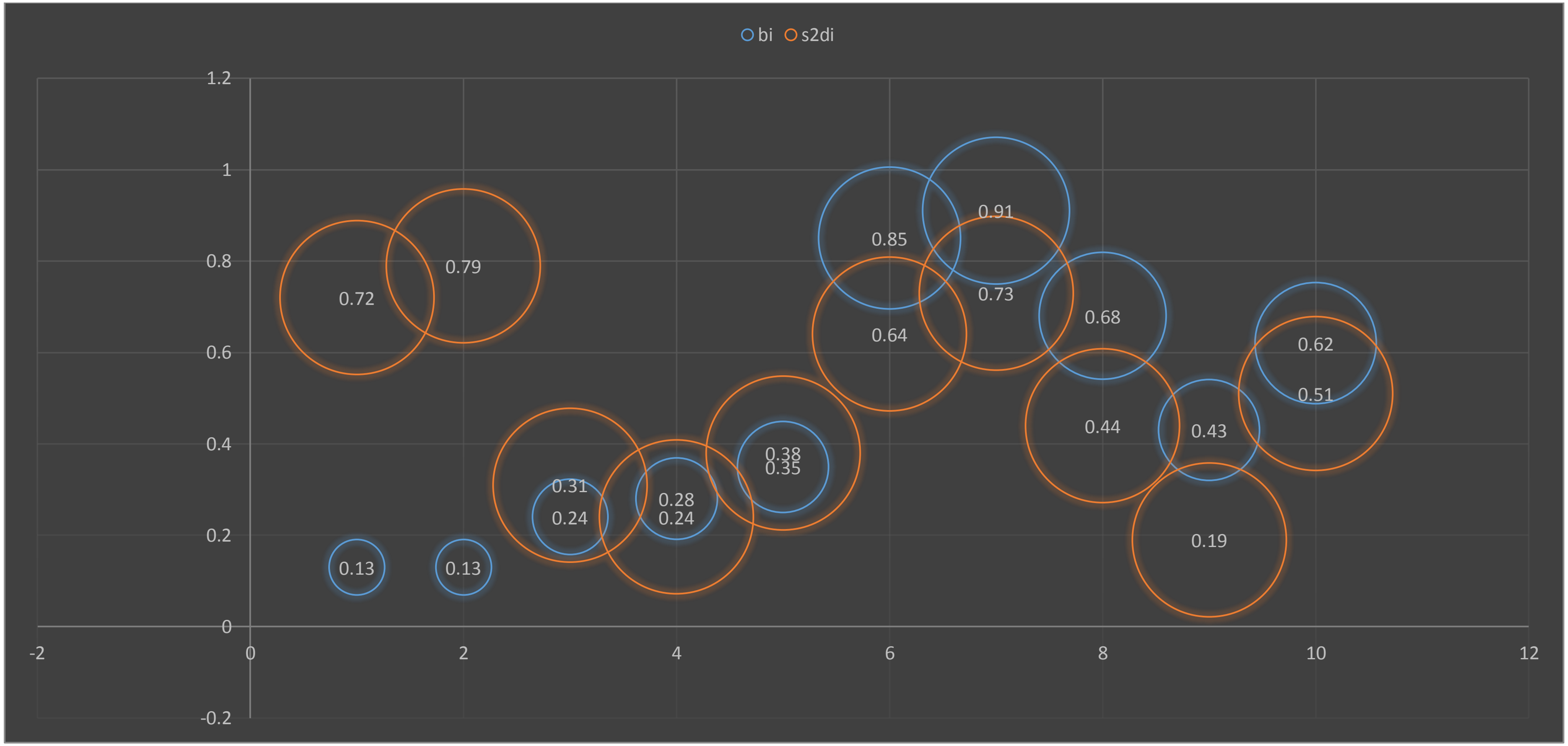
The mean of fertile grains/panicle of each of the three locations were 163.094 (Dinajpur), 160.143 (Nilphamari) and 157.987 (Faridpur). And the mean of each advance line over these three locations were PL1 (157.75), PL2 (165.3), PL12 (167.7), PL13 (153.4), PL15 (145.54), PL16 (154.12), PL17 (161.23), PL22 (180.54), PL24 (157.05), PL26 (161.45) **(Table 4.20)**. In case of environmental index, the highest positive value was found 2.686 in Dinajpur and the lowest negative value -2.421 in Faridpur where -0.265 in Nilphamari was moderate but negative. That means Dinajpur was the most suitable environment, Faridpur was the worst and Nilphamari was the moderate but bad environment for the corresponding genotypes in case of fertile grains/panicle **(Table 4.20)**. Also considerable differences were found in the values of phenotypic index for each of the line over the three locations. The highest positive value was found in PL15(14.868) followed by PL13 (7.008), PL16 (6.288) and PL24 (3.358) that means these lines were more stable and less sensitive for the three environments and the lowest negative value was found in PL22 (-20.132) followed by PL12 (-7.292), PL2 (-4.892), PL26 (-1.042) and PL17 (-0.822) that means these lines were less stable and more sensitive for the three environments in case of fertile grains/panicle **(Table 4.20)**. According to Eberhart and Russell model (1966), when a variety with unit regression coefficient (bi=1) and deviation not significantly different from zero (s^2di=0) is said to be the stable one. So PL16 was comparatively stable than others **(Figure 4.12)**.

4.4.2.5 Sterile grains/panicle

The mean of sterile grains/panicle of each of the three locations were 21.855 (Dinajpur), 22.305 (Nilphamari) and 23.937 (Faridpur). And the mean of each advance line over these three locations were PL1 (22.71), PL2 (22.07), PL12 (22.05), PL13 (20.82), PL15 (23.22), PL16 (19.86), PL17 (17.84), PL22 (27.11), PL24 (25.11), PL26 (26.2) **(Table 4.21)**.

Table 4.21. Environmental and phenotypic indices assessment for sterile grains/panicle

Advanced lines	Dinajpur	Nilphamari	Faridpur	Total	Mean	Phenotypic index (Grand mean – mean)
PL 1	24.45	23.13	20.55	68.13	22.71	-0.011
PL 2	21.07	21.88	23.26	66.21	22.07	0.629
PL 12	20.09	21.15	24.91	66.15	22.05	0.649
PL 13	19.65	19.93	22.88	62.46	20.82	1.879
PL 15	22.86	23.07	23.73	69.66	23.22	-0.521
PL 16	18.51	19.95	21.12	59.58	19.86	2.839
PL 17	16.15	16.95	20.42	53.52	17.84	4.859
PL 22	25.72	26.16	29.45	81.33	27.11	-4.411
PL 24	24.54	24.88	25.91	75.33	25.11	-2.411
PL 26	25.51	25.95	27.14	78.6	26.2	-3.501
Mean	21.855 (X_D)	22.305 (X_N)	23.937 (X_F)	68.097	22.699 (Grand mean)	
Environmental index (X_D/ X_N/ X_F – Grand mean)	-0.844	-0.394	1.238			



Here, in X-axis 1=PL1, 2=PL2, 3=PL12, 3=PL13, 4=PL15, 5=PL16, 7=PL17, 8=PL22, 9=PL24 and 10=PL26

Figure 4.13. Graphical representation of regression coefficient (bi) and deviation from regression (s^2di) of 10 genotypes in sterile grains/panicle

In case of environmental index, the highest positive value was found 1.238 in Faridpur and the lowest negative value -0.844 in Dinajpur where -0.394 in Nilphamari was moderate but negative. That means Faridpur was the most suitable environment, Dinajpur was the worst and Nilphamari was the moderate but bad environment for the corresponding genotypes in case of sterile grains/panicle **(Table 4.21)**.

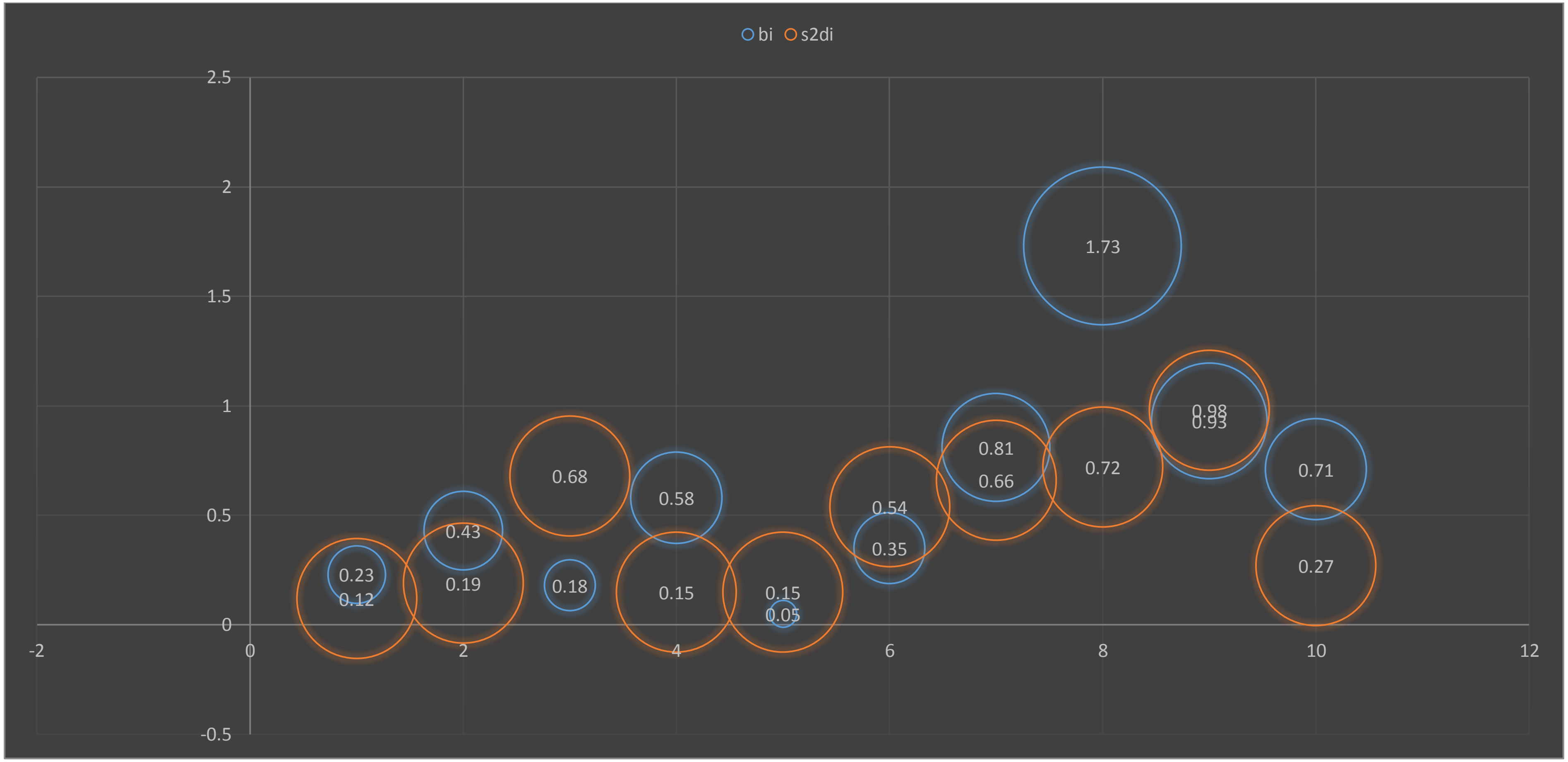
Also considerable differences were found in the values of phenotypic index for each of the line over the three locations. The highest positive value was found in PL17 (4.859) followed by PL16 (2.839), PL13 (1.879), PL12 (0.649) and PL2 (0.629) that means these lines were more stable and less sensitive for the three environments and the lowest negative value was found in PL22 (-4.411) followed by PL26 (-3.501), PL24 (-2.411), PL15 (-0.521) and PL1 (-0.011) that means these lines were less stable and more sensitive for the three environments in case of sterile grains/panicle **(Table 4.21)**. According to Eberhart and Russell model (1966), when a variety with unit regression coefficient (bi=1) and deviation not significantly different from zero (s^2di=0) is said to be the stable one. So PL12 and PL13 were comparatively stable than others **(Figure 4.13).**

4.4.2.6 Panicle weight

The mean of panicle weight of each of the three locations were 4.29 (Dinajpur), 3.89 (Nilphamari) and 3.52 (Faridpur). And the mean of each line over these three locations were PL1 (3.78), PL2 (3.97), PL12 (4.75), PL13 (3.22), PL15 (3.20), PL16 (3.16), PL17 (3.84), PL22 (4.21), PL24 (3.69), PL26 (4.52) **(Table 4.22)**. In case of environmental index, the highest positive value was found 0.462 in Dinajpur and the lowest negative value -0.317 in Faridpur where 0.059 in Nilphamari was moderate. That means Dinajpur was the most suitable environment, Faridpur was the worst and Nilphamari was the moderate environment for the corresponding genotypes in case of panicle weight **(Table 4.22)**. Also considerable differences were found in the values of phenotypic index for each of the line over the three locations. The highest positive value was found in PL15 (0.674), PL13 (0.634), PL22 (0.144), PL1 (0.054) that means these lines were more stable and less sensitive for the three environments and the lowest negative value was found in PL12 (-0.916) followed by PL24 (-0.686), PL26 (-0.686), PL17 (-0.376), PL2 (-0.136) and PL16 (-0.006) that means these lines were less stable and more sensitive for the three environments in case of panicle weight **(Table 4.22)**. According to Eberhart and Russell model (1966), when a variety with unit regression coefficient (bi=1) and deviation not significantly different from zero (s^2di=0) is said to be the stable one. So PL1 and PL15 were comparatively stable than others **(Figure 4.14).**

Table 4.22. Environmental and phenotypic indices assessment for panicle weight (g)

Advanced lines	Dinajpur	Nilphamari	Faridpur	Total	Mean	Phenotypic index (Grand mean – mean)
PL 1	4.19	3.69	3.45	11.33	3.78	0.054
PL 2	4.22	4.00	3.69	11.91	3.97	-0.136
PL 12	4.92	4.87	4.46	14.25	4.75	-0.916
PL 13	4.56	3.91	3.19	11.66	3.22	0.634
PL 15	3.65	3.10	2.88	9.63	3.2	0.674
PL 16	3.42	3.05	3.02	9.49	3.16	-0.006
PL 17	4.35	3.85	3.33	11.53	3.84	-0.376
PL 22	4.58	4.28	3.76	12.62	4.21	0.144
PL 24	4.25	3.68	3.14	11.07	3.69	-0.686
PL 26	4.82	4.50	4.25	13.57	4.52	-0.686
Mean	4.29 (X_D)	3.89 (X_N)	3.52 (X_F)	11.71	3.83 (Grand mean)	
Environmental index (X_D/ X_N/ X_F – Grand mean)	0.462	0.059	-0.317			

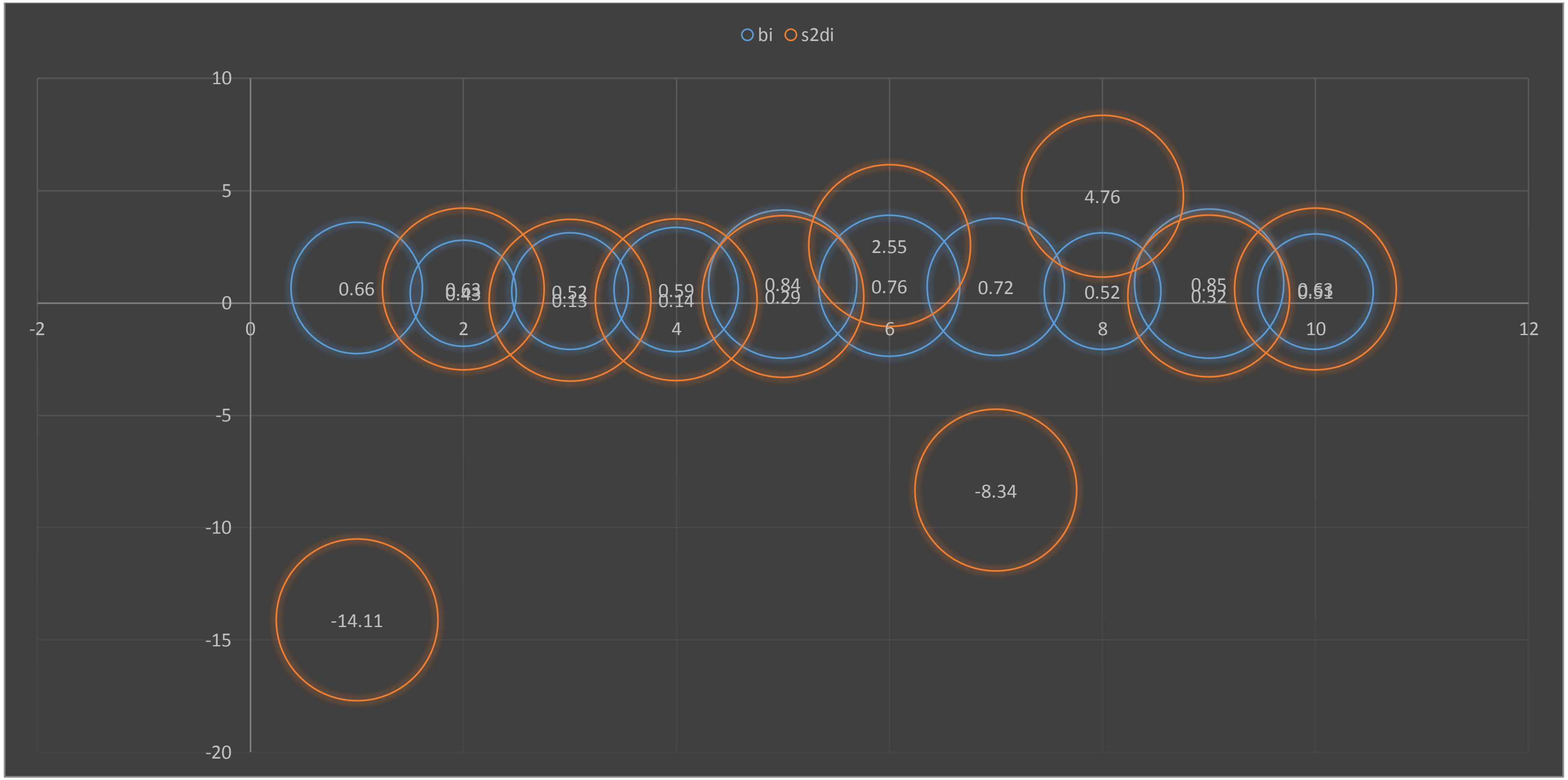


Here, in X-axis 1=PL1, 2=PL2, 3=PL12, 3=PL13, 4=PL15, 5=PL16, 7=PL17, 8=PL22, 9=PL24 and 10=PL26

Figure 4.14. Graphical representation of regression coefficient (bi) and deviation from regression (s^2di) of 10 genotypes in panicle weight.

Table 4.23. Environmental and phenotypic indices assessment for sterility percentage

Advanced lines	Dinajpur	Nilphamari	Faridpur	Total	Mean	Phenotypic index (Grand mean – mean)
PL 1	13.75	14.41	15.22	43.38	14.46	-2.555
PL 2	16.82	17.35	21.78	55.95	18.65	-6.745
PL 12	7.45	8.77	11.56	27.78	9.15	2.755
PL 13	6.65	7.24	12.81	26.70	8.90	3.005
PL 15	11.56	13.15	16.24	40.95	13.65	-1.745
PL 16	15.35	16.73	16.37	48.45	16.15	-4.245
PL 17	9.66	10.71	13.26	33.63	11.21	0.695
PL 22	7.89	8.12	12.67	28.68	9.56	2.345
PL 24	6.07	7.33	12.70	26.10	8.70	3.205
PL 26	6.93	8.02	10.91	25.86	8.62	-8.62
Mean	10.213 (X_D)	11.183 (X_N)	14.352 (X_F)	35.748	11.905 (Grand mean)	
Environmental index (X_D/ X_N/ X_F – Grand mean)	-1.692	-0.722	2.447			



Here, in X-axis 1=PL1, 2=PL2, 3=PL12, 3=PL13, 4=PL15, 5=PL16, 7=PL17, 8=PL22, 9=PL24 and 10=PL26

Figure 4.15. Graphical representation of regression coefficient (bi) and deviation from regression (s^2di) of 10 genotypes in sterility percentage.

4.4.2.7 Sterility percentage

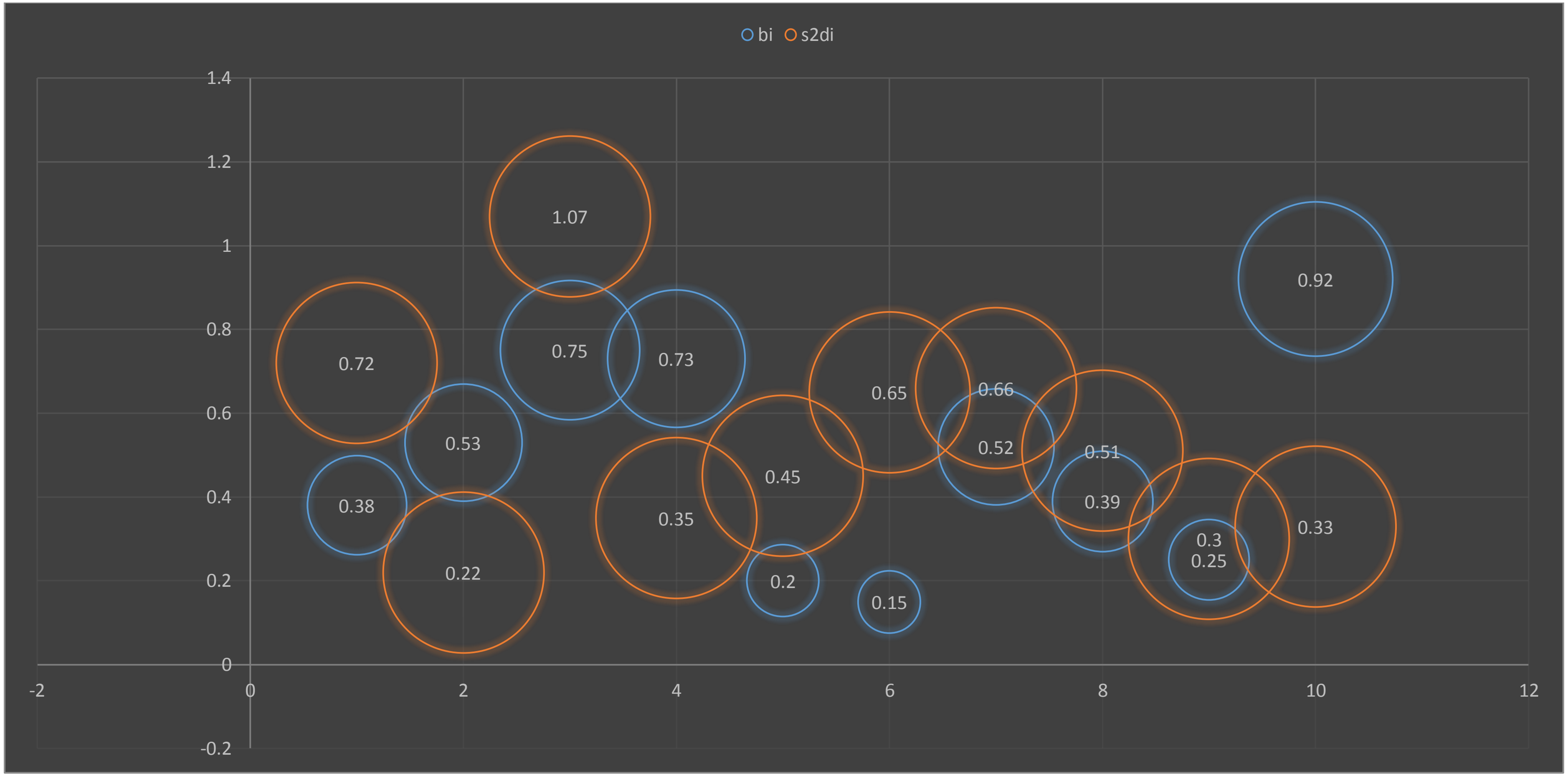
The mean of sterility percentage of each of the three locations were 10.213 (Dinajpur), 11.183 (Nilphamari) and 14.352 (Faridpur). And the mean of each line over these three locations were PL1 (14.46), PL2 (18.65), PL12 (9.15), PL13 (8.9), PL15 (13.65), PL16 (16.15), PL17 (11.21), PL22 (9.56), PL24 (8.7), PL26 (8.62) **(Table 4.23)**. In case of environmental index, the highest positive value was found 2.447 in Faridpur and the lowest negative value -1.692 in Dinajpur where -0.722 in Nilphamari was moderate but negative. That means Faridpur was the most suitable environment, Dinajpur was the worst and Nilphamari was the moderate but bad environment for the corresponding genotypes in case of sterility percentage **(Table 4.23)**. Also considerable differences were found in the values of phenotypic index for each of the line over the three locations. The highest positive value was found in PL24 (3.205) followed by PL13 (3.005), PL12 (2.755), PL22 (2.345) and PL17 (0.695) that means these lines were more stable and less sensitive for the three environments and the lowest negative value was found in PL26 (-8.62) followed by PL2 (-6.745), PL16 (-4.245), PL1 (-2.555) and PL15 (-1.745) that means these lines were less stable and more sensitive for the three environments in case of sterility percentage **(Table 4.23)**. According to Eberhart and Russell model (1966), when a variety with unit regression coefficient (bi=1) and deviation not significantly different from zero (s^2di=0) is said to be the stable one. So PL2, PL12, PL13, PL15, PL24 and PL26 were comparatively stable than others **(Figure 4.15).**

4.4.2.8 Lodging percentage

The mean of lodging percentage of each of the three locations were 9.268 (Dinajpur), 10.457 (Nilphamari) and 12.861 (Faridpur). And the mean of each line over these three locations were PL1 (19.67), PL2 (8.9), PL12 (7.03), PL13 (3.96), PL15 (8.9), PL16 (10.25), PL17 (11.75), PL22 (13.87), PL24 (11.25), PL26 (13.04) **(Table 4.24)**. In case of environmental index, the highest positive value was found 1.999 in Faridpur and the lowest negative value -1.594 in Dinajpur where -0.405 in Nilphamari was moderate but negative. That means Faridpur was the most suitable environment, Dinajpur was the worst and Nilphamari was the moderate but bad environment for the corresponding genotypes in case of lodging percentage **(Table 4.24)**. Also considerable differences were found in the values of phenotypic index for each of the advanced line over the three

Table 4.24. Environmental and phenotypic indices assessment for lodging percentage

Advanced lines	Dinajpur	Nilphamari	Faridpur	Total	Mean	Phenotypic index (Grand mean – mean)
PL 1	18.25	20.05	20.71	59.01	19.67	-8.808
PL 2	7.44	8.15	11.11	26.70	8.90	1.962
PL 12	6.15	6.61	8.33	21.09	7.03	3.832
PL 13	2.22	3.46	6.20	11.88	3.96	6.902
PL 15	6.72	8.57	11.41	26.70	8.90	1.962
PL 16	9.36	10.24	11.15	30.75	10.25	0.612
PL 17	9.57	10.71	14.97	35.25	11.75	-0.888
PL 22	11.65	13.23	16.73	41.61	13.87	-3.008
PL 24	9.36	10.55	13.84	33.75	11.25	-0.388
PL 26	11.96	13.00	14.16	39.12	13.04	-2.178
Mean	9.268 (X_D)	10.457 (X_N)	12.861 (X_F)	32.586	10.862 (Grand mean)	
Environmental index (X_D/ X_N/ X_F – Grand mean)	-1.594	-0.405	1.999			



Here, in X-axis 1=PL1, 2=PL2, 3=PL12, 3=PL13, 4=PL15, 5=PL16, 7=PL17, 8=PL22, 9=PL24 and 10=PL26

Figure 4.16. Graphical representation of regression coefficient (bi) and deviation from regression (s^2di) of 10 genotypes in lodging percentage.

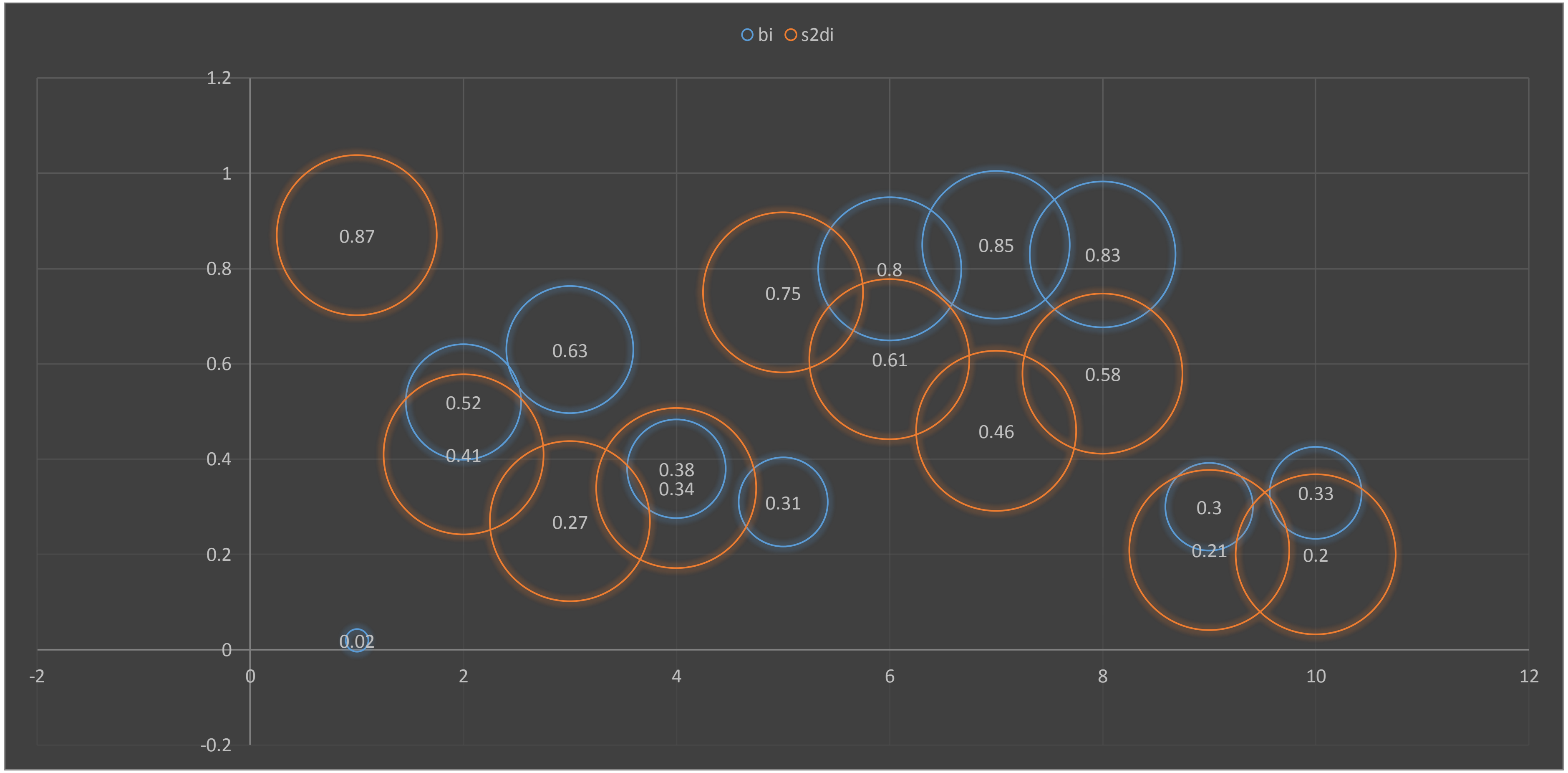
locations. The highest positive value was found in PL23 (6.902) followed by PL12 (3.832), PL2 (1.962), PL15 (1.962) and PL16 (0.612) that means these lines were more stable and less sensitive for the three environments and the lowest negative value was found in PL1 (-8.808) followed by PL22 (-3.008), PL26 (-2.178), PL17 (-0.888) and PL24 (-0.388) that means these lines were less stable and more sensitive for the three environments in case of lodging percentage **(Table 4.24)**. According to Eberhart and Russell model (1966), when a variety with unit regression coefficient (bi=1) and deviation not significantly different from zero (s^2di=0) is said to be the stable one. So PL24 was comparatively stable than others **(Figure 4.16).**

4.4.2.9 1000-grain weight

The mean of 1000-grain weight of each of the three locations were 14.535 (Dinajpur), 12.451 (Nilphamari) and 10.292 (Faridpur). And the mean of each advance line over these three locations were PL1 (10.87), PL2 (10.9), PL12 (13.9), PL13 (14.8), PL15 (10.12), PL16 (12.65), PL17 (10.94), PL22 (14.12), PL24 (11.7), PL26 (11.26) **(Table 4.25)**. In case of environmental index, the highest positive value was found 2.109 in Dinajpur and the lowest negative value -2.134 in Faridpur where 0.025 in Nilphamari was moderate. That means Dinajpur was the most suitable environment, Faridpur was the worst and Nilphamari was the moderate environment for the corresponding genotypes in case of 1000-grain weight **(Table 4.25)**. Also considerable differences were found in the values of phenotypic index for each of the line over the three locations. The highest positive value was found in PL1 (2.454) followed by PL17 (2.394), PL2 (2.264), PL16 (2.074), PL15 (1.034), PL26 (0.714) and PL24 (0.544) that means these lines were more stable and less sensitive for the three environments and the lowest negative value was found in PL12 (-7.516) followed by PL13 (-1.986) and PL22 (-1.976) that means these lines were less stable and more sensitive for the three environments in case of 1000-grain weight **(Table 4.25)**. According to Eberhart and Russell model (1966), when a variety with unit regression coefficient (bi=1) and deviation not significantly different from zero (s^2di=0) is said to be the stable one. So PL24 and PL26 were comparatively stable than others **(Figure 4.17).**

Table 4.25. Environmental and phenotypic indices assessment for 1000-grain weight

Advanced lines	Dinajpur	Nilphamari	Faridpur	Total	Mean	Phenotypic index (Grand mean – mean)
PL 1	13.87	10.75	7.99	32.61	10.87	1.556
PL 2	12.54	11.12	9.04	32.70	10.90	1.526
PL 12	15.15	14.15	12.40	41.70	13.90	-1.474
PL 13	16.47	14.95	12.98	44.40	14.80	-2.374
PL 15	12.26	10.20	7.90	30.36	10.12	2.306
PL 16	14.51	12.10	11.34	37.95	12.65	-0.224
PL 17	13.33	11.17	8.32	32.82	10.94	1.486
PL 22	16.61	13.88	11.87	42.36	14.12	-1.694
PL 24	13.83	11.65	9.62	35.10	11.70	0.726
PL 26	16.78	14.54	11.46	42.78	14.26	-1.834
Mean	14.535 (X_D)	12.451 (X_N)	10.292 (X_F)	37.278	12.426 (Grand mean)	
Environmental index (X_D/ X_N/ X_F – Grand mean)	2.109	0.025	-2.134			



Here, in X-axis 1=PL1, 2=PL2, 3=PL12, 3=PL13, 4=PL15, 5=PL16, 7=PL17, 8=PL22, 9=PL24 and 10=PL26

Figure 4.17. Graphical representation of regression coefficient (bi) and deviation from regression (s^2di) of 10 genotypes in 1000-grain weight

4.4.2.10 Days to 50% flowering

The days to 50% flowering in the advanced lines were measured from the number of days required after seeding in the seedbeds. The mean of days to 50% flowering of each of the three locations were 116.347 (Dinajpur), 114.698 (Nilphamari) and 113.454 (Faridpur). And the mean of each line over these three locations were PL1 (114.22), PL2 (112.98), PL12 (115.55), PL13 (109.42), PL15 (119.8), PL16 (114.4), PL17 (114.12), PL22 (117.6), PL24 (112.54), PL26 (117.7) **(Table 4.26)**. In case of environmental index, the highest positive value was found 1.514 in Dinajpur and the lowest negative value -1.379 in Faridpur where -0.135 in Nilphamari was moderate but negative. That means Dinajpur was the most suitable environment, Faridpur was the worst and Nilphamari was the moderate environment for the corresponding genotypes in case of days to 50% flowering **(Table 4.26)**. Also considerable differences were found in the values of phenotypic index for each of the line over the three locations.

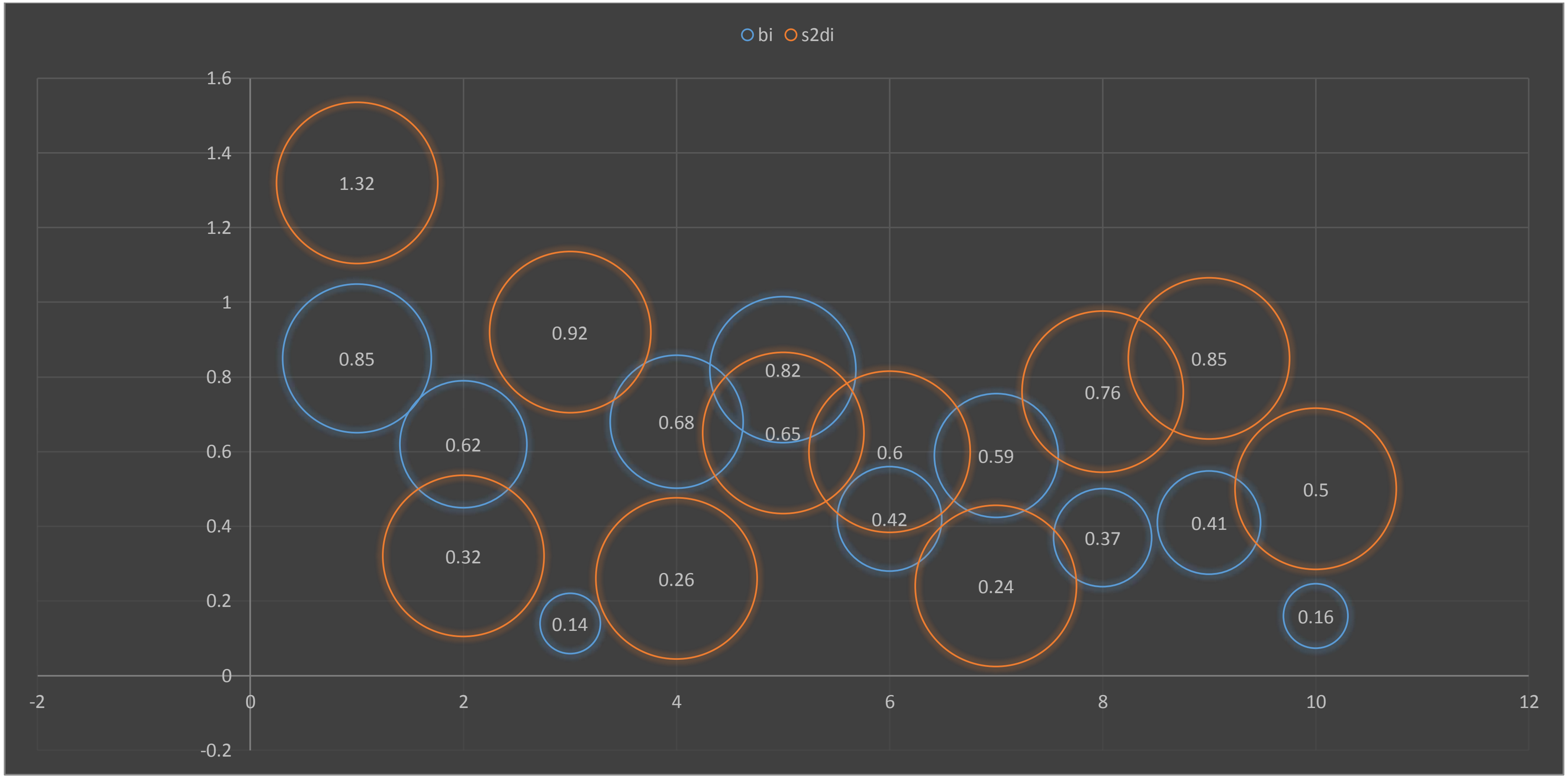
The highest positive value was found in PL13 (5.413) followed by PL24 (2.293), PL2 (1.853), PL17 (0.713), PL1 (0.613) and PL16 (0.433) that means these lines were more stable and less sensitive for the three environments and the lowest negative value was found in PL15 (-4.967) followed by PL26 (-2.867), PL22 (-2.767) and PL12 (-7.17) that means these lines were less stable and more sensitive for the three environments in case of days to 50% flowering **(Table 4.26).** According to Eberhart and Russell model (1966), when a variety with unit regression coefficient (bi=1) and deviation not significantly different from zero (s^2di=0) is said to be the stable one. So after analysis the graph there were no significant stable genotype in days to 50% flowering **(Figure 4.18).**

4.4.2.11 Days to maturity

The mean of days to maturity of each of the three locations were 146.211 (Dinajpur), 144.14 (Nilphamari) and 142.818 (Faridpur). And the mean of each line over these three locations were PL1 (144.75), PL2 (144.18), PL12 (143.4), PL13 (141.67), PL15 (145.94), PL16 (140.7), PL17 (146.95), PL22 (144.71), PL24 (143.4), PL26 (148.2) **(Table 4.27).** In case of environmental index, the highest positive value was found 1.821 in Dinajpur and the lowest negative value -1.572 in Faridpur where -0.25 in Nilphamari was moderate but negative. That means Dinajpur was the most suitable environment, Faridpur was the worst and Nilphamari was the moderate environment for the corresponding genotypes in case of days to maturity **(Table 4.27).** Also considerable

Table 4.26. Environmental and phenotypic indices assessment for days to 50% flowering (from seeding)

Advanced lines	Dinajpur	Nilphamari	Faridpur	Total	Mean	Phenotypic index (Grand mean – mean)
PL 1	116.12	116.02	110.52	342.66	114.22	0.613
PL 2	114.75	113.54	110.65	338.94	112.98	1.853
PL 12	118.65	115.76	112.24	346.65	115.55	-0.717
PL 13	110.43	108.88	108.95	328.26	109.42	5.413
PL 15	120.25	118.94	120.21	359.40	119.80	-4.967
PL 16	116.92	114.62	111.66	343.20	114.40	0.433
PL 17	116.00	113.74	112.62	342.36	114.12	0.713
PL 22	116.4	117.07	119.33	352.8	117.60	-2.767
PL 24	114.51	111.9	111.21	337.62	112.54	2.293
PL 26	119.44	116.51	117.15	353.10	117.70	-2.867
Mean	116.347(X_D)	114.698 (X_N)	113.454 (X_F)	344.499	114.833(Grand mean)	
Environmental index (X_D/ X_N/ X_F – Grand mean)	1.514	-0.135	-1.379			

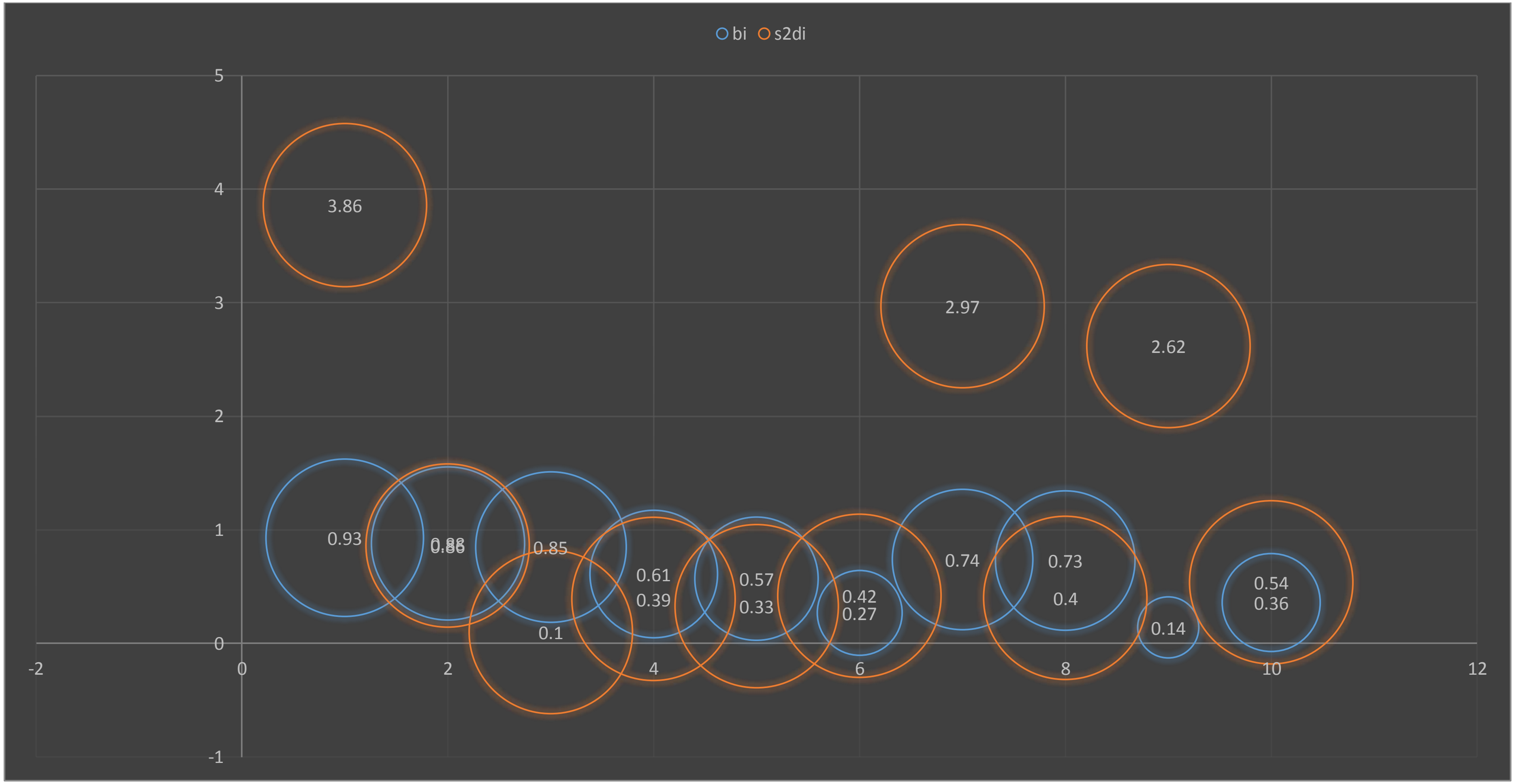


Here, in X-axis 1=PL1, 2=PL2, 3=PL12, 3=PL13, 4=PL15, 5=PL16, 7=PL17, 8=PL22, 9=PL24 and 10=PL26

Figure 4.18. Graphical representation of regression coefficient (bi) and deviation from regression (s^2di) of 10 genotypes in days to 50% flowering.

Table 4.27. Environmental and phenotypic indices assessment for days to maturity (from seeding)

Advanced lines	Dinajpur	Nilphamari	Faridpur	Total	Mean	Phenotypic index (Grand mean – mean)
PL 1	146.25	144.36	143.64	434.25	144.75	-0.36
PL 2	146.68	144.65	141.21	432.54	144.18	0.21
PL 12	145.18	144.20	140.82	430.20	143.40	0.99
PL 13	144.52	142.81	137.68	425.01	141.67	2.72
PL 15	147.25	145.00	145.57	437.82	145.94	-1.55
PL 16	142.22	140.42	139.46	422.10	140.70	3.69
PL 17	146.97	145.40	148.48	440.85	146.95	-2.56
PL 22	146.41	143.10	144.62	434.13	144.71	-0.32
PL 24	145.50	142.71	141.98	430.19	143.40	0.99
PL 26	151.13	148.75	144.72	444.60	148.20	-3.81
Mean	146.211 (X_D)	144.14 (X_N)	142.818 (X_F)	433.169	144.39 (Grand mean)	
Environmental index (X_D/ X_N/ X_F – Grand mean)	1.821	-0.25	-1.572			



Here, in X-axis 1=PL1, 2=PL2, 3=PL12, 3=PL13, 4=PL15, 5=PL16, 7=PL17, 8=PL22, 9=PL24 and 10=PL26

Figure 4.19. Graphical representation of regression coefficient (bi) and deviation from regression (s^2di) of 10 genotypes in days to maturity.

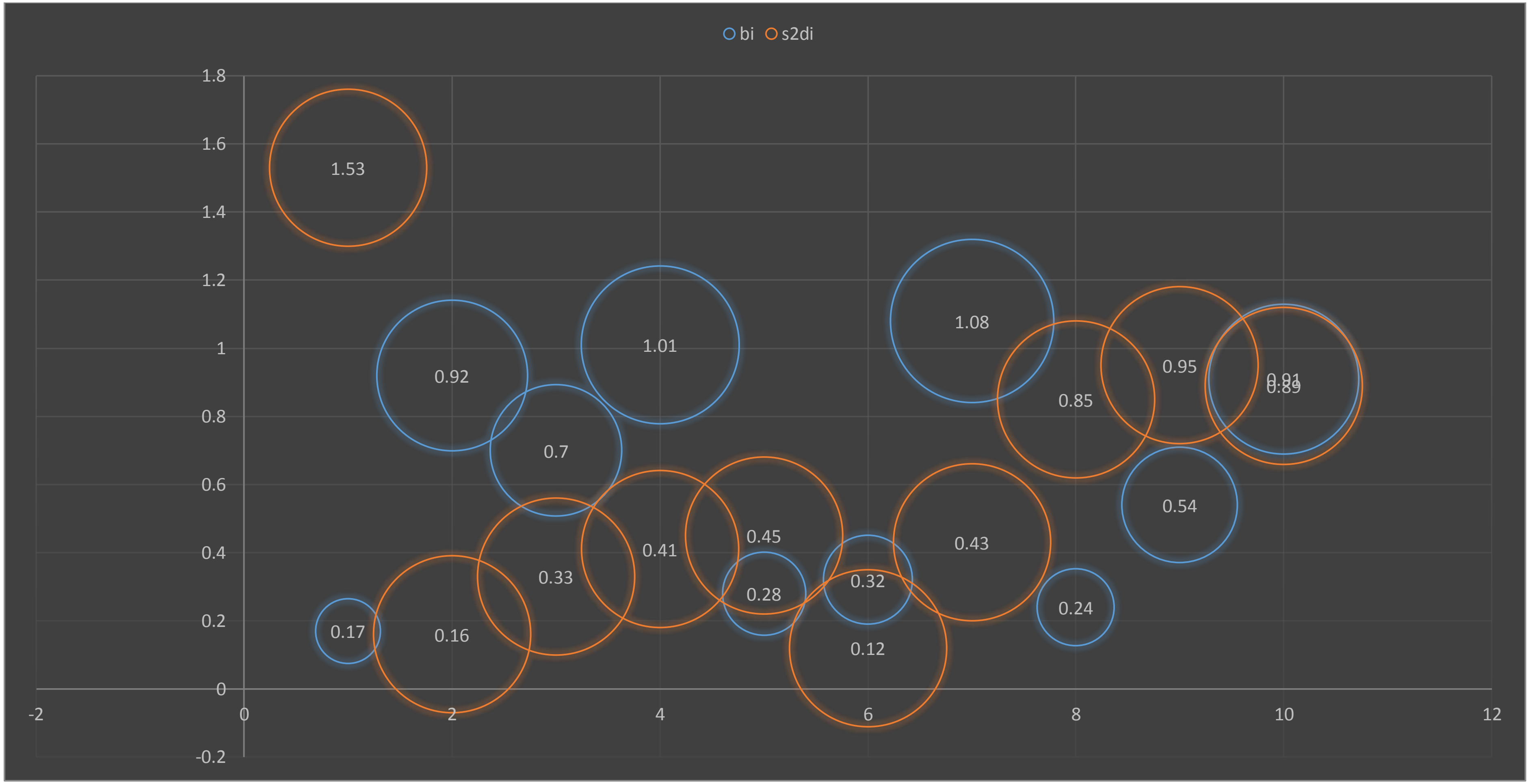
differences were found in the values of phenotypic index for each of the advanced line over the three locations. The highest positive value was found in PL16 (3.69) followed by PL13 (2.72), PL12 (0.99), PL24 (0.99) and PL2 (0.21) that means these lines were more stable and less sensitive for the three environments and the lowest negative value was found in PL26 (-3.81) followed by PL17 (-2.56), PL15 (-1.55), PL1 (-0.36) and PL22 (-0.32) that means these lines were less stable and more sensitive for the three environments in case of days to maturity **(Table 4.27).** According to Eberhart and Russell model (1966), when a variety with unit regression coefficient (bi=1) and deviation not significantly different from zero (s^2di=0) is said to be the stable one. So PL13, PL15, PL16 and PL26 were comparatively stable than others **(Figure 4.19).**

4.4.2.12 Harvest index

The mean of harvest index of each of the three locations were 33.075 (Dinajpur), 31.533 (Nilphamari) and 30.552 (Faridpur). And the mean of each advance line over these three locations were PL1 (27.43), PL2 (29.19), PL12 (32.16), PL13 (30.85), PL15 (34.92), PL16 (32.34), PL17 (30.54), PL22 (34.68), PL24 (32.80), PL26 (32.29) **(Table 4.28).** In case of environmental index, the highest positive value was found 1.355 in Dinajpur and the lowest negative value -1.168 in Faridpur where -0.187 in Nilphamari was moderate but negative. That means Dinajpur was the most suitable environment, Faridpur was the worst and Nilphamari was the moderate environment for the corresponding genotypes in case of harvest index **(Table 4.28)**. Also considerable differences were found in the values of phenotypic index for each of the line over the three locations. The highest positive value was found in PL1 (4.29) followed by PL2 (2.53), PL17 (1.18) and PL13 (0.87) that means these lines were more stable and less sensitive for the three environments and the lowest negative value was found in PL15 (-3.20) followed by PL22 (-2.96), PL24 (-1.08), PL16 (-0.62), PL26 (-0.57) and PL12 (-0.44) that means these lines were less stable and more sensitive for the three environments in case of harvest index **(Table 4.28).** According to Eberhart and Russell model (1966), when a variety with unit regression coefficient (bi=1) and deviation not significantly different from zero (s^2di=0) is said to be the stable one. So PL15 and PL16 were comparatively stable than others **(Figure 4.20).**

Table 4.28. Environmental and phenotypic indices assessment for harvest index

Advanced lines	**Dinajpur**	**Nilphamari**	**Faridpur**	**Total**	**Mean**	**Phenotypic index (Grand mean – mean)**
PL 1	28.68	27.43	26.18	27.43	27.43	4.29
PL 2	30.13	29.23	28.21	29.19	29.19	2.53
PL 12	33.21	32.35	30.92	32.16	32.16	-0.44
PL 13	31.82	30.56	30.17	30.85	30.85	0.87
PL 15	36.61	34.51	33.64	34.92	34.92	-3.2
PL 16	34.22	31.65	31.15	32.34	32.34	-0.62
PL 17	32.32	30.16	29.14	30.54	30.54	1.18
PL 22	35.69	34.52	33.83	34.68	34.68	-2.96
PL 24	34.62	32.54	31.24	32.80	32.80	-1.08
PL 26	33.45	32.38	31.04	32.29	32.29	-0.57
Mean	33.075 (X_D)	31.533 (X_N)	30.552 (X_F)	31.72	31.72 (Grand mean)	
Environmental index (X_D/ X_N/ X_F – Grand mean)	1.355	-0.187	-1.168			



Here, in X-axis 1=PL1, 2=PL2, 3=PL12, 3=PL13, 4=PL15, 5=PL16, 7=PL17, 8=PL22, 9=PL24 and 10=PL26

Figure 4.20. Graphical representation of regression coefficient (bi) and deviation from regression (s^2di) of 10 genotypes in harvest index.

4.4.2.13 Grain yield/hill

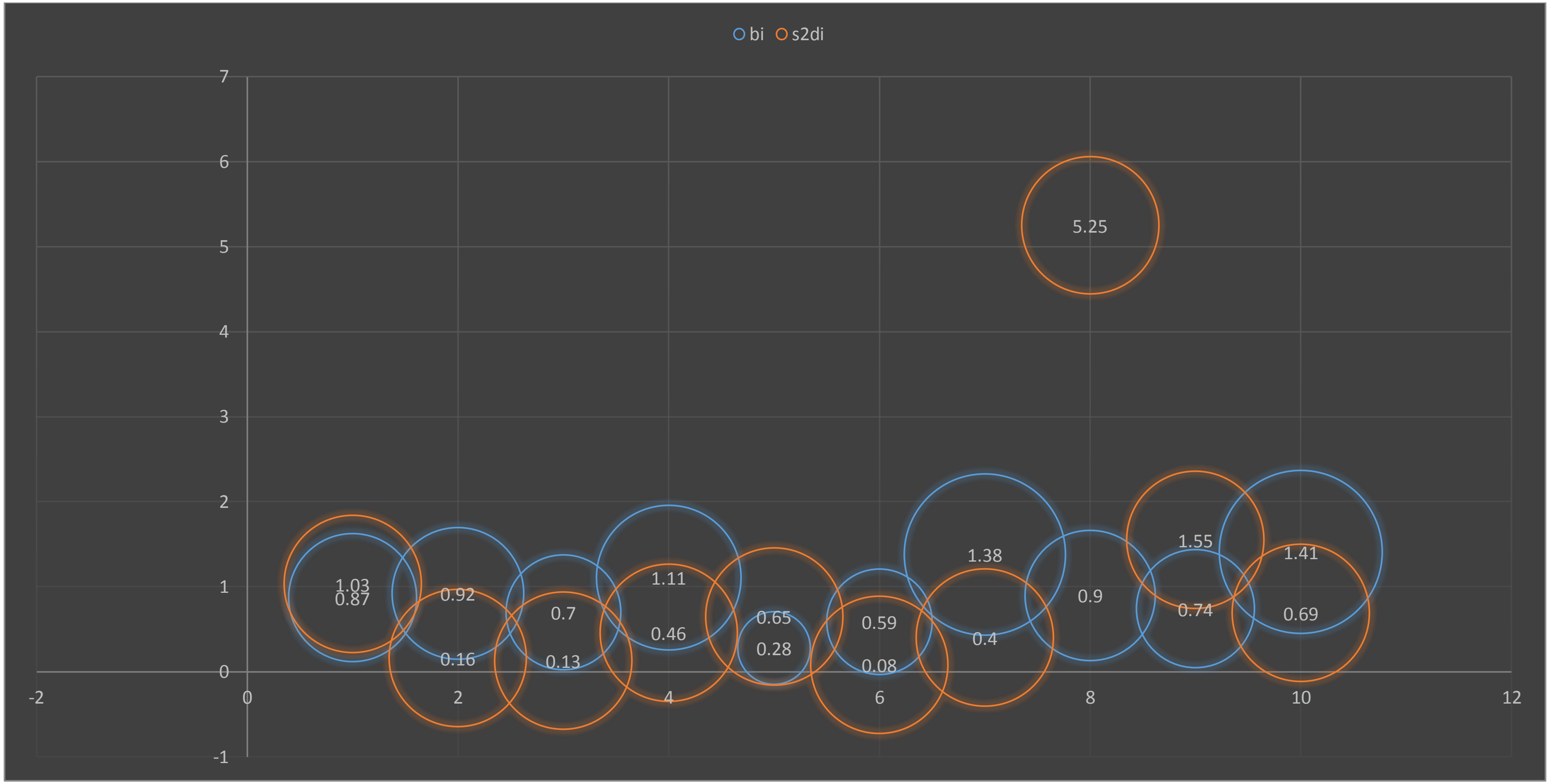
The mean of grain yield/hill of each of the three locations were 15.907 g/hill (Dinajpur), 14.959 g/hill (Nilphamari) and 14.088 g/hill (Faridpur). And the mean of each line over these three locations were PL1 (18.85), PL2 (13.10), PL12 (11.93), PL13 (16.12), PL15 (15.88), PL16 (18.10), PL17 (13.69), PL22 (17.19), PL24 (11.80), PL26 (13.21) **(Table 4.29)**. In case of environmental index, the highest positive value was found 0.92 in Dinajpur and the lowest negative value -0.899 in Faridpur where -0.028 in Nilphamari was moderate but negative. That means Dinajpur was the most suitable environment, Faridpur was the worst and Nilphamari was the moderate environment for the corresponding genotypes in case of grain yield/hill **(Table 4.29)**. Also considerable differences were found in the values of phenotypic index for each of the line over the three locations. The highest positive value was found in PL24 (3.187) followed by PL12 (3.057), PL2 (1.887), PL26 (1.777) and PL17 (1.297) that means these lines were more stable and less sensitive for the three environments and the lowest negative value was found in PL13 (-3.863) followed by PL16 (-3.113), PL22 (-2.203) and PL1 (-1.133) that means these lineswere less stable and more sensitive for the three environments in case of grain yield/hill **(Table 4.29).** According to Eberhart and Russell model (1966), when a variety with unit regression coefficient (bi=1) and deviation not significantly different from zero (s^2di=0) is said to be the stable one. So PL12, PL15 and PL16 were comparatively stable than others **(Figure 4.21).**

4.5 GGE biplot analysis for stability

The genotype x environment interaction structure is an important aspect of both plant breeding programme and the introduction of new crop cultivars (Freeman, 1985). ANOVA which is an additive model is effective in partitioning the total sum of squares into i) the genotype main effect, ii). The environment main effect and iii) the GEI, but it does not provide insight into GEI structure. To study the underlying the interaction component, more advance techniques such as principal component analysis are required. The AMMI model is a hybrid model involving both additive and multiplicative components of two way data structure. The AMMI model separates the additive variance and then applies Principal Component Analysis (PCA) to the interaction portion to extract a new set of co-ordinate axis which explain in more detail the interactions pattern. The effectiveness of AMMI procedure has been clearly demonstrated by various authors

Table 4.29. Environmental and phenotypic indices assessment for grain yield/hill

Advanced lines	Dinajpur	Nilphamari	Faridpur	Total	Mean	Phenotypic index (Grand mean – mean)
PL 1	19.12	18.05	17.03	54.20	18.10	-1.133
PL 2	14.21	13.03	12.06	39.30	13.10	1.887
PL 12	12.89	12.19	10.71	35.79	11.93	3.057
PL 13	19.84	18.83	17.88	56.55	18.85	-3.863
PL 15	16.96	15.83	14.87	47.66	15.88	-0.893
PL 16	17.05	16.11	15.21	48.37	16.12	-3.113
PL 17	14.44	13.41	13.22	41.07	13.69	1.297
PL 22	18.29	17.11	16.17	51.57	17.19	-2.203
PL 24	12.51	11.81	11.09	35.41	11.80	3.187
PL 26	13.76	13.22	12.64	39.62	13.21	1.777
Mean	15.907 (X_D)	14.959 (X_N)	14.088 (X_F)	44.954	14.987 (Grand mean)	
Environmental index (X_D/ X_N/ X_F – Grand mean)	0.92	-0.028	-0.899			



Here, in X-axis 1=PL1, 2=PL2, 3=PL12, 3=PL13, 4=PL15, 5=PL16, 7=PL17, 8=PL22, 9=PL24 and 10=PL26

Figure 4.21. Graphical representation of regression coefficient (bi) and deviation from regression (s^2di) of 10 genotypes in grain yield /hill

viz., in soybean Zobel *et al*. (1988) in maize Crossa *et al*. (1990), Nitch *et al*. (1992) and Crossa *et al*. (1991) in wheat, Shinde *et al*. (2002) in pearl millet and Zaval-Garcia *et al*. (1992) in rice, respectively using multi locational data. Yield potential of the selected advanced lines were evaluated over the locations, Dinajpur, Nilphamari and Faridpur. The PC1 was calculated to 99.53% and the straight line developed from GGE biplot analysis revealed strong effects of Faridpur environment as projected by far away and downward position of the interaction line from the base of horizontal axis with zero PC value (Fig.4.22). Moreover, the fig.4.22 exhibited thatDinajpur environment appeared as the best with upper spoke to cultivate the fine rice advanced lines.

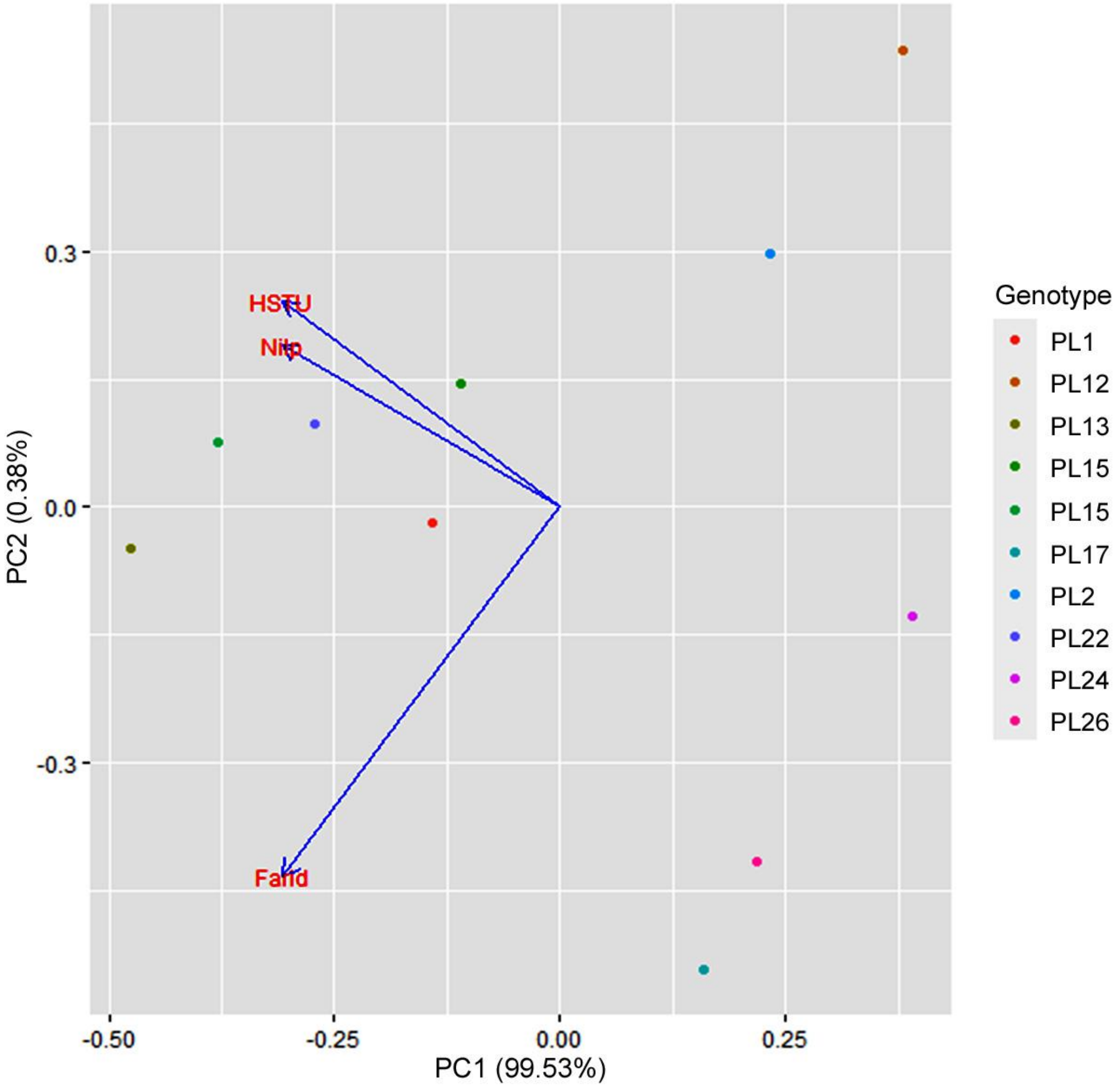


Figure 4.22. Yield potential comparison of the advanced lines over the locations under GGE biplot analysis

Comparing with horizintal axis with zero PC2 indicated that the advanced lines showed less sensitive in Nilphamari environment and strong effects of Faridpur environment (Figure 4.23). The main effects were paid by the advanced lines as well as by the locations and the interaction effects were the multiplicativenon-aditive effects. Most of the advanced lines performed better in Dinajpur environment as the GGE biplot straight line developed above the horizontal axis of PCA.

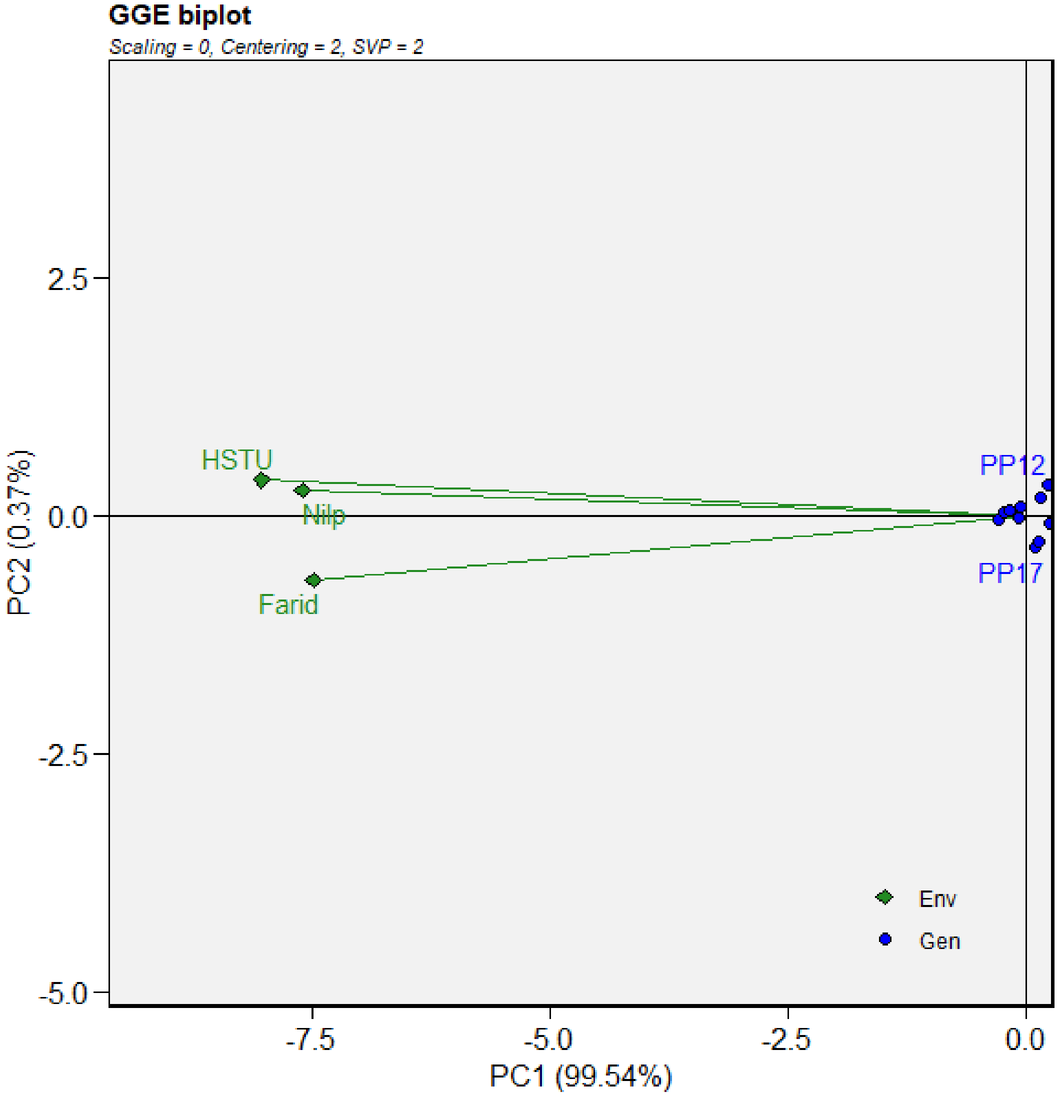


Figure 4.23. Discrimination and representative of G X E effects through GGE biplot analysis

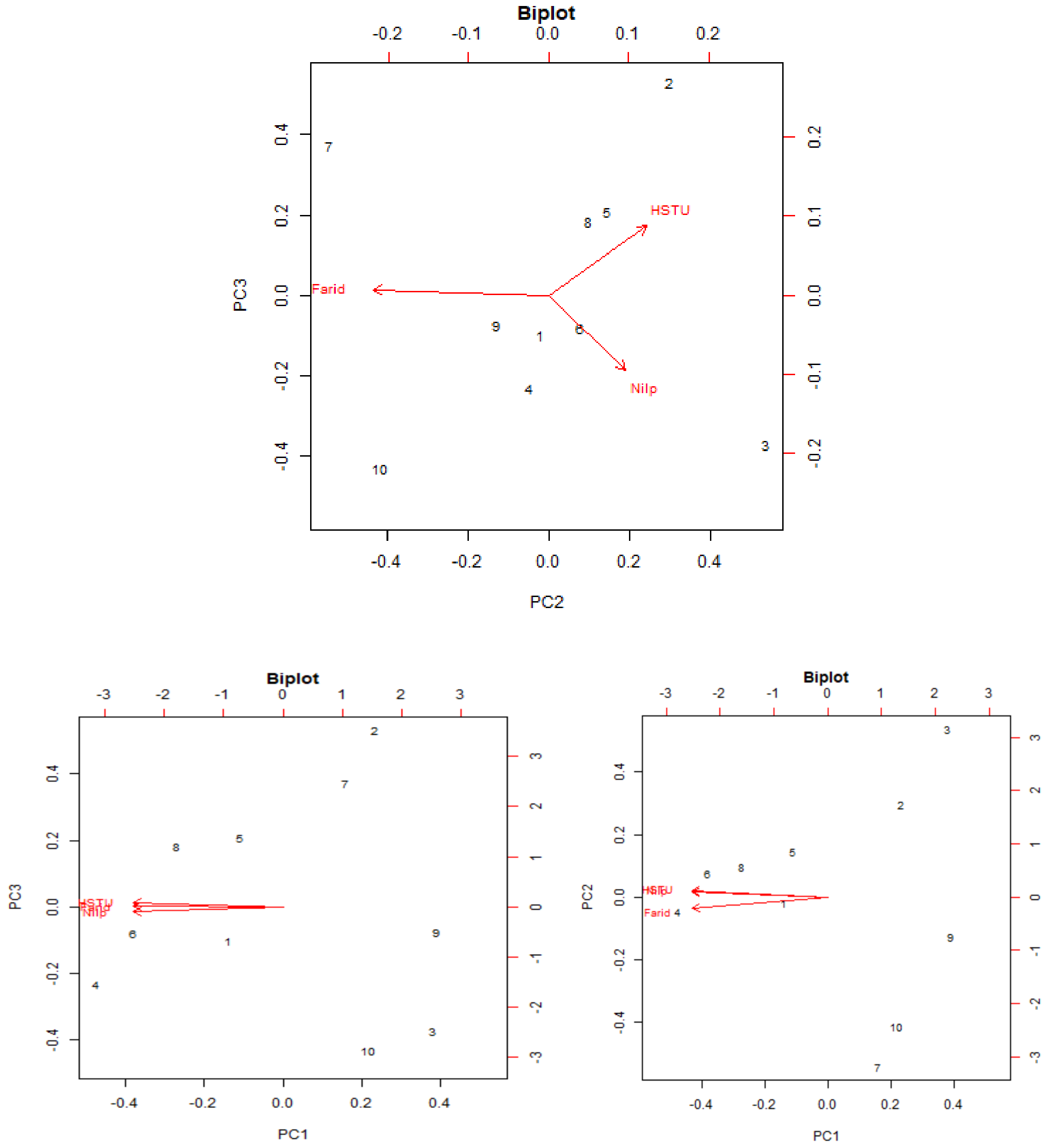


Figure 4.24. Interaction multiplicative effects derived from GGE biplot analysis

The multiplicative non-additive effects of G X E suggested that all the advanced lines showed similar trend of interactions for grain yield (Figure 4.24). The lengths of environmental vectors from the biplot origin were proportional to the standard deviation within each location and thus represented the discriminating ability of the three locations (22).

4.6 Estimation of aroma contents

Aroma contents were estimated from fresh leaves and grain powder and expressed in sensory method (Table 4.30). The results revealed that aroma contents were very minutely improved in F_6 generation over the locations. The highest aroma content (8.83) in PL16, was followed by PL12 and PL13. When the character was estimated over three locations, the maximum aroma was assessed fro PL13 with 9.00 the other pure lines possessed lower aroma content. However, aroma retaining in cooked rice is the most important to the consumers.

Table 4.30. Comparison of aroma contents in F_5 and F_6 in advanced lines of fine rice

Genotype	**Aroma in freshleave of F_5**	**Aroma in grain powder of F_5**	**Aroma in grain powder of F_6**
PL1	7.16 ab	6.39 c	8.33 c
PL2	6.86 c	6.95 bc	8.00 d
PL12	7.19 ab	7.94 ab	7.67 e
PL13	7.63 ab	7.94 ab	9.00 a
PL15	7.19 ab	7.06 b	8.67 b
PL16	8.75 a	8.83 a	7.67 e
PL17	7.41 ab	7.39 b	7.33 f
PL22	6.97 bc	7.5 b	8.33 c
PL24	7.19 ab	7.17 b	7.33 f
PL26	7.53 ab	7.28 b	7.00 g

The mean values bearing same letter (s) were not differ significantly at 5% level of probability

Figure 4.25. Thirty days' age after transplanting of ten F_6 generations at Plant breeding research

Figure 4.26. Supervisor is in HSTU research field at harvesting stage of F_6 generation for stability analysis.

Figure 4.27. I with my supervisor, co-supervisor, Departmental chairman and Farm manager, BADC at harvesting stage of F_6 generation at BADC seed multiplication farm Nilphamari for stability analysis

Figure 4.28. Harvesting stage of F_6 generation at BADC seed multiplication farm, Faridpur for stability analysis

Figure 4.29. I with my supervisor, Co-supervisor, Departmental chairman and others

Figure 4.30. Processing of selected rice grain for quality assessment

4.7 Experiment V: Estimation of cooking quality in F_6 generation

4.7.1 Analysis of variance

The analysis of variance (ANOVA) for 7 quantitative characters viz. rice length, cooked rice length, cooked rice weigh, aroma test, expansion of cooked rice, semi liquid starch weight, cooking time were accomplished to assess the variability pertained for a particular character among the selected 10 rice advanced lines. The sources of variation included genotype, replication and error presented in (**Table 4.31).** It was observed that mean sum of squares of the varieties for all the characters were significant indicating significant variation present in all the F_6 lines. There was a little significant variation found among the three replications in all the characters. Coefficient of variation in all the characters was equal to or less than 6.68 except for rice length (8.17), cooked rice length (8.78). Similar results were reported by Bekele *et al.,* 2013, Kumar *et al.,* 2006, Salgotra *et al.,* 2009 and Dhanwani *et al.* 2013. The mean squares for the lines exhibited strong and significant differences in each of the selected characters and therefore, breeder could drive the breeding methods either through selection or hybridization for the improvement of present yield status of the fine rice lines. Development of high yielding varieties in almost every year by the rice breeders and by different commercial agencies are being culminated through exploitable variability in the popular fine rice land races, that leads to erosion of these valuable rice germplasm.

4.7.2 Comparison of mean values of different cooking characteristics of rice

The mean performances of 7 characteristics in 10 advanced lines of rice were separated by DMRT test at 5% level of probability presented **(Table 4.31).** The characteristics evaluated were rice length (cm), cooked rice length (cm), cooked rice weight (g), aroma test, expansion of cooked rice (cm), semi liquid starch volume (ml), cooking time (min).

4.7.2.1 Rice length (cm)

Among all the F_6 lines PL26 showed highest rice length (0.60 cm) and PL2, PL13, PL24 showed lowest rice length (0.40 cm), with a grand mean of 0.47 cm. The highly performing group was constituted by the lines PL26 (0.60 cm), PL1, PL15, PL16, PL17, PL22 (0.50 cm) respectively. The group which showed lowest rice length was PL2, PL13, PL24 (0.40 cm), PL12 (0.45cm) respectively **(Table 4.31).** A comparative view of

Table 4.31. Analysis of variance (Mean Square) for cooking qualities in 10 advanced generation (F_6) of fine rice

Source of Variation	df	RL	CRL	CRW	AC	ECR	SLSV	CT
Replication	2	0.01*	0.001	0.0003	0	0.44***	3.6	1.43
Genotype	9	0.012***	0.025**	0.049***	3.2***	0.94***	395.2***	23.44***
Error	18	0.001	0.005	0.003	0	0.014	8.71	1.62
CV (%)		8.17	8.78	3.11	0.0001	2.2	0.81	6.68

Here, RL= Rice length (cm), CRL = Cooked rice length (cm), CRW = Cooked rice weight (g), AC = Aroma content, ECR = Expansion of cooked rice (cm), SLSV = Semi liquid starch volume (ml) and CT = Cooking time (min).

And ** and *** indicates significant at 1% and 0.1% level of probability respectively and df indicates degrees of freedom.

results of this trait has been presented in **Figure 4.31** with 20% of the lines showing highest and 80% producing least rice length.

4.7.2.2 Cooked rice length (cm)

Among all the lines PL1 showed the highest cooked rice length (1cm) and PL2, PL17 showed the lowest cooked rice length (0.70 cm), with a grand mean of 0.84 cm. The highly performing group was constituted by the genotypes PL1 (1 cm), PL12, PL16, (0.90 cm) and respectively. The group which showed the lowest cooked rice length was PL2, PL17 (0.70 cm), PL15, PL24 (0.80 cm) respectively **(Table 4.32).** Maximum parental lines exhibited the highest cooked rice length as shown in **Figure 4.31**.

4.7.2.3 Cooked rice weight (g)

Among all the F_6 lines PL 26 showed the highest cooked rice weight (0.79g) and PL 15 showed the lowest weight (0.33g), with a grand mean of 0.59g. The highly performing group was constituted by the lines PL 26 (0.79g), PL24 (0.72g) and respectively. The group which showed lowest cooked rice weight was PL 15 (0.33g), PL 16 (0.53g) respectively **(Table 4.32).** A comparative view of results of this trait has been presented in **Figure 4.31** with 90% of the lines showing highest and 10% producing least cooked rice weight.

4.7.2.4 Aroma content

Among all the advanced lines PL 13 (9.00) showed the highest aroma test followed by PL15 (8.67), PL1 (8.33), PL22 (8.33), PL2 (8.00), PL12 (7.67), PL16 (7.67) and PL26 (7.00) showed the lowest aroma test followed by PL17 (7.33), PL24 (7.33) with a grand mean of 7.93 **(Table 4.32).** Maximum advance lines exhibited lowest aroma content as shown in **Figure 4.31.**

4.7.2.5 Expansion of cooked rice (cm)

Among all the lines PL 13 showed the highest expansion of cooked rice (5.87cm) and PL 17 showed the lowest expansion of cooked rice (4.5 cm), with a grand mean of 5.36 cm. The highly performing group was constituted by the lines PL 13 (5.87 cm), PL 1 (5.5 cm) and respectively. The group which showed the lowest expansion of cooked rice was PL17 (4.5 cm), PL 15 (4.6 cm) respectively **(Table 4.32).** A comparative view of results of this trait has been presented in **Figure 4.32** with 55% of the lines showing highest and 45% producing least expansion of cooked rice.

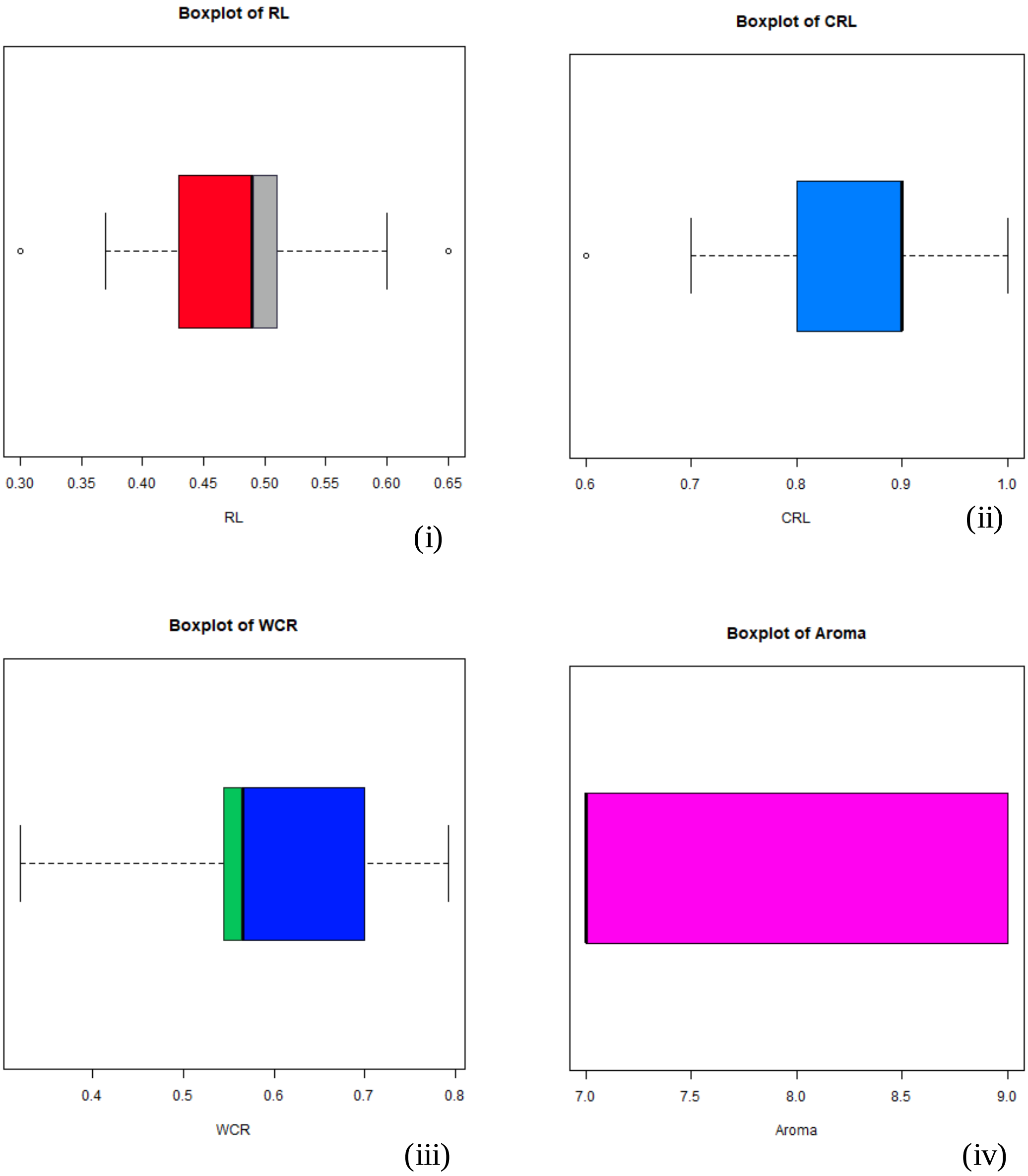


Figure 4.31. Boxplot showing (i) Rice length (cm), (ii) Cooked rice length (cm), (iii) Cooked rice weight (g) and (iv) Aroma content

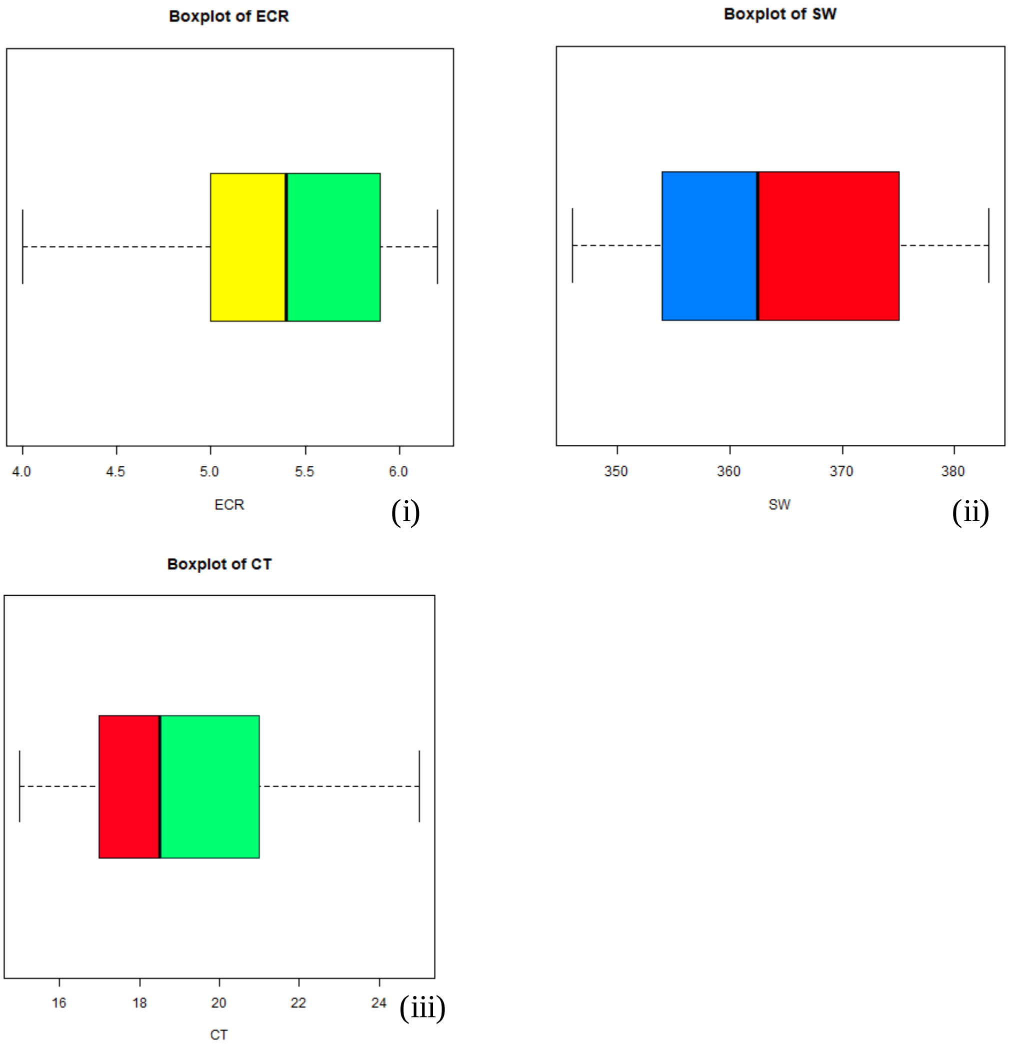


Figure 4.32. Boxplot showing (i) Expansion of cooked rice (cm) (ii) Semi liquid starch weight (ml) and (iii) Cooking time (min)

Table 4.32. Mean performances of different cooking characters in F_6 generation of fine rice

Genotypes	RL	CRL	CRW	AC	ECR	SLSV	CT
PL 1	0.50 b	1 a	0.58 cd	8.33 c	5.5 b	367 d	20 bc
PL 2	0.40 c	0.70 c	0.57 c-e	8.00 d	5 c	381 a	18 c-e
PL 12	0.45 bc	0.90 ab	0.55 d-f	7.67 e	5.8 a	373 bc	18 cd
PL 13	0.40 c	0.87 b	0.54 ef	9.00 a	5.87 a	358 e	21.67 b
PL 15	0.50 b	0.80 bc	0.33 f	8.67 b	4.6 d	353 ef	15.67 e
PL 16	0.50 b	0.90 ab	0.53 f	7.67 e	6 a	348 f	16 de
PL 17	0.50 b	0.70 c	0.59 c	7.33 f	4.5 d	355 e	17.67 c-e
PL 22	0.50 b	0.87 b	0.70 b	8.33 c	6 a	370 cd	24.33 a
PL 24	0.40 c	0.80 bc	0.72 b	7.33 f	5.13 c	355 e	21.67 b
PL 26	0.60 a	0.87 b	0.79 a	7.00 g	5.2 c	378 ab	17.33 de
Total	4.75	8.41	5.9	79.33	53.6	3638	190.34
Grand Mean	0.47	0.84	0.59	7.93	5.36	368.8	19.03
LSD	0.12	0.23	0.09	2.21	1.61	25.79	3.98

Here, RL= Rice length (cm), CRL = Cooked rice length (cm), CRW = Cooked rice weight (g), AC = Aroma content, ECR = Expansion of cooked rice (cm), SLSV = Semi liquid starch volume (ml) and CT = Cooking time (min).

4.7.2.6 Semi liquid starch volume (ml)

Among all the F_6 lines PL 16 showed the highest semi liquid starch weight (381ml) and PL 2 showed the lowest weight (348 ml), with a grand mean of 368.8 ml. The highly performing group was constituted by the advanced lines PL16 (381 ml), PL26 (378 ml) respectively. The group which showed the lowest semi liquid starch weight was PL2 (348 ml), PL15 (353 ml) respectively **(Table 4.32)**. A comparative view of results of this trait has been presented in **Figure 4.32** with 60% of the lines showing the highest and 40% producing least semi liquid starch weight.

4.7.2.7 Cooking time (min)

Among all the advanced lines PL22 showed highest cooking time (24.33 min) and PL15 showed lowest cooking time (15.67 min), with a grand mean of 19.03 min. The highly performing group was constituted by the lines PL 22(24.33 min), PL24 (21.67 min) and respectively. The group which showed the lowest cooking time was PL15 (15.67 min), PL16 (16 min) respectively **(Table 4.32)**. A comparative view of results of this trait has been presented in **Figure 4.32** with 70% of the lines showing highest and 30% producing least cooking time. Therefore, different cooking parameters particularly cooking time is very important for the fine rice consumers in our country.

CHAPTER V

SUMMARY AND CONCLUSION

Rice is the staple food for most of the Asian people and it is principally consumed as a whole grain after cooking. Despite being a major cereal grain, except yield potential, evaluation on rice quality has been given less priority. Huge varieties of rice exist and each variety differs in its agro-morphological, physico-chemical and cooking characteristics depending on the genetic background and growing environmental factors. Rice grain quality is influenced by all these parameters and consumer preference of rice varieties, differ from one region to another region of our country. To cope with the growing population, urbanization, climate change, food security, nutrient security, and changing food preference, there is a need for not only high yielding varieties but also for nutritionally improved rice varieties. In light of the facts, five experiments were sequentially conducted during July, 2015 to December, 2018. The Plant Breeding Research Field, BADC Seed Multiplication Farm, Nilphamari and BADC Seed Multiplication Farm, Faridpur and Genetics and Plant Breeding Laboratory were the experimental sites for accomplishing the total investigation. However, experiment wise results and output are described below-

Experiment I: Evaluation of F_4 generation for yield and yield promoting characters

The mean performances of thirteen characteristics in thirty-two advanced lines of rice were separated by DMRT test at 5% level of probability. The plant heights among the advanced lines were in general higher; the line, PL13 appeared as the tallest with 159.93 cm stature whereas, the shortest line was PL16 (123.66 cm) and the average was 137.33 cm. The group of advanced lines with higher plant height were constituted by PL13 (159.93 cm), PL17 (150.06 cm) and PL19 (144.23 cm) and group of lines that showed lower plant height were constituted by PL6 (123.66 cm), PL31 (125.70 cm) and PL24 (126.13 cm). The highest productive tillers/hill (8.90) was produced in PL2 and (8.50) was in PL8 and the lowest (4.90) was in PL8 and PL13. The grand mean value for the character was meseared to 6.75. The group of lines that showed higher number effective tillers /hill were constituted by PL2 (8.90), PL8 (8.50), PL9 (8.10), PL3 (7.80) and PL6 (7.70). The group of lines which showed the least number of productive tillers /hill were constituted by PL13 (4.90) and PL19 (4.90). The lines, PL13 and PL27 showed the highest lodging percentage (30.33%) and PL6 showed the lowest percentage (7.00%), with a grand mean of 18.57%. The highly performing group was constituted by the genotypes PL6 (7.00%), PL7 (11.33%), PL8 (11.33%), PL16 (11.33%), PL22 (11.33%) and PL31 (11.33%). The lines which showed the lowest performance of this trait were PL13 (30.33%), PL27 (30.33%), and PL3, PL4, PL12, PL14, PL18 and PL25 (26.330%). The group of F_4 lines which showed the lowest 1000-grain weight was PL30 (9.68 g), PL32 (11.68 g) and PL14 (12.47 g). The highest grain yield/hill (18.81 g/hill) was obtained in PL6 and the lowest yield (9.06 g/hill) was recorded in PL27. The group of lines that showed maximum days to maturity was constituted by PL29 (130.00 days) and PL24 (129.00 days). The group of genotypes which showed the least number of days to maturity was constituted by PL5 (99.00 days) and PL27 (121.00 days). The mean harvest index of the lines was recorded 31.62 percent and range varied from 26.71 percent (PL1) to 34.88 percent (PL5). Among all the F_4 lines, PL5 showed the maximum harvest index (34.88%) and PL1 showed the least harvest index (26.71%). The highly performing group included PL5 (34.88%), PL9 (34.69%) and PL15 (33.85%).

The analysis of variance (ANOVA) for thirteen quantitative characters including grain yield/hill were accomplished to assess the variability that existed for a particular character among the thirty-two F_4 lines. The sources of variation covered advanced lines, replications and experimental error. It was observed that mean sum of squares of the lines for all the characters were significant indicating significant variations present for the characters among the lines.

Different parameters such as genotypic variance (σ^2g), phenotypic variance (σ^2p), genotypic coefficient of variation (GCV %), phenotypic coefficient of variation (PCV %), heritability (%), genetic advance (GA) and genetic advance as percent of mean (GA %) for each of the thirteen characters were estimated to predict the variability existing among the characters. Most of the characters showed high heritability conjugated with low genetic advance, but high genetic advance (39.15) in fertile grains /panicle, indicates that the character may respond progressively well under favorable growing conditions. High phenotypic and genotypic variances were recorded with lodging percentage (LP) 33.85 and 33.71 respectively followed by grain yield /hill with 32.54 and 32.53; sterile grains/panicle 29.91 and 29.68; panicle weight 22.70 and 22.69. The lowest difference between GCV% and PCV% suggested strong inherent contribution of the lines and in general additive action of concerened alleles for the character. Again high heritability accompanied by high genetic advance indicates expected sustainable gain in the next generation after operating a selection program for the characters concerned. Accordingly, high heritability accompanied with high genetic advance as percent of the mean for productive tillers /hill, fertile grains/panicle, sterile grains/panicle, panicle weight, and sterility percentage, lodging percentage, 1000-grain weight, grain yield /hill and moderate genetic advance as plant height, days to 50% flowering, days to maturity, harvest index were measured.

Plant height revealed significant positive association with lodging percentage (rg=0.398**, rp=0.325**) but significant negative association with panicle weight (rg=-0.327**, rp=-0.539**) and grain yield /hill (rg=-0.514**, rp=-0.540**). Productive tillers /hill revealed significant positive association with grain yield /hill (rg=0.518**, rp=0.532**) but revealed significant negative association with lodging percentage (rg=-0.465**, rp=-0.543**). Fertile grains /panicle revealed significant positive association with panicle weight (rg=0.750**, rp=0.762**), grain yield /hill (rg=0.631**, rp=753**) and harvest index (rg=0.411**, rp=0.402**). Thousand grain weight showed significant positive association with grain yield /hill (rg=0.670**, rp=0.597**), harvest index (rg=0.211** rp=0.359**. The characters which showed positive significant association with grain yield /hill might may be considered for cocurrent improvement of those characters through simple selection breeding program.

From the path analysis, it was revealed that sterility percentage exhibited the lowest negative direct effect (-0.965) but 1000-grain weight paid the maximum direct effect (0.843) to develop strong genotypic correlation coefficients with grain yield /hill. Lodging percent also had negative direct effect on the development of a genotypic correlation with yield (-0.821) followed by days to 50% flowering (-0.646). Plant height had negative direct effect (-0.319) on grain yield/hill but showed negligible negative indirect effect through days to maturity and sterility percentage, productive tillers /hill had positive direct effect (0.303) on grain yield/hill but showed negligible negative indirect effect through sterile grains/panicle and showed negligible positive indirect effect through panicle length. Panicle length had positive direct effect (0.151) on grain yield/hill. It showed negligible negative indirect effect through productive tillers /hill, fertile grains/panicle, lodging percentage and showed negligible positive indirect effect through sterility percentage. Fertile grains /panicle had positive direct effect (0.381) on grain yield /hill. It showed negligible negative indirect effect through days to maturity and showed negligible positive indirect effect through plant height. The characters which exhibited positive indirect effects to develop strong association with grain yield /hill are considered as promising grain yield enhancing characters in fine rice. Most of the the positive or negative direct ditects were not compensated by indirect effects applied by yield related characters.

The thirty-two advanced lines were grouped following D^2 statistics on PCA superimposed. Maximum number of genotypes (twelve) were included in cluster III followed by cluster II with nine genotypes, cluster IV and V each comprising with five and two genotypes respectively, cluster I included four genotypes. The intra and inter cluster average distances among five clusters were variable. The highest intra-cluster distance was recorded for cluster V (1.322) followed by cluster IV (1.219) and cluster I (1.298) indicate genetic diversity among the lines belonging to these clusters. The genotypes belonging to the highest intra-cluster distance in the parenthesis (cluster IV) might develop good sergeants by crossing the genotypes of the cluster. The highest inter-cluster distance was observed between clusters I and V (13.534) suggests wide diversity present between the two clusters, followed by cluster IV and V (12.045), cluster II and V (11.853) and cluster I and IV (10.408). Therefore, advanced lines belonging to these clusters may be further used in hybridization program for the improvement of rice. The least inter- cluster distance was observed between clusters II and IV (2.258), followed by clusters I and III (2.307) indicate close relationship between the genotypes of these clusters and hence, may not be emphasized upon to be used in hybridization programs Fertile grains/panicle contributed maximum towards genetic divergence (16.378%) followed by sterile grains/panicle (15.691%), panicle length (11.034%) and 1000 grain weight (10.694%). Remaining traits had little contribution towards genetic divergence and hence, they were of less importance. Since the advanced lines with narrow genetic base are increasingly vulnerable to diseases and adverse climatic changes, availability of the genetically diverse genotypes for hybridization programs become more important. Since fertile grains/panicle, sterile grains/panicle, panicle length, 1000-grain weight contributed maximum towards the genetic divergence, we may initiate direct selection based on correlation with grain yield of these two characteristics for diversity purpose.

Experiment II: Assessment of selection response and realized heritability from F_4 to F_5 generation

Realized heritability decides the degree of resemblance between relatives and the rate of response to artificial and natural selections. Heritability mainly studied to determine how much variation in the phenotype in a population is due to genetic variation between individuals in that population. The highest realized heritability was found in grain yield /hill (93.58) with selection differential (1.87) and response to selection (1.75) followed by productive tillers /hill (91.45) with selection differential (1.04) and response to selection (0.95) and days to maturity (90) with selection differential (-0.10) and response to selection (-0.09). These values revealed that the offspring of the selected parents differed widely from the original population. Therefore, productive tillers/hill, grain yield/hill and days to maturity are the key components to evolve outstanding segregants at the end of several generations of selection.

Experiment III: Assessment of aroma in F_5 generation

Aroma was assessed from both young leaves and grain powder. Different scales such as, 9.00=very high, 7.00-<9.00=high, 5.00-<7.00=medium, 3.00-<5.00 and 1.00-<3.00=very low aroma content were applied for estimation of aromatic flavor The range of aroma varied 2.52 to 8.75 in fresh leaves and 3.39 to 8.83 in grain powder.

The advanced line, PL16 scored the highest rank (8.75) in fresh leaf and 8.83 in grain powder followed by PL12 (7.94), PL13 (7.94) and PL18 (7.94) in grain powder and PL14 (7.75) and PL13 (7.63) in fresh leaf and the lowest rank (3.39) scored by PL6 in grain powder and 2.52 by PL5 in fresh leaf followed by PL5 (3.94) in grain powder and PL6 (3.30), PL10 (3.52) and PL31 (3.75) in fresh leaf. The highest yield /hill 18.35 was scored by PL29, followed by PL23 (18.13), PL11 (18.11) and PL31 (18.07) where the lowest yield /hill in PL18 (13.26) followed by PL13 (13.46) PL32 (14.24). Therefore, joint consideration of aroma content either in green leaf or powder grain and grain yield /hill, the advanced lines PL13 and PL18 appeared as apparently outstanding to evolve superior progenies. However, it is very tough to improve aromatic rice jointly considering aroma content and yield potential, rather high aroma flavor with average yield potential variety development is more thoughtful in applied breeding of such advanced lines.

Experiment IV: Stability analysis of F_6 generation over the locations

A total of thirteen characters measured from ten fine rice advanced lines (F_6) were analyzed to assess G x E over three locations, like Plant Breeding Research Farm, HSTU, Dinajpur, Nilphamari and Faridpur. The advanced lines showing high mean yield, regression co-efficient (bi) around unity and deviation from regression (s^2di) near to zero are considered as suitable to evolve high yield as well as high aroma content varieties through further breeding. The advanced line, PL13 produced the highest yield (18.85g) and regression coefficient was around unity (1.11) with deviation from regression of 0.46 and was found to be suggests the most stable among the ten advanced lines across the three locations. Another line, PL16 produced a reasonable yield (18.10g) and its regression coefficient was close to unity (b=0.32) and deviation from regression was very nearer to zero (s^2d=0.12), hence the advance line was stabled irrespective of growing conditions and was suitable for general adaptation. Further GGE biplot analysis revealed Dinajpur was the best environment as compared to other two environments. The yield of PL1 was average but its deviation from regression was far away from zero, hence, the line intended to respond favorably to better environment like Plant Breeding Research Field, HSTU, Dinajpur and would be produced poor yield in unfavorable growing condition like BADC Seed Multiplication Farm, Faridpur and in a comparative view, PL15 was better than PL1. At the end of this investigation, it may be concluded that among the fine rice advanced lines, PL1 is suitable Dinajpur region and lines PL13 and PL16 are suitable across the three locations. In our country, very few advance line are adapted across the environments and the popular advance line are restricted to grow in a particular zone of the country. In such situation, new aromatic varieties may be developed exploiting the advanced lines shown average yield but considerable aroma flavor over the locations.

Experiment V: Estimation of cooking quality in F_6 generation

The mean performances of seven characteristics in ten advanced lines of rice were separated by DMRT test at 5% level of probability. Among all the genotypes PL26 showed the highest rice length (0.60 cm) and PL2, PL13, PL24 showed the lowest rice length (0.40 cm). PL1 showed the highest cooked rice length (1 cm) and PL2, PL17 showed the lowest cooked rice length (0.70 cm). PL26 showed the highest cooked rice weight (0.79g) and PL15 showed the lowest weight (0.33g). PL13 (9.00) showed the highest aroma test followed by PL15 (8.67), PL1 (8.33), PL22 (8.33), PL2 (8.00), PL12 (7.67), PL16 (7.67) and PL26 (7.00) showed the lowest aroma test followed by PL17 (7.33), PL24 (7.33) with a grand mean of 7.93. PL13 showed the highest expansion of cooked rice (5.87 cm) and PL17 showed the lowest expansion of cooked rice (4.5 cm). PL16 showed the highest semi liquid starch weight (381 ml) and PL2 showed the lowest weight (348 ml). PL22 showed highest cooking time (24.33 min) and PL15 showed the lowest cooking time (15.67 min). Larger expansion of cooked rice along with low requirement of heat energy are of great concerns during estimating the cooking qualities of rice; hence PL1 with highest cooked rice length, PL13 with highest expansion and PL16 with highest semi-liquid starch appeared to be superior to other advanced lines of rice.

Finally, the following conclusions are put down for further plant breeding activities-

I. Significant variation were revealed for 13 characters in 32 F_4 generation and productive tillers/hill, panicle weight and 1000-grain weight were strongly associated with grain yield/hill both at genotypic and phenotypic levels.

II. The 32 advanced lines (F_4) were grouped into five clusters where cluster I and V exhibited more diverse.

III. Variability of the characters gradually decreased with advancing the generation from F_4 to F_6.

IV. The advanced line PL13 (Kalozira×Chinigura) showed maximum aroma content (9.00) and medium grain yield (16.12 g/hill) and PL1 (Kataribhog×kalozira) with medium aroma content (8.33) but highest grain yield (18.85 g/hill) followed by PL16 (Kalozira×Chinigura) for yield potential and aroma content.

V. Among the three locations, HSTU (Dinajpur) appeared suitable for cultivation.

VI. Therefore three superior F_6 lines (PL1, PL13 and PL16) might incorporate in future breeding programs for the development of new fine rice varieties.

REFERENCES

Adams, M.W. (1967). Basis of yield component compensation in crop plants with special reference to the field bean, Phaseolus vulgaris 1. *Crop Science,* 7(5): 505-510.

Afiukwa, C.A., Faluyi, J.O., Atkinson, C.J., Ubi, B.E., Igwe, D.O. and Akinwale, R.O. (2016). Screening of some rice varieties and landraces cultivated in Nigeria for drought tolerance based on phenotypic traits and their association with SSR polymorphisms. *African Journal of Agricultural Research,* 11(29): 2599-2615.

Agrawal, P.K. (2003). Molecular approaches in evolutionary studies and speciation in genus Oryza—present status. In: Nanda, J.S. and S.D. Sharma (eds.) Monograph on Genus Oryza, Science Publishers, Inc. USA, pp. 139–170.

Ahmad, W.S., Loc, H.N., Mehran, Z., Wahida, Y., Tadashi, Y. and Yutaka, H. (2014). Comparative Analyses for Aroma and Agronomic Traits of Native Rice Cultivars from Central Asia. *Journal Crop Science Biotechnology,* 11(1): 17-22.

Ahmad, W.S., Shams, S., Mohammad, G.B. and Mohammad, G.S. (2015). Comparison of Yield and yield components among different Varieties of Rice. *Global Journal of Biology Agriculture and Helth Science,* 4(1): 158-163.

Ahmed (2019). ADB: Bangladesh continues to post high economic growth in 2019-20. Retrived at: https://www.dhakatribune.com/business/economy/2019/07/14/adb-Bangladesh-continues-to-post-high-economic-growth-in-2019-20. Published on July 14th, 2019.

Ahmed, M.S.K., Akter, M., Khalequzzaman, E.S.M.H., Rashid and Bashar, M.K. (2015). Diversity analysis in Boro rice (*Oryza sativa* L.) accessions. *Bangladesh Journal of Agricultural Research,* 35(1): 29-36.

Ahmed, S.U., Mohammad, M.K., Bashar, M.K. and Mohammad, A.K.S. (2016). Agro-Morphological, Physico-Chemical and Molecular Characterization of Rice Germplasm with Similar Names of Bangladesh. *Rice Science*, 23(4):

Ajmer, S., Jatasra, D.S., Ram, C., Battam, S. and Panwar, D.V.S. (1979). Genetic variability, correlation and path analysis in Maize (*Zea mays* L.) inbreds. *Bangladesh Journal of Pant Breeding and Genetics,* 10(2): 57-61.

Akhond, M.A.Y., Amiruzzaman, M., Bhuiyan, M.S.A., Uddin, M.N. and Hoque, M.M. (1998). Genetic parameters and character association in grain sorghum. *Bangladesh Journal of Agricultural. Research*, 23: 247-254.

Akinwale, M.G., Gregorio, G., Nwilene, F., Akinyele, B.O., Ogunbayo, S.A. and Odiyi, A.C. (2011). Heritability and correlation co-efficient analysis for yield and its components in rice (*Oryza sativa* L.). *African Journal of Plant Science*, 5(3): 207-212.

Al-kordy, M.A., Ibrahim, H.F., El-Mouhamady, A.B.A. and Abdel-Rahman, H.M. (2019). Genetic stability analysis and molecular depiction in elite entries of rice (*Oryza sativa* L.). *Bulletin of the National Research Centre*, 43(1): 85.

Allard, R. W. (1960) Principles of plant breeding. Wiley and Sons Inc., New York.

Amegan, E., Efisue, A., Akoroda, M., Shittu, A. and Tonegnikes, F. (2020). Genetic Diversity of Korean Rice (*Oryza sativa* L.) Germplasm for Yield and Yield Related Traits for Adoption in Rice Farming System in Nigeria. *Genomics, 8*(1), 19-28.

Anderson, J. (1987). The markedness differential hypothesis and syllable structure difficulty. *Interlanguage phonology: The acquisition of a second language sound system*, 279-291.

Anjali, K., Vanisree, S., Raju, C. and Sreedhar, M. (2014). Genetic Diversity Studies in Aromatic Rice (*Oryza sativa* L.) Germplasm. *Madras Agricultural Journal*, *101*.

Babu, N.N., Krishnan, S.G., Vinod, K.K., Krishnamurthy, S.L., Singh, V.K., Singh, M.P. and Bhowmick, P.K. (2017). Marker aided incorporation of Saltol, a major QTL associated with seedling stage salt tolerance, into *Oryza sativa* ‘Pusa basmati 1121’. *Frontiers in Plant Science,* 8: 41.

Bagheri, N., Babaeian-Jelodar, N. and Pasha, A. (2011). Path coefficient analysis for yield and yield components in diverse rice (*Oryza sativa* L.) genotypes. *Biharean Biologist*, 5(1): 32-35.

Bagudam, R., Eswari, K.B., Badri, J. and Rao, P.R. (2018). Correlation and Path Analysis for Yield and its Component Traits in NPT Core Set of Rice (*Oryza sativa* L.). *International Journal of Current Microbiology and Applied Sciences*, 7(9): 97-108.

Banumathy, S., Manimaran, R., Sheeba, A., Manivannan, N., Ramya, B., Kumar, D. and Ramasubramanian, G.V. (2010). Genetic diversity analysis of rice germplasm lines for yield attributing traits. *Electronic Journal of Plant Breeding*, 1(4): 500-504.

Baradhan and Thangavel. (2011). D2 analysis in rice (L.). *Plant Archives*, 11(1): 373-375.

Bartley, B.G. and Weber, C.R. (1952). Heritable and non heritable relationship and variability of agronomic characters in sucessive generations of soybean crosses. *Agronomy Journal*, 44(9): 487-493.

Basavaraja, T., Gangaprasad, S., Kumar D. and Hittlamani, S. (2011). Correlation and path analysis of yield and yield attributes in local rice cultivars (*Oryza sativa* L.), *Electronic Journal of Plant Breeding*, 2(4): 523-526.

Bates, L. S., Waldren, R. P., and Teare, I. D. (1973). Rapid determination of free proline for water-stress studies. *Plant and Soil*, *39*(1): 205-207.

BBS. (2019). The year book of agricultural statistics of Bangladesh. Stat. Div. Ministry. Plan., Govt. Peoples Rep. Bangladesh. Dhaka, pp. 123-127.

BBS. (2020). The year book of agricultural statistics of Bangladesh. Stat. Div. Ministry. Plan., Govt. Peoples Rep. Bangladesh. Dhaka, pp. 129-133.

Bekele, B.D., Rakhi, S., Naveen, G.K., Kundur, P.J. and Shashidar, H.E. (2013). Estimation of genetic variability and correlation studies for grain zinc concentrations and yield related traits in selected rice (*Oryza sativa* L.) genotypes. *Asian Journal of Experimental Biology*, 4(3): 391-397.

Bhandari, H.R., Bhanu, A.N., Srivastava, K., Singh, M.N., Shreya and Hemantaranjan, A. (2017). Assessment of genetic diversity in crop plants - an overview. *Advance Plants Agriculture Resserch*, 7(3): 279-286.

Bhuiyan, M.S.H., Zahan, A., Khatun, H., Iqbal, M., Alam, F. and Manir, M.R. (2014). Yield performance of newly developed test crossed hybrid rice variety. *International Journal of Agronomy and Agricultural Research*, 4(5): 48-54.

Bhutta, M.A., Munir, S., Qureshi, M.K., Shahzad, A.N., Aslam, K., Manzoor, H. and Shabir, G. (2019). Correlation and Path Analysis of Morphological Parameters Contributing to Yield in Rice (*Oryza sativa*) Under Drought Stress. *Pakistan Journal Botany*, 51(1): 73-80.

BINA (Bangladesh Institute of Nuclear Agriculture). (1993). Annual Report (1992-93). *Bangladesh Institute of Nuclear Agriculture*, 143.

Biswas, B.K., Azad, A.K., Hasanuzzaman, M., Begum, L.A. and Khandoker, R.A. (2008). Genetic Basis of Variability and Diversity Present in Fine Rice Available in Bangladesh. *Journal of Science and Technology* (Dinajpur), 6: 57-66.

Blanco, L., Casal, C., Akita, S. and Virmani, S.S. (1990). Biomass, grain yield and harvest index of F1 race hybrids and inbreeds. *International Rice Research Newsland*, 15(2): 9-10.

Bourgis, F., Guyot, R., Gherbi, H., Tailliez, E., Amabile, I., Salse, J., Lorieux, M., Delseny, M. and Ghesquiere, A. (2008). Characterization of the major fragance gene from an aromatic japonica rice and analysis of its diversity in Asian cultivated rice. *Theory and Applied Genetics,* 117: 353–368.

Bradbury, L. M. (2009). Identification of the gene responsible for fragrance in rice and characterisation of the enzyme transcribed from this gene and its homologs.

Buttery, R.G., Ling, L.C., Juliano, B.O. and Turnbaugh, J.G. (1983). Cooked rice aroma and 2-acetyl-1-pyrroline. *Journal of Agricultural and Food Chemistry*, 31(4): 823-826.

Chanbeni, Y., Ovung, G., Lal, M. and Rai, P.K. (2012). Studies on genetic diversity in Rice (*Oryza sativa* L.). *Journal of Agricultural Technology,* 8(3): 1059-1065.

Chandra, B.S., Reddy, T.D. and Ansari, N.A. (2007). Genetic divergence in rice (*Oryza sativa* L.). *Research on Crops,* 8: 600-603.

Chaubey, P.K. and Singh, R.P. (1994). Genetic variability, correlation and path analysis of filled components in rice. *Madras Agriculture Journal,* 81: 438-470.

Chowdhury, M.T.U., Sarker, A.U., Sarker, M.A.R. and Kashem, M.A. (1993). Effect of variety and number of seedlings hill -1 on the yield and its components on late transplanted *aman* rice. *Bangladesh Journal of Agricultural Science,* 20(2): 311-316.

Chowdhury, S., Khaled, N. B., Raghunathan, K., & Rashid, S. (2021). Public food transfers during pandemic: Insights from an IFPRI survey in Bangladesh.

Chuchert, S., Nualsri, C., Junsawang, N., and Soonsuwon, W. (2018). Genetic diversity, genetic variability, and path analysis for yield and its components in indigenous upland rice (*Oryza sativa* L. var. glutinosa). Songklanakarin *Journal Science and Technology*, 40(3): 609-616.

Chukwuemeka, A.I., Kelechi, A.J. and Bernard, A. (2015). Cooking and Physicochemical Properties of Five Rice Varieties Produced in Ohaukwu Local Government Area. *European Journal of Food Science and Technology,* 3(1): 1-10.

Clifford, H.T. and Stephenson, W. (1975). An Introduction to Numerical Classification. Academic Press, London, p. 229.

Comstock, K., & Robinson, P. R. (1952). Estimation of genetic advance. *Indian Journal of Hill Farming*, *6*(2): 171-174.

Correia, P., Alves, M., Lemos, D. and Guine, R. (2013). Contribution for Physical Characterization of Aromatic Rice. *Journal of Hygienic Engineering and Design*, UDC 633.18.

Crossa, J., H.G. Gauch and R.W. Zobel, 1990. Additive main effects and multiplicative interaction analysis of two international maize cultivar trials. *Crop Science,* 30: 493-500.

Crossa, J., P.N. Fox, W.H. Pfeiffer, S. Rajaram and H.G. Gauch Jr., 1991. AMMI adjustment for statistical analysis of an international wheat yield trial. *Theoretical and Applied Genetics,* 81: 27-37.

Cruz, C.D., Carneiro, P.C.S. and Regazzi, A.J. (2014). Modelos biométricos aplicados ao melhoramento genético. 3rd edition. Universidade Federal de Viçosa, 2: 668.

Cruz, C.D., Ferreira, F.M. and Pessoni, L.A. (2011). Biometria aplicada ao estudo da diversidade genética. Viçosa: Suprema, p. 620.

Danbaba, N., Anounye, J. C., Gana, A. S., Abo, M. E., Ukwungwu, M. N., and Maji, A. T. (2012). Physical and pasting properties of 'ofada' rice (*Oryza sativa* L.) varieties. *Nigerian Food Journal, 30*(1), 18-25.

Danbaba, N., Anounye, J.C., Gana, A.S., Abo, M.E. and Ukwungwu, M.N. (2011). Grain quality characteristics of Ofada rice (*Oryza sativa* L.): Cooking and eating quality. *International Food Research Journal,* 18: 629-634.

Das, S., Khanda, C.M., Mohanty, S.K., Parida, S. and Pradhan, B. (2014). Screening of indigenous aromatic rice cultivars for yield and aroma under moisture stress condition in western undulating zone of Odisha. *Journal of Pharmacognosy and Phytochemistry,* 7(3): 1958-1963.

Datta, D.S.K. (1981). Principles and Practices of Rice Production. John Wiley, New York.

De Datta, S. K. (1981). Principles and practices of rice production. International Rice Research Institute.

de la Hera, E., Gomez, M., & Rosell, C. M. (2013). Particle size distribution of rice flour affecting the starch enzymatic hydrolysis and hydration properties. *Carbohydrate Polymers, 98*(1), 421-427.

De la Hera, E., Martinez, M. and Gómez, M. (2013). Influence of flour particle size on quality of gluten-free rice bread. *LWT-Food Science and Technology*, 54(1): 199-206.

Debchoudhury, P.K. and Das, P.K. (1998). Genetic variability, correlation and path coefficient analysis in deep water rice. *Annals of Agricultural Research*, 19: 120-124.

Dessie, A., Zewdu, Z., Berie, A. and Atnaf, M. (2020). GGE Biplot Analysis of Genotype X Environment Interaction of Cold Tolerant Green Super Rice Genotypes in Ethiopia. *International Journal of Research and Review*, 7(1), 300-305.

Devi, B. (2016). Genetic divergence analysis for quantitative traits in rice (*Oryza sativa* L.), *European Journal of Biotechnology and Bioscience*, 4: 01-03.

Devi, K.R., Chandra, B.S., Lingaiah, N., Hari, Y. and Venkanna, V. (2017). Analysis of variability, correlation and path coefficient studies for yield and quality traits in rice (*Oryza sativa* L.). *Agricultural Science Digest-A Research Journal*, 37(1): 1-9.

Devi, K.R., Parimala, K., Venkanna, V., Lingaiah, N., Hari, Y., and Chandra, B.S. (2016). Estimation of variability for grain yield and quality traits in rice (*Oryza sativa* L.). *International Journal of Pure and Applied Bioscience*, 4(2): 250-255.

Devi, R. K., Venkanna, V., Hari, Y., Chandra, S. B., Lingaiah, N., & Rajendra, K. P. (2020). Studies on genetic diversity and variability for yield and quality traits in promising germplasm lines in rice (*Oryza sativa* L.). *The Pharma Innovation Journal*, *9*(1), 391-399.

Dewey, D.R. and Lu, K.H. (1959). A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agronomy Journal*, 51(9): 515-518.

Dhanwani, R.K., Sarawgi, A.K., Solanki, A. and Tiwari, J.K. (2013). Genetic variability analysis for various yield attributing and quality traits in rice (*Oryza sativa* L.). *The Bioscan*, 8(4): 1403-1407.

Dutta, B.C., Nath, A. and Dasgupta, T. (1998). Characterization and variability analysis of Rice genotypes with reference to Cooking Quality Parameters. *Journal of Agriculture and Veterinary Science,* 9(4 Ver. II): 08-12.

Dwivedi, J.L. (1985). Heterosis in rice and its exploitation. In: Genetics and Rice Improvement. National Symposium held at Directorate of Rice Research, Hyderabad, India, 40-42.

Eberhart, S.T. and Russell, W.A. (1966). Stability parameters for comparing varieties 1. *Crop Science,* 6(1): 36-40.

Eeuwijk, F. A., Bustos-Korts, D. V., and Malosetti, M. (2016). What should students in plant breeding know about the statistical aspects of genotype× environment interactions? *Crop Science*, *56*(5), 2119-2140.

Ekka, H., Padhee, D., Sharma, L., Diwakar, M., Lahari, R. and Tiwari, S. (2016). Study of cooking quality of selected varieties of rice at varying temperature using induction heater. *International Journal of Food Science and Nutrition,* ISSN: 2455-4898, Impact Factor: RJIF 5.14.

Ekka, H., Padhee, D., Sharma, L., Diwakar, M., Lahari, R. and Tiwari, S. (2010). Study of cooking quality of selected varieties of rice at varying temperature using induction heater.

Ekka, R.E., Sarawgi, A.K. and Kanwar, R.R. (2011). Correlation and path analysis in traditional rice accessions of Chhattisgarh. *Journal of Rice Research*, 4(1): 11-18.

Falconer, D.S. and Mackay, T.F.C. (1996). Introduction to Quantitative Genetics. 4th ed. Longman Group Limited, Harlow, UK.

Faruq, G., Khalid, N., Jennifer, A.H., Subha, B., Zulqarnain, M., Osman, M. and Mohammad, O. (2010). Evaluation of kernel elongation ratio and aroma association in global popular aromatic rice cultivars in tropical environment. *African Journal of Agricultural Research*, 5(12): 1515-1522.

Faruq, G., Prodhan, Z.H. and Nezhadahmadi, A. (2015). Effects of Ageing on Selected Cooking Quality Parameters of Rice. *International Journal of Food Properties,* 18: 922–933.

Fernandez, R. (2002). Unlad-Ani Program: Hybrid Rice Program Now in Full Swing. Philippine Star, 7.

Financial Express Report (2018). Imported fine varieties making inroads into local rice market. Middle-class drives demand for pricey staple. Retrived at: https://thefinancialexpress.com.bd/trade/imported-fine-varieties-making-inroads-into-local-rice-market-1526064965. Published on May 12, 2018.

Foreign Agricultural Service (2019). Scheduled Reports – 2019. Retrived at: https://www.fas.usda.gov/data-analysis/scheduled-reports-2019.

Frankel, O.H. (1935). Analytical Yield Investigations on New Zealand Wheat: II. Five Years' Analytical Variety Trials. *The Journal of Agricultural Science*, 25(4): 466-509.

Freeman, G.H. (1985). The analysis and interpretation of interaction. *Journal of Applied Statistics*, 12: 3-10.

Gana A.S. (2006). Variability studies of the response of rice varieties to biotic and abiotic stresses. Ph.D Thesis, University of Ilorin.

Gana, A.S., Shaba, S.Z. and Tsado, E.K. (2013). Principal component analysis of morphological traits in thirty-nine accessions of rice (*Oryza sativa* L.) grown in a rainfed lowland ecology of Nigeria. *Journal of Plant Breeding and Crop Science,* 4(6): 120-126.

Ganapati, R. K., Rasul, M. G., Sarker, U., Singha, A., & Faruquee, M. (2020). Gene action of yield and yield contributing traits of submergence tolerant rice (*Oryza sativa* L.) in Bangladesh. *Bulletin of the National Research Centre, 44*(1), 1-7.

Ganapati, R.K., Rasul, M.G., Mian, M.A.K. and Sarker, U. (2014). Genetic variability and character association of T-Aman rice (*Oryza sativa* L). *International Journal of Plant Biology and Research*, 2(2): 1-4.

Ganapati, R.K., Rasul, M.G., Sarker, U., Singha, A. and Faruquee, M. (2020). Gene action of yield and yield contributing traits of submergence tolerant rice (*Oryza sativa* L.) in Bangladesh. *Bulletin of the National Research Centre*, 44(1): 1-7.

Garcia, D.M., Bassinello, P.Z., Ascheri, D.R.P., Ascheri, J.L.R., Trovo, J.B.T. and Cobucci, R.D.M.A. (2011). Cooking quality of upland and lowland rice characterized by different methods. *Food Science and Technology,* 31(2): 341-348.

Garg, P., Pandey, D.P. and Kaushik, R.P. (2011). Genetic divergence for yield and quality traits in rice (*Oryza sativa* L.). *Journal of Rice Research,* 4(1): 1-5.

Girma, C. (2018). Genotype X Environment Interaction and Yield Stability in Improved Rice Varieties (*Oryza sativa* L.) Tested Over Different Locations in Western Oromia, Ethiopia, *Global Journal of Science Frontier Research,* 18(5): 39-44.

Golam, F., Yin, Y.H., Masitah, A., Afnierna, N., Majid, N.A., Khalid, N. and Osman, M. (2011). Analysis of aroma and yield components of aromatic rice in Malaysian tropical environment. *Australian Journal of Crop Science,* 5(11): 1318-1325.

Golam, F., Zulaani, K.N., Jennifer, A.H., Subha, B., Zulqarnain, M., Nazia, A.M., Zulqarnian, M. and Mohammad, O. (2010). *African Journal of Agricultural Research,* 5(12): 1515-1522.

Govintharaj, P., Tannidi, S., Swaminathan, M. and Sabariappan, R. (2017). Effectiveness of selection, parent-offspring correlation and regression in bacterial blight resistance genes introgressed rice segregating population. *Ciência Rural,* 47(9).

Gravois, K.A. and Mcnew, R.M. (1993). Genetic relationship among and selection for rice yield and yield components. *Crop Science,* 33(2): 249-252.

Guei, R.G., Sanni, K.A. and Fawole, A.F.J. (2005). Genetic diversity of rice (*Oryza sativa). Agronomie Africaine,* 5: 17–28.

Hairmansis, A., Kustianto, B. and Suwarno, S. (2013). Correlation analysis of agronomic characters and grain yield of rice for tidal swamp areas. *Indonesian Journal of Agricultural Science*, 11(1): 11-15.

Haripriya, A., Mercy, L., Radhika, V. and Darshini, M.P.R. (2017). Quality characteristics of indigenous organic Indian rice variety: Kouni nel. *International Journal of Home Science,* 3(1): 75-81.

Hasan, M.J., Kulsum, M.U., Akter, A., Masuduzzaman, A.S.M. and Ramesha, M.S. (2010). Genetic Variability and Character Association forAgronomic Traits in Hybrid Rice (*Oryza sativa* L.), *Bangladesh Journal Plant Breeding and Genetics,* 24(1): 45-51.

Hasan, M.J., Kulsum, M.U., Akter, A., Masuduzzaman, A.S.M. and Ramesha, M.S. (2013). Genetic variability and character association for agronomic traits in hybrid rice (*Oryza sativa L.*). *Bangladesh Journal of Plant Breeding and Genetics*, 24(1): 45-51.

Hien, N. L., Yoshihashi, T., Sarhadi, W. A., and Hirata, Y. (2006). Sensory test for aroma and quantitative analysis of 2-acetyl-1-pyrroline in Asian aromatic rice varieties. *Plant Production Science*, *9*(3), 294-297.

Horna, J.D., Smale, M. and Von Oppen, M. (2005). Farmer willingness to pay for seed-related information: rice varieties in Nigeria and Benin. Washington DC.: International Food Policy Research Institute (IFPRI), EPT Discussion 142 pp.

Hossain, M.S., Singh, A.K. and Zaman, F.U. (2009). Cooking and eating characteristics of some newly identified inter sub-specific (indica/japonica) rice hybrids. *Science Asia Journal,* 35: 320–325.

Hossain, S., Haque, M. and Rahman, J. (2015). Genetic Variability, Correlation and Path Coefficient Analysis of Morphological Traits in some Extinct Local Aman Rice (*Oryza sativa* L), *Journal of Rice Research,* 4: 1.

IRRISTAT (2017). Statistical data base. International Rice Research Institute, Manila, Philippines.

Islam, M. Z., Khalequzzaman, M., Bashar, M. K., Ivy, N. A., Haque, M. M., & Mian, M. A. K. (2016). Variability assessment of aromatic and fine rice germplasm in Bangladesh based on quantitative traits. *The Scientific World Journal*, *2016*.

Islam, M.R., Mustafi, B.A.A. and Hossain, N. (1996). Socio-economic aspects of fine quality rice cultivation in Bangladesh (Rice Res. Prioritization), BRRI/IRRI.

Jadhav, S., Balakrishnan, D., Beerelli, K., Chandu, G. and Neelamraju, S. (2019). Genotype by Environment (G×E) Interaction Study on Yield Traits in Different Maturity Groups of Rice. *Journal of Crop Science and Biotechnology*, 22(5): 425-449.

Jeger MI, Garethojies D, Griffiths E. Components of partial resistance of wheat seedling of Septoria nodorum. Euphytica. 1983;32:575–84

Jiang, L.G., Wang, W.J. and Xu, Z.S. (2015). Study on development patterns, dry matter production and yield of indica rice varieties. *Huazhong Agricultural University,* 14(6): 549-554.

Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Estimates of genetic and environmental variability in soybean. *Agronomy Journal*, 47(7): 314- 318.

Johnson, P.L., Sharma, R.N. and Nanda, H.C. (2015). Genetic diversity and association analysis for yield traits chickpea (*Cicer arietinum* L.) under rice based cropping system. *The Bioscan*, 10(2): 879-884.

Juliano, B.O., Bautista,G.M., Lugay, J.C. and Reyes, A.C. (1964). Studies on the physicochemical properties of rice. *Journal of Agricultural and Food Chemistry*, 12: 131-138.

Kabir, M. S., Salam, M. U., Chowdhury, A., Rahman, N.M. F., K M Iftekharuddaula, K. M., Rahman, M. S., Rashid, M.H., Dipti, S. S., Islam, A., Latif, M. A., Islam, A. K. M. S., Hossain, M. M., Nessa, B., Ansari, T. H., Ali, M. A. and Biswas, J. K. (2015). Rice Vision for Bangladesh: 2050 and Beyond. *Bangladesh Rice Journal*, 19(2):1-18.

Kalyan, B., Radha Krishna, K.V. and Subba Rao, L.V. (2017). Correlation coefficient analysis for yield and its components in rice (*Oryza sativa* L.) genotypes. *International Journal of Current Microbiology and Applied Sciences*, 6(7): 2425-2430.

Kar, R.K., Mishra, T.K., Pandey, R.K. and Das, S.R. (2016). Assessment of Genetic Variability in Low Land Sub-1 Introgressed Rice Genotypes Showing Tolerance to Submergence and Stagnant Flooding. *Journal of Agriculture and Veterinary Science,* 9(6 Ver. I): 42-46.

Karthikeyan, P., Anbuselvam, Y., Elangaimannan, R., Venkatesan, M. (2009). Variability and heritability studies in rice (*Oryza sativa* L.) under coastal salinity. *Electronic Journal of Plant Breeding,* 1: 196-98.

Kato, T. (1997). Selection responses for the characters related to yield sink capacity of rice. *Crop Science*, 37(5): 1472-1475.

Kaur, J., Mahal, S. S.and Kaur, A. (2016). Yield and quality evaluation of direct seeded basmati rice (*Oryza sativa* L.) under different irrigation and nitrogen regimes. *Cereal Research Communications,* 44(2): 330-340.

Khammari, M., Khani, M.M., Khammari, D.A. and Nia, M.R. (2016). The Eating and Cooking Qualities of Rice: A Review. *International Journal of Science and Technology,* 2(2): 134-139.

Khatun, M., Hanafi, M.M., Yusop, M.R., Wong, M.Y., Salleh, F.M. and Ferdous, J. (2015). Genetic variation, heritability, and diversity analysis of upland rice (*Oryza sativa* L.) genotypes based on quantitative traits. *BioMed Research International,* ID 290861.

Khush, G. S. (2001). Green revolution: the way forward. *Nature Reviews Genetics*, *2*(10): 815-822.

Khush, G.S. (1997). Origin, dispersal, cultivation and variation of rice. *Plant Molecular Biology*, 35: 25-34.

Kiniry, J.R., McCauley, G., Xie, Y. and Arnold, J.G. (2001). Rice parameters describing crop performance of four U.S. cultivars. *Agronomy Journal,* 93(6): 1354-1361.

Kishore, N.S., Babu, V.R., Ansari, N.A. and Chandran, R. (2007). Genetic divergence analysis using yield and quality traits in rice (*Oryza sativa* L.). *Crop Improvement,* 34: 12-15.

Kohnaki, E.M., Kiani, G. and Nematzadeh, G. (2016). Relationship between Morphological Traits in Rice Restorer Lines at F3 Generation using Multivariate Analysis. *International Journal of Advanced Biological and Biomedical Research,* 1(6): 572-577.

Kole, P.C., Chakraborty, N.R., Bhat, J.S. (2008). Analysis of variability, correlation and path coefficients in induced mutants of aromatic non-basmati rice. *Tropical Agricultural Research and Extension,* 11: 60-64.

Konate, A.K., Zongo, A., Kam, H., Sanni, A. and Audebert, A. (2016). Genetic variability and correlation analysis of rice (*Oryza sativa* L.) inbred lines based on agro-morphological traits, *African Journal of Agricultural Research,* 11(35): 3340-3346.

Krishnaveni, B., Shobharani, N. and Ramprasad, A.S. (2006). Genetic parameters for quality characteristics in aromatic rice. *Oryza.,* 43(3): 234-237.

Kulsum, M.U., Hasan, M.J., Akter, A., Rahman, H. and Biswas, P. (2013). Genotype-environment interaction and stability analysis in hybrid rice: an application of additive main effects and multiplicative interaction. *Bangladesh Journal of Botany*, 42(1): 73-82.

Kumar, A., Singh, N.K. and Sharma, V.K. (2006). Combining ability analysis for identifying elite parents for heterotic rice hybrids. *Oryza,* 43(2): 82-86.

Kumar, M., Prakash, N. and Sharma, P.R. (2009). Effectiveness of F2 and F3 plant selection for yield and its components in rice. *ORYZA-An International Journal on Rice,* 46(1): 17-20.

Kumar, P.S. and Saravanan, K. (2012). Genetic variability, correlation and path analysis in rice (*Oryza sativa* L.). *International Journal of Current Research,* 4(9): 82-85.

Kumar, S., Chauhan, M.P., Tomar, A., Kasana, R.K. and Kumar, N. (2018). Correlation and path coefficient analysis in rice (*Oryza sativa* L.). *The Pharma Innovation Journal*, 7(6): 20-26.

Kumar, V. (2015). Genetic diversity and character association studies for some economic traits in rice (*Oryza sativa* L.). *The Bioscan*, 10(2): 899-904.

Lakew, T., Dessie, A. Desta, S.T. and Abebe. (2017). Evaluation of Performance and Yield Stability Analysis Based on AMMI and GGE Models in Introduced Upland Rice Genotypes Tested Across Northwest Ethiopia, *International Journal of Research Studies in Agricultural Sciences,* 3(2): 17-24.

Lakshmi, M.V., Suneetha, Y., Yugandhar, G. and Lakshmi, N.V. (2014). Correlation studies in rice (*Oryza sativa* L.). *International Journal of Genetic Engineering and Biotechnology,* 5(2): 121-126.

Lang, N.T., Xa, T.T.T., Luy, T.T. and Buu, B.C. (2013). Rice Breeding for Grain Quality In The Mekong Delta. *Omonrice,* 19: 54-60.

Laxami, J., Kumar, B. and Razdan, A.K. (2017). GGE Biplot Analysis of Genotype x Environment Interaction in Basmati Rice (*Oryza sativa* L.). *International Journal of Current Microbiology and Applied Sciences,* 6(12): 3345-3350.

Laxuman, S., PM, S., HE, M., HD, P., and SS, V. HM and Janagoudar, B.S. (2011). Character association and path coefficient analysis among the backcross inbred lines derived from Indica× NERICA cross for productivity traits in rice (*Oryza sativa* L.). *Karnataka Journal of Agricultural Sciences,* 24(5), 626-628.

Lestari, A.P., Abdullah, B., Junaedi, A. and Aswidinnoor, H. (2011). Performance of Grain Quality and Aroma of Aromatic New Plant Type Promising Rice Lines. *Indonesian Journal of Agricultural Science,* 12(2): 84-93.

Li, R., Li, M., Ashraf, U., Liu, S. and Zhang, J. (2019). Exploring the relationships between yield and yield-related traits for rice varieties released in China from 1978 to 2017. *Frontiers in Plant Science*, 10: 543.

Liang, J., Lu, Y., Xiao, P., Sun, M., Corke, H. and Bao, J. (2010). Genetic diversity and population structure of a diverse set of rice germplasm for association mapping. *Theoretical and Applied Genetics*, 121: 475–87.

Light Castle Analytics Wing (2019). Rice Industry Essential for Rural Development. Retrived at: https://databd.co/stories/rice-industry-essential-for-rural-development-5556. Published on August 25, 2019.

Lstiburek, M., Bittner, V., Hodge, G.R., Picek, J. and Mackay, T.F. (2018). Estimating realized heritability in panmictic populations. *Genetics*, 208(1): 89-95.

Lu, B.R. (1998). Diversity of rice genetic resources and its utilization and conservation. *Chin Biodiversity*, 6(1): 63–72.

Madhavilatha, L., Sekhar, R.M., Suneetha, Y. and Srinivas, T. (2005). Genetic variability, correlation and path analysis for yield and quality traits in rice (*Oryza sativa* L.). *Research on Crops*, 6(3): 527-534.

Mahalanobis, P. C. (1936). On the generalized distance in statistics. National Institute of Science of India.

Mahmud, I. (2019). Bangladesh not in a position to export rice: IFPRI. Retrived at: https://en.prothomalo.com/bangladesh/Bangladesh-not-in-a-position-to-export-rice-IFPRI. Published on 1 June 2019.

Maji, A.T. and Shaibu, A.A. (2012). Application of principal component analysis for rice germplasm characterization and evaluation. *Journal of Plant Breeding and Crop Science*, 4(6): 87-93.

Manikyaminnie, C., Dayakar reddy, T and Surendra Raju, Ch. (2013). Correlation and path analysis for yield and its components in rice (*Oryza sativa* L.). *The Journal of Research ANGRAU*, 41(1): 132-134

Matsuo, T. (1997). Science of the rice plant. Food and Agriculture Policy Research Center, Tokyo (Japan), 3: 69–88.

Megha, C.P., Ramesh, D. and Prakash, J. (2019). Physico-Chemical and Cooking Properties of Selected Rice Varieties. *Acta Scientific Nutritional Health,* 3(3): 23-30.

Mishra, L.K. and Pravin, J. (2004). Variability and genetic diversity in rice (*Oryza sativa* L.). *Mysore Journal Agriculture Science,* 38: 367-375.

Mo, Z., Ashraf, U., Tang, Y., Li, W., Pan, S., Duan, M., ... & Tang, X. (2018). Nitrogen application at the booting stage affects 2-acetyl-1-pyrroline, proline, and total nitrogen contents in aromatic rice. *Chilean Journal of agricultural Research,* 78(2): 165-172.

Mrshra, S. K., Maurya, D. M. and Vrshwakarma, D. N. (1993). Selection model in rice (*Oryza sativa* L.). *The Indian Journal of Genetics and Plant Breeding,* 53(2): 131-134.

Mustafa, M.A. and Elsheikh, M.A.Y. (2007). Variability, correlation and path coefficient analysis for yield and its components in rice. *African Crop Science Journal,* 15(4): 183-189.

Nadaf, A. B., Wakte, K. V. and Zanan, R. L. (2014). 2-Acetyl-1-pyrroline biosynthesis: from fragrance to a rare metabolic disease. *Journal of Plant Science and Research,* 1, 102.

Nádvorníková, M., Banout, J., Herák, D. and Verner, V. (2018). Evaluation of physical properties of rice used in traditional Kyrgyz Cuisine. *Food Science and Nutrition*, 6(6): 1778-1787.

Nagaraju, M., Chaudhary, D. and Rao, M.J.B. (1975). A simple technique to identify scent in rice and inheritance pattern of scent. *Current Science.* 44: 599.

Nath, A., Nath, D., Santra, C.K. and Dasgupta, T. (2019). Post-Harvest Evaluation of Rice Hybrids for Grain and Cooking Qualities. *International Journal of Current Research and Review,* DOI: http://dx.doi.org/10.31782/IJCRR.2019.11124

Nayak, A.R., Chaudhury, D. and Reddy, J.N. (2001). Correlation and path analysis in scented rice (*Oryza sativa* L.). *Indian Journal of Agricultural Research.* 35(3): 186-189.

Nguyen, H.L., Tran, P.D. and Tran, D.H. (2020). Path analysis for agronomic traits and yield of salt tolerant rice cultivars under moderate salinity condition in Central Vietnam. *Indian Journal of Agricultural Research*, *54*(1): 107-111.

Nguyen, T., Fu, K., Mou, C., Yu, J., Zhu, X., Huang, Y. and Wang, P. (2020). Fine mapping of qSdr9, a novel locus for seed dormancy (SD) in weedy rice, and development of NILs with a strong SD allele. *Molecular Breeding*, *40*(8), 1-11.

Nikhil, B.S.K., Rangare, N.R. and Saidaiah, P. (2019). Correlation and Path Analysis in Rice (*Oryza sativa* L.). *International Journal of Tropical Agriculture,* 32(1-2).

Nitch, M.M., G. Nitch, H. Ketata, H.G. Gauch and R.W. Zobel, 1992. Use of AMMI and their regression models to analyze genotype environment interaction in durum wheat. *Theoretical and Applied Genetics,* 83: 597-601.

Ogunbayo, S.A., Sié, M., Ojo, D.K., Sanni, K.A., Akinwale, M.G., Toulou, B., Shittu, A., Idehen, E.O., Popoola, A.R., Daniel, I.O. and Gregorio, G.B. (2014). Genetic variation and heritability of yield and related traits in promising rice genotypes (*Oryza sativa* L.). *Journal of Plant Breeding and Crop Science,* 6(11): 153-159.

Ohtsubo, K. and Nakamura, S. (2017). Evaluation of Palatability of Cooked Rice. *International Technology Open Journal,* DOI: http://dx.doi.org/10.5772/66398.

Ojo, D.K., Omikunle, O.A., Ajala, M.O. and Ogunbayo, S.O. (2006). Heritability, character correlation and path co-efficient analysis among six-linked of maize. *World Journal of Agricultural Science,* 2: 352-358.

Oka, H.I. (1988). Origin of Cultivated Rice. Japan Scientific and Social Press, Tokyo. 254.

Oko, A.O., Ubi, B.E. and Dambaba, N. (2012). Rice Cooking Quality and Physico-Chemical Characteristics: a Comparative Analysis of Selected Local and Newly Introduced Rice Varieties in Ebonyi State, Nigeria. *Food and Public Health,* 2(1): 43-49.

Okpala, N.E., Duan, L., Shen, G., Zhang, G. and Qi, X. (2017). Comparisons of Cooking and Eating Qualities of Two Indica Rice Cultivars, *Journal of Rice Research,* 5: 2.

Ovung, C.Y., Lal, G.M. and Rai, P.K. (2012). Studies on genetic diversity in rice (*Oryza sativa* L.). *Journal of Agricultural Technology*, 8(3): 1059-1065.

Palaniraja, K. and Anbuselvam, Y. (2010). D2 Analysis in Rice (*Oryza sativa* L.). *Agriculture Science Digest*, 30(3): 182-185.

Pandey, V. and Shukla, A. (2015). Acclimation and tolerance strategies of rice under drought. *Stress Rice Science,* 22(4): 147-161.

Panse, V.G. (1957). Genetics of quantitative characters in relation to plant breeding. *Indian Journal of Genetics and Plant Breeding*, 17: 318-28.

Patterson, H.D. and Thompson, R. (1971). Recovery of inter-block information when block sizes are unequal. Biometrika pp. 545–554.

Perween, S., Kumar, A., Prasad, B.D. and Choudhary, M. (2020). Assessment of Genetic Diversity in Rice (*Oryza sativa* L.) under Irrigated and Drought Stress Condition. *Current Journal of Applied Science and Technology*, 39(1): 112-125.

Phukon, R., Baishya, S., Rathi, S. and Sarma, A. (2019). Characterization of Rice Landraces from Dibrugarh District of Assam. *Indian Journal of Plant Genetic Resources*, 32(3): 368-376.

Phukon, R., Baishya, S., Rathi, S., & Sarma, A. (2019). Characterization of Rice Landraces from Dibrugarh District of Assam. *Indian Journal of Plant Genetic Resources*, 32(3): 368-376.

R Core Team. 2017. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL https://www.R-project.org/.

Rahman, A. and Shah, S.M.A. (2019). Genotype × Environment interaction for yield and associated traits in rice. *Sarhad Journal of Agriculture,* 35(2): 532-538

Rahman, M.A. and Bahl, P.N. (1986). Evaluation of early generation testing in chickpea. *Plant Breeding*, 97(1): 82-85.

Rai, S.K., Suresh, B.G., Rai, P.K., Lavanya, G.R., Kumar, R. and Sandhya (2014). Genetic variability, correlation and path coefficient studies for grain yield and other yield attributing traits in rice (*Oryza sativa* L.). *International Journal of Life Sciences Research,* 2(4): 229-23.

Rai, V.P., Singh, A.K. and Jaiswal, H.K. (2015). Evaluation of molecular markers linked to fragrance and genetic diversity in Indian aromatic rice. *Turkish Journal of Botany,* 39: 209-217.

Raji, A.A. (2002). Assessment of genetic diversity and heterotic relationships in African improved and local cassava germplasm. PhD thesis. University of Ibadan, Nigeria.

Ramya, B., Saravanan, K. and Kumar, P.S. (2012). Genetic parameters of variability, correlation and path coefficient studies for grain yield and other yield attributes traits in rice (*Oryza sativa* L.). *Plant Archives*, 12(2): 711-715.

Ramya, K. and Senthilkumar, K. (2008). Genetic divergence in rice. *Crop Improvement*, 35(2): 119-121.

Ranawake, A.L. and Amarasinghe, U.G.S. (2014). Relationship of Yield and Yield Related Traits of Some Traditional Rice Cultivars in Sri Lanka as Described by Correlation Analysis, *Journal of Scientific Research and Reports*, 3(18): 2395-2403.

Rao, C. R. 1964. Statistical genetic consideration for maintaining germplasm collection. *Theoretical and Applied Genetics,* 86: 673-678.

Rao, C.R. (1952). Advanced statistical methods in biometrical research. Edn. I. John Wiley and Sons, New York. Pp. 390.

Rao, S.A., McNeilly, T., Khan, M.A. and Khan, A.A. (1997). Cause and effect relations of yield and yield components in rice (*Oryza sativa* L.) [Pakistan]. *Journal of Genetics and Breeding* (*Italy*). 51(1): 1-5.

Rashid, M.M., Ghosh, A.K., Roni, M.N., Islam, M.R. and Alam, M.M. (2017). Yield performance of seven aromatic rice varieties of Bangladesh. *International Journal of Agriculture and Environmental Research.* 3(2): 2637-2642.

Rashid, M.M., Hassan, L., Das, B. and Begum, S.N. (2017). Correlation and Path Coefficient Analysis of Yield and Yield Contributing Traits in Rice. *International Journal of Sustainable Crop Production*, 12(2): 1-6.

Rashid, M.M., Nuruzzaman, M., Hassan, L. and Begum, S.N. (2017). Genetic variability analysis for various yield attributing traits in rice Genotypes. *Journal of the Bangladesh Agricultural University,* 15(1): 15–19.

Rasool, N., Baba, W.N., Muzzaffar, S., Masoodi, F.A., Ahmad, M. and Bhat, M.M. (2015). A correlation study of proximate composition, physical and cooking properties of new high yielding and disease resistant rice varieties. *Journal of Food Science and Technology*. http://dx.doi.org/10.1080/23311932. 2015.1099175

Ren, Y., Ashraf, U., He, L. X., Mo, Z. W., Wang, F., Wan, X. C., ... & Tang, X. R. (2017). Irrigation and nitrogen management practices affect grain yield and 2-acetyl-1-pyrroline content in aromatic rice. *Applied Ecology and Environmental Research*, *15*(4), 1447-1460.

Resende, M.D.V. (2007). Matemática e estatística na análise de experimentos e no melhoramento genético. Embrapa Florestas, Colombo.

Resende, M.D.V. (2015). Genética Quantitativa e de Populações. Suprema, Visconde do Rio Branco, 463.

Ritika, B.Y., Satnam, M. and Baljeet, S.Y. (2016). Physicochemical, Pasting, Cooking and Textural Quality Characteristics of Some Basmati and Non-Basmati Rice Varieties Grown in India. *International Journal of Agricultural Technology,* 12(4): 675-692.

RK, G. and MAK, M. (2014). Genetic variability and character association of T-aman rice (*Oryza sativa* L). *International Journal of Plant Biology and Research*. 2(2): 1013.

Robertson, A. (1959). The sampling variance of the genetic correlation coefficient. *Biometrics*, 15: 469-485.

Romesburg, H. C. (1984). Cluster analysis for researchers. Wadsworth. *Inc., Belmont, CA*.

Rosniyana, A., Hazila, K.K., Hashifah, M.A. and Norin, S.A.S. (2010). Quality characteristics of organic and inorganic Maswangi rice variety. *Journal of Tropical Agriculture and Food Science,* 38(1): 71-79.

Roy, A. and Ponwar, D.V.S. (1993). Genetic divergence in rice. *Oryza,* 30: 197-201.

Roy, A., Panwar, D.V.S. and Sarma, R.N. (1995). Genetic variability and causal relationship in rice. *Madras Agricultural Journal,* 82(4): 251-255.

Roy, S. C. and Shil, P. (2020). Assessment of Genetic Heritability in Rice Breeding Lines Based on Morphological Traits and Caryopsis Ultrastructure. *Scientific Reports*, 10(1): 1-17.

Roy, S., Banerjee, A., Mawkhlieng, B., Misra, A.K., Pattanayak, A., Harish, G.D., Singh, S.K., Ngachan, S.V. and Bansal, K.C. (2015). Genetic Diversity and Population Structure in Aromatic and Quality Rice (*Oryza sativa* L.) Landraces from North-Eastern India. *Plos One,* 10(6): e0129607.

Sabesan, T., Suresh, R. and Saravanan, K. (2009). Genetic variability and correlation for yield and grain quality characters of rice grown in coastal saline low land of Tamilnadu. *Electronic Journal of Plant Breeding,* 1: 56-59.

Sabesan, T., Suresh, R., & Saravanan, K. (2009). Genetic variability and correlation for yield and grain quality characters of rice grown in coastal saline low land of Tamilnadu. *Electronic Journal of Plant Breeding*, 1(1): 56-59.

Sadeghi, S.M. (2011). Heritability, phenotypic correlation and path coefficient studies for some agronomic characters in landrace rice varieties. *World Applied Sciences Journal,* 13(5): 1229-1233.

Saha, S.R., Hassan, L., Haque, A., Islam, M.M. and Rasel, M. (2019). Genetic variability, heritability, correlation and path analyses of yield components in traditional rice (*Oryza sativa* L.) landraces, *Journal of Bangladesh Agriculture University*, 17(1): 26–32.

Saleh, M. M., Salem, K. F. and Elabd, A. B. (2020). Definition of selection criterion using correlation and path coefficient analysis in rice (*Oryza sativa* L.) genotypes. *Bulletin of the National Research Centre*, *44*(1): 1-6.

Salgotra, R.K., Gupta, B.B. and Singh, P. (2009). Combining ability studies for yield and yield components in basmati rice. *Oryza.* 46(1): 12-16.

Sankar, D.P., Sheeba, A. and Anbumalarmathi, J. (2006). Variability and character association studies in rice. *Agricultural Science Digest*, 26(3): 182-184.

Sarawgi, A.K., Rastogi, N.K. and Soni, D.K. (1997). Correlation and path analysis in rice accessions from Madhya Pradesh. *Field Crops Research*, 52(1-2): 161-167.

Sawant, D.S., Patil, S.L., Sadhar, B.B. and Bhare, S.G. (1995). Genetic divergence, character association and path analysis in rice. *Journal of Maharashtra Agricultural University,* 20: 412-414.

Sellamuthu, R., Liu, G.F., Ranganathan, C.B. and Serraj, R. (2011). Genetic analysis and validation of quantitative trait loci associated with reproductive-growth traits and grain yield under drought stress in a doubled haploid line population of rice (*Oryza sativa* L.). *Field Crops Research,* 124: 46-58.

Setyaningsih, W., Majchrzak, T., Dymerski, T., Namieśnik, J. and Palma, M. (2019). Key-Marker Volatile Compounds in Aromatic Rice (*Oryza sativa*) Grains: An HS-SPME Extraction Method Combined with GC× GC-TOFMS. *Molecules*, 24(22): 4180.

Shamim, F., Raza, M. A. and Akhtar, M. (2017). Grain quality attributes of new Rice Basmati lines of Pakistan. *Journal of Applied Agriculture and Biotechnology*, *2*(1): 37-47.

Shinde, G.C., M.T. Bhingarde and S.S. Mehetre, 2002. AMMI analysis for stability of grain yield of pearl millet (*Pennisetum typhoides* L.) hybrids. *Indian Journal of Genetics and Plant Breeding*, 62: 215-217.

Siddi, S. (2020). Genetic variability and trait association studies for gall midge incidence, yield and its traits in rice (*Oryza sativa* L.) genotypes. *Journal of Entomology and Zoology Studies*, 8: 30-34.

Sidhu, J. S., Gill, M. S. and Bains, G. S. (1975). Milling of paddy in relation to yield and quality of rice of different Indian varieties. *Journal of Agricultural and Food Chemistry*, 23(6): 1183-1185.

Silva, G.N., Silva Júnior, A.C. da; Sant'anna, I. de C., Cruz, C.D., Nascimento, M. and Soares, P.C. (2019). Projeção de distâncias como método auxiliar na classificação de arroz irrigado quanto a adaptabilidade e estabilidade. *Revista Brasileira de Biometria,* 37: 229-243.

Silva, G.N., Silva Júnior, A.C.D., Sant'Anna, I.D.C., Cruz, C.D., Nascimento, M. and Soares, P.C. (2020). Similarity networks for the classification of rice genotypes as to adaptability and stability. *Pesquisa Agropecuária Brasileira*, 55.

Simonelli, C., Abbiati, A. and Cormegna, M. (2016). Physicochemical Characterization of some Italian rice varieties. *La Rivista di Scienza dell'Alimentazione* No 1: Anno 45.

Simonelli, C., Galassi, L., Cormegna, M. and Bianchi, P. (2017). Chemical, Physical, Textural and Sensory Evaluation on Italian Rice Varieties. *Universal Journal of Agricultural Research,* 5(2): 104-112.

Singh, A. and Sengar, R.S. (2015). Fragrance Gene Overview in Aromatic Rice and Strategies for Characterization. *Journal of Agricultural Engineering and Food Technology,* 2(1).

Singh, A., Singh, A.K., Singh, V., Singh, N., Singh, V.N., Shamin, M., Vikram, P. and Singh, S. (2014). Genetic variability among traits associated with grain yield of rice (*Oryza sativa* L.) exposed to drought at flowering stage. *African Journal of Agricultural Research*, 9(16): 1252.

Singh, D., Kumar, A., Sirohi, A., Kumar, P., Singh, J., Kumar, V., Jinda, A., Kumar, S., Kumar, N., Kumar, V., Sharma, V., Gupta, S. and Chand, S. (2011). Improvement of Basmati rice (*Oryza sativa* L.) using traditional breeding technology supplemented with molecular markers. *African Journal of Biotechnology,* 10(4): 499-506.

Singh, M.K., Thakur, R., Verma, U.N., Upasani, R.R. and Pal, S.K. (2000). Effect of planting time and nitrogen on production potential of Basmati rice cultivars in Bhiar Plateau. *Indian Journal of Agronomy*. 45(2): 300-303.

Singh, N., Choudhury, D.R., Singh, A.K., Kumar, S., Srinivasan, K. and Tyagi, R. (2013). Comparison of SSR and SNP markers in estimation of genetic diversity and population structure of Indian rice varieties. *PloS One,* 8(12): e84136.

Singh, P.K., Mishra, M.N., Hore, D.K. and Verma, M.R. (2006). Genetic divergence in lowland rice of north eastern region of India. *Communications in Biometry and Crop Science,* 1(1): 35-40.

Singh, R., Yadav, V., Mishra, D.N. and Yadav, A. (2018). Correlation and Path Analysis Studies in Rice (*Oryza sativa* L.). *Journal of Pharmacognosy and Phytochemistry,* SP1: 2084-2090.

Singh, R.K. and Chaudhary, B.D. (2010). Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, New Delhi, India. P.57.

Singh, R.K., and Choudhury, B.D. (2010). Biometrical Method in Quantitative Genetic Analysis. Kalyani Publishers, Ludhiana, New Delhi, pp. 54-57.

Singh, R.K., Singh, U.S., Singh, N., Singh, H.N. and Singh, G. (2003). Kalanamak: a scented black pearl of eastern Uttar Pradesh. In: Singh RK, Singh US, editors. A Treatise on the Scented Rices of India. New Delhi, India: Kalyani Publishers, pp. 421–431.

Singh, S.K., Maurya, V., Vennela, P.R. and Singh, D.K. (2018). Genetic Divergence Studies in High Zinc and Drought Tolerant Rice (*Oryza sativa* L.) AccessionsUsing Morphological Traits, *International Journal of Genetics,* 10: 478-481.

Singh, V., Singh, A.K., Mohapatra, T., Krishnan, G.S. and Ellur, R.K. (2018). Pusa Basmati 1121 – a rice variety with exceptional kernel elongation and volume expansion after cooking. *Journal of Rice,* 11: 19.

Sinha, T. S. and Bhattacharyya, R. K. (1980). Note on genetic variability in Sundarban rice varieties under saline soil. *Indian Journal of Agricultural Sciences*, 50(9): 719-721.

Sinha, T.S. and Bhattacharya, R.K. (1980). Note on genetic variability in Sundarban rice varieties under saline soil. *Indian Journal of Agricultural Science,* 50(9): 719-721.

Sivasubramanian, S. and Menon, M. 1973. Heterosis and inbreeding depression in rice. *Madras Agricultural Journal,* 60:1139.

Sood, B. C. and Siddiq, E. A. (1978). A rapid technique for scent determination in rice [India]. *Indian Journal of Genetics and Plant Breeding,* 38(2): 268-271.

Sorensen, D. and Kennedy, B. (1984). Estimation of genetic variances from unselected and selected populations. *Journal of Animal Science,* 59: 1213–1223.

Souroush, H.R., Mesbah, M., Hossainzadeh, A. and Bozorgipour, R. (2004). Genetic and phenotypic variability and cluster analysis for quantitative and qualitative traits of rice. *Seed and Plant Karaj,* 20: 167-182.

Sowbhagya, C. M., Ramesh, B. S., & Bhattacharya, K. R. (1987). The relationship between cooked-rice texture and the physicochemical characteristics of rice. *Journal of Cereal Science*, *5*(3): 287-297.

Sowmiya, C.A. and Venkatesan, M. (2017). Studies on Genetic Diverity in Rice (*Oryza sativa* L.). *International Journal Current Microbiology Application Science,* 6(9): 1749-1756.

Srivastava, D., Shamim, M., Mishra, A., Prashant, Y., Deepak, K., Pandey, P., Khan, N.A. and Singh, K.N. (2019). Introgression of semi-dwarf gene in Kalanamak rice using marker-assisted selection breeding. *Current Science,* 116(4): 597.

Srivastava, P., Singh, S.K., Habde, S., Singh, D.K., Vennela, P.R. and Khaire, A. (2019). Studies on genetic diversity in rice (*Oryza sativa* L.) using SSR markers. *Journal of Pharmacognosy and Phytochemistry,* 8(3): 922-928.

STAR, version 2.0.1. (2014). Biometrics and Breeding Informatics, PBGB Division, International Rice Research Institute, Los Baños, Laguna, Philippines.

Steel, R.G. and Torrie, J.H. (1984). Principles and procedure of statistics, pp. 137-167.

Subedi, U., Karki, R., Mishra, A. and Shrestha, M.B. (2016). Quality Assessment of Some Rice Varieties Newly Adopted in Nepal. *Journal of Food Science Technology, Nepal,* 9: 48-54.

Subrahmanyam, D., Murty, V.S. and Rao, A.V. (1986). Heritability of yield and other traits and inter-relationships among traits in F_2 to F_5 generation of three crosses of rice. *Indian Journal of Genetics and Plant Breeding,* 46(2): 390-393.

Sudeepthi, K., Srinivas, T., Ravi Kumar, B.N.V.S.R., Jyothula, D.P.B. and Nafeez Umar, Sk. (2020). Assessment of genetic variability, character association and path analysis for yield and yield component traits in rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding,* 11(01): 144-148.

Sudharani, M., Reddy, P.R., Reddy, G.H. and Chaudhary, S.R. (2013). Correlation and path coefficient analysis for yield and physiological attributes in rice (*Oryza sativa* L.) hybrids under saline soil conditions. *The Journal of Research ANGRAU,* 41(1): 105-108.

Sun, S.H., Gao, F.Y., Lu, X.J., Wu, X.J., Wang, X.D., Ren, G.J. and Luo, H. (2008). Genetic analysis and gene fine mapping of aroma in rice (*Oryza sativa* L. Cyperales, Poaceae). *Genetics and Molecular Biology,* 31: 532–538.

Sun, X.C. (1979). Estimates of heritability for some major economic characters in hybrid generation of Indica rice. *Scientia Agricluturae Sinica,* 4: 45-50.

Surek, H. and Beser, N. (2005). Selection for grain yield and its components in early generation in rice (*Oryza sativa* L.). *Trakia University Journal of Science,* 6(1): 51-58.

Takahashi, N. (1984). Seed germination and seedling growth. In S. Tsunoda and N. Takahashi, eds. Biology of Rice. Tokyo, Japan: *Japan Science Society Press and Elsevier,* pp. 71-88.

Takeda, K. and Saito, K. (1983). Heritability and genetic correlation of kernel weight and white belly frequency in rice. *Japanese Journal of Breeding,* 33: 468-480.

Talwar, S.N. (1976). Selection index for grain yield and its contributing characters in parietal collection of rice. *Indian Agriculture Journal,* 20(1): 35-37.

Tamu, A., Asante, M.D., Akromah, R. and Soe, I. (2017). Evaluation of physicochemical characteristics of rice (*Oryza sativa* L.) Varieties in Ghana Alex. *International Journal of Agricultural Sciences,* 7(8): 1342-1349.

Tejaswini, K.L.Y., Manukonda, S. and Rao, P.V.R. (2018). Genetic divergence and cluster analysis studies in rice (*Oryza sativa* L.) using D2 statistics, *Journal of Pharmacognosy and Phytochemistry,* SP4: 108-116.

Tiruneh, A., Gebrselassie, W. and Tesfaye, A. (2019). Genetic Diversity Study on Upland Rice (*Oryza sativa* L.) Genotypes Based on Morphological Traits in Southwestern Ethiopia. *Asian Journal of Crop Science*, 11(1): 17-24.

Tiwari, A. and Priya, B. (2018). Correlation and Path Analysis for Yield Determing Traits in Sabita/Sambamahsuri Derivatives of Rice (*Oryza sativa* L.) Genotypes, *Biotechnology Journal International,* 21(3): 1-7.

Tiwari, D.N., Santosh, R.T., Mahendra, P.T., Narayan, K. and Bishwas, B. (2019). Genetic Variability and Correlation Coefficients of Major Traits in Early Maturing Rice under Rainfed Lowland Environments of Nepal. Preprint · January 2019 DOI: 10.1101/520338.

Traore, K. (2006). Characterization of novel rice germplasm from West Africa and genetic marker associations with rice cooking quality (Doctoral dissertation, Texas AandM University).

Tripathi, A., Kumar, S., Singh, M.K., Kumar, A. and Karnwal, M.K. (2017). Phenotypic assessment of rice (*Oryza sativa* L.) genotypes for genetic variability and varietal diversity under direct seeded condition. *Journal of Applied and Natural Science,* 9(1): 6-9.

Tripathi, R.S. and Rao, M.J.B.K. (1979). Inheritance and linkage relationship of scent in rice. *Euphytica*, 28(2): 319-323.

Tukey, J.W., Kempthorne, T.A., Bancroft, J.W., Gowen and Lush, J.L. (1954). Causation, regression and path analysis in *Oryza sativa*. *Statistics and Mathematics in Biology*, 35–66.

Ullah, M.Z., Bashar, M.K., Bhuiyan, M.S.R., Khalequzzaman, M. and Hasan, M.J. (2011). Interrelationship and cause-effect analysis among morpho-physiological traits in biroin rice of Bangladesh. *International Journal of Plant Breeding and Genetics*, 5(3): 246-254.

Umadevi, M., Veerabadhiran, P., Manonmani, S. and Shanmugasundaram, P. (2010). Physico-chemical and cooking characteristics of rice genotypes. *Electronic Journal of Plant Breeding*, 1(2): 114-123.

Van Eeuwijk, F.A., Bustos-Korts, D.V. and Malosetti, M. (2016). What should students in plant breeding know about the statistical aspects of genotype× environment interactions? *Crop Science*, 56(5): 2119-2140.

Varthini, V., Robin, S., Sudhakar, D., Raveendran, M., Rajeswari, S. and Manonmani, S. (2014). Evaluation of rice genetic diversity and variability in a population panel by principal component analysis. *Indian Journal of Science and Technology*, 7(10): 1555–1562.

Vennila, S., Anbuselvam, Y. and Palaniraja, K. (2011). D2 analysis of rice germplasm for some quantitative and quality traits. *Electronic Journal of Plant Breeding*, 2(3): 392- 403.

Venuprasad, R., Cruz, M.S., Amante, M., Magbanua, R., Kumar, A. and Atlin, G.N. (2008). Response to two cycles of divergent selection for grain yield under drought stress in four rice breeding populations. *Field Crops Research*, 107(3): 232-244.

Whan, B.R. Rathjen, A. J. and Knight, R. (1981). The relation between wheat lines derived from F_2, F_3, F_4 and F_5 generations for grain yield and harvest index. *Euphytica*, 30: 419-430.

Wolie, A., Dessalegn, T. and Belete, K. (2013). Heritability, variance components and genetic advance of some yield and yield related traits in Ethiopian collections of finger millet (*Eleusine coracana* (L.) genotypes. *African Journal of Biotechnology,* 12(36): 5529–5534.

Woodworth, C. M. (1931). Breeding for Yield in Crop Plants 1. *Agronomy Journal*, 23(5): 388-395.

Wright, S. (1921). Correlation and causation. *Journal of Agriculture and Research,* 20: 557-585.

Yadav, S.K., Suresh, B.G., Pandey, P. and Kumar, B. (2010). Assessment of genetic variability, correlation and path association in rice (*Oryza sativa* L.). *Journal of Biological Science,* 18: 1-8.

Yan, W. and Tinker, N.A. (2006). Biplot analysis of multi-environment trial data: Principles and applications. *Canadian Journal of Plant Science*, 86: 623–645.

Yang, J., Benyamin, B., McEvoy, B.P., Gordon, S., Henders, A.K., Nyholt, D.R., Madden, P.A., Heath, A.C., Martin, N.G. and Montgomery, G.W. (2010). Common SNPs explain a large proportion of the heritability for human height. *Nature Genetics,* 42: 565–569.

Yanjie, X., Yining, Y., Shuhong, O., Xiaoliang, D., Hui, S., Shukun, J., Shichen, S. and Jinsong, B. (2018). Factors Affecting Sensory Quality of Cooked Japonica Rice. *Journal of Rice Science,* 25(6): 330-339.

Yolanda, J.L. and Das, L.D.V. (1995). Correlation ad path analysis in rice (*Oryza sativa* L). *Madras Agricultural Journal,* 82: 576-578.

Yonezawa, K. and Yamagata, H. (1981a). Selection strategy in breeding of self–fertilized crops. I. Theoretical considerations on the efficiency of single plant selection in early generations. *Japan Jpurnal of Breeding,* 31: 35-48.

Yonezawa, K. and Yamagata, H. (1981b). Selection strategy in breeding of self–fertilized crops. II. On the use of selection among F2 populations by the presence and absence of promising phenotypes. *Japan Journal of Breeding,* 31: 215-225.

Zahid, M.A., Akhter, M., Sabar, M., Manzoor, Z. and Awan, T. (2006). Correlation and path analysis studies of yield and economic traits in Basmati rice (*Oryza sativa* L.). *Asian Journal of Plant Science*, *5*(4): 643-645.

Zain, N.A.M., Ismail, M.R., Mahmood, M., Puteh, A. and Ibrahim, M.H. (2014). Alleviation of water stress effects on MR220 rice by application of periodical water stress and potassium fertilization. *Molecules*, 19: 1795-1819.

Zaval-Garcia, P., Bramel-Cox, P.J. and Eastin, J.D. (1992). Potential gain from selection for yield stability for grain sorghum populations. *Theoretical and Applied Genetics*, 85: 112-119.

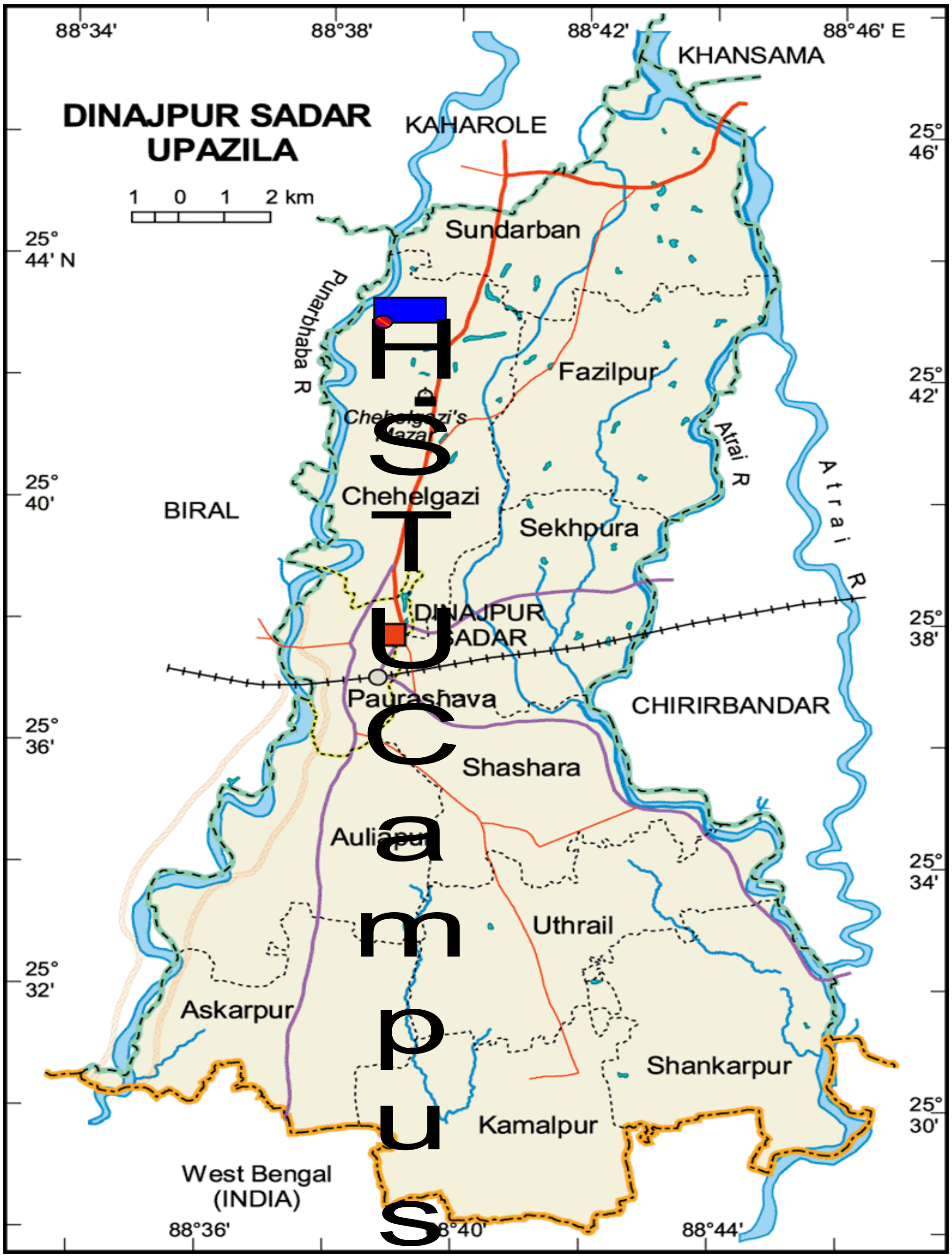
Zhende, Y. (1988). Agronomic Management of Rice Hybrids Compared with Conventional Varieties. Proceedings of the International Symposium on Hybrid Rice Changsha, Hunan, China, 27-35.

Zhou, C., Huang, Y., Jia, B., Wang, Y., Xu, Q., Li, R., Wang, S. and Dou, F. (2018). Effects of Cultivar, Nitrogen Rate, and Planting Density on Rice-Grain Quality. *Journal of Agronomy,* 8(11): 246.

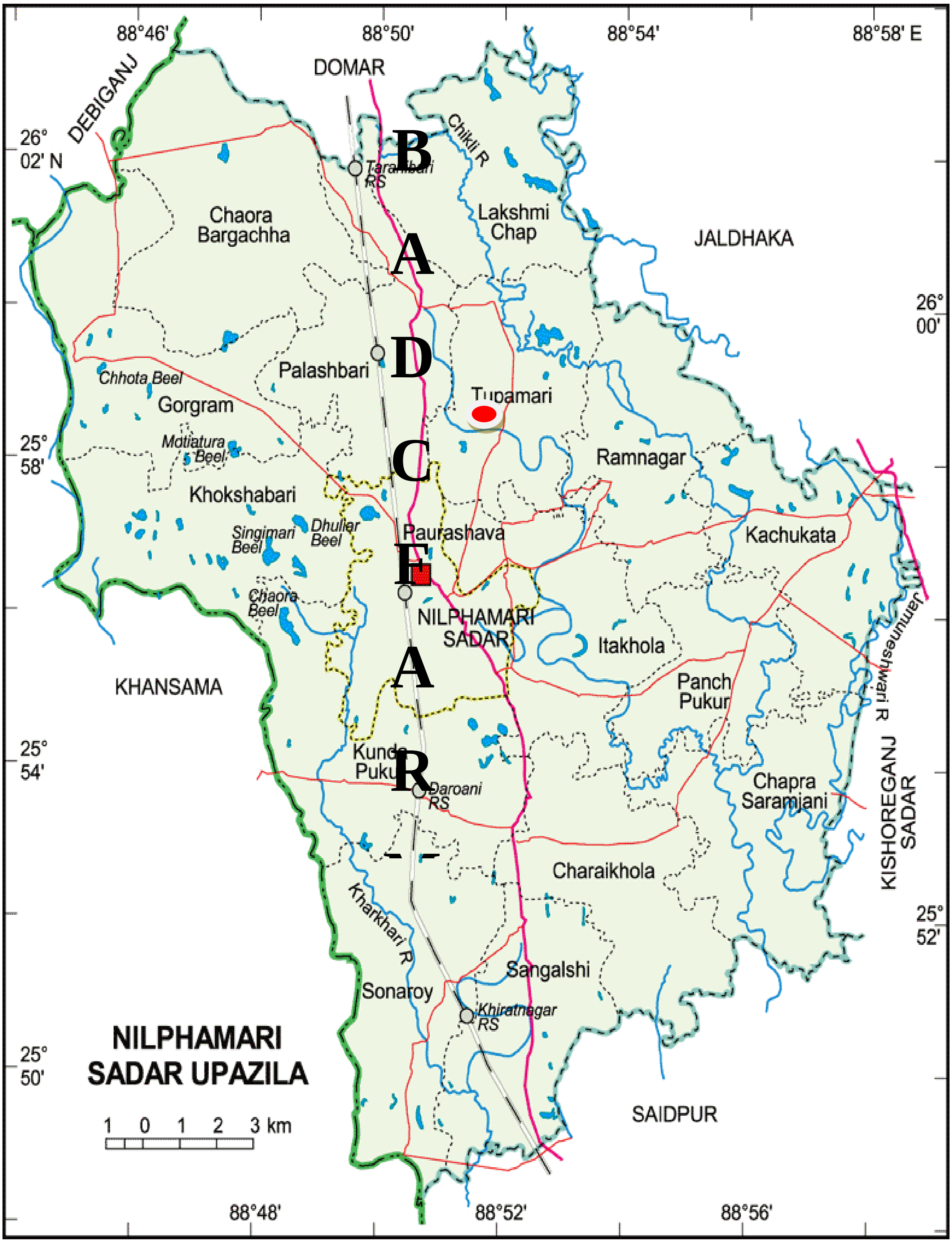
Zobel, R.W., Wright, M.J. and Gauch, H.G. (1988). Statistical analysis of a yield trial. *Agronomy Journal,* 80: 388-393.

APPENDICES

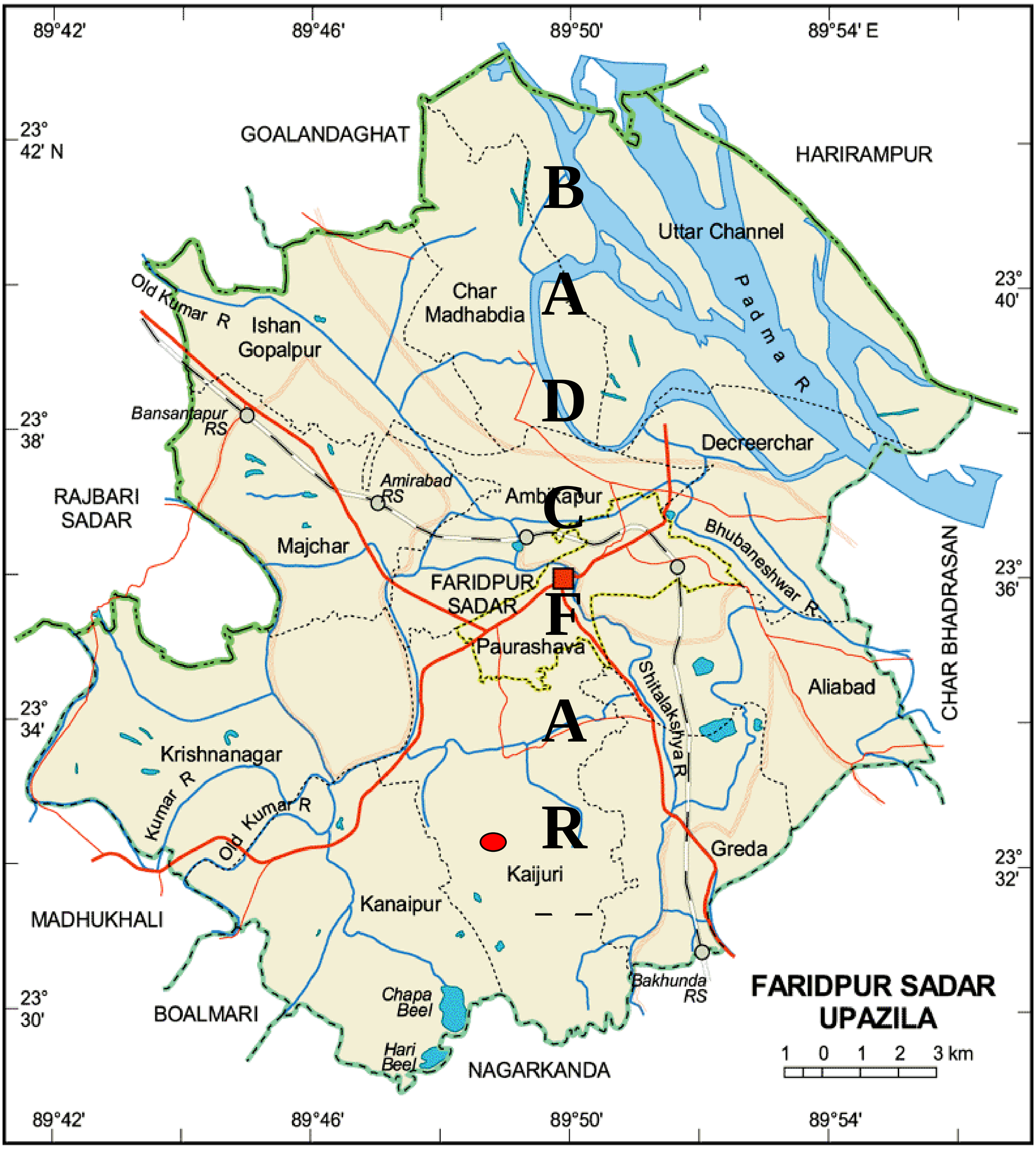
Appendix-I: Location of the experimental site (map of Dinajpur Sadar Upazila showing the research plot).



Appendix-II: Location of the experimental site (map of Nilphamari Sadar Upazila showing the research plot).



Appendix-III: Location of the experimental site (map of Faridpur Sadar Upazila showing the research plot).



Appendix-IV: Climate data of Dinajpur, Nilphamari and Faridpur for 2017

Item	June			July			Aug			Sep			Oct			Nov			Dec		
	Din	Nil	Far	Din	Nil	Far	Din	Nil	Far	Din	Nil	Far	Din	Nil	Far	Din	Nil	Far	Din	Nil	Far
Average high °C	33.8	32.9	33.6	32.7	32.6	32.6	33.1	33.1	33.2	33.8	32.8	33.6	31.4	32.2	31.7	29.5	28.8	30.0	26.9	26.5	26.6
Average low °C	26.0	26.7	26.0	26.6	26.3	26.3	26.8	26.6	26.8	26.4	26.3	26.6	23.6	23.6	24.6	16.4	22.4	18.9	13.5	14.1	15.6
Average rainfall in mm	335.3	335.2	345.1	433.6	435.2	399.8	387.7	350.0	304.5	383.8	350.0	264.2	115.1	456.3	156.1	7.0	139.7	31.8	10.2	11.8	11.3
Average humidity (%)	82.0	82.0	85.0	84.0	83.0	87.0	84.0	83.0	85.0	85.0	83.0	85.0	82.0	80.0	82.0	78.0	75.0	78.0	78.0	76.0	78.0
Average Wind speed(m/s)	1.74	3.73	3.76	1.62	3.56	3.62	1.43	3.05	3.31	1.18	2.74	2.66	0.81	2.12	1.53	0.66	2.04	1.09	0.69	2.24	1.12
Sun-shine(hr)	3.0	3.0	2.95	2.0	2.0	2.99	2.0	2.0	2.0	3.0	3.01	3.0	6.0	6.0	5.9	8.0	8.10	8.50	9.0	9.15	9.5

Source: Bangladesh Meteorological Department, Meteorological Complex, Agargaon, Dhaka-1207, Bangladesh