

**Evaluation of a Set of Rice (*Oryza sativa* L.)
Genotypes for Grain Yield and Some
Important Grain Mineral Content *viz.*,
Calcium (Ca), Magnesium (Mg), Iron (Fe) and
Zinc (Zn)**

Thesis

Submitted to the
Central Agricultural University, Imphal
in partial fulfillment of the requirements
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Master of Science (Agriculture)

In

Genetics and Plant Breeding

by

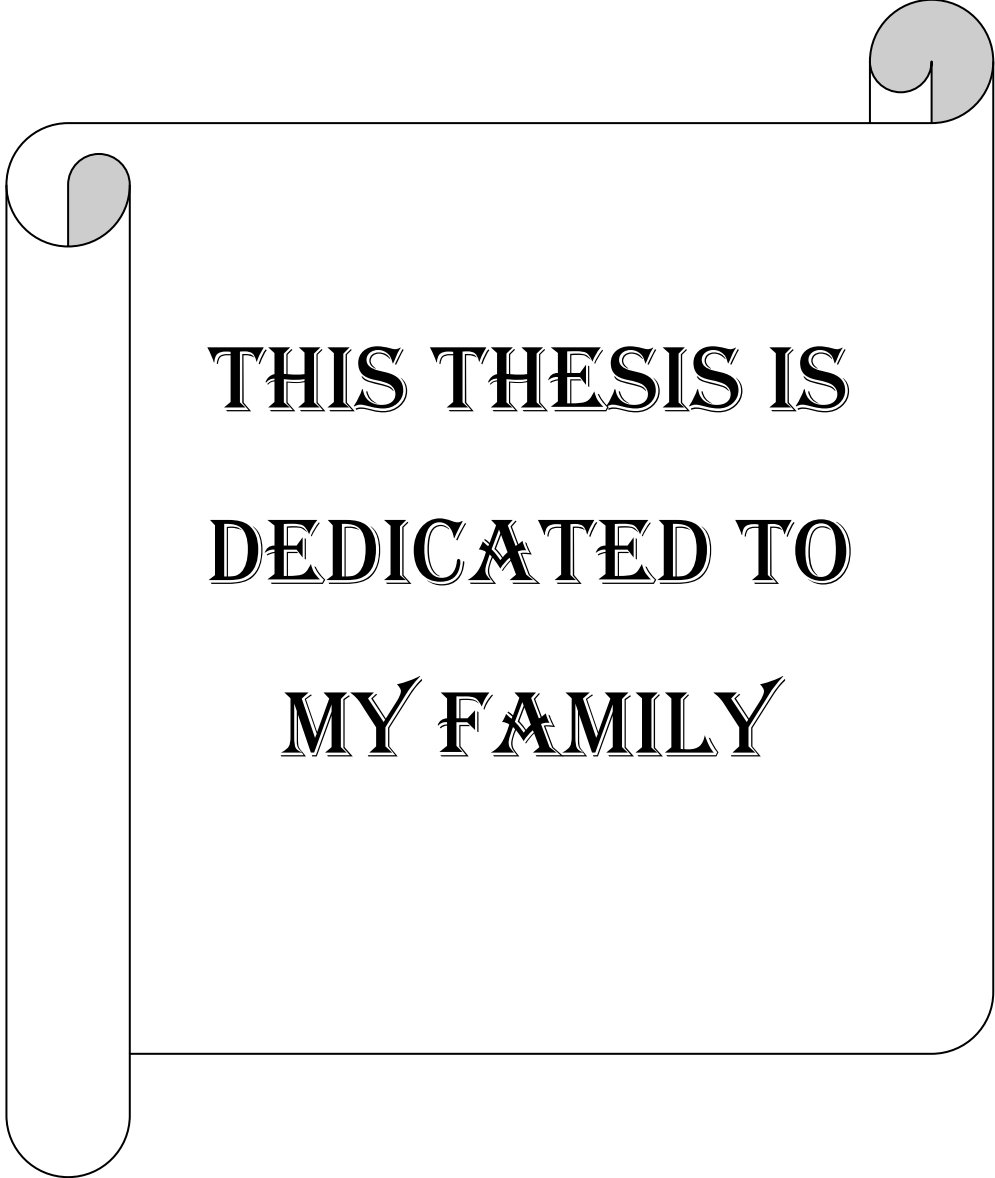
SHUBHRATA GOSWAMI, B.Sc. (Ag.)

U-21-ML-01-010-M-A-003



**SCHOOL OF CROP IMPROVEMENT
COLLEGE OF POST GRADUATE STUDIES
IN AGRICULTURAL SCIENCES
CENTRAL AGRICULTURAL UNIVERSITY, IMPHAL
Umiam, Pin: 793103, Meghalaya, India**

October, 2022



**THIS THESIS IS
DEDICATED TO
MY FAMILY**



CERTIFICATE – I

Certified that **Ms. Shubhrata Goswami** {Admission No. **CAU/CPGS-AS/GPB/M20/02**; Registration No. **U-21-ML-01-010-M-A-003**} has satisfactorily prosecuted her course of research for a period of not less than two semesters and that the thesis entitled **“Evaluation of a Set of Rice (*Oryza sativa* L.) Genotypes for Grain Yield and Some Important Grain Mineral Content viz., Calcium (Ca), Magnesium (Mg), Iron (Fe) and Zinc (Zn)”** submitted by her to the Central Agricultural University, Imphal – 795 004 (Manipur) in partial fulfilment of the requirements for the award of the degree of **Master of Science (Agriculture)** in the subject of **Genetics and Plant Breeding** is the result of original research work conducted by her under my supervision and is sufficiently of high standard to warrant its presentation to the examination.

I also certify that the thesis or part thereof has not been previously submitted by her for a degree of any University.

Date

(K. Noren Singh)

Chairperson

Student advisory's committee



CERTIFICATE- II

This is to certify that the thesis entitled “**Evaluation of a Set of Rice (*Oryza sativa* L.) Genotypes for Grain Yield and Some Important Grain Mineral Content viz., Calcium (Ca), Magnesium (Mg), Iron (Fe) and Zinc (Zn)**” submitted by **Ms. Shubhrata Goswami [Regn. No. U-21-ML-01-010-M-A-003]** submitted to the Central Agricultural University, Imphal – 795 004 (Manipur) in partial fulfillment of the requirements for the award of the degree of **Master of Science (Agriculture)** in the subject of **Genetics and Plant Breeding** has been approved by the Student’s Advisory Committee after oral examination jointly with a Dean’s Nominee.

(Mahesh Pathak)

Professor,
School of Crop Protection
Dean’s Nominee

(K. Noren Singh)

Professor,
School of Crop Improvement
Chairperson,
Student’s Advisory Committee

In-Charge,
School of Crop Improvement

(Mayank Rai)

Professor,
School of Crop Improvement
Member,
Student’s Advisory Committee

Dean of Faculty

(Wricha Tyagi)

Professor,
School of Crop Improvement
Member,
Student’s Advisory Committee

Date :

DECLARATION

I hereby declare that the thesis entitled“**EVALUATION OF A SET OF RICE (*Oryza sativa* L.) GENOTYPES FOR GRAIN YIELD AND SOME IMPORTANT GRAIN MINERAL CONTENT viz., CALCIUM (Ca), MAGNESIUM (Mg), IRON (Fe) AND ZINC (Zn)**” is an authentic record of the work done by me and that no part thereof has been presented for the award of any other degree, diploma, associateship, fellowship or any other similar title.

Date:

(ShubhrataGoswami)

Place: Umiam, Meghalaya

Student

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Date:

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Shubhrata Goswami

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LIST OF ABBREVIATIONS

%	Percent
µg	Microgram
°C	Degree Celsius
ANOVA	Analysis of variance
CD	Critical difference
cm	Centimetre
CRD	Completely Randomized design
D50F	Days to 50% flowering
D80M	Days to 80% maturity
df	Degrees of freedom
et al	Et alibi
Fig	Figure
g	Gram
h ²	Heritability
ha	Hectare
HCL	Hydrochloric acid
hr	Hour
M	Molar
mg	Milligram
min	Minute
ml	Millilitre
mm	Millimetre

Mol.wt	Molecular weight
MSL	Mean sea level
MSS	Mean sum of squares
N	Normality
NaOH	Sodium hydroxide
NE	North East
NETP	Number of panicles per plant
NTPP	Number of tillers per plant
PH	Plant height
PL	Panicle length
PCV	Phenotypic coefficient of variation
RBD	Randomized Block Design
SE(d)	Standard Error of mean difference
SS	Sum of squares
TNGPP	Total number of grains per panicle
TNFGPP	Number of filled grains per panicle
UPGMA	Unweighted Pair Group Method of Arithmetic Mean
Ve	Error variance
Vg	Genotypic variance
Vp	Phenotypic variance
YPP	Yield per plant

ABSTRACT

One of the main sources of dietary carbohydrates for billions of people worldwide, rice (*Oryza sativa* L.) is the main food for close to 3.5 billion people. Understanding the assessment of yield variability and its component aspects is crucial before executing any breeding programme for the genetic improvement of crop plants. To improve grain yield of rice in a specific condition, the contribution and relationship of its component characters viz., plant height, filled grains /panicle, days to 50% flowering and maturity, panicle length, 1000-grain weight and grain size are to be understood. Grain quality of rice plays a major role in the consumer acceptability and it is the second major breeding objective after yield. It also contributes in popularization of a variety as well as security in nutrition and health of those who consume it. 43 genotypes were used in the current investigation to study the grain yield and the mineral content of the kernel. Four minerals, namely Ca, Mg, Fe, and Zn, as well as yield and its component characteristics, made up the total of 10 characters that were examined. Maximum variations were seen among the genotypes for important characters namely total number of grains/panicle (90.75 cm to 184.25 cm) followed by total number of filled grains/panicle (62.75 cm to 141.25 cm) and plant height (73.78cm to 150.31 cm). Heritability (broad sense) coupled with GAM was seen to be maximum in plant height (70.43%, 29.37%). Heritability (broad sense) coupled with GAM was recorded to be maximum in Mg (97.27%, 82.34%) for mineral content. In correlation study, positive and significant correlation was seen between grain yield to total no. of tillers/plant, total no. of effective tillers/plant, total no. of grains/panicle and total no. of filled grains/panicle whereas it showed significant negative correlation with days to 80% maturity and days to 50% flowering. The results of the Path Analysis showed that the total no. of effective tillers/plant (0.7592) had the maximum positive direct effects followed by total number filled grains/panicle (0.6633) to grain yield/plant. Maximum positive and indirect effects were recognized in no. of tillers/plant (0.7497) to grain yield/plant through no. of effective tillers/plant. For yield and its attributing characters, the intra cluster distance was observed maximum in the cluster V (70.621) containing 4 genotypes while the inter cluster distance was found to be maximum between the clusters IV and IX (911.174). Genotypes from the clusters I, II, IV and VII had higher mean values for grain yield and these can be used as a parent in hybridization programme. For mineral content, the intra cluster distance was observed maximum in the cluster V (18.972) containing 3 genotypes and the inter cluster distance was found to be maximum between the clusters IV and VI (274.390). Genotypes belonging to the clusters III and V were high in Ca, I and VI in Mg, IV and V for Fe and cluster VII for Zn. The study revealed that the genotypes NEH-2, NEH-12, CAU-R1, NEH-1, NEH-4, NEH-6, NEH-13, NEH-17 and CAU-R4 performed better for yield and attributing characters. Genotypes NEH-11, M-6T, NEH-1 and M-9 had better mineral content for Ca, Mg, Fe and Zn, respectively based on mean performance. However, the genotypes NEH-2, NEH-12, CAU-R1, NEH-4, NEH-13, M-11, and CAU-R4 were statistically at par for mineral content. Considering yield and attributing traits and mineral content together the genotypes CAU-R4, CAU-R1, NEH-1, NEH-2, NEH-4, NEH-12 and NEH-13 showed better performance and hence, these genotypes can be used for cultivation as well as can be utilized as a parent for further hybridization programmes.

Key words: Yield, Heritability, Zinc, Iron, Calcium, Magnesium, Genetic variability

Chapter 1

Introduction

Rice (*Oryza sativa* L.) is a staple food for most people in most countries numbering about 3.5 billion people worldwide and one of the key sources of dietary carbohydrate. Rice is a main *kharif* crop for North East India having about 10,000 landraces of it. Rice grain quality is vital for consumer acceptance and is the second most significant breeding goal after yield. India is regarded as one of the world's major rice producers. Rice agriculture covers around 43,388,000 acres of land and produces approximately 689 and 780 kcal per day of food for India and Asia, respectively (Rathna *et al.*, 2019). The agricultural industry in India consumes the most energy, and rice plays a key role in this.

Grain quality influences both the popularity of a variety and the health and nutritional security of those who consume it. The seeds come in a variety of colours, including red, brown, purple, and black. Unmilled rice has a thicker coating of bran with a higher nutritious content than milled rice. However, attention of most consumers are drawn to milled rice because of its size, shape, and appearance (Rathna *et al.*, 2019).

Modern, high-yielding cultivars have largely supplanted older kinds, particularly in the irrigated rice habitat, resulting in a smaller genetic basis and hence increased genetic susceptibility. It is critical to diversify the genetic base of this vital crop by introducing genes from various sources. As a result, character associations of various component traits with yield and among themselves should be considered in breeding programmes (Veni *et al.*, 2013).

From the knowledge of component of variances, the breeder must isolate desired genotype. Genetic factors such as the genotypic coefficient of variation (GCV) and the phenotypic coefficient of variation (PCV) can be used to detect the degree of diversity in a germplasm sample (Singh *et al.*, 2011). The most important feature is the partitioning of total variation into phenotypic, genotypic, and environmental components, and determining the magnitude of these components for various traits, which is a measure of the type of gene action and thus aids in the selection of a breeding procedure for the genetic improvement of a trait (Gour *et al.*, 2017).

In the hybridization programme genetic diversity plays an important role in selection of parents and helps in selecting the desirable characters and their right combinations in the succeeding generations. Crosses between two parents having high genetic diversity will lead to the production of desirable combination in the segregating generations. Based on their magnitude of diversity and variability it is considered as an effective tool to select parents in breeding programmes (Guru *et al.*, 2017).

Younger leaves will become yellow and wither if the plant is deficient in calcium (Ca). Split or rolled tips, together with white discolouration, are also possible. The plant's growth is hindered when older leaves bend over. Magnesium (Mg) insufficiency in plants impacts various enzyme activities, including CO₂ absorption and protein synthesis, as well as cellular pH and cation-anion balance activation. It could degrade grain quality (percent milled rice, protein, and starch content). Plant growth is greatly hampered by an iron (Fe) deficit. Iron (Fe) is an essential micronutrient for all living things. It's an important micronutrient that helps with metabolic processes like DNA synthesis, respiration, and photosynthesis. Zinc (Zn) is a necessary nutrient for various metabolic activities in rice plants, including chlorophyll synthesis and membrane integrity. Plant colour and turgor are affected by Zn deficiency. Existing rice varieties (whether white or brown) do not contain adequate micronutrients for optimal health.

IRRI is producing healthier rice to help increase the nutritional content of rice. This rice could deliver extra vitamin A, iron, and zinc to individuals in rice-consuming countries that don't get enough of these minerals now. Ca is necessary for the mineralization of bones and teeth, as well as neuromuscular conduction and the maintenance of body fluid balance within cells. Inadequate calcium intake in the diet can lead to bone loss and osteoporotic fractures in later life. As an enzyme cofactor, magnesium is involved in over 300 metabolic activities in the body. It helps in energy production, neuromuscular transmission, bone mineralization, and DNA and RNA synthesis, among other things. Inadequate magnesium consumption raises the risk of developing a variety of chronic conditions, including insulin resistance, type 2 diabetes, hypertension, Alzheimer's disease, and osteoporosis. Fe is an important component in hematopoiesis. Furthermore, Fe is required for oxygen transport in the human body and plays a role in a number of metabolic activities, including the creation of deoxyribonucleic acid (DNA) and electron transport.

Fe deficiency can cause anaemia, which has a negative impact on cognitive processes, learning abilities, and immune responses. Anemia is especially harmful during pregnancy since it has been linked to a number of unfavourable consequences,

including low birth weight and maternal and perinatal mortality. Zn has a variety of activities in the human body, including regulatory, catalytic, and structural functions. The effect on wound healing, supporting the immunological and reproductive systems, regulation of blood pressure and heart rate, and appropriate insulin secretion are cited as some of the most essential Zn functions. A lack of zinc can cause problems with the immunological, reproductive, neurological, and gastrointestinal systems (Bielecka *et al.*, 2021).

In view of this, this research entitled, “Evaluation of a set of rice (*Oryza sativa* L.) genotypes for grain yield and some important grain mineral content *viz.*, Calcium (Ca), Magnesium (Mg), Iron (Fe) and Zinc (Zn)” was conducted with the following two major objectives:

1. To estimate the different genetic variability parameters of yield and its component characters for a set of rice genotypes
2. To estimate the content of some important minerals namely Calcium (Ca), Magnesium (Mg), Iron (Fe) and Zinc (Zn) in the rice grain by using Atomic Absorption Spectrophotometer

Chapter-2

Review of Literature

Rice (*Oryza sativa* L.) is the important staple food crop among the cereals. To meet out the food requirement of growing population, development of high yielding varieties through crop improvement is essential. Crop improvement depends on the available genetic variability and the extent to which the traits are heritable. The germplasm provides immense scope for wide variability. An extensive survey of genetic variability and a thorough understanding of the genetic makeup of the crop with the help of biometrical tools are indispensable for initiating an effective breeding programme.

The literature related to the objectives of the present study has comprehensively reviewed and is presented in this chapter under the following subheadings:

2.1 Genetic variability in rice genotypes for yield and its contributing traits

Yadav *et al.* (2010) observed high heritability coupled with high to moderate genetic advance as per cent of the mean was seen on plant height, seed yield per plant, straw yield per plant, harvest index, test weight and number of spikelets per panicle.

Akinwale *et al.* (2011) studied the germplasm pool having sufficient genetic variability and reported the high to moderate heritability, genetic advance, significantly lower GCV than PCV indicating the considerable influence of the environment for traits viz., a number of grains per panicle, grain yield, panicle weight and number of panicles per plant.

Ghosh and Sharma (2012) reported the narrow difference between PCV and GCV for days to fifty per cent flowering, sterile spikelet per panicle, fertile spikelet per panicle, panicle length, grain yield per plant, test weight and head rice recovery indicating less environmental influence. All the characters reportedly exhibited high broad sense heritability. High heritability along with higher genetic advance as per cent of the mean for grain yield per plant, sterile spikelet per panicle, fertile spikelet per panicle and 1000 seed weight was also reported.

Khalid *et al.* (2012) reported high genotypic coefficient of variation and estimated genetic advance for plant height, number of tillers per plant and 1000 grain weight; high heritability with low genetic advance for days to fifty per cent flowering and days to maturity.

Pandey *et al.* (2012) evaluated fifty-two rice genotypes to know the genetic relationship of various polygenetic traits on yield. Their results revealed that substantial amount of variability exists in entire gene pool for all characters studied, magnitude of PCV and GCV were high for straw yield per plant, moderate for grain yield per plant, number of spikelet per panicle, however days to fifty per cent flowering, days to maturity, plant height, panicle length, per cent spikelet per panicle and harvest index had low estimates. They reported high heritability combined with high genetic advance in per cent mean for biological yield, grain yield per plant and spikelet per panicle.

The studies conducted in upland rice on genetic variability, heritability and correlation coefficients of grain yield and yield contributing traits and reported the highly significant ($p < 0.01$) GCV & PCV for days to fifty per cent flowering, days to 85 per cent maturity, plant height, panicle length, spikelets per panicle and thousand grains weight. High heritability and genetic advance for plant height, days to fifty per cent flowering, panicles per plant, spikelets per panicle, grains per panicle and thousand grains weight, indicating the role of additive gene action (Seyoum *et al.*, 2012).

Yaqoob *et al.* (2012) evaluated the ten hybrid rice and two high yielding varieties under drought conditions. Studies found the high range of significant genetic variation among various hybrids for plant height, number of grains per panicle, number of productive tillers per plant, 1000 grain weight and grain yield whereas for days to fifty per cent panicle initiation, panicle length, spikelet fertility and days to maturity recorded non-significant genetic variation.

Vanisree *et al.* (2013) reported high estimates of GCV for productive tiller per plant and filled grain per panicle where as low estimates of GCV were noticed for panicle length, days to fifty per cent flowering kernel breadth and kernel elongation ratio. Productive tiller per plant and filled grain per panicle exhibited high heritability and genetic advance.

Toshimenla and Sapu Changkija (2014) conducted study on seventy four upland rice accessions of Nagaland (India) were evaluated for 13 quantitative traits. All the genotypes differed significantly with respect to all the quantitative

characters. Maximum genotypic and phenotypic variances were observed for days to fifty per cent flowering, days to maturity, plant height, leaf length, number of filled grains, and yield per plant. High estimates of heritability coupled with moderate or high value of genetic advance as percentage of means was observed for yield per plant, 100 seed weight, leaf length, days to fifty per cent flowering, leaf width, number of unfilled grains, days to maturity and panicle weight.

The studies among 52 genotypes showed significant differences for yield and quality contributing traits except for early seedling vigour, spikelet sterility and coleoptile length. This indicated the presence of substantial amount of genetic variability in the study material and there is scope for selection. The results showed that PCV (Phenotypic Coefficient of Variation) in general was higher than GCV (Genotypic Coefficient of Variation) for various characters (Prasad *et al.*, 2013).

Roy and Sharma (2014) concluded the results shows that there were high variations in the growth of local upland rice crosses (F_2), both on the components of growth such as plant height, number of productive tillers and the yield components such as panicle length, number of grains per panicle, filled grain percentage and 1000-grain weight.

Shahriar *et al.* (2014) studied to know variability in yield and its contributing characters and also to identify short duration rice genotypes at F_9 generation. The genotypes differed significantly for plant height (cm), length of panicle, total number of tiller per hill, effective tiller number per hill, filled grains per panicle, unfilled grains per panicle, days to fifty per cent flowering, days to maturity, 1000 grains weight and yield per plot (kg plot^{-1}).

Paikhomba *et al.* (2014) evaluated thirty F_1 rice hybrids along with complete set of thirteen parents and checks for variability, heritability and genetic advance in different yield and yield components. The estimates of GCV were lower than the respective PCV, indicating the influence of environmental factors on the expression of the traits studied. Characters like per cent pollen fertility, grain yield per hill, harvest index and number of filled grains per panicle showed high heritability coupled with moderate genetic advance as per cent of mean.

Studies on genetic variability, correlation and path coefficient analysis were conducted on 30 elite rice (*Oryza sativa* L.) genotypes. Analysis of variance among 30 genotypes showed significant difference for all the characters studied. Correlation studies revealed that correlation between grain yield per hill was positively significant with harvest index, biological yield per hill, test weight and plant height at

both genotypic and phenotypic level. The estimates of phenotypic coefficient of variation (PCV) were slightly higher than those of genotypic coefficient of variation (GCV) for all the traits studied. In this study slight differences indicated minimum environmental influence and consequently played a greater role in expression of the traits. Genotypic coefficient of variation and phenotypic coefficient of variation was highest for grain yield per plant followed by harvest index, flag leaf length and test weight. Path coefficients revealed the harvest index, biological yield per hill, number of spikelets per panicle, number of tillers per hill and plant height had high positive direct effect on grain yield at both genotypic and phenotypic level (Bhati *et al.*, 2015).

A field experiment was conducted to find out the genetic variation for grain yield and their associated traits of Aman rice varieties. Among the cultivars BR10 recorded the highest grain yield (3.83 t/ha) and their associated traits *viz.*, plant height (107.8 cm), number of effective tillers/hill (8.33), panicle length (28.3 cm), 1000 grain weight (22.45 g) compared to other cultivars. (Begum *et al.*, 2015).

Islam *et al.* (2015) studied 23 genotypes of rice and 3 check varieties. Grain yields are found to be positively and significantly associated with filled grains per panicle, plant height, days to 50% flowering and days to maturity at both genotypic and phenotypic level suggesting that the importance of these characteristics to enhance rice yield capacity.

Sameera *et al.* (2015) conducted studies on Twenty five rice genotypes were evaluated in randomized block design with three replications to examine the nature and magnitude of variability, heritability and genetic advance. Analysis of variance revealed that differences among the genotypes were significant for all the characters studied. Further, the traits, number of tillers per plant, productive tillers per plant, number of grains per panicle and number of filled grains per panicle showed higher estimates of genotypic and phenotypic co-efficient of variation, while high estimates of heritability were recorded for all the characters under study.

Bhatt *et al.* (2016) conducted an experiment to study variability in rice genotypes. The study revealed that phenotypic coefficient of variation was highest for grains yield per plant followed by number of fertile grain per panicle, flag leaf length, length breadth ratio and text weight exhibited moderate high phenotypic coefficient. High heritability values were also recorded for test weight, plant height at maturity and vegetative plant height. Estimate of genetic advance was highest for number of grains per panicle, followed by plant height. Genetic advance as per cent of mean was, however, highest for no of grains per panicle followed by grain yield per plant. Number

of tillers exhibited positive and significant association with test weight, positive and non significant association with length breadth ratio and grain yield per plant.

Onyia *et al.* (2017) estimated the magnitude of genetic variability and relationship of some agronomic traits of rice and their contributions to yield. The results obtained showed high broad sense heritability was associated with grain yield, number of spikelets per panicle, plant height for the first year planting, whereas in the second year planting, days to fifty per cent flowering, days to maturity and grain yield were among the traits that showed high broad sense heritability.

Rashid *et al.* (2017) investigated 10 rice genotypes for genetic variability. The results showed that plant height had substantial phenotypic and genotypic variations, with values of 750.58 and 741.49, respectively. Number of full grains per panicle (569.64 and 541.39), days to maturity (144.50 and 142.12), and days to 50 percent blooming (103.39 and 102.09), all had high phenotypic and genotypic variability. The parameters yield per panicle (0.16 and 0.13), number of effective tillers per plant (0.372 and 0.279), and panicle length (0.620 and 0.575) had minimal phenotypic and genotypic variations, respectively. For all of the characteristics, phenotypic variants were higher than genotypic variances.

Umarani *et al.* (2017) conducted research to evaluate the variability parameters in seventy rice landraces. The total number of grains per panicle (35.94/35.85), single plant yield (24.07/23.28), 100grain weight (22.30/11.16), and number of productive tillers per plant (21.88/20.13) all had high phenotypic and genotypic coefficients, while total number of tillers per plant (19.92/18.24) and panicle length (11.29/10.43) had moderate phenotypic and genotypic coefficients.

Behera *et al.* (2018) conducted an experiment to study genetic variability in forty-nine elite slender grain rice genotypes for thirteen component characters including grain yield. Majority of the traits showed the smaller difference between phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV). Both PCV and GCV were high for grain yield and fertile grains per panicles indicating less effect of environment on these characters. PCV and GCV were moderate for characters like harvest index, fertility percentage, flag leaf area (cm²) and days to fifty per cent flowering indicating that there is considerable amount of environmental effect on such characters. Moderate to a high degree of heritability estimates were observed for the majority of the traits under study except for a number of effective tillers per plant indicating the low or negligible influence of environment in the expression of these traits and may respond to selection for their improvement.

High heritability (H^2) estimates were associated with moderate to high genetic advance as per cent mean (GAM) for days to fifty per cent flowering, plant height, panicle length, flag leaf area, fertile grains per panicle, fertility percentage, 100 seed weight and grain yield per plant indicating the presence of additive gene effect and hence selection based on phenotypic performance for these traits would be effective.

Adhikari *et al.* (2018) used 26 advance genotypes of lowland irrigated rice in an experiment to quantify genotypic and phenotypic diversity on grain yield and yield-related characteristics. Days until blooming, maturity, plant height, panicle length, thousand grain weight, and grain yield all showed significant differences after analysis of variance. Days to blooming (88%), maturity (79%), thousand grain weight (48%) and plant height (43%) were all shown to have substantial heritability, indicating that these parameters are under strong genetic influence.

Patel *et al.* (2018) evaluated F3 segregating progenies of two cross of one traditional landrace (Lalkada) and two high yielding varieties (IR-28 and Jaya) viz., Cross I (IR-28 x Lalkada) and Cross II (Jaya x Lalkada) of rice to assess the genetic variability, heritability and genetic advance, correlation and direct and indirect effects among yield and yield components. The progenies of the both crosses had higher values of GCV and PCV for grain yield per plant and straw yield per plant. The progenies of both the crosses had high heritability coupled with high genetic advance as per cent mean for grain yield per plant and straw yield per plant was observed.

Ranjith *et al.* (2018) studied the variability in 30 rice genotypes. The results revealed that high estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for fertile grains followed by flag leaf area and tillers per hill. High heritability coupled with high genetic advance was recorded for plant height.

Hosagoudar and Kovi (2018) carried out an experiment at Agricultural and Horticultural Research Station, Ponnampet, University of Agricultural and Horticultural Sciences, Shivamogga during 2015. The experimental material comprised of 15 advanced varietal lines including existing variety as check. Mean performance of individual rice genotypes revealed that the days to 50 per cent flowering found to vary from 85.00 days to 114.50. Plant height was found to vary from 59.84 cm to 91.33 cm with average height of 75.42 cm. Number of panicles per m^2 area ranged from 304.52 (IET-1912) to 580.80 (IET-1902) with mean of 432.21 panicles / m^2 area. The genotype IET-1912 produced maximum grain yield (5172.60 kg / ha) and found to be 20.77 per cent superior in

grain yield than local check Tunga (3096.09 kg / ha) followed by IET-1914 (5059.61 kg / ha) which found 19.64 per cent superior, whereas IET-1908 was found to be 3.74 per cent inferior in grain yield (2722.42 kg / ha) than local check. Analysis of variance revealed highly significant sum of squares due to genotypes for all the characters indicating existence of ample variability among the genotypes. The traits such as plant height, number of panicles and grain yield which showed high heritability coupled with high genetic advance could be used as selection criteria for their improvement since these are governed by additive gene action. The traits like plant height and days to 50% flowering could be used as indirect selection criteria for their simultaneous improvement.

Rao *et al.* (2020) conducted this study with 30 rice genotypes to investigate yield variability and its component attributes. The findings suggested that there was a lot of variation in the germplasm. For number of productive tillers per plant, yield per plant, and 100 grain weight, high estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were reported, indicating considerable amounts of diversity among the germplasm.

A study was conducted with fifteen genotypes of rice (*Oryza sativa* L.) to evaluate yield component characteristics by Naik *et al.*(2020). Results showed high genetic advance (>20) for number of filled grains per panicle (83.14), days to fifty percent flowering (31.84), plant height (28.67), single plant yield (20.85) and low genetic advance (0-10) for number of productive tillers (6.93), 1000 grain weight (6.67) and panicle length (4.64). Analysis of variance among lines, significant differences was observed for plant height, number of productive tillers per plant, panicle length, number of filled grains per panicle, single plant yield and 1000 grain weight

Devi *et al.* (2020) conducted an experiment using 71 rice genotypes to assess the genetic diversity and variability for agronomic traits such as plant height, effective tillers, panicle length and filled grains per panicle and plot yield. PCA analysis were done for above agronomic traits along with some quality traits which showed that 82.23% of total variation in these genotypes were exhibited by first five principal components and also very high correlation among them. High PCV and GCV were exhibited by traits like panicle density, filled grains per panicle and yield per plant. Traits like panicle density, filled grains panicle were recorded for high genetic advance coupled with high heritability. Maximum genetic divergence along with high mean values were showed by some genotypes like RCPR32- HHZ-5-DT-20-DT-3 and RGL

7011 for both agronomic and quality traits which can be used for further crop improvement programmes.

To examine the nature and magnitude of genetic variability for yield and grain quality features, Nanda *et al.* (2021) evaluated twenty-nine rice genotypes along with three checks. Number of full grains per panicle had a high phenotypic coefficient of variance, while grain production, 100-grain weight, plant height, and number of effective tillers per plant had a low phenotypic coefficient of variance.

A study was conducted to evaluate 72 germplasm accessions along with three local checks in rice for yield and yield attributing characters in rice by Chamar *et al.* (2021). High estimates of phenotypic coefficient of variations (PCV%) and genotypic coefficient of variations (GCV%) were recorded for number of tillers per plant, number of productive tillers per plant, number of grains per panicle and grain yield per plant.

2.2 Studies on association and path analysis among yield and its contributing traits

Nandan and Singh (2010) study was undertaken with the objective to determine the nature and magnitude of variability, degree of association between yield and its component characters and their direct, indirect effects on grain yield in rice (*Oryza sativa* L.). Thirty three genotypes were evaluated for identifying their efficiency with respect to 20 yield and quality traits.

Akhtar *et al.* (2011) studied ten rice genotypes for yield contributing traits and noted that yield had strong *genetic* correlation with number of grains per panicle, days to maturity and 1000-grain weight.

Pratap *et al.* (2012) reported components like panicle per hill, grain yield per hill, biological yield per hill, and harvest-index showed significant and positive associations with yield.

Ramya *et al.* (2012) reported significant and positive associations of grain yield per plant with total number of tillers per plant and number of productive tillers per plant. Path coefficients analysis revealed that total number of tillers per plant had direct contribution to grain yield.

Vanisree *et al.* (2013) reported significant correlation of productive tiller per plant, filled grain per panicle, panicle length and days to fifty per cent flowering with harvest index.

Venkanna *et al.* (2014) studied association between yield traits in F₂ generation in 36 crosses of rice which revealed Seed yield had highly significant positive correlations with total biomass both phenotypically and genotypically and 1000 weight genotypically. Path analysis revealed that number of filled grains per panicle had the highest positive and direct effect on grain yield followed by total biomass, kernel length and harvest index.

Ratna *et al.* (2015) conducted study on correlation and path coefficients analyses among fourteen morphological characters were studied in six advanced lines of Basmati rice and one commercial check namely BRRI Dhan 29. In general, genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients suggesting that the environmental influence reduces the relationship between yield and yield contributing characters of rice.

Naseer *et al.* (2015) studied the path coefficient and reported the highest positive direct effect on yield per plant by number of grains per panicle, weight of the filled grains per panicle, weight of 1000 grains per panicle and plant height. While traits such as the number of filled grains per panicle and weight of 1000 grains per panicle will be useful in future breeding programs to obtain superior genotypes with excellent yield potential.

Sameera *et al.* (2016) studied character associations and path coefficients analyses among 25 rice genotypes. Study showed that yield was positively associated with number of tillers per plant, productive tillers per plant, number of grains per panicle and number of filled grains per panicle.

Tejaswini *et al.* (2016) conducted study on correlation and path coefficients analyses among forty two F₅ families. The study revealed that panicle length had positive direct effect coupled with positive significant correlation with grain yield per plant and hence direct selection can be made based on this trait for improving yield.

Rathod *et al.* (2017) studied the correlation and path analysis in fifty-six high iron and zinc genotypes of rice. Character association studies revealed that the characters grain yield per plant showed significant positive association with number of productive tillers per plant, panicle length, number of filled grains per panicle and grain iron concentration. Path coefficient analysis revealed that the traits 1000-grain weight, numbers of filled grains per panicle, number of productive tillers per plant, grain iron concentration, grain zinc concentration, days to fifty per cent flowering and plant height

were directly influencing the grain yield per plant.

2.3 Genetic divergence, heritability and genetic advance among the rice genotypes

Banumathy *et al.* (2010) evaluated fifty-three rice genotypes to identify diverse genotypes. Based on the D^2 analysis, the genotypes were grouped into 11 clusters. Maximum number of 16 and 15 genotypes were grouped under cluster XI and I respectively, while clusters II, IV, V, VI, VIII, IX and X had only two genotypes each and clusters III and VII consisting of three and five genotypes respectively. Maximum inter cluster D^2 value was observed between cluster I and X (32.96) followed by cluster I and IV (32.90). The intra cluster distance was maximum in cluster VII (24.62) followed by cluster XI (22.15).

Anandan *et al.* (2011) studied diversity of forty four salt tolerant rice genotypes from different geographic regions were assessed using Mahalanobis D^2 analysis. The D^2 statistics grouped the genotypes into 12 distinct clusters. Consisting of 19 genotypes, Cluster I was the largest cluster, followed by Cluster II with nine genotypes. Meanwhile, Clusters III, IV, VI, VII, IX, and XII were mono-genotypic clusters. The maximum intercluster distance was exhibited between Cluster IX and X (144.91), followed by Clusters II and X (131.87), as well as clusters VII and X (126.27). The number of grains per panicle (42.71 %), followed by the grain yield per plot (29.81 %), was the major contributor to the total divergence.

Nature and magnitude of genetic diversity among 23 genotypes of rice was assessed in the present study by using Mahalanobis D^2 statistics. Significant variation for all the traits revealed presence of notable genetic variability among genotypes. Estimates of components of variance indicated that genotypic variance contributed maximum to phenotypic variance which suggested that available genetic variability can be exploited through selection and hybridization (Kumar *et al.*, 2014).

Praveen *et al.* (2016) studied genetic divergence among 100 local landraces of rice along with five check varieties based on nineteen quantitative characters. This analysis allowed the 105 genotypes of rice to be identified into ten distinct clusters. Among the different clusters, cluster III contained maximum of 46 genotypes and cluster I, II and X contained a minimum of 1 genotype each. The highest inter cluster distance was observed between cluster II and VIII while the lowest between III and IX. The lowest intra cluster distance was observed in cluster I, II and X while highest intra cluster distance was observed in cluster IX.

Meena *et al.* (2017) studied genetic divergence among thirty-eight maintainer lines through Mahalanobis's D^2 and principal component analysis for eleven characters. Genotypes were grouped into five different clusters. Cluster IV comprised maximum number of genotypes (thirteen) followed by cluster V and III. The inter-cluster distance was maximum between clusters I and V (35.700) indicating wide genetic diversity between these two clusters followed by the distance between cluster I and IV (30.090), cluster I and cluster III (26.530) and cluster II and cluster V (22.800). The minimum inter-cluster distance was observed between cluster III and cluster IV (3.600) followed by cluster IV and cluster V (5.920) and cluster V and cluster III (9.450) indicating that the genotypes of these clusters were genetically close.

Yadav *et al.* (2017) conducted a study to evaluate 35 different genotypes of rice (*Oryza sativa* L.) with two checks for twelve quantitative features in sodic soil. Plant height (97.13 percent) had the highest heritability, followed by days to 50 percent flowering (95.39 percent), days to maturity (94.60 percent), grain yield per plant (94.52 percent), and 1000 grain weight (91.26 percent). Plant height (37.60 percent) had the highest genetic advance as a percentage of mean, while panicle length (5.44 percent) had the lowest.

Ranjith *et al.* (2018) studied the nature and magnitude of genetic divergence in 30 rice genotypes. Mahalanobis D^2 analysis revealed considerable amount of diversity in the material. The genotypes were grouped into six clusters. Cluster I constituted maximum number of genotypes (19). The genotypes falling in cluster II had the maximum divergence. The inter cluster distance was maximum between cluster II and V (228.14) followed by cluster III and V (214.44), suggesting that the genotypes constituted in these clusters may be used as parents for future hybridization programme.

Sandeep *et al.* (2018) looked at the genetic variability, heritability, and progress of 200 rice genotypes. Plant height, single plant yield, number of grains per panicle, number of tillers per hill, number of productive tillers per hill, panicle length, and 1000 grain weight all had high heritability estimates and high genetic advance as a percent of mean, indicating that these traits could be improved further using simple selection methods.

Agbowuro *et al.* (2021) conducted a study on eleven landrace upland rice accessions that are primarily produced in Nigeria's agro-ecological zone. Grain yield had a heritability estimate of 61.4393 percent, whereas plant height had a heritability estimate of 99.6028 percent. For all of the qualities tested in the

experiment, broad sense heritability values of more than 60% were achieved. This revealed that additive genetic genes are in charge of all of these features' inheritance.

2.4 Biochemical characteristics of rice

Ahmed *et al.* (1998) revealed considerable variation in mineral contents in some rice cultivars. They also found a considerable variation in chemical composition of rice cultivars and iron content that ranged from 1.5 to 5.0 mg per 100g with an average value of 3.2 mg/100g.

Graham *et al.* (1999) noticed higher Fe content trait is expressed in all rice environments tested such as dry season in normal and saline soils, in acid and neutral soils grain Fe generally varied much more with genotype, than with environment and genotype x environment interactions.

Glahn *et al.* (2002) observed that bioavailability of iron in rice varied with genotypes and that it was not correlated with grain iron concentration. Further, they noticed high grain iron concentration in unpolished rice but lesser availability due to the presence of an inhibitor in unpolished grain.

Although, rice is not a major source of mineral in the diet, any increase in its mineral concentration could significantly help to reduce iron and zinc deficiency because of the high levels of rice consumption in Asia (Gregorio, 2002).

The variation of grain Fe concentration in brown rice among Australian and Thai rice varieties was found to be in a similar range, from 10 to 20 mg Fe/ kg and from 7 mg to 22 mg Fe/ kg (Prom-u-Thai and Rerkasem, 2004).

Ya-wen *et al.* (2005) reported that mineral element contents of 653 Yunnan rice accessions were closely related to most quality traits, including significant correlations between amylose content and potassium, gel consistency and iron or zinc content and gelatinization temperature and manganese content.

Meng *et al.* (2005) have reported that black rice contains iron, zinc, calcium, copper and manganese higher than those in red rice.

Rosniyana *et al.*, (2006) conducted a study to compare the nutritional composition of brown rice and milled rice. The study revealed that the highest nutrient content were observed in brown rice viz., phosphorus (201mg/100g) and iron (6.05mg/100g).

Eight varieties of pigmented rice grown in southern Thailand were studied for their chemical compositions, antioxidant properties and color parameters as

a dehusked grain by Yawadio *et al.* (2007). The iron and polyphenol contents in these rice samples were in the range of 0.900 -11.66 mg/100 g and 58-329 mg GAE/100 g sample respectively. The results showed that dark purple grain had higher iron content, polyphenol content and antioxidant capacity than red brown grain.

Four Pakistani coarse rice varieties namely Irri-6, Irri-9, Sarshar and DR-83 were milled to obtain different fractions *viz.* brown rice, white rice, polished rice, bran and polishing. Chemical components such as moisture, ash, fat, fiber and NFE (Nitrogen Free Extract) differed significantly due to differences in milling fractions as well as rice cultivars. Mineral contents were significantly higher in bran followed by polishing. Iron, zinc, manganese, copper contents ranged from 0.59 to 3.98 mg/100g, 1.12 to 4.69 mg/100g, 0.51 to 5.12 mg/100g, 0.28 to 1.69 mg/100g respectively among different milling fractions. The mineral contents ranged from 1.57 to 1.94 mg/100g, 1.44 to 2.97 mg/100g, 1.57 to 2.33 mg/100g and 0.58 to 0.92 mg/100g among different varieties. The rice varieties Sarshar (more protein @ 8.80%) and Irri-6 (more Fe @ 1.94% and Zn @ 2.97%) must be given more attention by the rice breeders to use in their hybridization programs as these varieties exhibit more proteins and minerals which are required to maintain normal body metabolism (Anjum *et al.*, 2007).

Shabbir *et al.*, (2008) analyzed the mineral contents of four rice varieties namely IRRI-6, KS-282, Basmati 2000 and Super Basmati that were milled to obtain brown rice and white rice. Mineral components were significantly higher in brown rice than white rice. Minerals components were significantly higher in brown rice than white rice. Sodium, potassium, iron and zinc contents in brown rice ranged from 3.87 to 4.88 mg/100g, 102.0 to 229.0mg/100mg, 0.77 to 1.72 mg/100g and 1.31 to 2.01 mg/100g respectively.

A total of 29 different food samples were selected by convenience sampling. The contents of Ca, Zn and Fe in foods were measured by atomic absorption spectrophotometer (AAS). These results showed that although the foods analyzed had high mineral content, they also had a high phytate content which may impair the bioavailability of minerals to the body. Therefore, optimal food processing and cooking methods should be chosen to minimize this effect (Norhaizan *et al.*, 2009).

Babu *et al.* (2013) observed huge variations in grain quality among the new hybrids. Mean micronutrient iron concentration of hybrids (68.4 ppm) was found to be 1.83 times that of zinc (37.3 ppm). Two hybrids with both high iron and zinc concentration (DRRH-2 with 125.8 ppm and 43.8 ppm; and Sahyadri-4 with 104.8 and 43.0 ppm) were identified.

Roy and Sharma (2014) estimated Fe and Zn content in rice accessions. The Iron concentration varies from 0.25 µg/g to 34.8 µg/g and zinc from 0.85 µg/g to 195.3 µg/g among 84 rice landraces. Highest iron was in Swetonunia (34.8 µg/g) and highest Zn was found in Nepali Kalam (195.3 µg/g).

Bielecka *et al.* (2021) obtained a total of 99 samples from 12 groups of rice products (basmati, black, brown, parboiled, red, wild, white rice and expanded rice, rice flakes, flour, pasta, and waffles). The atomic absorption spectrometry method (AAS) was used to determine the content of Ca, Cu, Fe, Mg, Mn, Se and Zn in the study material. The average measured contents of Ca, Cu, Fe, Mg, Mn, Se and Zn were 226.3 ± 160.6 mg/kg, 3.6 ± 2.8 mg/kg, 9.4 ± 7.0 mg/kg, 618.0 ± 498.4 mg/kg, 16.7 ± 10.0 mg/kg, 242.9 ± 140.4 µg/kg and 19.5 ± 15.0 mg/kg respectively. Statistical analyses confirmed the differences in the levels of the studied elements between the subgroups of processed and unprocessed products. Considering the tolerable upper intake level of studied elements, the tested products could be regarded as safe to consume. All tested products can be recommended as a source of Cu, Mn, and Se, while a majority of studied products can be considered a source of Mg and Zn in the diet of the adult European population.

Chapter-3

Materials and Methods

During the *kharif* season 2021, an experiment was conducted entitled “Evaluation of a set of rice (*Oryza sativa* L.) genotypes for grain yield and some important grain mineral content *viz.*, Calcium (Ca), Magnesium (Mg), Zinc (Zn) and Iron (Fe)”.The following are the research materials, methodologies and procedures used throughout the investigation:

3.1 Experimental site

The experiment was conducted at two locations:

- 1) At research cum instructional farm, College of Post Graduate Studies In Agricultural Sciences, (Central Agricultural University, Imphal), Umiam, Meghalaya, India
- 2) At Farmers field, Umiet, Ri-Bhoi District, Meghalaya, India

The locations are located at an elevation of 964m and 835m above mean sea level (MSL) respectively. A schematic layout of the experiment site is shown in Fig. 3.1.

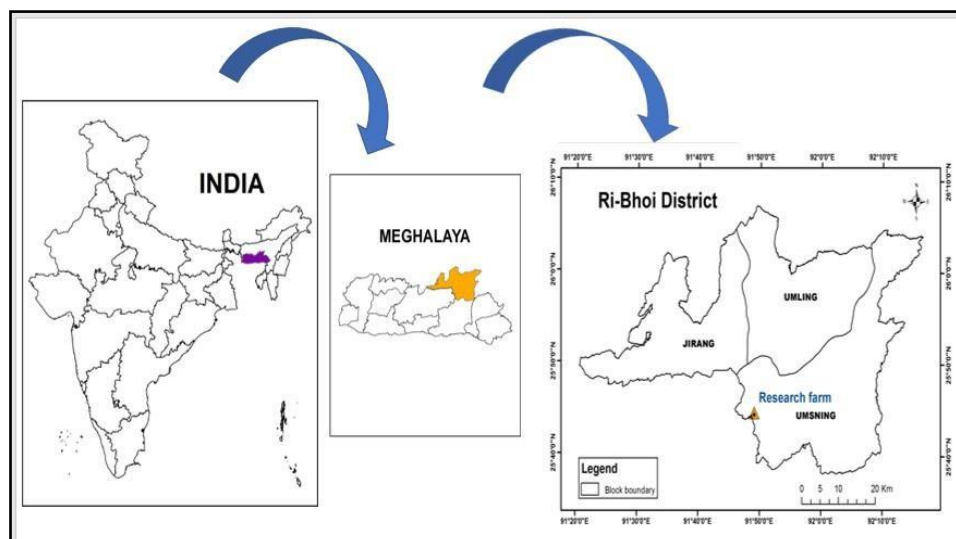


Fig. 3.1: Location of experimental site

3.2 Climate and weather

Meghalaya is located between 25°1'N and 26°5' N latitude and 85°8' E and 92°52' E longitude. The temperature range is approximately 2°C to 36°C depending upon the altitude ranging between 300 m above MSL to 2000 m above MSL. Meghalaya is one amongst the highest rainfall areas in the country with an annual rainfall of 11,000 mm during the period of 1980-1991 and the state is predominantly mountainous, lying between the Brahmaputra valley in the North and the Surma valley (Bangladesh) in the South. Shillong is the capital of Meghalaya and lies at 25°34' N latitude and 91°53'E longitude at an average altitude of 4908 feet (1496 m) above mean sea level (MSL), with the highest level being Shillong peak at 6449 feet (1966 m).

3.3 Experimental materials

The experimental materials comprised of 43 rice genotypes which are presented in Table 3.1. The experimental materials including all the genotypes and the breeding lines were collected from School of Crop Improvement, College of Post Graduate Studies in Agricultural Sciences, Umiam, (Central Agricultural University, Imphal), Meghalaya.

Table 3.1 List of genotypes evaluated in the study

Sl. No.	Genotype code
1	CAU-R1
2	CAU-R2
3	CAU-R3
4	CAU-R4
5	NEH-1
6	NEH-2
7	NEH-3
8	NEH-4
9	NEH-5
10	NEH-6
11	NEH-7
12	NEH-8
13	NEH-9
14	NEH-10
15	NEH-11
16	NEH-12

17	NEH-13
18	NEH-14
19	NEH-15
20	NEH-16
21	NEH-17
22	NEH-18
23	NEH-19
24	M-1
25	M-2
26	M-3
27	M-6S
28	M-6T
29	M-7
30	M-8
31	M-9
32	M-10
33	M-11
34	M-12B
35	M-12G
36	IRRI-8
37	IRRI-15
38	IRRI-16
39	IRRI-18
40	IRRI-22
41	IRRI-31
42	IRRI-34
43	IRRI-42

3.4 Methods

3.4.1 Layout and design for objective 1

All the selected genotypes were evaluated in an experimental field design whose details are given below. The soil was made homogenous after proper land preparation.

Experimental design: Randomized Block Design (RBD)

Replications : 2

Number of treatments: 43

3.4.2. Recording of data

3.4.2.1. Yield and its component characters

The detailed description on the methods of recording observations is elaborated for each character as below-

3.4.2.1.1 Plant height (cm)

Plant height was measured in centimeters (cm) from soil surface to tip of the tallest panicle in the randomly selected ten plants in plot from all the genotypes and averaged.

3.4.2.1.2 Days to 50 % flowering

The total number of days taken from the date of sowing (DOS) to the date when primary panicles of 50 % plants in a plot were flowered was taken as days to 50 % flowering by visual means.

3.4.2.1.3 Days to 80% maturity

The total number of days taken from the date of sowing to the date when panicles of 80% plants in a plot were matured was taken as days to 80 % maturity by visual means.

3.4.2.1.4 Number of tillers per plant

Ten plants were randomly selected in a plot excluding border rows. The total number of tillers per plant at the time of harvest were counted in randomly selected plants of all the 43 rice genotypes in each replication.

3.4.2.1.5 Number of panicles per plant

Ten plants were randomly selected in a plot excluding border rows. The total number of panicles per plant were counted at the time of harvest for randomly selected plants and averaged for each replication.

3.4.2.1.6 Panicle length (cm)

Single panicle length of five randomly selected plants from each replication was measured in centimeters from the base of panicle to the tip of last spikelet after harvesting. The data was averaged in each replication to calculate the length of the panicle.

3.4.2.1.7 Total number of grains per panicle

Total number of grains per panicle were counted in five randomly

selected panicles from each replication of each genotype and the data was averaged in each replication.

3.4.2.1.8 Number of filled grains per panicle

Total number of filled grains per panicle were counted in five randomly selected panicles from each replication of each genotype and the data was averaged in each replication.

3.4.2.1.9 Thousand grain weight (g)

Thousand well-developed whole grains of each entry having about 12%-13% moisture content were counted manually and weighed in gram (g) on a precision weighing balance.

3.4.2.1.10 Grain yield per plant (g)

After harvesting, grain from five randomly selected plants in each replication were dried in sun for 5 – 8 days, then the grain yield was measured in gram (g) using a weighing balance and the mean was estimated.

3.4.3 Layout and design for objective 2

Experimental design : Completely Randomized Design (CRD)

Replication : 2

Number of treatment : 43

CRD was used to assign treatments fully at random, ensuring that each experimental unit has an equal chance of receiving any of the treatments during observation and analysis.

3.4.4 Recording of data

3.4.4.1 Digestion of Iron, Zinc, Calcium and Magnesium:

These four elements were determined in the di-acid digest of plant tissues using the Atomic Absorption Spectrophotometer (AAS) as in case of soil analysis.

3.4.4.2 Procedure for wet digestion:

Wet digestion for estimation of Ca, Mg, Zn and Fe-

- 0.5 of the plant sample was taken in digestion tube or breaker.

- 15 mL of diacid mixture (conc. $\text{HNO}_3:\text{HClO}_4$ in the ratio of 3:1) was added to it.
- The sample was heated until the solution became colourless (evolution of copious dense white fumes).
- It was cooled and then filtered using Whatman No.1 paper and final volume is made upto 100 mL.
- Similarly we ran a blank digestion and blank solution following the above mentioned procedure.

3.4.4.3 Atomic Absorption Spectrophotometry

“The ground state” atom absorbs light energy of a specific wavelength as it enters the “excited state”. As the number of atoms in the light path increases, the amount of light absorbed also increases. By measuring the amount of light absorbed, a quantitative determination of the amount of analyte can be made. The use of special light sources and careful selections of wavelengths allow the specific determination of individual elements.

3.4.4.4 Instrumentation

There are five basic components of an atomic absorption instrument:

1. The light source (hollow cathode lamp/Electrode less discharge lamp) that emits the spectrum of the element of interest.
2. An absorption cell in which atoms of the sample are produced (flame, graphite furnace).
3. A Monochromator for light dispersion.
4. A detector which measures the light intensity and amplifies the signal.
5. A display that shows the reading after it has been processed by the instrument electronics.

Atomic Absorption Spectrophotometer (ELICO, SL 194 DOUBLE BEAM AAS) was used for analysis of Calcium, Magnesium, Zinc and Iron contents in powdered rice grains.

3.4.4.5 Methodology

The method for estimating Calcium, Magnesium, Zinc and Iron was created in the computer program as per the standard operating procedure of AAS using the parameters mentioned below and then respective hollow cathode lamp for

Calcium, magnesium, zinc and iron was switched on for 10 minutes.

- Linearity Range: 0.2 ppm to 6 ppm standard.
 - Recommended flame: Air Acetylene (for Mg, Zn, Fe) and Air Acetylene and Nitrous Oxide for Ca.
 - Wavelength: 423.1(Ca), 285.7(Mg), 214.4(Zn), 248.8(Fe).
1. The burner was aligned by aspirating the standard solution of the specified element. A linearity range of 0.2 ppm to 6.0 ppm standards was used.
 2. The sample information file and result data names were set and the manual analysis window was opened.
 3. The result window and calibration window were also opened.
 4. Flame was switched on.
 5. Nebulizer sample tube was dipped in the solutions and then blank, standards and samples were analysed.
 6. The readings were noted down and the printout of the results generated by the computer program were taken.
 7. The instrument itself tabulated the concentration of the samples in ppm using different concentrations of standard.

3.4.4.6 Calculation

$$\text{Element(ppm)} = \frac{\text{Concentration of solution (ppm)} \times \text{Dilution factor (mL)}}{\text{Weight of sample (g)}}$$

3.5 Statistical analysis

3.5.1 Pooled Analysis Of Variance (Pooled ANOVA)

Pooled Analysis Of Variance is used in estimating the different components of variance. It also provides basis for the test of significance. The mean data was worked out for all traits of each genotype. These mean data were further utilized for calculation of range, standard deviation, coefficient of variation etc.. ANOVA is a tool which helps in subdividing the total variance into three sub components which are “treatment”, “replication” and “error”.

Table 3.2 Pooled Analysis Of Variance (Pooled ANOVA) table

Sources of Variation	Degrees of Freedom (Df)	Sum of Squares (SS)	Mean Sum of Squares (MSS)	F
Replication	$s(r-1)$	RSS	RMS	RMS/EMS
Environment	$s-1$	EnSS	EnMS	EnMS/EMS
Treatment	$t-1$	TSS	TMS	TMS/TEMS
TXE	$(t-1)(s-1)$	TESS	TEMS	TEMS/EMS
Pooled Error	$s(t-1)(r-1)$	ESS	EMS	
Total	$rst-1$	Total SS		

Where,

s = location

r = replication

t = Number of genotypes

TSS = Treatment sum of squares

ESS = Error sum of squares

Total SS = Total sum of squares

TMS = Treatment mean squares

EMS = Error mean squares

Test of Significance

Test of significance was computed by comparing the 'f' calculated values with 'f' tabulated values at 5% significance level. If calculated values are more than the tabulated values, then it was supposed to be significant otherwise it was non-significant if calculated values were less than the table value.

3.5.2 Mean performance

The mean performance and range of 43 genotypes for all the characters studied was estimated by dividing the sum total of observation by total number of observations.

Arithmetic Mean, AM (\bar{X})= $\Sigma(X/N)$

Where,

ΣX =Total observations for character

N= Observation number

3.5.3 Range

Difference between the maximum and the minimum mean value of each trait is known as the range.

Range= $X_n - X_t$

Where,

X_n =highest mean for trait

X_t =lowest mean for trait

3.5.4 Standard error of mean difference

$$SE_d = \sqrt{\frac{2 \text{ EMS}}{r}}$$

Where,

r=number of replications

EMS=Error mean sum of squares

3.5.5 Coefficient of variation

CV is described as the proportion of standard deviation to its mean value and is measured in percentage(%).

$$CV(\%) = \frac{\text{Standard deviation}}{\text{Mean}} \times 100$$

3.5.6 Estimation of genetic variability

Both genotypic and phenotypic coefficients of variability for all the characters were computed as per the method given by Burton and De Vane (1953).

i. Genotypic Coefficient of Variability (GCV)

$$GCV(\%) = \frac{\sqrt{\text{Genotypic variance (Vg)}}}{\text{General mean of population (x)}} \times 100$$

ii. Phenotypic Coefficient of Variability (PCV)

$$\text{PCV (\%)} = \frac{\sqrt{\text{Phenotypic variance (Vp)}}}{\text{General mean of population (x)}} \times 100$$

GCV and PCV were classified as follows, (Robinson *et al.*, 1949)

Low = 0 - 10%

Moderate = 10-20%

High = > 20%

iii. Heritability (in broad sense, h^2)

Heritability in broad sense was calculated by the formula as suggested by Allard (1960).

$$\text{Heritability (\%)} = \frac{V_g}{V_p} \times 100$$

Where,

V_g = Genotypic variance [$V_g = (\text{TMS} - \text{EMS}) / r$]

V_p = Phenotypic variance [$V_g + V_e$]

r = Number of replication

Heritability was classified as follows, (Robinson *et al.*, 1949)

Low = 0 - 30%

Moderate = 30 - 60%

High = > 60%

iv. Genetic advance

The expected genetic advance under selection for the different characters was estimated as suggested by Allard (1960).

$$\text{G.A.} = h^2 (b) \times \sigma_p \times k$$

G.A. = Expected genetic advance

h^2_b = Heritability in broad sense

σ_p = Phenotypic standard deviation ($\sqrt{\sigma_p^2}$)

K = Intensity of selection, the value of which is 2.06 when 5 percent of the individual are selected from the population as given by Lush (1940).

Genetic advance as percent of mean for each character was calculated as suggested by Johnson *et al.* (1955).

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

3.5.7 Correlation

Pearson's Correlation Coefficient was calculated by the following formula

$$r = [n(\sum xy - (\sum x)(\sum y))] / [n\sum x^2 - (\sum x)^2][n\sum y^2 - (\sum y)^2]$$

Where, x and y are variables

n = number of observations

Significance was checked at 5% and 1% level of significance at df (n-2).

3.5.8 Path analysis

The direct and indirect relationship of variables on independent variable can be identified through path studies suggested by Dewey and Lu (1959).

$$r_{1y} = p_{1Yr11} + p_{2Yr12} + p_{3Yr13} + \dots + p_{6Yr16}$$

$$r_{2y} = p_{1Yr21} + p_{2Yr22} + p_{3Yr23} + \dots + p_{6Yr26}$$

$$\dots = \dots + \dots + \dots + \dots + \dots$$

$$r_{6y} = p_{1Yr61} + p_{2Yr62} + p_{3Yr63} + \dots + p_{6Yr66}$$

Where ,

1,2,...,6 = Independent variables,

Y= Dependent variable (grain yield per plant)

r_{1y}, r_{2y}....r_{6y} = Correlation coefficient

p_{1Y}, p_{2Y}....., p_{6Y} = Correlation coefficient between independent and dependent variable 'y'

3.5.9 Genetic Diversity (D²)

This is numerical approach which is used for measuring genetic divergence from collected data of different character, this statistical method developed by Mahalanobis (1936).

3.5.9.1 Determination of group constellations or clusters

The population was divided into distinct clusters using the tocher's approach, as explained by Rao (1952). This method's clustering criterion is that any two variables belonging to the same cluster should have a lower D^2 value on average than those belonging to separate clusters. D^2 values of each genotype combination were sorted in ascending order of magnitude in a tabular format for this purpose.

To begin, two populations with the shortest distance between them were selected, followed by a third population with the lowest D^2 value of the first two populations. The nearest fourth population was then considered, and the process was repeated. When it was determined that adding a certain population resulted in an abrupt increase in the average D^2 , that population was removed from consideration for that cluster. The first cluster's groups were then eliminated, and the rest were processed similarly. This method was repeated until all of the populations were assigned to one of two clusters. The averages of inter and intra cluster divergence (distances) were calculated after the clusters were formed. The distance (D) between and within clusters is represented by the square root of the D^2 values obtained from the above.

3.5.9.2 Average intra and inter- cluster distances

The intra cluster D^2 was determined by combining all possible genotype combinations in a cluster and dividing by the number of genotypes in the cluster, whereas the inter cluster distance was obtained by adding all possible D^2 values between the genotypes of two clusters and dividing by $n_1 \times n_2$. Where n_1 and n_2 are the number of genotypes in two clusters, respectively. The cluster mean for a given trait is calculated by multiplying the sum of the mean values of the genotypes in a cluster by the number of genotypes in the cluster.

3.5.9.3 Cluster diagram

Cluster diagrams depicting the relationship between distinct populations were constructed based on D^2 values between and within clusters.



Fig.3.2: Experimental field at different stages of plant growth



Digestion Unit



Atomic Absorption Spectrophotometer



Samples after digestion

Fig. 3.3. Working in the laboratory

Chapter – 4

Results

Fourty three rice genotypes were used in the current experiment. The genetic variability parameters for grain yield, yield component traits and mineral content were evaluated to determine the genetic potential of the genotypes under study. Correlation analysis was performed to determine the level of character linkage. However, path coefficient analysis will offer sufficient details on the direct and indirect effects of the features that are influencing the yield. One of the most useful tools for breeding programme parent selection is diversity analysis. Therefore, the goal of the current study was to concentrate on finding and choosing better parents, and the outcomes are provided under the following headings.

- 4.1. Grain yield and its component characters
- 4.2. Grain mineral content
- 4.3. Analysis of variance
- 4.4. Genetic variability parameters
- 4.5. Correlation
- 4.6. Path coefficient analysis for yield characters
- 4.7. Diversity analysis for yield and mineral content

4.1 Grain yield and its component characters

The pooled mean data for grain yield and related traits were studied and presented below in table 4.1.

4.1.1 Plant height (PH) (cm)

The trait varied from 73.78 cm to 150.31 cm along with average performance of 100.09 cm. The maximum plant height was recorded in CAU-R4 (150.31 cm) followed by NEH-19 (148.04 cm) and the minimum plant height was recorded in NEH-7 (73.78 cm).

4.1.2 Days to 50% flowering (D50F)

The maximum days for the trait was observed for M-1 (125.50) followed by IRRI-16 (125.25) and the minimum no. of days was recorded for CAU-R3 (86.75). The trait varied from 86.75 to 125.50 days with the average performance of 111.66 days.

4.1.3 Days to 80% maturity (D80M)

The maximum days for the trait was observed for M-12G and M-12B (154.75) followed by NEH-19 (153.00) and the minimum no. of days was recorded for CAU-R3 (121.75). The trait ranges from 121.75 to 154.75 days with the average performance of 143.06 days.

4.1.4 No. of tillers/plant (NTPP)

The trait varied from 5.25 to 9.75 along with average performance of 7.88. The maximum no. of tillers was observed for NEH-17 (9.75) followed by IRRI-34 (9.50) and the minimum was observed for NEH-19 (5.25).

4.1.5 No. of effective tillers/plant (NETPP)

The maximum no. of panicles was observed for IRRI-8 (9.50) followed by IRRI-16 (9.25) and the minimum was observed for NEH-19 (5.00). The trait varied from 5.00 to 9.50 with the average performance of 7.70.

4.1.6 Total no. of grains/panicle (TNGPP)

The maximum no. of grains was observed for NEH-2 (184.25) followed by NEH-12 (180.25) and the minimum was observed in M-11 (90.75). Total grains/panicle varied from 90.75 to 184.25 along with the average performance of 135.01.

4.1.6.1 No. of filled grains/panicle (TNFGPP)

The trait varied from 62.75 to 141.25 along with the average performance of 101.92. The maximum filled grains was observed in NEH-12 (141.25) followed by NEH-6 (137.25) and the minimum filled grains was observed in IRRI-15 (62.75).

4.1.7 Panicle length (PL) (cm)

The length varied from 19.13 to 26.29 cm with the mean performance of 22.60 cm. The maximum length was recorded in M-11 (26.29 cm) followed by NEH-19 (26.21 cm) and the minimum length was recorded in IRRI-31 (19.13 cm).

4.1.8 Thousand grain weight (1000GW) (g)

The trait varied from 20.15 to 28.73 g along with the average performance of 24.83 g. The maximum test weight was observed in NEH-10 (28.73 g) followed by NEH-12 (28.25 g) and the minimum test weight was observed in M-12G (20.15 g).

4.1.9 Grain yield/plant (GYPP) (g)

The maximum yield per plant was observed in NEH-2 (22.60 g) followed by NEH-12 (22.50 g) and the minimum yield per plant was observed in IRRI-15 (10.10 g). The trait ranged from 10.10 to 22.60 g along with the average performance of 17.58 g.

Table 4.1 Pooled mean performance of 43 rice genotypes for yield and its component characters

Sl. No.	Genotypes	PH	D50F	D80M	NTPP	NETPP	TNGPP	TNFGPP	PL	1000GW	GYPP
1	CAU-R1	98.70	107.25	138.25	7.50	7.50	165.00	119.00	21.26	23.65	21.45
2	CAU-R2	75.40	87.00	130.00	7.25	7.00	142.25	100.25	20.40	25.98	19.18
3	CAU-R3	80.95	86.75	121.75	8.00	7.75	124.00	83.75	20.45	24.80	17.43
4	CAU-R4	150.31	114.25	143.25	7.00	7.00	145.50	113.00	25.23	27.73	20.95
5	NEH-1	97.88	108.50	138.50	9.50	9.25	137.00	114.00	24.25	27.40	21.33
6	NEH-2	93.86	107.75	139.75	9.00	8.75	184.25	136.75	24.35	27.05	22.60
7	NEH-3	95.48	110.75	141.25	7.75	7.75	128.25	107.25	24.07	20.78	18.33
8	NEH-4	99.75	111.25	140.50	8.00	8.00	133.75	112.25	22.19	23.45	21.00
9	NEH-5	85.74	111.75	143.50	6.50	6.50	98.75	73.00	23.09	27.03	16.30
10	NEH-6	125.98	104.75	134.50	7.75	7.75	168.50	137.25	24.20	26.03	21.33
11	NEH-7	73.78	113.25	146.00	7.25	7.00	111.75	83.50	19.96	28.23	16.58
12	NEH-8	100.32	111.25	141.50	6.25	6.00	122.25	86.75	22.79	24.00	14.15
13	NEH-9	93.14	114.75	143.50	8.25	8.25	159.00	113.00	23.56	27.95	20.45
14	NEH-10	103.83	116.00	143.50	7.00	7.00	167.50	105.00	23.71	28.73	19.08
15	NEH-11	90.16	108.75	142.50	9.25	8.75	130.00	113.00	22.29	22.98	20.45

16	NEH-12	103.75	112.50	144.00	9.25	9.25	180.25	141.25	22.91	28.25	22.50
17	NEH-13	83.70	111.00	141.00	6.50	6.50	149.75	128.50	21.62	26.35	21.38
18	NEH-14	85.85	125.25	148.25	6.00	6.00	178.25	124.75	22.02	23.38	17.33
19	NEH-15	81.12	114.75	145.25	8.25	7.75	134.00	84.25	21.74	21.75	12.85
20	NEH-16	98.34	107.50	139.50	8.00	7.75	114.25	82.75	22.60	24.28	15.18
21	NEH-17	93.24	105.00	140.00	9.75	9.00	120.25	101.75	22.53	28.05	21.10
22	NEH-18	89.98	110.25	140.50	8.50	8.50	114.00	87.00	22.71	27.08	17.53
23	NEH-19	148.04	105.75	153.00	5.25	5.00	114.75	96.75	26.21	25.13	13.08
24	M-1	94.62	125.50	147.75	9.50	9.25	124.75	91.25	23.13	26.28	20.78
25	M-2	91.25	122.00	144.25	8.75	8.25	118.25	92.00	21.62	22.05	16.68
26	M-3	91.40	104.50	137.75	6.50	6.25	139.50	94.75	21.06	27.95	16.53
27	M-6S	110.23	101.75	141.50	7.75	7.50	146.25	122.75	23.99	27.88	19.35
28	M-6T	123.34	105.00	138.25	5.50	5.25	151.00	121.75	25.52	25.33	15.23
29	M-7	102.34	110.25	141.00	8.25	8.25	155.25	120.00	23.05	24.25	20.15
30	M-8	131.19	111.75	140.50	7.75	7.50	112.50	101.50	22.61	23.28	15.58
31	M-9	135.20	111.75	145.50	8.25	8.00	115.75	86.00	24.74	25.58	14.63
32	M-10	116.50	125.00	148.75	7.00	7.00	129.00	97.25	24.68	23.98	14.18

33	M-11	127.55	117.25	150.00	7.75	7.50	90.75	65.50	26.29	24.65	10.95
34	M-12B	86.75	123.00	154.75	8.00	8.00	131.25	113.25	21.37	24.85	15.45
35	M-12G	82.19	122.50	154.75	6.00	5.75	143.50	102.50	20.08	20.15	10.58
36	IRRI-8	113.30	106.50	143.75	9.50	9.50	131.25	87.75	21.93	21.70	16.68
37	IRRI-15	98.29	123.75	149.50	7.75	7.50	126.25	62.75	20.20	21.98	10.10
38	IRRI-16	92.02	125.25	148.50	9.25	9.25	122.00	87.50	21.80	23.30	17.13
39	IRRI-18	105.39	108.50	144.00	8.50	8.50	159.25	116.75	22.07	23.68	18.83
40	IRRI-22	84.98	116.00	141.50	9.00	8.75	122.50	102.50	22.05	21.50	19.23
41	IRRI-31	79.06	121.50	148.75	8.25	8.00	114.50	92.75	19.13	21.73	15.33
42	IRRI-34	95.16	104.50	147.00	9.50	9.00	122.75	86.75	20.36	24.75	19.95
43	IRRI-42	94.02	109.25	144.25	8.50	8.25	125.75	92.75	21.95	23.01	17.01
	Mean	100.09	111.66	143.06	7.88	7.70	135.01	101.92	22.60	24.83	17.58
	SE(d)±	4.95	1.26	1.44	0.59	0.56	12.92	10.37	0.58	0.26	1.93
	CD	9.85	2.50	2.86	1.18	1.11	25.71	20.64	1.16	0.51	3.85

4.2 Grain mineral content

The pooled mean data for grain mineral content were studied and presented below table 4.2.

4.2.1 Calcium (Ca) in ppm

The Ca concentration varied from 35 to 195 along with average performance of 102.83. The maximum Ca concentration was recorded for NEH-11 (195) followed by NEH-4 (177.5) and the minimum was recorded for NEH-8 (35).

4.2.2 Magnesium (Mg) in ppm

The maximum Mg concentration was recorded in M-6T (561.5) followed by CAU-R4 (550) and the minimum concentration recorded in NEH-5 (59.75). The concentration in ppm varied from 59.75 to 561.5 along with average mean performance of 281.73.

4.2.3 Iron (Fe) in ppm

The range of Fe concentration varied from 17.25 to 52.25 with average mean performance of 35.85. The maximum was recorded for NEH-4 (52.25) followed by IRRI-8 (50) and the minimum concentration was recorded for NEH-6 (17.25).

4.2.3 Zinc (Zn) in ppm

The range of Zn concentration varied from 19.75 to 59.5 with average mean performance of 42.35. The maximum was recorded for M-9 (59.5) followed by M-11 (58.5) and the minimum concentration was recorded for M-2 (19.75).

Table 4.2 Pooled mean performance of 43 rice genotypes for grain mineral content

Sl. No.	Genotypes	Ca	Mg	Fe	Zn
1	CAU-R1	46.25	166.75	20.75	57.50
2	CAU-R2	173.25	447.75	36.50	50.75
3	CAU-R3	72.50	543.00	27.00	43.50
4	CAU-R4	175.75	550.00	26.25	43.25
5	NEH-1	79.25	238.75	47.25	39.25
6	NEH-2	126.25	66.50	46.75	54.75
7	NEH-3	57.50	78.75	32.50	36.50
8	NEH-4	177.50	218.50	52.25	42.25
9	NEH-5	131.75	59.75	28.75	44.00
10	NEH-6	70.50	444.25	17.25	39.25
11	NEH-7	84.25	462.25	30.50	50.75
12	NEH-8	35.00	532.50	29.25	36.00
13	NEH-9	49.00	341.00	46.00	35.75
14	NEH-10	92.50	232.50	35.25	52.50
15	NEH-11	195.00	158.25	38.25	51.00
16	NEH-12	75.00	241.25	35.50	54.50
17	NEH-13	111.00	348.00	48.00	43.00
18	NEH-14	125.50	338.50	26.50	36.50
19	NEH-15	95.75	98.50	45.50	29.00
20	NEH-16	96.25	179.75	34.75	49.25
21	NEH-17	99.50	280.75	35.25	50.50
22	NEH-18	70.00	427.50	27.50	58.50
23	NEH-19	99.00	82.00	42.75	21.75
24	M-1	72.00	222.75	44.00	32.25
25	M-2	125.00	264.50	34.50	19.75
26	M-3	123.25	355.50	38.75	28.50
27	M-6S	58.50	425.50	42.00	37.00

28	M-6T	74.50	561.50	33.25	47.25
29	M-7	162.25	353.50	37.00	37.50
30	M-8	88.25	449.00	25.00	47.50
31	M-9	46.00	132.75	45.75	59.50
32	M-10	98.75	150.50	34.75	49.00
33	M-11	165.25	351.00	33.25	58.50
34	M-12B	89.50	233.25	49.00	26.00
35	M-12G	127.75	71.50	22.00	25.75
36	IRRI-8	118.50	100.25	50.00	22.50
37	IRRI-15	129.50	84.75	21.75	47.25
38	IRRI-16	166.00	497.00	43.00	41.50
39	IRRI-18	64.50	232.75	20.25	33.25
40	IRRI-22	92.50	71.00	39.00	34.25
41	IRRI-31	83.25	337.00	38.75	55.00
42	IRRI-34	105.25	227.00	36.00	46.50
43	IRRI-42	93.00	456.75	43.50	52.25
	Mean	102.83	281.73	35.85	42.35
	SE(d)±	10.73	15.96	5.57	4.43
	CD	21.45	31.92	11.14	8.85

4.3 Pooled Analysis of variance (Pooled ANOVA)

Variability among 43 rice genotypes was evaluated by ANOVA and presented below in table 4.3 for yield characters viz. plant height, days to 50% flowering, days to 80% maturity, total no. of tillers/plant, total no. of effective tillers/plant, total no. of grains/panicle, total no. of filled grains/panicle, panicle length, 1000 grain weight and grain yield/plant and table 4.4 for grain mineral content viz. Ca, Mg, Fe and Zn. The mean sum of squares of ten quantitative traits under study showed significant differences for the yield and yield attributing traits and for grain mineral content. From the pooled analysis of variance, it was revealed that the genotype x environment mean square was highly significant for all the characters studied. The highest significant value of genotype x environment for yield attributes was recorded in total no. of grains/panicle followed by total no. of filled grains/panicle and plant height whereas the lowest significant value was recorded in total no. of effective tillers/plant followed by panicle length. The highest significant value of genotype x environment for mineral content was recorded in Mg whereas the lowest was recorded in Fe. Maximum coefficient of variance for yield attributes was recorded in grain yield/plant followed by total no. of filled grains/panicle and total no. of grains/panicle whereas minimum coefficient of variance was recorded in days to 80% maturity followed by 1000 grain weight. Maximum coefficient of variance for mineral content was recorded in Zn and minimum was recorded in Mg.

Table 4.3 Pooled ANOVA for yield and yield component characters

Source of Variation	Degrees of freedom					MSS					CV(%)
	Replication/ Blocks	Genotype (G)	Environ- ment (E)	G x E	Pooled Error	Replication /Blocks	Genotype (G)	Environment (E)	G x E	Pooled Error	
PH	2	42	1	42	84	521.42	1347.37**	17393.54**	193.24**	49.05	6.99
D50F	2	42	1	42	84	14.94	300.20*	241.95	146.28**	3.16	1.59
D80M	2	42	1	42	84	22.47	143.89	843.95	89.01**	4.13	1.42
NTPP	2	42	1	42	84	0.99	5.34	10.25	3.80**	0.70	10.63
NETPP	2	42	1	42	84	0.22	5.03	13.95	3.70**	0.61	10.22
TNGPP	2	42	1	42	84	2286.22	1896.05**	1816.75	687.86**	333.89	13.53
TNFGPP	2	42	1	42	84	1446.80	1387.05*	749.31	386.19**	215.08	14.38
PL	2	42	1	42	84	0.05	11.72**	17.29	3.74**	0.68	3.66
1000GW	2	42	1	42	84	0.02	21.89**	7.22	10.02**	0.13	1.46
GYPP	2	42	1	42	84	26.87	42.72**	0.67	19.34**	7.48	15.56

** Significance at 1% level
* Significance at 5% level

Table 4.4 Pooled ANOVA for mineral content

Source of Variation	Degrees of freedom					MSS					CV(%)
	Replication /Blocks	Genotype (G)	Environment (E)	G x E	Pooled Error	Replication /Blocks	Genotype (G)	Environment (E)	G x E	Pooled Error	
Ca	2	42	1	42	84	260.73	6412.60**	6397.68	400.96*	230.13	14.75
Mg	2	42	1	42	84	186.28	96639.33**	939.56	834.55*	509.60	8.01
Fe	2	42	1	42	84	31.35	327.06	36.28	213.50**	62.03	21.97
Zn	2	42	1	42	84	31.27	466.28	436.49	419.10**	39.17	14.78

** Significance at 1% level
 * Significance at 5% level

4.4 Genetic variability parameters among yield character and mineral content

The genetic variability parameters for yield & its component characters and mineral content were estimated and presented below table 4.5.

4.4.1 Genotypic and phenotypic coefficient of variation

The genotypic coefficient of variation in percentage for yield characteristics was found to be maximum in plant height (16.97) followed by grain yield/plant (13.76) and minimum in days to 80% maturity (2.59) whereas the phenotypic coefficient of variation was found to be maximum in grain yield/plant (24.97) followed by total no. of filled grains/panicle (24.54) and minimum in days to 80% maturity (5.43).

Similarly, the genotypic and phenotypic coefficient of variation for mineral content was found to be maximum in Mg (54.93, 55.70) and GCV was found to be minimum in Zn (8.11) while PCV was found to be minimum in Fe (35.95).

4.4.2 Heritability and Genetic advance percent mean

Heritability in broad sense was calculated for all yield characters and mineral content. The maximum heritability estimates in percentage for all yield characters was observed in plant height (70.43%) followed by panicle length (47.41%) and minimum in total no. of effective tillers/plant (13.31%). The maximum heritability in percentage for mineral content was observed in Mg (97.27%) and minimum in Zn (4.90%).

The genetic advance as percent of mean was found to be maximum in plant height (29.37%) followed by total no. of grains/panicle (21.82%) and minimum in total no. of effective tillers/plant (0.43%) for yield characters whereas for mineral content it was found to be maximum for Mg (82.34%) and minimum in Zn (3.70%).

Table 4.5 Estimates of genetic variability parameters for yield and its component characters and mineral content in 43 rice genotypes

Sl.No	Characters	Mean	Range		GCV%	PCV%	Heritability (%) (bs)	GA % mean
			Min	Max				
1	PH	100.09	73.78	150.31	16.97	20.22	70.43	29.37
2	D50F	111.66	86.75	125.50	5.56	9.53	33.99	7.45
3	D80M	143.06	121.75	154.75	2.59	5.43	22.76	3.64
4	NTPP	7.88	5.25	9.75	7.89	20.61	14.64	0.49
5	NETPP	7.70	5.00	9.50	7.48	20.51	13.31	0.43
6	TNGPP	135.01	90.75	184.25	12.87	21.12	37.16	21.82
7	TNFGPP	101.92	62.75	141.25	12.99	24.54	28.00	14.43
8	PL	22.60	19.13	26.29	6.25	9.08	47.41	2.00
9	1000GW	24.83	20.15	28.73	6.94	11.42	36.87	2.15
10	GYPP	17.58	10.10	22.60	13.76	24.97	30.35	2.74
11	Ca	124.8	35	195	37.70	41.47	82.65	70.60
12	Mg	440.4	59.75	561.5	54.93	55.70	97.27	82.34
13	Fe	314.8	17.25	52.25	14.86	35.95	17.09	12.65
14	Zn	123.3	19.75	59.50	8.11	36.65	4.90	3.70

4.5 Correlation

Plant breeders utilize correlation analysis to uncover relationships between yield traits and to increase grain production, which is a crucial part of plant breeding. Correlation analysis was carried out to check the relationship for ten yield attributing traits amongst 43 rice genotypes represented in the table 4.6. Correlation analysis revealed positive and negative relationship between two traits. Days to 80% maturity was found to be highly significant and positively correlated to days to 50% flowering. No. of effective tillers/plant was found to be highly significant and positively correlated to no. of tillers/plant. Total no. of filled grains/panicle was found to be highly significant and positively correlated to total no. of grains/panicle. Panicle length was found to be highly significant and positively correlated to plant height. 1000 grain weight was found to be significant and positively correlated to panicle length. Grain yield/plant was found to be significant and positively correlated to no. of tillers/plant, no. of effective tillers/plant, total no. of grains/panicle, total no. of filled grains/panicle and 1000 grain weight. Grain yield/plant was found to be significant and negatively correlated to days to 50% flowering and days to 80% maturity.

Table 4.6 Correlation coefficients among yield and yield component characters

Sl.No.	Characters	PH	D50F	D80M	NTPP	NETPP	TNGPP	TNFGPP	PL	1000GW	GYPP
1	PH	1									
2	D50F	-0.025	1								
3	D80M	0.124	0.796**	1							
4	NTPP	-0.208	0.010	-0.086	1						
5	NETPP	-0.189	0.040	-0.082	0.987**	1					
6	TNGPP	-0.013	-0.082	-0.190	-0.072	-0.014	1				
7	TNFGPP	0.101	-0.130	-0.197	-0.020	0.031	0.830**	1			
8	PL	0.756**	-0.004	0.049	-0.165	-0.142	0.067	0.221	1		
9	1000GW	0.137	-0.295	-0.261	-0.032	-0.018	0.234	0.254	0.328*	1	
10	GYPP	-0.103	-0.313*	-0.461**	0.430**	0.471**	0.535**	0.677**	0.065	0.466**	1

** Significance at 1% level

* Significance at 5% level

4.6 Path analysis for yield and its attributing traits

The indirect and direct effects of variable characters impacting the yield are provided by the path coefficients. The path coefficient analysis were estimated and presented below in Table 4.7 and Figure 4.1.

4.6.1 Direct effects

The characters days to 50% flowering, no. of tillers/plant, no. of effective tillers/plant, total no. of grains/panicle, total no. of filled grains/panicle and 1000 grain weight were found to have direct and positive effects towards grain yield/plant whereas, plant height, days to 80% maturity and panicle length were found to have negative and direct effects with grain yield/plant. Path analysis affirmed that the character total no. of effective tillers/plant (0.7592) had the maximum positive direct effects followed by total no. filled grains/panicle (0.6633), total no. of tillers/plant (0.3529) and 1000 grain weight (0.3033) to grain yield/plant.

4.6.2 Indirect effects

Maximum positive indirect effects was observed in no. of tillers/plant (0.7497) to grain yield/plant through no. of effective tillers/plant followed by total no. of grains/panicle (0.5508) to grain yield/plant through total no. of filled grains/panicle.

The direct and indirect negative effects were very low and the residual effect was estimated as 0.4111 (41%).

Table 4.7 Path coefficient analysis for yield and yield component characters

Characters	PH	D50F	D80M	NTPP	NETPP	TNGPP	TNFGPP	PL	1000GW	GYPP
PH	-0.0657	-0.0007	-0.0319	0.0733	-0.1434	0.0019	0.0668	-0.0451	0.0416	-0.1033
D50F	0.0016	0.0266	-0.2043	-0.0036	0.0304	0.0120	-0.0864	0.0002	-0.0896	-0.3131*
D80M	-0.0082	0.0212	-0.2568	0.0302	-0.0623	0.0277	-0.1305	-0.0029	-0.0792	-0.4606**
NTPP	0.0137	0.0003	0.0220	0.3529	0.7497	0.0106	-0.0132	0.0099	-0.0096	0.4304**
NETPP	0.0124	0.0011	0.0211	-0.3484	0.7592	0.0020	0.0207	0.0085	-0.0055	0.4710**
TNGPP	0.0008	-0.0022	0.0489	0.0256	-0.0103	0.1457	0.5508	-0.0040	0.0709	0.5347**
TNFGPP	-0.0066	-0.0035	0.0505	0.0070	0.0237	-0.1210	0.6633	-0.0132	0.0769	0.6771**
PL	-0.0497	-0.0001	-0.0126	0.0583	-0.1076	-0.0098	0.1463	-0.0597	0.0995	0.0645
1000GW	-0.0090	-0.0079	0.0670	0.0112	-0.0137	-0.0341	0.1682	-0.0196	0.3033	0.4656**

*Residual effect = **0.4111**

** Significance at 1% level

* Significance at 5% level

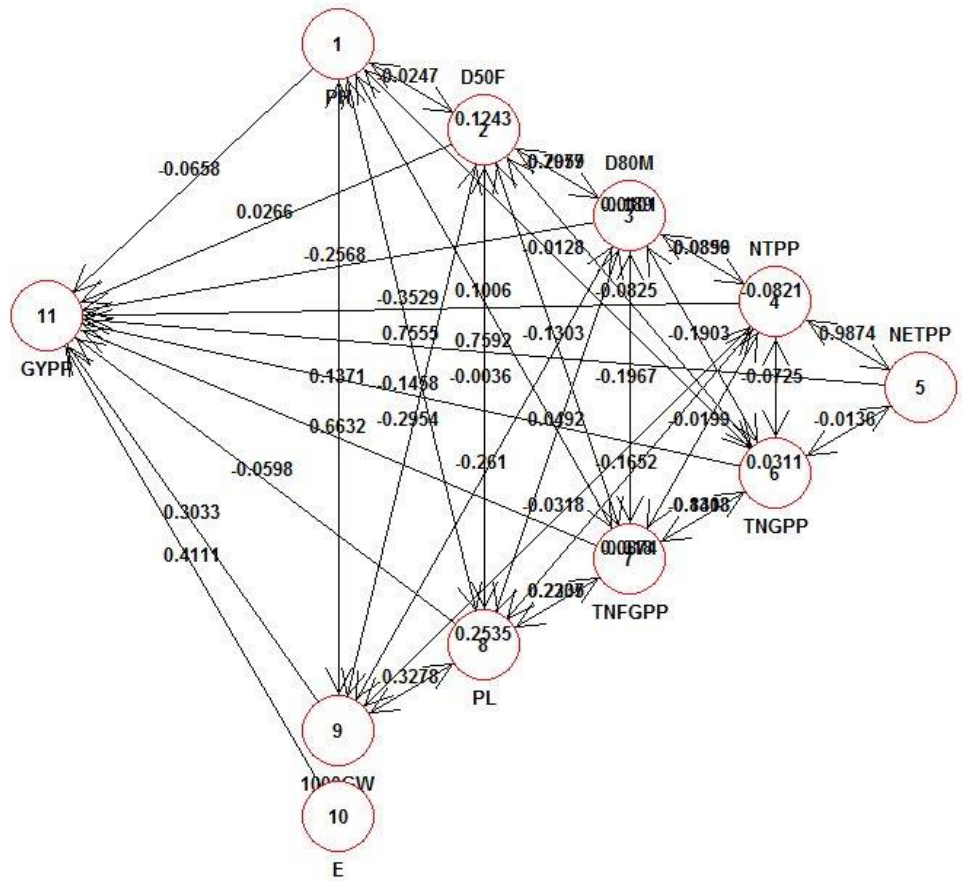


Figure 4.1: Path diagram for yield and yield attributing characters

4.7 Diversity analysis among yield and quality characteristics

In the present study, genetic diversity analysis grouped all 43 genotypes into nine clusters for yield characters and eight clusters for mineral content and presented below in table 4.7 and 4.8 respectively. The no. of genotypes were observed maximum in the cluster II and the no. of genotypes were observed minimum in cluster VI, VII, VIII and cluster IX for yield characters. For mineral content no. of genotypes were observed maximum in the cluster I and minimum in cluster VII and cluster VIII.

The intra and inter cluster distance for yield characters was presented in table 4.9. The intra cluster distance observed maximum in the cluster V (70.621) containing 4 genotypes whereas the minimum distance observed in the Cluster VI (0), VII (0), VIII (0) and XI (0) each consisting of only one genotype. The inter cluster distance was found to be maximum between the clusters IV and IX (911.174) and the minimum distance found between the cluster VI and VII (87.162).

The intra and inter cluster distance for mineral content was presented below table 4.10. The intra cluster distance observed maximum in the cluster V (18.972) containing 3 genotypes whereas the minimum distance observed in the Cluster VII (0) and VIII (0) each consisting of only one genotype respectively. The inter cluster distance found maximum between the clusters IV and VI (274.390) and minimum distance found between the cluster IV and VIII (25.765).

A significant variation was observed for yield characters among the cluster mean and presented below in the table 4.11. For cluster I the maximum values was found for days to 80% maturity (142.35) and minimum for no. of effective tillers/plant (8.08). For cluster II the maximum values was found for total no. of grains/panicle (144.37) and minimum for no. of effective tillers/plant (7.81). For cluster III the maximum values was found for days to 80% maturity (145.91) and minimum for no. of effective tillers/plant (7.91). For cluster IV the maximum values was found for total no. of grains/panicle (133.13) and minimum for no. of effective tillers/plant (7.38). For cluster V the maximum values was found for days to 80% maturity (150.31) and minimum for no. of effective tillers/plant (7.94). For cluster VI the maximum values was found for total no. of grains/panicle (151.00) and minimum for no. of effective tillers/plant (5.25). For cluster VII the maximum values was found for plant height (150.31) and minimum for no. of tillers/plant and no. of effective tillers/plant (7.00). For cluster VIII the maximum values was found for days to 80% maturity (153.00) and minimum for no. of effective tillers/plant (5.00). For cluster XI the maximum values was

found for days to 80% maturity (154.75) and minimum for no. of effective tillers/plant (5.75).

For quality characters, the cluster mean values were presented in table 4.12. For cluster I, II, V, VI and VII the maximum values were found for Mg (540.49, 384.25, 504.58, 555.25 and 342.50 respectively) while for cluster III, IV and VIII the maximum values were found for Fe (294.81, 452.00 and 293.00 respectively).

Table 4.8 Clustering pattern of 43 rice genotypes for yield and yield component characters

Cluster No.	No. of Genotypes	Genotypes
I	12	NEH-11, IRRI-42, NEH-4, IRRI-18, NEH-16, M-7, NEH-8, CAU-R1, M-8, IRRI-8, IRRI-34, M-9
II	13	NEH-1, NEH-2, NEH-18, NEH-9, NEH-12, NEH-5, NEH-13, NEH-17, M-3, NEH-7, NEH-10, M-6S, NEH-6
III	8	M-2, IRRI-22, IRRI-31, NEH-15, IRRI-16, IRRI-15, NEH-14, NEH-3
IV	2	CAU-R2, CAU-R3
V	4	M-10, M-11, M-12B, M-1
VI	1	M-6T
VII	1	CAU-R4
VIII	1	NEH-19
IX	1	M-12G

Table 4.9 Clustering pattern of 43 rice genotypes for mineral content

Cluster No.	No. of Genotypes	Genotypes
I	19	CAU-R3, M-6T, NEH-6, NEH-8, NEH-9, M-3, M-6S, NEH-7, NEH-12, M-2, IRRI-42, M-8, M-10, NEH-18, NEH-14, NEH-15, NEH-17, NEH-2, NEH-11
II	11	NEH-10, NEH-16, M-9, IRRI-15, IRRI-18, IRRI-31, CAU-R1, M-1, NEH-1, NEH-13, M-12G
III	4	NEH-4, M-11, NEH-5, M-12B
IV	2	NEH-3, NEH-19
V	3	M-7, IRRI-8, CAU-R4
VI	2	CAU-R2, IRRI-16
VII	1	IRRI-34
VIII	1	IRRI-22

Table 4.10 Intra and inter cluster distances among yield and yield component characters

Cluster No.	I	II	III	IV	V	VI	VII	VIII	IX
I	47.781	180.906	139.158	288.798	117.339	117.659	235.647	189.954	276.711
II		52.039	423.379	231.536	218.229	105.696	113.741	232.138	705.628
III			55.034	623.938	136.873	344.500	489.319	434.427	93.071
IV				36.877	550.979	236.166	423.389	410.532	911.174
V					70.621	193.898	223.401	253.956	267.979
VI						0	87.162	87.490	558.585
VII							0	156.436	774.207
VIII								0	566.417
IX									0

Table 4.11 Intra and inter cluster distances among mineral content

Cluster No.	I	II	III	IV	V	VI	VII	VIII
I	17.374	38.399	97.560	212.486	40.068	42.923	68.653	192.344
II		14.319	36.635	99.594	39.980	70.004	30.935	85.320
III			13.466	63.673	54.214	101.600	57.685	47.042
IV				12.885	173.732	274.390	94.709	25.765
V					18.972	31.040	69.576	164.451
VI						17.406	97.701	239.824
VII							0	105.632
VIII								0

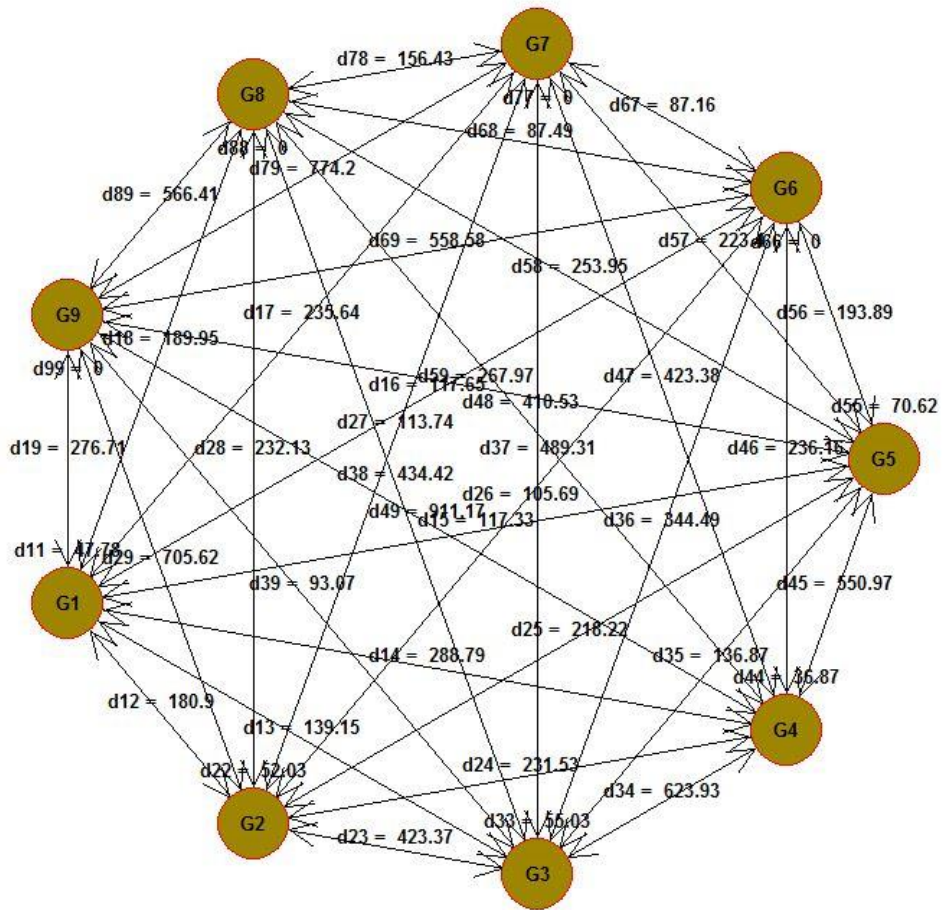


Figure 4.2: Cluster diagram for yield and yield attributing characters

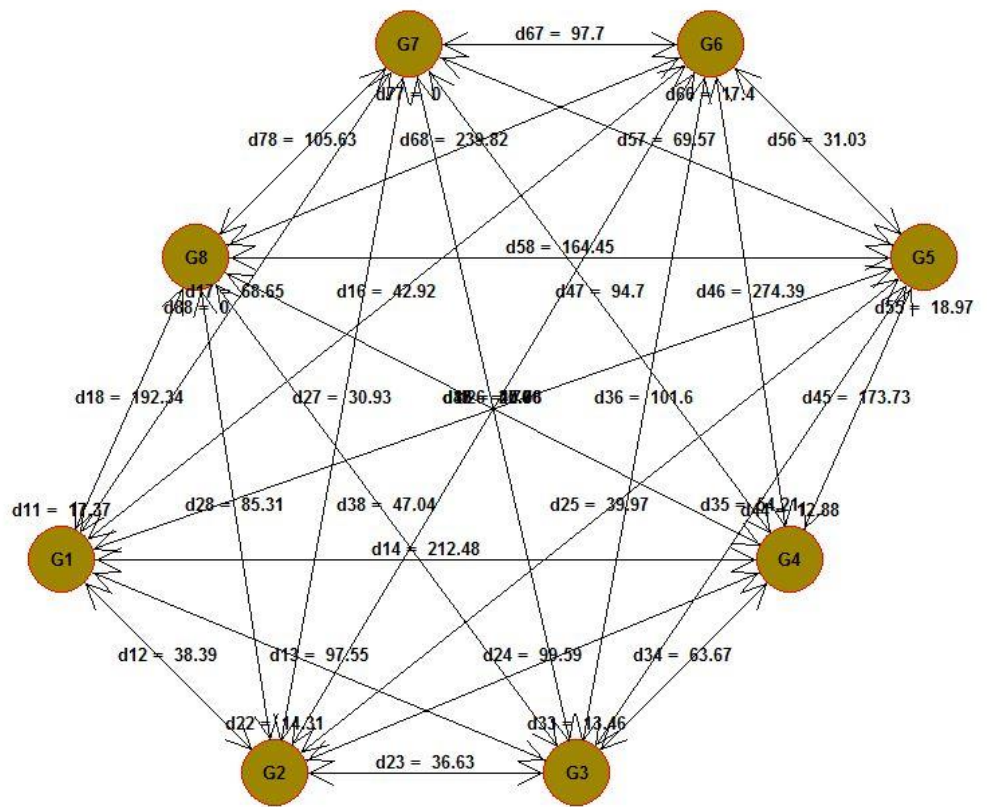


Figure 4.3: Cluster diagram for mineral content

Table 4.12 Cluster mean values for yield and its component characters

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX
PH	105.32	95.88	88.50	78.17	106.35	123.34	150.31	148.04	82.19
D50F	109.04	109.37	119.91	86.88	122.69	105	114.25	105.75	122.50
D80M	142.35	141.08	145.91	125.88	150.31	138.25	143.25	153.00	154.75
NTPP	8.27	7.96	8.13	7.63	8.06	5.50	7.00	5.25	6.00
NETPP	8.08	7.81	7.91	7.38	7.94	5.25	7.00	5.00	5.75
TNGPP	132.31	144.37	130.50	133.13	118.94	151.00	145.5	114.75	143.50
TNFGPP	100.44	110.65	94.22	92.00	91.81	121.75	113	96.75	102.50
PL	22.32	22.92	21.58	20.42	23.87	25.52	25.225	26.21	20.08
1000GW	23.72	27.53	22.06	25.39	24.94	25.32	27.725	25.12	20.15
GYPP	17.92	19.69	15.87	18.30	15.34	15.22	20.95	13.08	10.58

Table 4.13 Cluster mean values for mineral content

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Ca	102.61	113.11	186.38	137.25	198.25	175.50	84.00	122.00
Mg	540.49	384.25	281.06	127.5	504.58	555.25	342.50	96.00
Fe	313.75	319.23	294.81	452.00	332.75	187.75	315.25	293.00
Zn	116.49	123.48	115.94	141.75	132.83	141.00	225.50	75.25

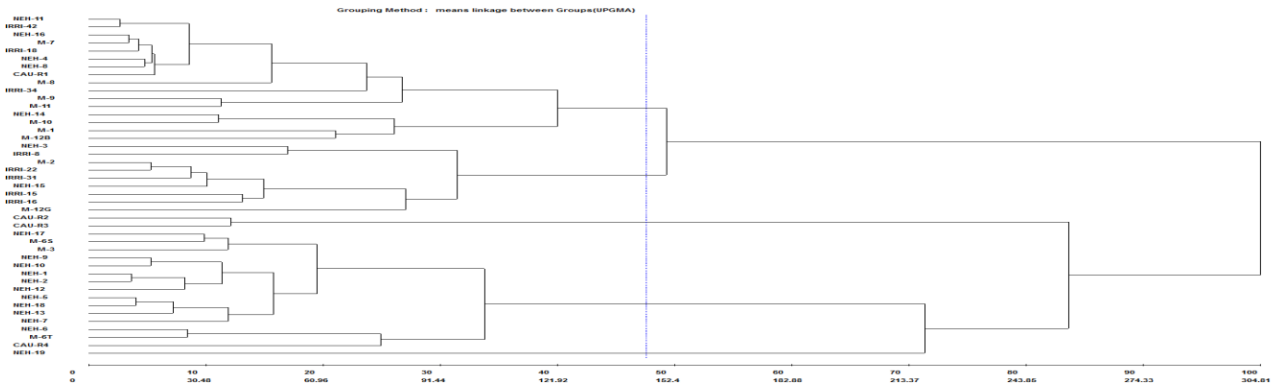


Figure 4.4: Dendrogram for yield characters using UPGMA clustering method

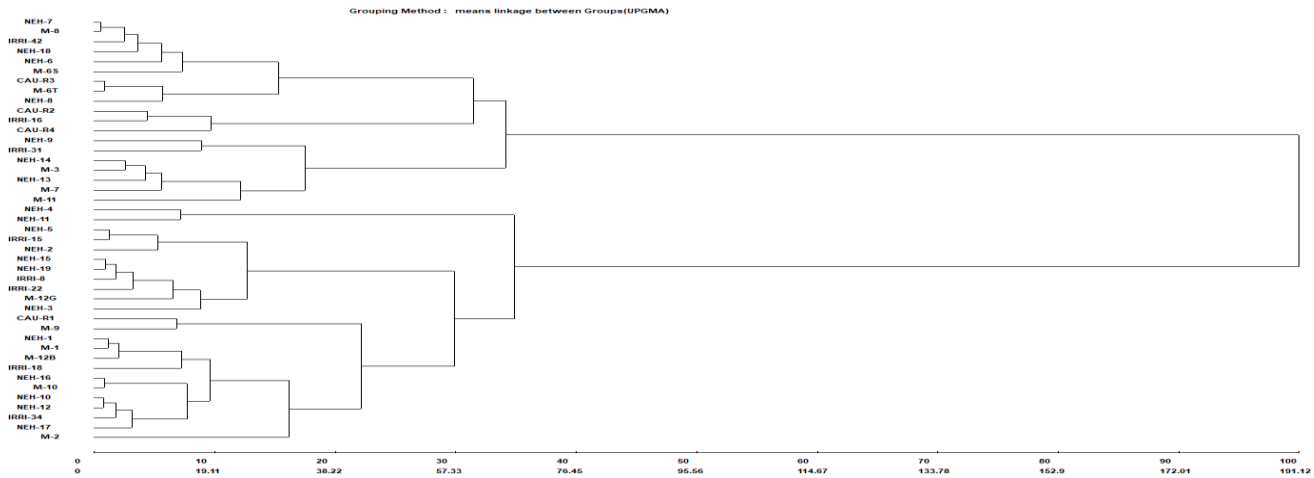


Figure 4.5: Dendrogram for mineral content using UPGMA clustering method

Chapter 5

Discussion

Rice has a significant role in daily life and is virtually always used in Indian rituals. India currently has a population of around 135 crore, but by 2050, that number is projected to grow closer to 160 crore. In contrast, there is a shortage of land, and expanding existing land is also impossible owing to urbanization. Therefore, adopting better and high yielding varieties will provide increased production and productivity of rice, which may help to meet the needs of the Indian people. Due to growing public knowledge of the health advantages and beneficial nutritional qualities of brown or hulled rice, such as its high concentration of minerals, proteins, and phytochemicals, consumption has grown to demand more production recently.

After the yield factor, quality is a crucial criterion that breeders should take into account because of its significant influence on marketing and consumer acceptance. Due to variations in terrain, soil, climate, etc., the mineral composition may vary from one country to the next. Breeders should, therefore develop rice varieties with sufficient mineral content and high yielding varieties. Rice genotypes were evaluated, characterized, and identified through a research programme for yield and mineral content taking into considerations of this significance into account.

In the current study, 43 rice genotypes were evaluated for ten agronomic characters pertaining to yield and its component characters, as well as four minerals. The findings of the study, "Evaluation of a set of rice (*Oryza sativa* L.) genotypes for grain yield and some important grain mineral content viz., Calcium (Ca), Magnesium (Mg), Iron (Fe) and Zinc (Zn)" is discussed as below.

5.1 Grain yield, its component characters and mineral content evaluation

5.1.1 Mean per se performance of 43 rice genotypes for 14 characters under study (10 agronomic traits and 4 mineral contents)

The top performers out of the 43 rice genotypes evaluated mentioned below can be used as parents in breeding programmes in conformance with the breeder's preferences and the demands of the intended consumers.

The rice genotypes used in the study showed sufficient variability for the yield and its component traits. The maximum value for the plant height was recorded in CAU-R4 (150.31 cm) followed by NEH-19 (148.04 cm) and the minimum value for the plant height was recorded in NEH-7 (73.78 cm) indicating wide variability for plant height. The maximum days to 50% flowering was observed for M-1 (125.50) followed by IRRI-16 (125.25) and the minimum no. of days was recorded for CAU-R3 (86.75). The maximum days to 80% maturity was observed for M-12G and M-12B (154.75) followed by NEH-19 (153.00). The minimum number of days was recorded for CAU-R3 (121.75) being the earliest rice genotype among others in 50% flowering also. The no. of tillers varied from 5.25 to 9.75 along with average performance of 7.88. The maximum no. of tillers was observed for NEH-17 (9.75) followed by IRRI-34 (9.50) and the minimum was recorded for NEH-19 (5.25). The maximum total no. of effective tillers/plant was observed for IRRI-8 (9.50) followed by IRRI-16 (9.25) and the minimum was observed for NEH-19 (5.00). The maximum no. of grains per panicle was observed for NEH-2 (184.25) followed by NEH-12 (180.25) and minimum was observed in M-11 (90.75). The total no. of filled grains/panicle varied from 62.75 to 141.25 along with the average performance of 101.92. The maximum filled grains was observed in NEH-12 (141.25) followed by NEH-6 (137.25). The minimum filled grains was observed in IRRI-15 (62.75) though there was a total of 126.25 grains per panicle. This may be due to a huge number of chaffy grains resulted from poor adaptation of the genotype in the prevailing condition. The results of varied performance of yield and its component traits in the studied experimental materials agreed with the report of Adhikari *et al.* (2018) and Chamar *et al.* (2021) in rice.

The panicle length varied from 19.13 to 26.29 cm with the mean of 22.60 cm. The maximum length was recorded in M-11 (26.29 cm) followed by NEH-19 (26.21 cm) and the minimum length was recorded in IRRI-31 (19.13 cm). The maximum test weight was observed in NEH-10 (28.73 g) followed by NEH-12 (28.25 g) and the minimum test weight was observed in M-12G (20.15 g). The maximum yield/plant was observed in NEH-2 (22.60 g) followed by NEH-12 (22.50 g) and the minimum was observed in IRRI-15 (10.10 g). The above findings indicated that the genotype NEH-12 performed better in yield as well as its component traits like grain weight, number of filled grains per panicle. The results obtained were similar to the report of Devi *et al.* (2020), Roy and Sharma (2014) and Shahriar *et al.* (2014) in rice.

The Ca concentration varied from 35 to 195 along with average performance of 102.83. The maximum Ca concentration was recorded for NEH-11 (195) followed by NEH-4 (177.5) and minimum was recorded for NEH-8 (35). The

maximum Mg concentration was recorded in M-6T(561.5) followed by CAU-R4(550) and the minimum concentration recorded in NEH-5(59.75).The concentration in ppm varied from 59.75 to 561.5 along with average mean performance of 281.73. The results are in conformance with the results of Bielecka *et al.* (2021) in rice. The range of Fe concentration varied from 17.25 to 52.25 with average mean performance of 35.85. The maximum was recorded for NEH-4 (52.25) followed by IRRI-8(50.00) and the minimum concentration was recorded for NEH-6(17.25).The range of Zn concentration varied from 19.75 to 59.5 with average mean performance of 42.35. The maximum was recorded for M-9(59.5) followed by M-11 (58.5) and the minimum concentration was recorded for M-2(19.75).The results obtained were in similar with the report of Ahmed *et al.* (1998) and Anjum *et al.* (2007) in rice.

5.2 Analysis of variance (ANOVA)

ANOVA revealed the maximum and significant variation among the examined attributes. Maximum variability for yield characteristics was noted in grain yield/plant (15.56).For analysis of variance among genotypes, significant differences was observed for plant height, length of panicle, no. of filled grains/panicle, grain yield/plant and 1000-grain weight. The results obtained in this study were related to the observations of Naik *et al.* (2020), Sameera *et al.* (2015) and Roy and Sharma (2014) in rice.

5.3 Genetic variability parameters

5.3.1 GCV and PCV (%)

For every trait examined in the current study, the PCV was more than the GCV. PCV is typically higher than GCV, showing that the environment has an impact on the traits that are studied. All of the characters in the study displayed low, medium, and high GCV and PCV values. The GCV in percentage for yield and its component characteristics was maximum in plant height (16.97%) followed by grain yield/plant (13.76%) and minimum in days to 80% maturity (2.59%) whereas the PCV was maximum in grain yield/plant (24.97%) followed by total no. of filled grains per panicle (24.54%) and minimum in days to 80% maturity (5.43%). High GCV and PCV indicated the potential for selection to improve the observed characteristics. In our study most values for GCV and PCV were found to be moderate and low. A sufficient level of diverseness among the qualities under study is indicated by moderate GCV and PCV, which can be used to generate advanced generation via selection. Low GCV and PCV revealed little variation in the traits examined. Therefore, techniques like

induced mutation or hybridization can be used to increase the genetic diversity among those genotypes under investigation. The outcomes were consistent with research on rice genotypes conducted by Akinwale *et al.* (2011), Bhati *et al.* (2015), Paikhomba *et al.* (2014) and Prasad *et al.* (2013) in rice.

5.3.2 Heritability and genetic advance per cent mean

Heritability is the degree to which a trait can be passed down to the next generation. The heritability of all yield and quality characters was examined in the current study in a broad sense. High heritability (>60%) in yield characters was recorded for the trait plant height (70.43%), moderate heritability (30-60%) was observed for no. of days to 50% flowering (33.99%), total no. of grains/panicle (37.16%), panicle length (47.41%), 1000-grain weight (36.87%) and grain yield/plant (30.35%). Low heritability (0-30%) was recorded for no. of days to 80% maturity (22.76%), no. of tillers (14.64%) and effective tillers/plant (13.31%) and total no. of filled grains/panicle (28.00%). The results obtained for heritability were in agreement to Seyoum *et al.* (2012) and Ranjith *et al.* (2018) in rice.

Since it contains both the additive and non-additive effects, estimating heritability only is not taken into account. Consequently, estimating genetic advance offers knowledge of the desirable feature in the population following selection. High GAM was noted for plant height (29.37%) and total number of grains/panicle (21.82%), moderate GAM was found for total no. of filled grains/panicle (14.43%) while low values were observed for the days to 50% flowering (7.45%), days to 80% maturity (3.64%), total no. of tillers (0.49%) and effective tillers/plant (0.43%), panicle length (2.00%), 1000 grain weight (2.15) and grain yield/plant (2.74%) which was similar to the results of Bhatt *et al.* (2016). High heritability combined with a high GAM indicates that features are governed by additive gene effects, making phenotypic selection more successful and it was recorded for the trait plant height.

5.4 Correlation

Through the use of correlation analysis, the association between the yield and its attributing characters was investigated, enabling breeders to identify the desired traits to concentrate on enhancing. The correlation analysis showed both negative and positive correlation between characters. Days to 80% maturity was highly significant and positively correlated to days to 50% flowering. No. of effective tillers/plant was found to be highly significant and positively correlated (0.987) to number of tillers per panicle. Total number of filled grains/panicle turned out to be highly significant and positively correlated to total number of grains/panicle. Panicle

length was found to be highly significant and positively correlated to plant height. 1000 grain weight was found significant and positively correlated to panicle length. Grain yield/panicle was found significant and positively correlated to no. of tillers/plant, no. of panicles/plant, total no. of grains per plant, total no. of filled grains/panicle and 1000-grain weight. Grain yield/plant was significant and negatively correlated to days to 50% flowering and days to 80% maturity with the values of 0.313 and 0.461, respectively. This negative correlation of crop duration with grain yield indicated negative impacts of flowering and maturity on grain yield. The results obtained was in conformance with the report of Adhikari *et al.*(2018), Rathod *et al.* (2017), Sameera *et al.* (2016) and Akhtar *et al.* (2011)for different rice genotypes for genotypic correlation.

5.5 Path analysis

The indirect and direct effects of variable characters impacting the yield are provided by the path coefficients. The characters days to 50% flowering, no. of effective tillers/plant, total no.of filled grains/panicle and 1000-grain weight were found to have direct and positive effects towards grain yield/plant whereas, plant height, days to 80% maturity, no. of tillers/plant, total no. of grains/ panicle and panicle length were found to have negative and direct effects with grain yield per plant. Path analysis affirmed that the character total no. of effective tillers/plant (0.7592) had the highest positive direct effects and then by the total number filled grains/per panicle (0.6633), total number of tillers/plant (0.3529) and 1000-grain weight (0.3033) to grain yield/plant. The maximum positive indirect effects was observed in number of tillers/plant (0.7497) to grain yield/plant through no. of effective tillers /plant followed by total no. of grains/plant (0.5508) to grain yield/plant through total no. of filled grains/panicle. The results obtained were in similar to the report of Venkanna *et al.* (2014) in rice.

5.6 Diversity analysis

The choice of parents and the selection of the desirable traits and their appropriate combinations in following generations are greatly influenced by genetic diversity. The intra cluster distance observed maximum in the cluster V (70.621) containing 4 genotypes whereas the minimum distance observed in the Cluster VI (0), VII (0), VIII (0) and XI (0) each consisting of only one genotype. The inter cluster distance was obtained to be maximum between the clusters IV and IX (911.174) and the minimum distance found between the cluster VI and VII (87.162). For cluster I the maximum mean values was found for days to 80% maturity (142.35) and minimum for number of effective tillers/plant (8.08).For cluster II the maximum values was found for

total no. of grains/panicle (144.37) and minimum for no. of effective tillers/plant (7.81). For cluster III the maximum values was recorded for days to 80% maturity (145.91) and minimum for no. of effective tillers/plant (7.91). For cluster IV the maximum values was obtained for total no. of grains/ panicle (133.13) and minimum for no. of effective tillers/plant (7.38). For cluster V the maximum values was obtained for days to 80% maturity (150.31) and minimum for no. of effective tillers/plant (7.94). For cluster VI the maximum values was found for total no. of grains/panicle (151.00) and minimum for no. of effective tillers/plant (5.25). For cluster VII the maximum values was found for plant height (150.31) and minimum for no. of tillers/plant and no. of effective tillers/plant (7.00). For cluster VIII the maximum values was found for days to 80% maturity (153.00) and minimum for no. of effective tillers/plant (5.00). For cluster IX the maximum values was found for days to 80% maturity (154.75) and minimum for no. of effective tillers per plant (5.75). The results obtained were unanimous with Devi *et al.* (2020) and Guru *et al.* (2017) in rice. The intra cluster distance observed maximum in the cluster V (18.972) containing 3 genotypes whereas the minimum distance observed in the Cluster VII (0) and VIII (0) each consisting of only one genotype respectively. The inter cluster distance found to be maximum between the clusters IV and VI (274.390) and minimum distance found between the cluster IV and VIII (25.765). For quality characters, the mean values of cluster were presented in table 4.12. For cluster I, II, V, VI and VII the maximum values were found for Mg (540.49, 384.25, 504.58, 555.25 and 342.50 respectively) while for cluster III, IV and VIII the maximum values were found for Fe (294.81, 452.00 and 293.00 respectively). The results obtained were similar with Banumathy *et al.* (2010), Meena *et al.* (2017), Praveen *et al.* (2016) and Roy and Sharma (2014) in rice.

Chapter-6

Summary and Conclusion

The research work entitled, “**Evaluation of a set of rice (*Oryza sativa* L.) genotypes for grain yield and some important grain mineral content viz., Calcium (Ca), Magnesium (Mg), Iron (Fe) and Zinc (Zn)**” was performed using 43 rice genotypes. In order to identify, assess, and choose rice genotypes that perform better, in yield, its component features, and mineral content, this 43 rice genotypes were evaluated and analyzed. The experiment was conducted in two locations—the farmers field in Umiet and the experimental research farm at CPGS-AS in Umiam, Ri-Bhoi District, Meghalaya during the *kharif* season 2021.

The current study aimed to identify and evaluate 43 rice genotypes in order to determine the yield performance of various breeding lines and to assess the mineral content of rice in order to pick the top genotypes for use in further breeding programmes.

The following are the key findings from the current study:

- ✓ Days to 80% maturity was found to be maximum in M-12G and M-12B (154.75) followed by NEH-19 (153.00). The maximum filled grains was observed in NEH-12 (141.25) followed by NEH-6 (137.25) and the maximum yield/plant was observed in NEH-2 (22.60 g) followed by NEH-12 (22.50 g).
- ✓ Through field testing, it was concluded that the genotypes with the maximum filled grains per panicles in the current set of genotypes had the maximum yield.
- ✓ From the pooled analysis of variance, it was stated clearly that the genotype x environment mean square was highly significant for all the traits studied. The highest significant value for genotype x environment was recorded in the total no. of grains/panicle followed by total no. of filled grains/panicle and plant height whereas the significant value was lowest in total no. of effective tillers/plant followed by panicle length.
- ✓ Maximum coefficient of variance for yield attributes was recorded for grain yield/plant, then came to total no. of filled grains/panicle and total no. of

grains/panicle whereas minimum coefficient of variance was recorded in days to 80% maturity followed by 1000 grain weight.

- ✓ Heritability (broad sense) was found to be maximum in plant height (70.43%) followed by panicle length (47.41%) and GAM was regarded high for plant height (29.37%) followed by total no. of grains/panicle (21.82%). Hence, these traits might be effective for selection.
- ✓ The GCV in percentage for yield and its component characteristics was found to be maximum in plant height (16.97) then by grain yield/plant (13.76) and minimum in days to 80% maturity (2.59) thus, selection of genotypes based on these characteristics will be successful as they are based on genotypic variation only whereas the PCV was found to be maximum in grain yield/plant (24.97) followed by total no. of filled grains/panicle (24.54) and minimum in days to 80% maturity (5.43).
- ✓ In correlation study, positive and significant correlation between grain yield and total no. of tillers/plant was observed, total no. of panicles/plant, total no. of grains/panicle and total no. of filled grains/panicle whereas it showed significant and negative correlation with days to 80% maturity and days to 50% flowering.
- ✓ Path analysis affirmed that the character total no. of effective tillers/plant (0.7592) had the highest positive direct effects and then by total no. filled grains/panicle (0.6633) and also 1000 grain weight (0.3033) to the grain yield/plant. Maximum positive and indirect effects was seen in no. of tillers/plant (0.7497) to grain yield/plant through no. of panicles/plant followed by total no. of grains/panicle (0.5508) to grain yield/plant through total no. of filled grains/panicle.
- ✓ The intra cluster distance was observed maximum in cluster V (70.621) containing 4 genotypes while the inter cluster distance was found to be maximum between the clusters IV and IX (911.174). Hence, crosses can be made between these genotypes to obtain desirable recombinants.
- ✓ Genotypes in the clusters I, II, IV and VII had high grain yield mean values and these can be used for cultivation as well as a parent in further hybridization programme.
- ✓ Ca concentration varied from 35 to 195 along with average performance of 102.83. The maximum Ca concentration was recorded for NEH-11 (195)

followed by NEH-4(177.5) and minimum was recorded for NEH-8 (35).

- ✓ The maximum Mg concentration was recorded in M-6T(561.5) followed by CAU-R4(550) and the minimum concentration recorded in NEH-5(59.75).The concentration in ppm varied from 59.75 to 561.5 along with average mean performance of 281.73.
- ✓ The range of Fe concentration varied from 17.25 to 52.25 with average mean performance of 35.85. The maximum was recorded for NEH-4 (52.25) followed by IRRI-8(50) and the minimum concentration was recorded for NEH-6(17.25).
- ✓ The range of Zn concentration varied from 19.75 to 59.5 with average mean performance of 42.35. The maximum was recorded for M-9(59.5) followed by M-11 (58.5) and the minimum concentration was recorded for M-2(19.75).
- ✓ The genotype x environment interaction for mineral content showed the highest significant value in Mg and the lowest in Fe.
- ✓ Maximum coefficient of variance for mineral content was recorded in Zn and minimum was recorded in Mg.
- ✓ The GCV and PCV for mineral content was found to be maximum in Mg (54.93, 55.70) and GCV was recorded to be minimum in Zn (8.11) while PCV was found to be minimum in Fe (35.95).
- ✓ Heritability in broad sense was maximum for Mg (97.27%) and minimum for Zn (4.90%)The GAM was found to be maximum for Mg (82.34%) and minimum in Zn (3.70%) in case of mineral content.
- ✓ The intra cluster distance was observed maximum in the cluster V (18.972) containing 3 genotypes and the inter cluster distance was observed to be maximum between the clusters IV and VI (274.390).
- ✓ Genotypes from the clusters III and V were high in Ca, I and VI in Mg, IV and V for Fe and cluster VII for Zn. Thus, these can be used as a parent in further hybridization programmes.

Future scope of research

According to the observations of genetic variability parameters, correlation, path coefficient analysis, and diversity analysis, the following traits—plant height, no. of tillers, no. of effective tillers, length of panicles, total no. of grains and thousand grain weight can be effectively used to develop rice genotypes with high yields. When choosing prospective genotypes, traits with high heritability (broad sense) and GAM should be given more consideration. Genotypes NEH-2, NEH-12, CAU-R1, NEH-1, NEH-4, NEH-6, NEH-13, NEH-17, CAU-R4 performed better for yield and its attributing characters. The genotypes NEH-11, CAU-R4, M-6T, NEH-1, NEH-13, M-9, M-11 performed better for mineral contents. These genotypes can be used in a future breeding programme to develop superior lines. The exact measurement of genetic diversity and the confirmation of significant mineral and yield traits should be obtained in the future by molecular characterization.

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Appendix I

Weekly data prevailed during crop growing season

SMW	Month and date	Total Rainfall (mm)	Avg. Max. temperature (°C)	Avg. Min. temperature (°C)	Relative Humidity (%)
23	June 4-10	30.30	29.21	27.71	80.37
24	11-17	54.60	29.07	28.43	79.09
25	18-24	59.20	29.57	28.43	79.61
26	25-1	81.80	28.00	27.86	80.37
27	July 2-8	29.80	27.57	20.50	89.20
28	July 9-15	35.40	29.14	18.21	89.64
29	16-22	129.70	29.71	17.93	88.71
30	23-29	39.10	33.14	18.86	83.00
31	30-5	120.90	32.43	18.21	90.09
32	August 6-12	80.90	30.08	18.79	91.57
33	13-19	30.00	29.07	19.07	91.69
34	20-26	84.90	29.07	18.07	88.83
35	27-2	134.40	23.86	19.07	71.27
36	September 3-9	57.70	31.50	17.00	76.47
37	10-16	28.60	32.07	16.71	77.26
38	17-23	181.60	29.64	16.29	76.03
39	24-30	25.60	30.21	16.07	68.31
40	October 1-7	106.00	29.14	15.71	80.69
41	8-14	64.60	33.64	16.43	80.60
42	15-21	80.40	31.14	16.64	85.23
43	22-28	0.00	28.07	11.50	69.43
44	29-4	0.00	28.36	10.00	77.76

45	November 5-11	0.00	26.93	8.79	72.17
46	12-18	0.00	27.50	14.64	76.40
47	19-25	0.00	25.86	16.35	68.13
48	26-2	0.00	25.36	NA	67.71

