VARIABILITY AND STABILITY STUDIES FOR NITROGEN USE EFFICIENCY IN UPLAND RICE (*Oryza sativa* L.) GENOTYPES OF NAGALAND

Thesis

submitted to

NAGALAND UNIVERSITY

in partial fulfillment of requirements for the Degree

of

Doctor of Philosophy

in

Genetics and Plant Breeding

by

B. LALHRUAITLUANGI
Admn. No. Ph – 288/19 Regn. No. Ph.D./GPB/00341

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School of Agricultural Sciences
Nagaland University, Medziphema Campus – 797106
Nagaland
2024

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DECLARATION

I, **B. Lalhruaitluangi,** hereby declare that the subject matter of this thesis is the record of work done by me, that the contents of this thesis did not form the basis of the award of any previous degree to me or to the best of my knowledge to anybody else, and that the thesis had not been submitted by me for any research degree in any other university/institute.

This is being submitted to Nagaland University for the degree of Doctor of Philosophy in **Genetics and Plant Breeding**.

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CERTIFICATE – I

This is to certify that the thesis entitled ***"Variability and stability studies for nitrogen use efficiency in upland rice (Oryza sativa L.) genotypes of Nagaland"*** submitted to Nagaland University in partial fulfillment of the requirements for the award of degree of Doctor of Philosophy in **Genetics and Plant Breeding** is the record of research work carried out by Miss **B. Lalhruaitluangi,** Registration No. **Ph.D./GPB/00341** under my personal supervision and guidance.

The result of the investigation reported in the thesis have not been submitted for any other degree or diploma. The assistance of all kinds received by the student has been duly acknowledged.

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CERTIFICATE – II

VIVA VOCE ON THESIS OF DOCTOR OF PHILOSOPHY IN GENETICS AND PLANT BREEDING

This is to certify that the thesis entitled **"Variability and stability studies for nitrogen use efficiency in upland rice (*Oryza sativa* L.) genotypes of Nagaland"** submitted by B. LALHRUAITLUANGI Admission No. Ph-288/19 to the NAGALAND UNIVERSITY in partial fulfillment of the requirements for the award of degree of Doctor of Philosophy in Genetics and Plant Breeding has been examined by the Advisory Board and External examiner on …….....

The performance of the student has been found **Satisfactory/Unsatisfactory.**

Member	Signature
1. Dr. M.B. Sharma (Supervisor and Chairman)	…….
2. …… (External examiner)	…….
3. Pro-Vice Chancellor Nominee (Dean, SAS)	…….
3. Dr. Pankaj Shah	…….
4. Dr. Kigwe Seyie	…….
5. Dr. Tongpang Longkumer	…….
6. Dr. Sanjoy Das	…….

Head
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Dean
School of Agricultural Sciences

Dedicated

to my beloved parents

and brothers

ACKNOWLEDGEMENTS

I am deeply grateful as I stand at the culmination of my journey by the grace of God and through the realm of Genetics and Plant Breeding, undertaken at SAS. This incredible journey would not have been possible without the unwavering support and guidance of a multitude of individuals and resources. It is with immense gratitude that I extend my heartfelt acknowledgments to each of them.

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In closing, the completion of this thesis marks not just the culmination of an academic pursuit, but also a reflection of the collective effort and encouragement from a multitude of individuals. Each of you has played an indispensable role in shaping my academic and personal growth, and for that, I am eternally thankful.

Date:

Place: Medziphema **(B. LALHRUAITLUANGI)**

CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF PLATES

LIST OF ABBREVIATIONS

%	: Per cent
/	: Per
@	: at the rate
AC	: Amylose content
ANOVA	: Analysis of Variance
b_i	: regression coefficient
BY	: Biological Yield
CD	: Critical Difference
cm	: Centimeter
Df	: Degree of freedom
DMSO	: Dimethyl sulphoxide
E_1	: Environment 1
E_2	: Environment 2
E_3	: Environment 3
et al.	: Et alilbi and others
G	: Gram
GA	: Genetic Advance
GCV	: Genotypic Coefficient of Variation
GN%	: Grain nitrogen%
h^2_{bs}	: heritability in broad sense
ha	: Hactare
HI	: Harvest Index
HSW	: hundred grain weight
ICAR	: Indian Council of Agricultural Research
Kg	: Kilogram
KOH	: Potassium hydroxide
Max.	: Maximum

Min.	: Minimum
MSS	: Mean sum of sqaures
N	: Nitrogen
NaOH	: Sodium hydroxide
NEH	: North Eastern Hill
NHI	: Nitrogen harvest index
NPK	: Nitrogen Phosphorous Potassium
NS	: Non-significant
NUE	: Nitrogen use efficiency
NUpE	: Nitrogen uptake efficiency
NUtE	: Nitrogen utilization efficiency
^{O}C	: Degree Celsius
PCV	: Phenotypic Coefficient of Variation
PNUE	: Physiological nitrogen use efficiency
RBD	: Randomized Block Design
S^2_{di}	: mean square deviations
SAS	: School of Agricultural Sciences
SEm	: Standard error of mean
SS	: Sum of Square
TGW	: thousand grain weight
UI	: Utilization index
via.	: through

ABSTRACT

The present investigation under the topic 'Variability and stability studies for nitrogen use efficiency for upland rice (*Oryza sativa* L.) genotypes of Nagaland" was conducted in the Experimental farm of Department of GPB, SAS, Medziphema campus, Nagaland University. A set of 28 upland rice genotypes was evaluated in three different nitrogen doses in two years (*Kharif* 2021 and *Kharif* 2022) using randomized block design with three replications *viz.*, E_1: zero N (N: P: K @ 0: 30: 30 kg/ha), E_2: low N (N: P: K @ 40: 30: 30 kg/ha) and E_3: high N (N: P: K @ 60: 30: 30 kg/ha). Characterization of 11 qualitative traits revealed variability in early plant vigour, basal leaf sheath, panicle exsertion, stigma colour, panicle type, seed coat colour and hull (husk) colour but no variability in case of leaf pubescence, apiculus colour and awning. For 29 quantitative traits, mean for NUE, yield and yield attributing traits like panicles per plant, amylose content, spikelet fertility, harvest index, Grain N%, PNUE, NutE, Biological yield, NHI, 100 grain weight and grain yield per plant were highest in Thupfu Lha, Thangma White, Manen Red (SARS-5), Taposen Youli, Thangmo Red, Ngoni, Yarba (SARS-3) and Tsushvuri. Similarly, GCV was highest for chlorophyll a, germination percentage, flag leaf area, total chlorophyll, harvest index, chlorophyll b and flag leaf length whereas PCV was highest in biological yield, chlorophyll a, germination percentage, grain weight, amylose content, harvest index, flag leaf area, chlorophyll, chlorophyll b and flag leaf length indicating high variability among these traits. Heritability was also high for many important characters associated with NUE yield and yield attributes. High heritability coupled with high genetic advance as per cent of mean were also observed in NUE yield and yield attributing traits which shows the presence of additive genes. Grain yield expressed strong positive correlation with 100 grain weight, spikelet fertility, NUtE, harvest index and panicle weight at both genotypic and phenotypic level which indicated that these traits could be used as selection criteria for higher

yield for NUE. Highest value of positive direct effects at genotypic and phenotypic path analysis were also observed in grain N%, harvest index and NUtE and highest negative direct effects were in PNUE, NUtE, amylose content and biological yield. Genetic diversity studies revealed 5 number of clusters with maximum inter-cluster distance between cluster 3 and 5. Genotypes such as Kezie (SASRS-94), Moyatsuk, Yarba (SARS-3), Tsushvuri, Shyekenyii, Moya Chali, Longkhum Tsuk (SARS-2) and Amusu were also showing high mean and stability for NUE yield and yield attributing characters.

CHAPTER - I

INTRODUCTION

INTRODUCTION

Rice is a dietary staple food for billions of people in the world and is recognized as the most significant food crop, particularly in a country like India. A 100 gram of rice contains mainly carbohydrate (28g), protein (2.7 g) and total fat (0.3g) (USDA, 2019) and supplies the daily dietary needs of mankind. India has the largest area under rice cultivation and is both the second-largest producer and the biggest exporter of rice worldwide. China and India together produced 52% of the total global production of rice in 2020 which is 756.7 million metric tonnes. There was an enormous increase in production of rice in India from 1980 to 2022, a total of 53.6 million tonnes was produced in 1980 whereas 130 million tonnes was recorded in 2021-2022 and production of rice per hectare in 2021–22 was 2809 kg (NFSM, 2022).

Rice is also a major staple food in Nagaland and is cultivated in terrace and jhum system which occupies about 86% of the state's arable land and has over 400 accessions of rice germplasm (Konjengbam, 2021). Traditional rice cultivars are grown in altitudes between 300 and 2500 metre and rice production in Nagaland was 5.51 million tonnes in 2020-2021(The Naga Republic, 2021). Since, the indigenous cultivars of Nagaland are low yielders with high genetic variability; they are employed for incorporating biotic and abiotic stress resistant gene, better quality, adaptability, and other aspects that can ultimately improve yield. SARS, Mokokchung has been actively involved in germplasm conservations and conducting research on upland and lowland rice and these rice cultivars were evaluated within different agro-climatic regions. Sungmangtsuk (SARS-1) is one of the promising upland rice cultivar that is now being registered with the PPV&FRA, New Delhi and SARS is currently maintaining 51 lowland and 89 upland rice cultivars (SARS, Nagaland). Upland rice has a unique habitat where crops are grown in rainfed conditions without the accumulation of surface water. Due to dearth of research

articles on upland rice, the success of lowland cultivars has little bearing on upland rice and since upland rice has low production costs, finding lines with improved yield and agronomically favourable traits is essential in solving the productivity problems. Nitrogen deficiency is also common in upland rice due to uneven distribution of rainfall during cropping season. Most destructive diseases of upland rice are brown spot (*Bipolaris oryzae*) and blast (*Magnaporthe grisea*).

Nitrogen is one of the most essential elements for plant productivity, along with phosphorus and potassium. The crucial stages when rice needs nitrogen are early vegetative and panicle initiation stages. Grain yield is increased by applying nitrogen during early vegetative or panicle initiation stages and insufficient N availability induces biomass production, smaller leaves, lower chlorophyll content and ultimately decreased yield and poorer grain quality.

Moll *et al*. (1982) defined nitrogen use efficiency as grain yield per unit of nitrogen supply, whereas its efficiency might be defined as grain yield per unit of nitrogen uptake (Muchow, 1998). Nitrogen use efficiency (NUE) of the genotypes is demonstrated as genotypes that perform better when exposed to low soil N levels. Breeding for improving grain yield and NUE is a primary objective of many rice breeding initiatives (Wei *et al*., 2011) and these efficient genotypes are used to increase rice production in subpar rice soils, which is beneficial for farmers with limited resources and access to N fertilizer. Recently, selection and analyzing for improvements in nitrogen use efficiency (NUE) has been done by breeders. Breeding and selection of improved varieties are carried out in environments with abundant nitrogen (N), where the amount is not a yield-limiting factor. Therefore, cultivars with higher yields and greater crop NUE that function well in low N environments are suitable for improvement programmes.

A genotype is N-efficient if it transforms high N intake into yield more efficiently than other genotypes (Sattelmacher *et al*., 1994). Therefore, it is necessary to evaluate plants under both low and high nitrogen environments in order to find a NUE-efficient genotype and compare its performance to that of other genotypes under varied N situations in order to produce genotypes with higher nitrogen use efficiency along with yield.

The whole production of the rice crop depends on NUE, and its improvement necessitates a thorough knowledge of the mechanisms influencing NUE (Ladha *et al*., 1998). For selection of genotypes with high NUE factors such as relationships between N absorption, water availability, and interactions between various macro- and micronutrients are taken into account. Nitrogen harvesting index (NHI) is another factor that influences nitrogen use efficiency (NUE). If NHI remains stable, nitrogen uptake efficiency (NUtE) increases which decreases grain nitrogen (N) content. Therefore, NUtE should be increased when grain nitrogen concentration is lower because higher photosynthesis occurs per unit of absorbed nitrogen which indicates the capacity of a genotype to retain greener leaf longer during grain filling.

The increase in nitrogen intake from fertilizer, especially N fertilizers, has improved crop yields worldwide (Cassman, 1999). Hence, in order to optimize crop development and increase grain yield, farmers frequently apply more N fertilizers than is necessary (Lemaire and Gastal, 1997). Therefore, in order to boost rice production with less nitrogen fertilizer application, research on increasing NUE of the rice crop has been done over the past 30 years and this has been done by improving N use efficiency (NUE) through improved N fertilizer management. It is also essential to improve the timing and rate of N treatment in order to balance the crop's need for N and supply of N (Cassman *et al*., 1998).

The results of NUE's efforts and dedication to germplasm development, however, have not been very notable. Breeders have found it challenging to create crops that utilize nitrogen more effectively due to increased environmental concerns and rising cost of fertilizer. Genetic diversity is a vital pre-requisite for any hybridization programmes that aimed at increasing yield, especially for self-pollinated crops (Joshi and Dhawan, 1966). Grain yield is also a complex trait with considerable environmental effects where variety selection based on performance in a single environment is not sufficient for variety identification (Shrestha *et al*., 2012.) and therefore selection must be carried out when there are more than one or two environments while taking yield evaluation of stability into account as contrary to average performance analysis.

Keeping these points in view, the following objectives were undertaken:

1) To characterize upland rice genotypes of Nagaland for NUE with yield and yield attributing traits.
2) To estimate genetic divergence in the genotypes for NUE, yield and yield attributing traits.
3) To assess GxE interactions affecting NUE and other traits through stability analysis.

CHAPTER - II

REVIEW OF LITERATURE

REVIEW OF LITERATURE

The investigations to be carried out are reviewed under different headings:

2.1 Importance and constraints in rice production with respect to nitrogen use

By 2050, it is expected that there will be 9.3 billion people on the planet and we will need to produce 60 per cent more food (FAO, 2012). To fulfill the rising demand for food, it is necessary to maintain yield improvement on current land due to the restricted capacity for arable land growth. For about half of the world's population, rice is one of the primary food crops. To meet the demands of the expanding global population, rice output must be greatly boosted. The demands of declining arable land, a changing climate, more frequent natural disasters, and an increase in diseases and pests make it difficult for us to increase rice production. One of the fundamental macro-elements needed for plant development and growth is nitrogen (N). In the majority of agricultural cropping systems, soil N availability typically limits plant yield. As a result, the use of N fertilizer has emerged as a crucial and practical method for raising crop yield in intensive agricultural systems all over the world. To increase crop yield, N fertilizer addition has historically reached a plateau. Although excessive nitrogen fertilizer use may not boost yield, it will have a negative impact on the environment. Due to the quick N losses via ammonia volatilization, denitrification, surface runoff, and leaching in the soil-flood water system, high N fertilizer input results in low nitrogen usage efficiency (NUE). Significant environmental issues, such as soil acidification, air pollution, and water eutrophication, resulted as a result. New approaches to boost yields while maintaining or, preferentially, reducing applied N is critically needed if we are to continue to attain high crop productivity and high NUE under well-fertilized circumstances.

2.2 Nitrogen Cycle

Nitrogen cycle circulates nitrogen in various forms through nature. Nitrogen, a component of proteins and nucleic acids, is essential to life on Earth. Although 78 percent by volume of the atmosphere is nitrogen gas, this abundant reservoir exists in a form unusable by most organisms. Through a series of microbial transformations, however, nitrogen is made available to plants, which in turn ultimately sustain all animal life. The steps, which are not altogether sequential, fall into the following classifications: nitrogen fixation, nitrogen assimilation, ammonification, nitrification, and denitrification. Nitrogen fixation, in which nitrogen gas is converted into inorganic nitrogen compounds, is mostly (90 percent) accomplished by certain bacteria and blue-green algae. A much smaller amount of free nitrogen is fixed by abiotic means (e.g., lightning, ultraviolet radiation, electrical equipment) and by conversion to ammonia through the Haber-Bosch process. Nitrates and ammonia resulting from nitrogen fixation are assimilated into the specific tissue compounds of algae and higher plants. Animals then ingest these algae and plants, converting them into their own body compounds. The remains of all living things and their waste products are decomposed by microorganisms in the process of ammonification, which yields ammonia (NH_3) and ammonium (NH_4^+). Ammonia can leave the soil or be converted into other nitrogen compounds, depending in part on soil conditions. Nitrification, a process carried out by nitrifying bacteria, transforms soil ammonia into nitrates (NO_3^-), which plants can incorporate into their own tissues. Nitrates also are metabolized by denitrifying bacteria, which are especially active in water-logged anaerobic soils. The action of these bacteria tends to deplete soil nitrates, forming free atmospheric nitrogen.

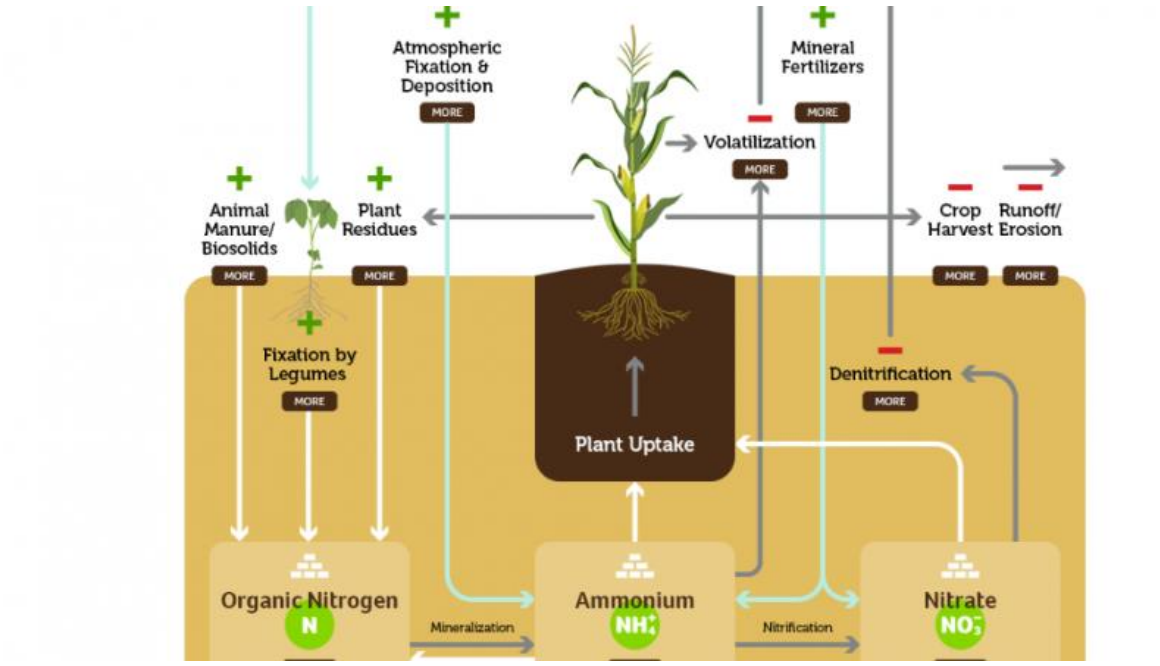


Figure 2.1: Nitrogen cycle

Source: Nitrogen cycle https://smartnitrogen.com/smart-talk/the-nitrogen-cycle-explained/

2.3 Nitrogen deficiency

When a significant amount of N fertilizer is applied, but at the incorrect time or in the incorrect manner, nitrogen deficit results. Total chlorosis in older leaves, premature leaf withering, stunted growth, field-wide yellowing, and narrow leaves are the principal signs of a nitrogen deficit. Older leaves begin to yellow gradually at the tips, followed by light brown necrosis. Compared to the healthy variety, there is less aerial growth. The root system is also lengthier but less bulky than usual. Leaching, low organic matter, drought conditions, high rainfall or heavy irrigation, addition or high levels of non-decomposed organic matter or manures, and rapid crop growth are some of the factors that can contribute to deficiencies.

2.4 Nitrogen Use Efficiency

The combination of several genes with environmental conditions causes NUE, which is intrinsically complicated. NUE equation components include N usage, N content, and N availability in a variety of definitions and estimates of NUE. N utilization efficiency (NUtE), which is the efficiency of assimilation

and remobilization of plant N to finally generate grain, and N uptake efficiency (NUpE), which is the efficiency of absorption/uptake of given N, are the two main components of plant NUE. The grain yield per unit of supplied N, which also integrates NUpE and NUtE, is the simplest definition of plant NUE. The utilization index (UI), which measures the exact quantity of biomass generated per unit of nitrogen, is another way to define NUE. NUE is also known as NUEg, which stands for grain production per unit of available nitrogen, and HI, which stands for grain production of total plant biomass. A crop plant could, however, produce a lot of biomasses per unit of nitrogen (high UI) without using the nitrogen for seed production, resulting in low NUEg and HI. In conclusion NUpE, NUtE, or both should be increased for improving NUE of a crop. It is challenging to determine the "true" amount of N fertilizer accessible or actually ingested by plants due to changes in the rhizosphere caused by microorganisms, root exudates, and the volatile loss of gaseous N from the soil/plant canopy.

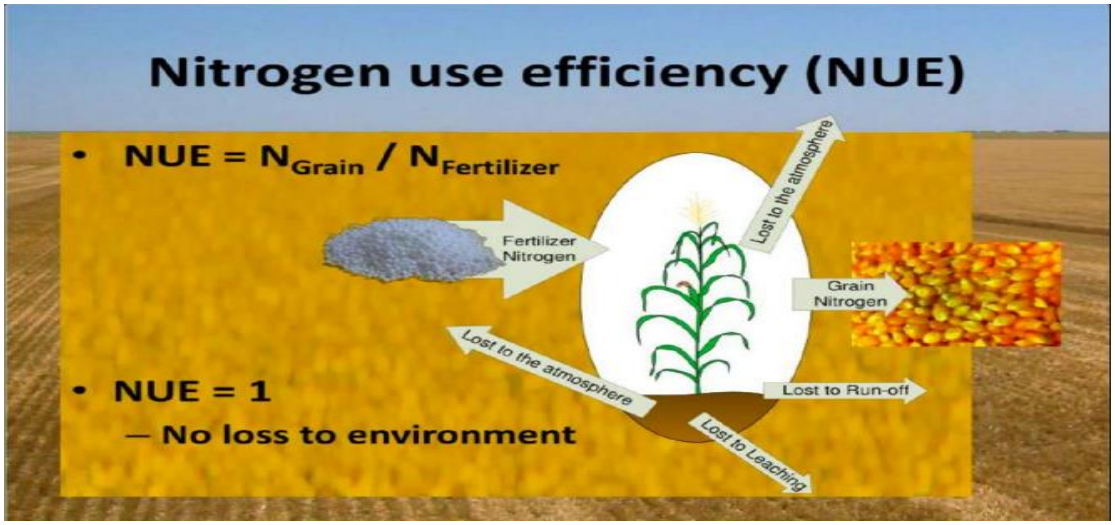


Figure 2.2: Nitrogen use efficiency (NUE)

Source: https://www.civilsdaily.com/news/what-is-nitrogen-use-efficiency-nue/

2.4.1 Nitrogen role in growth and development

Increased nitrogen doses of up to 144 kg N ha^{-1} considerably enhanced plant development, yield, and yield components, according to Ebaid and

Ghanem's (2000). According to El-Batal *et al*. (2004), increasing nitrogen delivery from 120 to 190 kg ha^{-1} resulted in considerable improvements in plant height, panicle length, number of filled grains/panicle, and grain yields at the rates of 100, 200, and 300 kg N ha^{-1}. According to Salem (2006), all grain specimens considerably increased in weight and protein content when nitrogen was maximized through cultural and agronomic approaches, chemical fertilizers containing N can be used more effectively. The most significant way to reduce the risk of environmental and soil water pollution with low nitrogen inputs is to breed varieties with maximum NUE (Fageria *et al*., 2008; Sachiko *et al*., 2009). According to Shaiful Islam *et al*. (2009), applying the right amount of nitrogen can save costs while maintaining a secure environment. Nitrogen fertilizer has a lingering effect on soil and the ecosystem when it is used excessively. Yoseftabar (2013) discovered nitrogen caused significant increase in plant development characteristics, yield attributes, and grain production. An essential component for rice's development and metabolic activities is nitrogen (Ghoneim and Ebid, 2015). Prior to recommending a nitrogen fertilizer dose for any crop, it is important to assess the effectiveness and optimal rate for various treatment levels in order to improve the growth and yield of each rice variety that has been released (Noor, 2017).

2.4.2 Nitrogen losses

In crop production, nitrogen is a nutrient that limits yield. First is denitrification (19%), which involves the anaerobic reduction of nitrogen in its nitrate form by microorganisms. Soils with a heavy texture and inadequate drainage are vulnerable to this loss (Mosier *et al*., 2001). Second is erosion, runoff, and wind erosion where loss occurs by water in humid and sub-humid environments as well as arid and semi-arid areas. Nitrogen nitrate will be lost during heavy rain through runoff (Fageria, 2002). Thirdly, where organic manure and chemical fertilizer are applied, volatilization (21%) happens, where nitrogen is lost as ammonia gas (Bolan and Hedley, 2003). Only 30-40% of

sprayed nitrogen is taken up by crops, the rest is lost to the environment. Fourth is leaching (20%), where the nitrate form of nitrogen is mobile and not strongly absorbed, can result in the loss of nitrogen. In sandy soil, N is pushed away from the soil profile by enough water. Nitrogen is used by plants in two different forms: nitrate, or NO_3^- in anaerobic conditions, and ammonia, or NH_4^+ in aerobic conditions (Oldroyd and Dixon, 2014). Crop production requires nitrogen fertilization, but because soil levels are insufficient and external application is necessary, there is a demand for N fertilizer.

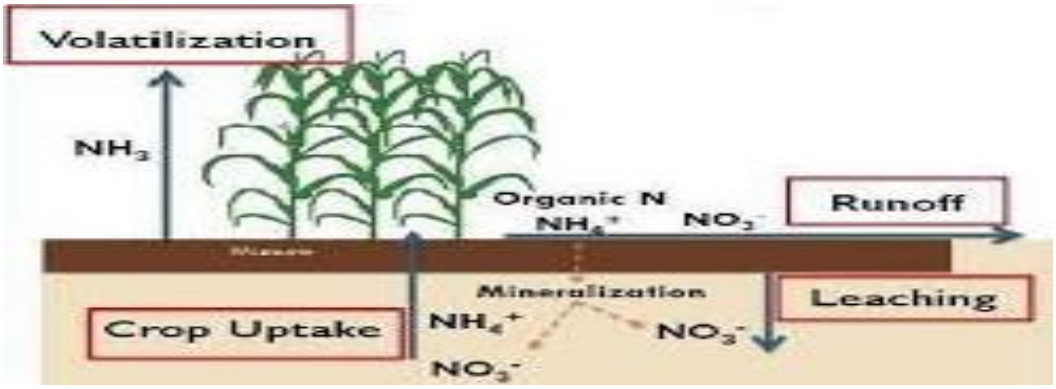


Figure 2.3: Loss of nitrogen

2.4.3 Consequences due to low NUE

Low NUE may be the result of groundwater pollution, where N is lost in nitrate form outside the root zone. The process of eutrophication involves enriching water bodies with chemicals, particularly nitrogen and phosphorus, which can result in excessive algal growth, which reduces oxygen availability and is hazardous to aquatic species. In the case of the greenhouse effect, nitrous oxide, which is formed through denitrification, is a significant greenhouse gas that is responsible for 5% of the global climatic change (Shoji *et al*., 2001). Ammonia is released into the atmosphere in the case of nitrogen deposition through volatilization, which then returns to the earth's surface as co-deposition with sulphur dioxide gas (Buresh *et al*., 2004). Additionally, there are various

sources of variation in NUE, such as species and cultivars, which are important in situations where genotype influences both the uptake and the utilization of absorbed nitrogen because each genotype has unique morphological and functional traits for roots, leaves, and other plant parts (Schenk, 2006). Environmental factors such as crop management, crop density (plant population), spatial arrangement, N fertilization rate, application methods, and water management, as well as abiotic and biotic stresses are additional sources. N availability is also affected by mineralization and leaching (Agostini *et al*., 2010).

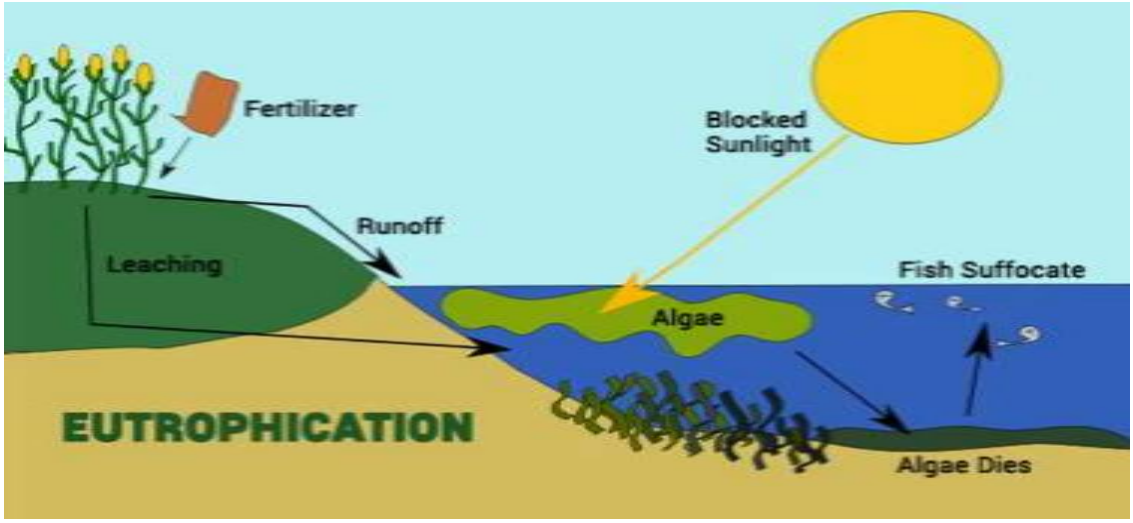


Figure 2.4: Eutrophication

Source:https://www.google.com/url?sa=i&url=https%3A%2F%2Fwww.pioneer.com%2Fus%2Fagronomy%2Fnitrogen_losses.html&psig=AOvVaw1J1cs29X5vQ_KN_SN2e4n&ust=1669297378785000&source=images&cd=vfe&ved=2ahUKEwitr8i7t8T7AhVRTmwGHXcSB5QQj

2.5. Morpho-physiological understanding of NUE

Because N is crucial for growth and development, high yielding cultivars are thought to benefit from nitrogen use efficiency. The availability of N, which increases the nitrogen harvest index, is one internal and external element that affects NUE (NHI). Understanding legislative mechanisms to control plant N is crucial for enhancing NUE as well as reducing fertilizer consumption and delivering a satisfactory yield.

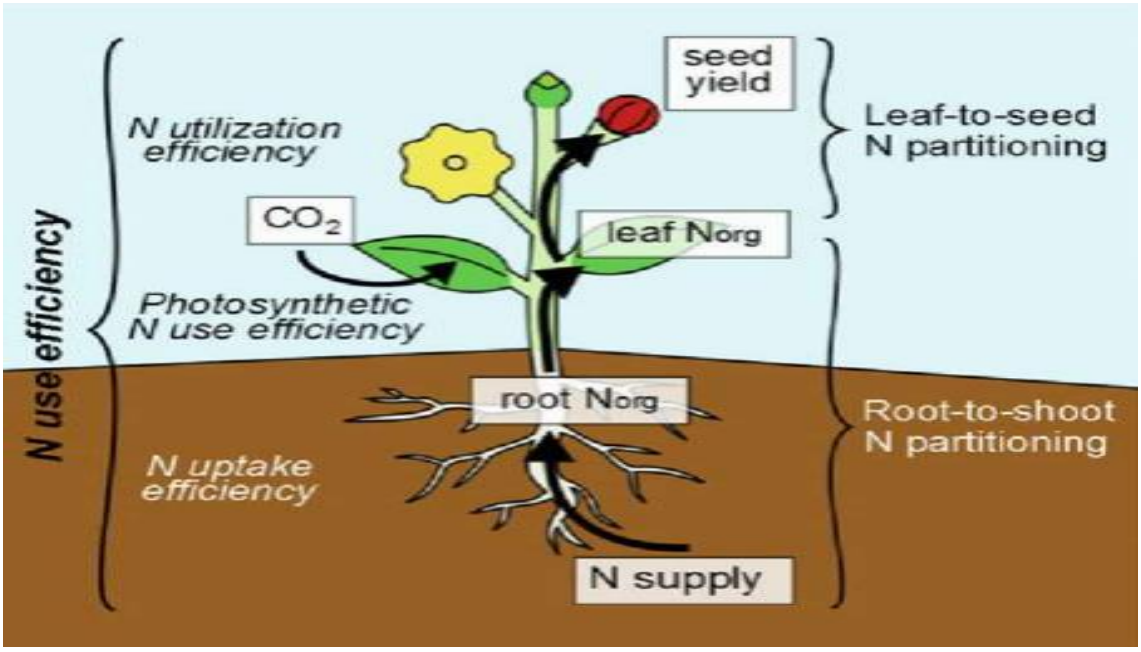


Figure 2.5: Nitrogen use efficiency in leaf and shoot

Source: https://link.springer.com/chapter/10.1007/978-3-319-92958-3_13

2.5.1 Importance of root architecture for NUE

Cereals are the most consumed food gains in the world. But among cereals, rice has lowest NUE as compared to other cereals. Root morphology is important for acquiring nutrients with low mobility in the soil (Nye and Tinker, 1977) but for more mobile nutrients, such as NO_3^- and NH_4^+, root morphology is often considered of lesser importance (Burns, 1980; Robinson and Rorison, 1983). Root architecture is also significantly influenced by nutrient availability, heterogeneity of nutrient supply and symbiotic microorganisms. Root growth parameters are associated with NUE but the evaluation of different rice genotypes with their different doses of N is lacking. The responses of urease in N have not been much studied. At normal level of N, urea suppressed root length and its effect increased when the concentration was doubled and vice versa. The suppressive effect has been found to be more in fast germinating genotypes and relatively low in the slow germinating genotypes and sometimes these differences would not be significant in some genotypes, except in genotypes like Panvel 1 (Sharma *et al.*, 2018).

In soil, inorganic N is available as nitrate (NO_3^-) in aerobic uplands and ammonium (NH_4^+) in flooded wetland or acidic soils. Rice roots in paddy soils release oxygen which generates nitrification on their surface, and thus absorb N as NO_3^- at a rate comparable with that of NH_4^+ uptake. But this uptake in roots commonly results in alkalization or acidification which results in lesser N soil availability. Increasing the uptake capacity of roots is not easy because of the tight regulation of N uptake. The capacity of the root for uptake depends on the degree to which the root extends and its absorption area, which is determined by complex root morphology. Root hairs can make up 70–80% of the root surface area and are also thought to play an important role in nutrient uptake (Marschner, 1995). In crops like rice, wheat and maize, root responses to low N availability by enhanced root elongation and deeper root systems to absorb nitrate, which is mobile mineral nutrient ions. Similarly, in maize higher NUE was related to higher N uptake efficiency and this was due to plants maintaining root growth and N uptake during flowering and early grain fill. Thus, soil N availability fluctuates in both space and time which affects root morphology, which could make plants uptake N efficiently. Studies have also shown that NH_4^+ can improve the capacity to tolerate water stress in rice in comparison with NO_3^- (Guo *et al.,* 2007), and has been shown to act as an inducer of resistance against salinity conditions in other species (Fernandez-Crespo *et al.,* 2012). But NH^{4+} can also affect plant growth negatively and this negative effects result in stunted root growth, yield depression, and chlorosis of leaves. Similarly the lateral roots occupy more than 90% of the total length of the root system which play a major role in water uptake (Han *et al.,* 2015). The root traits, especially the deeper roots, greater root oxidation activity and higher photosynthetic NUE at lower N rates, could be used in selection for N-efficient rice varieties.

2.5.2 Relationship between leaf characteristics and N content

Leaf chlorophyll content is estimated using chlorophyll meter and evaluated using simple and partial regression coefficients (SPAD) to study relation with leaf nitrogen concentration which could provide an indirect assessment of leaf nitrogen status (Chapman and Barreto, 1997). There is a close relationship between maximum leaf photosynthetic rate under saturating light, leaf N content, leaf N distribution and leaf photosynthesis such that the effect of light interception depends on N availability in different plants (Field and Mooney, 1986). Leaf nitrogen is also closely related to photosynthesis rate and grain yield in rice. It is necessary to detect the leaf N status and detect the precise time and rate of nitrogen fertilizer top dressing.

Turner and Jund (1991) also indicated that the chlorophyll meter could be used to predict the requirement of nitrogen topdressing prior to panicle initiation and panicle differentiation stages in semi-dwarf rice cultivars. Many studies have also shown that the regression equations and correlations for leaf chlorophyll content using the chlorophyll meter reading differed depending on growth stage, genotype and environmental conditions. From the results of Esfahani (2008) strong evidence was provided that there was a statistically significant relationship between leaf N concentration and chlorophyll meter (SPAD-502) readings. Total chlorophyll and chlorophyll stability index also revealed high direct effect on yield. Characters like yield are an important yield determinants and each of these characters can increase the yield of grain along with other yield components (Gopikannan and Ganesh, 2013). Ghoziladeh *et al.* (2017) studied that there was a better relationship between rice leaf N content as well as yield with SPAD reading at the panicle formation stage and this reading is more reliable than in the booting stage. Different types of chlorophyll depend on chemical substituents where chlorophyll a and b depends on only one substituent while chlorophyll a has methyl substituent and

chlorophyll b has aldehyde substituent. Presence of chlorophyll a and chlorophyll b gives green part in plants.

2.6 NUE and yield and yield attributing traits

Nitrogen is needed for the development of spikelets and later for the reduction of the spikelet degeneration. Reports of significant increase of spikelets per panicle with the increase of N application are made. Grain yield also depends mostly on the total number of fertile and sterile spikelets (Matsushima, 1970). Among yield and yield attributing traits in rice, panicle or spikelet number per unit area is the most variable among the yield components (Fageria *et al.,* 1997). Singh *et al.* (1998) reported that tillering, panicle number and total spikelet number increased with increasing level of applied N. Average tiller, panicle and spikelet differed significantly among genotypes and N supply conditions in medium and long duration genotypes. Thus the genotypes exhibit high yield potential under non-limiting N supply. Higher accumulation of N in vegetative and early reproductive growth stage is useful in production of more number of spikelets and top dressing of N at panicle initiation stage is most efficient in increasing spikelet number (Yoshida *et al.,* 2006). Analysis of panicle under low N in wet season has also shown decrease in spikelets and grains on secondary branches. Yield attributes of rice also differed significantly according to different N levels. Each increase in the N level increases plant height as well as effective tillers and 1000 grain weight which increases grain yield. When N was applied at 120kg/ha, it produces the highest grain yield as well as straw yield (Shukla *et al.,* 2015). Ju *et al*. (2015) also showed that varieties HD-5 and LJ-7 can maintain grain yield at lower N rates as N-efficient varieties which results in greater root and shoot biomass, deeper root distribution, longer root, greater root density, root oxidation activity and crop growth rate, higher photosynthetic NUE, and more remobilization of non-structural carbohydrate from stems during grain filling at lower N rates. Grain yield and yield components results in significantly higher biomass production

and harvest index (Zhu *et al.*, 2016). Among the yield components, there was a significant increase in spikelets m^{-2} and grain filling percentage which accounted for the genetic improvement in grain yield. It was also demonstrated that N uptake was significantly higher in newer varieties and NUE for grain yield was also significantly increased. Therefore, increase in N uptake may have contributed to the improvement in radiation use efficiency (RUE) which depends on photosynthesis and respiration.

2.7 Variability in NUE

There are many studies on rice that revealed a significant genetic variability for nitrogen use efficiency (NUE) particularly in irrigated and lowland rice. Shoot dry weight, grain yield, number of panicles, number of grains per panicle, 1000 grain weight, spikelet sterility, N uptake in grain, N harvest index and N use efficiency were significantly affected by genotype and N treatment (Singh *et al.*, 1998; Fageria and Barbosa Filho, 2001). Genetic variation is the base of plant breeding and assorts genotypes that can be chosen for developing new varieties or breeding materials (Pandey *et al.*, 2009). Heritability also helps plant breeders to anticipate the genetic make-up of the succeeding generation, as well as to make an appropriate selection and to evaluate the magnitude of genetic improvement through selection. From the studies of Manikya and Reddy (2011) if there is a small difference between GCV and PCV for all the traits under study, it indicated that there is less influence of environment over expression of the traits. High heritability along with high genetic advance was found for all the characters except for traits like spikelet fertility. Pratap *et al*. (2012) showed PCV and GCV values were moderate for panicle length, plant height and harvest index. The estimates of PCV were higher than GCV for all the traits.

On the other hand, Lingaiah *et al.* (2014) found that all traits under study have higher phenotypic coefficient of variation than genotypic coefficient of variation. The magnitude of phenotypic coefficient of variation and

genotypic coefficient of variation was moderate to high for the traits no. of grains per panicle, test weight and yield. High PCV was observed for no. of grains per panicle, test weight and yield whereas high GCV was obtained for no. of grains per panicle indicating the improvement is possible through selection. Heritability estimates were also high for all the characters except for number of productive tillers per plant. High magnitude of genetic advance as percent of mean was observed among traits like number of grains per panicle, test weight, yield and plant height whereas traits like number of grains per panicle, test weight, plant height and yield have high heritability along with genetic advance as percent of mean which indicate that these characters contribute to additive gene effects which are fixable revealing that improvement in these characters would be possible through direct selection.

Plant traits having genotypic variation in NUE are associated with high grain yield and traits having high NUE can be used as a selection criteria in breeding programmes to develop nitrogen use efficient varieties with high yield potential. Variability studies in rice provide information on genotypic and environmental effect on yield and nitrogen use efficiency which gives information about heritability of character. Many researchers on rice for significant genetic variability for NUE is mostly done in irrigated rice or rainfed lowland rice but little is known about variability of NUE in upland rice. Selecting NUE for any variation in the environmental conditions could be significant as a genotype (Han *et al.,* 2015). Ju *et al*. (2015) also revealed a significant genotype x nitrogen supply level interaction for grain yield and N uptake in irrigated conditions. A high nitrogen use efficiency was linked between two lowland japonica varieties which have greater root biomass, deeper root, increase root length, better root oxidation activity. Rakotosona *et al.* (2017) revealed significant genetic variability for NUE, nitrogen uptake efficiency (NUPE) and nitrogen utilization efficiency (NUTE) in both high N and low N treatments but a low level of G × N interaction. There was no

correlation between NUPE and NUTE, either under high N or under low N and no negative relationship between grain yield and grain N concentration under low N which varies under different climatic conditions whereas two traits, the number of panicles per m^2 and the harvest index were correlated with NUE. This study revealed significant varietal differences for NUE between component traits and complex interactions with environmental conditions. However, difference in N uptake between flowering and maturity were found to be negative values suggesting that some N was lost despite increase in total above ground biomass between flowering and harvest. Manjunatha *et al.* (2017) revealed that phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV). PCV was high for yield per hectare whereas GCV was high for number of panicles per square metre and high GCV indicates the degree of variability percent for a character. Heritability evaluation were high for all the traits and traits like days to 50% flowering, yield and plant height revealed high magnitude of genetic advance as percent of mean. Savitri *et al.* (2018) also reveals high genotypic coefficient of variability (gcv) and phenotypic coefficient of variability (pcv) value for nitrogen use efficiency in the cross kaduvakalongi × banavasi selection indicating less influence of environmental factors on their expression. Similarly, high heritability and genetic advance as percent mean were observed for the following traits, number of tillers per plant, number of productive tillers per plant, panicle length, test weight, yield per plant, nitrogen use efficiency. Interactions between N uptake and water availability and the interaction between different macro and micronutrients are the factors to be considered to determine the level of genetic variation.

Adhikari *et al.* (2018) observed high phenotypic coefficient of variation estimated as compared to genotypic coefficient of variation and high heritability for days to flowering, maturity, thousand grain weight and plant height suggesting these traits are under high genetic control. High phenotypic

variation was observed for grain yield, number of grains per panicle, number of panicles per m^2 and straw yield while grain yield had medium while genotypic coefficient of variation was low for some traits. Grain yield and days to flowering also showed medium genetic advance as percent of mean. High broad-sense heritability estimates were also observed by Iqbal *et al.* (2018) for characters like number of days to maturity, culm length, flag leaf area, days to heading, secondary branches per panicle, panicle length and primary branches per panicle. Genetic advance estimation also showed that flag leaf area exhibited high genetic advance followed by secondary branches per panicle and culm length among studied traits of rice genotypes. High heritability coupled with high genetic advance as percent of mean was also observed for number of tillers per hill, number of panicles per plant, number of grains per panicle, 1000-grain weight (TGW), filled grains per panicle, flag leaf length, stigma breadth, filament length indicating preponderance of additive gene action in the expression of these characters (Hossain *et al*., 2020). Genotypic and phenotypic coefficients of variation were high for the flag leaf area, spikelet number, grain number, test weight and grain yield and moderate for plant height, days to flowering, number of panicle and primary branches per panicle. Heritability was also high for days to flowering, plant height and test weight while genetic advance as per cent of mean was very high for test weight and grain yield, moderate for plant height, flag leaf area and the number of grains, and low for spikelet fertility (%) (Nath and Kole, 2021).

Demeke *et al*. (2023) also studied genetic variability based on the yield performance, good physical appearance, medium maturity date, high filled grain per panicle, and productive tillers to find out promising genotypes for further breeding purpose. From their study, unfilled grain per panicle had the highest GCV and PCV values, while days to maturity had the lowest value and all quantitative traits studied exhibited high heritability percentage. Plant height, productive tillers, non-productive tillers, filled grain per panicle,

unfilled grain per panicle, thousand grain weight, grain yield, biomass, and harvest index were having high heritability and high genetic advance as percent of mean, indicating the presence of additive gene effects for these traits. High mean, range, and genotypic variances was observed by Faysal *et al*. (2022) for most of the characters which indicates there is a wide range of variation for these traits studied. Therefore, all the characters have minimum influence of environment on the expression of the trait and genetic factors had a significant role in the expressivity of these characters i.e., high heritability in broad sense and high to moderate genetic advance as percent of the mean were recorded for all the characters except for panicle length (PL). On the other hand Akshay *et al*. (2022) revealed that the estimates of GCV for all the characters studied were slightly less than PCV estimates indicating influence of environment on the genotype performance. Traits like plant height, number of productive tillers per plant, panicle length, number of grains per panicle, 1000 grain weight, grain yield per plant, head rice recovery percentage, grain length, grain width, length/breadth ratio, protein content, iron and zinc content showed moderate to high variability, high heritability coupled with high genetic advance as per cent of mean revealing the role of additive gene effect but low PCV and GCV were recorded for the traits like days to 50% flowering, hulling percentage and milling percentage. High heritability coupled with moderate genetic advance as per cent of mean was observed for days to 50% flowering, hulling percentage and milling percentage which indicates the presence of both additive and non-additive gene effects in the inheritance of these traits.

2.8 Correlation and Path analysis

Path analysis allows partitioning of correlation coefficient into its components, one component being the path coefficient that measures the direct effect of a predictor variable on a response variable whereas the second component being the indirect effect of a predictor variable on the response variable through another predictor variable (Dewey and Lu, 1959). Correlation

and path analysis initiate the degree of relationship between yield and its components and also shows comparative significance of their direct and indirect effects, giving us a clear understanding of their relationship with grain yield. Basically, this kind of analysis allows breeder to create selection program to improve grain yield. Sometimes negative correlations and non-significant associations also arise due to competition for a common possibility, such as nutrient supply. If one component gets advantage over the other, a negative correlation may arise (Adams and Grafius, 1971). A non-significant association was observed with 1000-grain weight and negative and significant associations were also recorded for panicle length and 1000-grain weight (Yang, 1986). Grain yield has been reported to be influenced by high direct effects of flag leaf area, 1000 grain weight and plant height (Ruben and Katuli, 1989). Highly significant relationship of grain yield was also detected with number of tillers per plant and flag leaf area (Rasheed *et al.*, 2002; Surek and Beser, 2003). Deepa *et al*. (2006) and Singh *et al.* (2006) observed that days to 50 per cent flowering exhibited a positive and significant association with days to maturity, plant height and panicle length indicating a scope for simultaneous improvement of the traits. A character association in rice genotypes for yield improvement was studied by Watoo *et al.* (2010) and recorded grain yield to be significantly correlated like flag leaf area. Path analysis also revealed that days to maturity had the highest direct effect (0.751) on grain yield per plant. From the studies of Shanthi and Jebaraj (2011) number of filled grains per panicle revealed significant correlation with proline content, total chlorophyll content and chlorophyll stability index but in days to 50 per cent flowering there was a negatively non-significant association with yield of single plant. In case of path analysis, number of tillers per plant and number of filled grains per panicle showed high as well as positive direct effect of yield on grain. Spikelet fertility percentage, panicle length and chlorophyll content have high and indirect effect on yield of plant. These characters can enhance yield of grain and other

components of yield. Padmaja *et al*. (2011) also showed that number of grains per panicle showed positive and significant association with single plant yield and it had a negative correlation with spikelet fertility whereas spikelet fertility had positive and significant association with single plant yield and positive association with 100-grain weight. 100-grain weight exhibited maximum positive direct effect as against its highest positive significant correlation value with single plant yield due to high positive indirect effects of 100-seed weight via panicle length, spikelet fertility and grains per panicle. Similar results were also reported by Gopikannan and Ganesh (2013) whereby yield of a single plant showed positive and significant correlation with seven characters viz., number of productive tillers per plant, panicle length, spikelet fertility percentage, number of filled grains per panicle and total chlorophyll content. Similar results were reported by Lakshmi *et al.* (2014). A significant positive correlation was also found between total nitrogen accumulation and total root length, root superficial area as well as in the volume of roots in rice (Pan *et al*., 2016). Biological yield per plant, harvest index, 1000-grain weight, panicle bearing tillers/plant and panicle length showed positive and significant correlation with grain yield per plant while path analysis identified biological yield per plant followed by harvest index as most important direct as well as indirect yield effects (Singh *et al*., 2018). Shrestha *et al*. (2018) also revealed positive and significant association of 1000 grain weight, flag leaf area and SPAD reading on yield while plant height showed negative and non-significant correlation with yield. Path analysis also showed flag leaf senescence, 1000 grain weight, flag leaf area and SPAD had positive and high direct effect on grain yield respectively.

From the study of Soe *et al.* (2019) correlation analyses also revealed that out of the 14 morphological and agronomic characters only 100 grain weight, tiller number, days to 50% flowering, panicle number, days to 80% grain maturity, ligule length and panicle length showed significant positive

association with grain yield. There was significant positive correlation of 100 grain weight with grain yield and also significant positive relation between grain yield and panicle number. The correlation coefficient between grain yield per plant and other quantitative characters attributing to yield showed that grain yield was significantly and positively associated with number of grains per panicle, TGW, spikelet fertility, filament length and pollen fertility at both genotypic and phenotypic levels. Path coefficient at genotypic level also revealed that panicle length, number of effective tillers/plants, number of grains per panicle, TGW, filled grains per panicle, spikelet fertility, stigma length, stigma breadth, filament length and pollen fertility had direct positive effect on grain yield indicating importance of these parameters as the main contributors to yield (Hossain *et al*., 2020). Saleh *et al.* (2020) also showed that grain yield per plant had a high positive and significant correlation with panicle number per plant, full grain number per panicle, and 1000 grain weight. There was a negative correlation between days to heading and panicle number per plant and with1000 grain weight. Path coefficient analysis showed high positive and significant correlation between grain yield per plant. Traits with positive and significant correlation and with a high direct effect on grain yield per plant were 1000 grain weight followed by panicle number per plant and full grain number per panicle.

Nath and Cole (2021) revealed genotypic and phenotypic correlations of seed yield with plant height, flag leaf area, days to flowering, the number of primary and secondary branches per panicle, the number of spikelets and filled grains per panicle, spikelet fertility (%) and test weight were significant and positive. Genotypic path analysis also indicated that direct selection for test weight, the number of primary and secondary branches per panicle in a positive direction with restricted selection for panicle number and spikelet fertility would increase the grain yield of rice in the population. The direct positive effect of test weight was highest, followed by secondary branches, plant height,

panicle number and primary branches which show these characters had a highly significant and positive association with grain yield. From the studies of Faysal *et al.* (2022) genotypic coefficient of correlation was generally a little bit higher than the corresponding phenotypic coefficient of correlation which indicates that there is apparent association due to genetic reasons. Spikelet fertility (%) showed a direct path coefficient in a negative direction which shows that direct selection through these characters would be effective for improving the grain yield of rice. Although genotypic correlation with grain yield for plant height, number of effective tillers per hill, panicle length, number of filled spikelets per panicle, flag leaf length, spikelet fertility (%) and harvest index were significant but considering three analyses, such as genotypic correlation for grain yield, phenotypic coefficient and principal component analysis revealed that direct selection of number of filled spikelets per panicle, spikelet fertility (%), flag leaf length and harvest index would be effective for improving the grain yield of rice.

2.9 Genetic divergence in rice

'Divergence in character' was used by Darwin (1859) for variation in genera and species. To quantify the nature and magnitude of genetic diversity for germplasms Multivariate analysis (Rao, 1952) based on Mahanlanobis D^2 statistics are used. These analyses help in measurement of different components of diversity both at intra and inter cluster level drawn from divergent clusters. The more diverse the parents, greater the diversity and for development of any genotype with traits of interest, divergent parents are necessary to be included in the breeding programme as they have the capability to produce superior recombinants. Grouping of genotypes provides a clear understanding about the inter relationship of genotypes and helps to give appropriate divergent genotype/parents to be used in future hybridization programme.

Genetic divergence is used for determination and discrimination among genotypes which is useful for selecting genotypes for hybridization to establish high yielding potential variety (Bhatt, 1970). About 95% of rice is cultivated in Asia, and Asian-cultivated rice is mainly two distinct subspecies, indica and japonica. Not only in developmental and physiological traits, NUE is also different between these two subspecies, with indica generally having much higher NUE than japonica. In 1980s, some research had already indicated that indica and japonica rice varieties have the differential nitrate uptake and nitrate assimilation capacity (Chanh *et al.,* 1981; Li *et al.,* 1981). The patterns of clusters of genotypes were reported by Chandra *et al.* (2007) and Bhanumathi *et al.* (2010) showing that there is lack of relationship between genetic diversity as well as geographical origin. Banumathi *et al*. (2010) and Latif *et al*. (2011) reported that the traits like spikelets per panicle, biological yield per plant, grain yield per plant and tillers/plant were the major contributors to genetic divergence.

Cluster analysis based on agro-morphological diversity assessment in rice was reported in several studies by Li *et al*. (2010) and Zhang *et al*. (2010). Wellington *et al*. (2011) also studied cluster analysis for the quantitative traits using the Euclidean distance and from the results three groups were formed. Group I was classified to be more divergent for higher number of panicles, fertile spikelets and plant production, which are important agronomic characters. The analysis of the descriptors used also showed that number of panicles per plant was the most important character in this group classification. No duplicates were also identified among the studied accessions for quantitative traits in the cluster analysis which means there is a high diversity among the accessions for these traits. From the study of Sohrabi *et al.* (2012) fifty accessions of upland rice were also clustered into six groups by 12 quantitative traits. Cluster III was the biggest and cluster VI was the smallest group. Cluster III showed highest average for five traits such as plant height,

days to flowering, days to maturity, flag leaf length-to-width ratio and panicle length. Group VI also included the highest average for four traits such as number of tillers, 1000 grain weight, yield of plant, and spikelet fertility while accessions with cluster VI showed the lowest average values in the characters such as plant height, days to maturity, flag leaf length-to width ratio, number of panicles, panicle length, and spikelet per panicle. From the studies of genetic divergence in rice by Nikhil and Rangare (2012), clustering pattern and geographical distribution has no relationship. Pratap *et al.* (2012) also found that among the traits, harvest index is also an important trait which shows significant and positive associations between yield and yield components. Mau *et al*. (2017) also studied 40 upland rice accessions and revealed that the rice accessions were clustered in various sub-clusters with mixed accession members from various origin except the clusters III and V that consisted only of a single accession. Accessions from the same place were not always grouped into the same cluster or sub-clusters, indicating high quantitative trait diversity of red and black upland rice germplasm. Mishra *et al.* (2018) studies also revealed that out of twenty-one traits studied, maximum variability was contributed by biological yield per plant, amylose content and 1000-grain weight. Singh *et al.* (2019) also revealed that highest contribution in manifestation of genetic divergence was exhibited by spikelet per panicle followed by biological yield per plant, grain yield per plant and tillers/plant. Other characters like plant height, flag leaf length and width, panicles/plant, days to maturity, days to 50 % maturity, test weight contributed least towards the genetic divergence.

Understanding the extent of genetic diversity among genotypes and organizing individuals into groups whose members are similar in some ways have importance in plant breeding program. With this aim, a study was conducted by Altaye *et al*. (2019) to estimate the genetic diversity of 36 upland rice genotypes based on quantitative morphological traits. Cluster analysis

indicated that 36 genotypes were grouped into 6 clusters and divergences between all pairs were significant. Similarly, genetic diversity among 30 upland rice genotypes (*Oryza sativa* L.) was evaluated using morphological traits by Syiemlieh *et al.* (2019). The diverse genotypes revealed from morphological-based dendrogram were the following pairs viz., Aizawng New and Majinlu, Aizawng New and Mima-Mitong-Jang, Mibisa and Chakhao Poireiton, Chakhao Poireiton and Vepvu Tsuk, Buh Pui (Tuirel) and Chakhao Poireiton, Marow and Chakhao Poireiton, Kba Tlang and Majinlu, Lokhumo (Tall) and Chakhao Poireiton. While Aizawng New and Mibisa, IC 583129 and Mibisa, Bhalum-1 and Mibisa, Bhalum-2 and Mibisa, Marow and Mibisa pairs. These were identified as the diverse genotypes based on molecular dendrogram which may be used as parent for hybridization during further rice improvement. Soe *et al.* (2019) also studied 87 rice accessions and were classified into seven main clusters at a similarity coefficient of 0.21 based on morphological traits which indicates genetic variation among the accessions. Therefore, variation observed among the accessions revealed that there is morphological diversity existing among rice accessions. Variability for morphological traits in 20 upland rice varieties was also studied by Zeleke and Worede (2022) and cluster analysis using un-weighted Pair Group Method using Arithmetic Average linkage (UWPGMA) classified the twenty varieties into five distinct groups. The maximum inter-cluster distances recorded were 8.05 between cluster I and V, 6.67 between cluster I and IV; and 5.5 between Cluster I and III, indicating that the possibility of high heterosis if individuals from these clusters are cross bred.

2.10 Stability in rice

According to Eberhart and Russell (1966) a stable genotype means a high trait mean, unit regression (b_i=1) and least deviation from regression (S^2_{di}=0). If regression coefficient is greater than unity (b >1) it is considered to below average stable and if regression coefficient is less than unity (b<1) it is

considered to be above average stable. Sometimes desirably important traits show low GxE but high on other traits such that they adjust in response to changing environment. Therefore, stability in certain yields components and other yield components can result in stability in yielding ability as they compensate each other. Significant variation due to environment (linear) showing linear assessment of environmental effects and additive environment variance were also reported by Lavanya *et al*. (2005), Deshpande and Dalvi (2006) and Arumugam *et al*. (2007). Pooled analysis of variance for grain yield over environments showed highly significant differences among genotypes, environments and genotype-environment (GxE) interaction indicating diverse and variable nature of cropping environments (Bhakta and Das, 2008). Similar result was also found in a study by Saidaiah *et al*. (2010). They made an attempt to study stability of rice hybrids developed and they are evaluated at three different agro-climatic zones using Eberhart and Russel (1966) model based on the magnitude of heterosis over different environments and identify hybrids that shows stability in yield and which shows less influence by the environmental effects. According to their result, the genotypes and environments were significant for all the traits excluding 1000 seed weight and spikelet fertility percentage for varieties which shows that there is diversity among the genotypes and environments studied. Similarly, Bastia *et al.* (2010) revealed that the stability analysis showed significance in linear component of variation for grain yield where the stability yield performance of the genotypes was found to be associated with the stability of yield components like effective tillers m^{-2} and grains $panicle^{-1}$.

Therefore, analysis of variance of GxE interaction using Eberhart and Russell's model shows highly significant differences among genotypes and among environments and significant GxE interaction indicated differential performance of genotypes over environments (Das *et al.*, 2010). Balestre *et al*. (2010) also studied stability and adaptability of 20 upland rice genotypes using

GGE Biplot method. From the result of GGE biplot analysis it revealed that varieties BRS Pepita and MG1097 were the best adapted genotypes whereas BRA 042160, BRSMG Caravera and BRSMG lightning were the most stable genotypes. It is necessary to screen and identify phenotypically stable genotypes that could perform uniformly under different environmental conditions. Twenty genotypes including hybrids and aromatic rice were evaluated in 8 environments in two production systems viz; System of Rice Intensification (SRI) and normal cultivation environments by Gritlahre and Sarial (2011). The G x E interaction was significant for six traits including all key components of SRI except number of tillers. Both linear and non-linear components contributed towards G x E interaction. Stability parameters identified genotypes PR-114 and HKR-47 as stable for grain yield per plant and HKR-127, HKR-120, CSR-30, Pusa-1121 and IR-64 for test grain weight. Genotypes identified suitable for favourable environments were HKR-126, HSD-1, PAU-201 and Govind whereas HSD-1, HKRH-1094, HKR-48 and PAU-201 were suited for unfavourable environments.

As grain yield is a complex quantitative trait, with high environmental interaction; selection of genotypes based on performance in single environment is not effective for varietal identification (Shrestha *et al*., 2011). It is essential to carry out selection based on yield stability evaluation than average performance in multiple environment conditions. Genotype × environmental interaction and stability estimate were investigated on grain yield of 30 upland rice by Maji *et al*. (2015) and AMMI anova for grain yield revealed no significant different among genotypes but there is significant difference on environments and the interaction. AMMI 2 biplot revealed that, genotype ART16-9-3-15-3-B-1-1 (8) has the highest mean yield with high main additive effect better than the check varieties. Hence, this genotype is considered more adapted to wide environments than the rest of genotypes. Another study of stability was done by Balakrishnan *et al.* (2016) where a wide range of

variation was observed for yield traits among the varieties studied across the environments. Combined analysis data of three environments showed significant genotypic and genotype × environment interactions for all the traits except for 1000 grain weight where the G × E interactions were not significant. Oladosu *et al*. (2017) studied G × E interaction over ten environments for yield stability in fifteen rice genotypes comprising twelve mutant lines and three established varieties. The pooled analysis of variance showed highly significant differences among genotypes, locations, seasons, and genotypes by environment (G × E interaction) for all the traits. Based on univariate and multivariate stability parameters, rice genotypes were classified into three main groups viz., genotypes having high stability along with high yield (widely adapted to diverse environmental conditions), genotypes that exhibited high yield but low stability (suitable for specific environments) and genotypes with low yield and high stability. The genotype x environment (GxE) interaction for grain yield and some associated traits was studied by Paul *et al*. (2018) and pooled analysis of variance revealed that the mean sum of square due to genotypes for all the traits and GXE interaction for many traits were significant which clearly indicated that the genotypes differ in their adaptability and stability. The significant G x E interaction (linear) of many traits indicates there was differential response of the genotype to environmental changes and pooled deviations were also significant for all the traits studied which suggested that these genotypes differed in their deviation from linearity. Stability parameters (mean, bi and s^2_{di}) of genotypes were estimated separately over eight environments and seven genotypes namely BAU 438-6-2, OR 2084-2, BAU 363-96, RR410-79-1-B-D2-B, NDR-1054-4-1, BAU/GVT 435-06 and UPRI-2004-6 were showing stability and proves to be desirable for rainfed upland condition.

Poli *et al*. (2018) also studied to identify stable rice genotypes in multi environment under both irrigated and stress conditions. The most stable lines

based on the combined analysis of 12 seasons were G125 (NH210) under normal condition, G17 (NH686), G176 (NH363) and G284 (NH162) in low phosphorus condition and G176 (NH363) under water limited condition. G176 was performing the best considering all 3 conditions. Findings of Das *et al.* (2019) for the stability analysis revealed that four genotypes Kalabor, Aki Bora, Rongdoi and Luha Sali shows average stability for grain yield while Betguti sali shows below average stability. In case of nitrogen uptake efficiency, Lothabor, Luha Sali, Kolabor, Aki Bora and Gitesh show average stability while Betguti Sali shows below average stability. For Harvest Index (HI) four genotypes namely Luha Sali, Kolabor, Aghoni Bora and Gitesh are showing average stability. Since grain yield changes with the change in environment a genotype showing stability in yield can minimize the loss in yield in case of fluctuating environment. Similarly, for grain yield genotypes like Kolabor, Aki Bora, Rongdol and Luha Sali show average stability. Among all the genotypes, Koliabor shows average stability for most of the trait studied. Zewdu *et al.* (2020) also studied thirteen rice genotypes in multi-environments using AMMI model. Analysis of variance also showed a highly significant difference for genotypes, environment, and genotype x environment (GE) interaction for grain yield. Based on the GGE, AMMI analysis genotype variety Hidassie (G4) and NERICA-4 (G3) were the most stable and high yielding genotypes and recommended for production for the testing sites and similar upland rice-producing areas of Ethiopia. In another study by Phapumna *et al*. (2020) eight indigenous upland rice varieties, including ULR026, ULR042, ULR075, ULR078, ULR080, ULR081, ULR089, and ULR105 showed superior stable grain yield performance over the Sew Mae Jan (ULR008) check variety. From the study some of the high-yielding varieties also presented favorable qualities such as high amylose content (ULR081 and ULR075), high aroma (ULR078), and intermediate gelatinization temperature

(GT) (ULR078, ULR026, and ULR105) which has proven to be beneficial for future trait selection in upland rice breeding programs.

By using the methods of Eberhart and Russell, multiple centroids and GGE biplot Silva Junior *et al.* (2020) studied eighteen genotypes which were evaluated for grain yield under 12 environments. From the results, genotypes behaved differently regarding stability and adaptability in the different environments. Both methodologies identified BRA 02691 and MGI 0607-1 as promising genotype which can be released as a cultivar but genotypes like BRA 011001 are found to have inconsistent classification. Furthermore, these methods simultaneously provide an innovative approach for interpretation of GxE interactions and are a viable alternative for genotype classification. The genotype MGI 0607-1 also showed promising behavior independent of the methodology used. Therefore, different methods shows different classifications when ranking genotypes which indicate that using of more than one methodology would give greater credibility to the results. According to Mengistu *et al.* (2022), genotypes YIN LU20 and WABC165 (IAC165) were also found to be stable and widely adaptable whereas genotype YIN LU20 was found to be a high yielder in most locations. Regression analysis and AMMI models also revealed that CNAX3031-15-2-1-1 was the most stable genotype.

CHAPTER - III

MATERIALS AND METHODS

MATERIALS AND METHODS

The experimental study entitled "Variability and stability studies for nitrogen use efficiency in upland rice (*Oryza sativa* L.) genotypes of Nagaland" are detailed under the following heads:

3.1 Location

The field experiment was carried out during *Kharif* 2021 and *Kharif* 2022 at the Experimental farm, Department of GPB, SAS, Nagaland University. The experimental site is located in Medziphema, in the foothills of Nagaland having an elevation of 310m above mean sea levels with geographical location of 25º 45' 43''N latitude and 95º 53' 04''E longitudes respectively.

3.2 Experimental materials

A set of 28 materials from SARS, Mokokchung, Nagaland and ICAR (RC) for NEH region, Jharnapani was used in the present study and details are in table 3.1.

3.3 Meteorological data

The meteorological data during the period of study was obtained from Department of Agronomy, School of Agricultural Sciences, Medziphema, Nagaland University as given in the Appendix I and II.

3.4 Experimental design and methodology

The present study was carried out with three different nitrogen doses in two years (*Kharif* 2021 and *Kharif* 2022) using randomized block design (Fig 4.1) with three replications keeping planting dates in the main field as below:

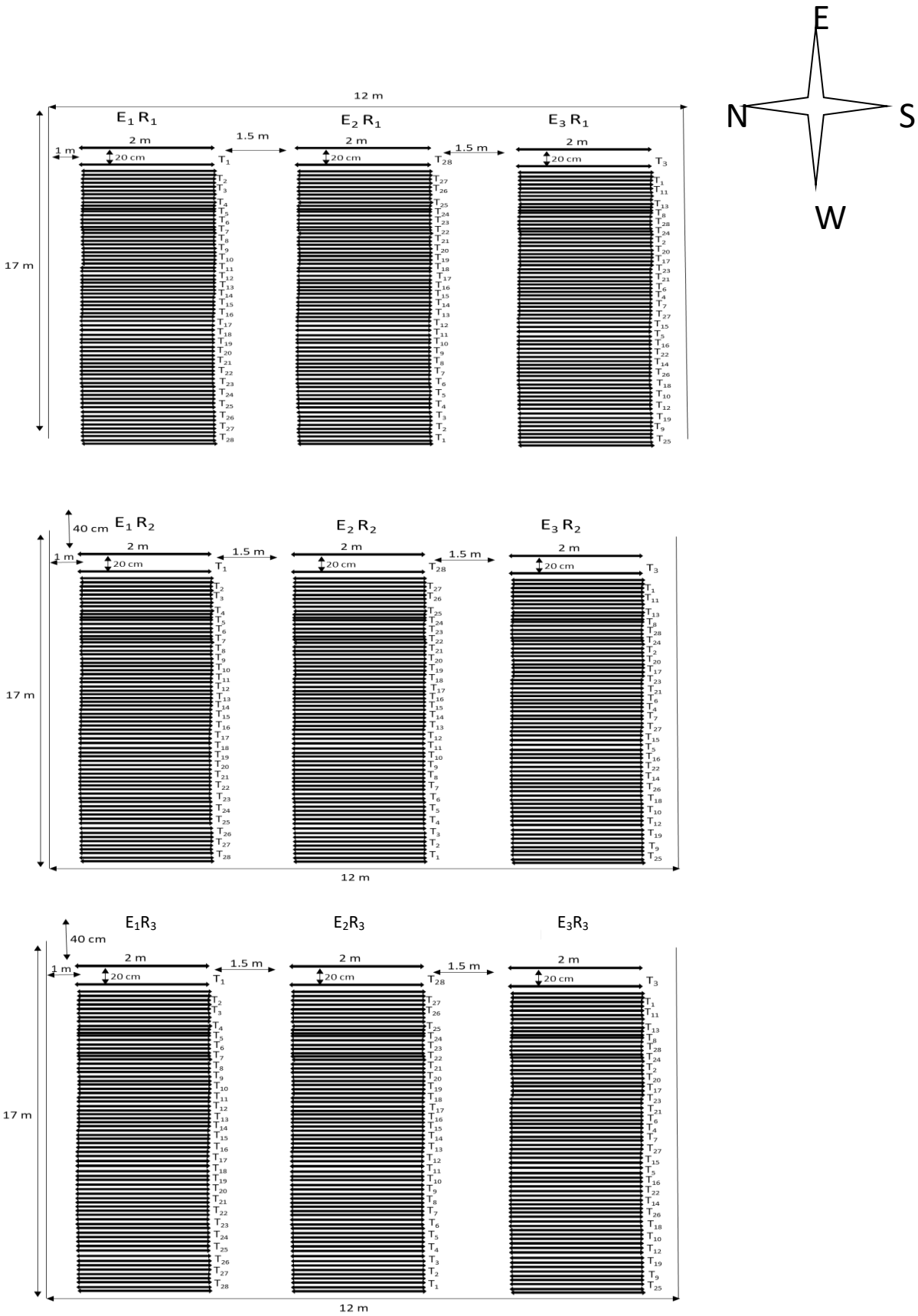


Fig 3.1: Layout of the experimental field (RBD)

Table 3.1: Genotypes used in study

S.No	Name	Source of collection
1	Sungmangtsuk (SARS-1)	SARS, Mokochung, Nagaland
2	Apuapa (SARS-61)	SARS, Mokochung, Nagaland
3	Kezie (SASRS-94)	SARS, Mokochung, Nagaland
4	Korea Tsuk	SARS, Mokochung, Nagaland
5	Longkhum Tsuk (SASRS-2)	SARS, Mokochung, Nagaland
6	Yarba (SARS-3)	SARS, Mokochung, Nagaland
7	Tsushvuri	SARS, Mokochung, Nagaland
8	Chali	SARS, Mokochung, Nagaland
9	Chishoghi	SARS, Mokochung, Nagaland
10	Thangmo Red	SARS, Mokochung, Nagaland
11	Thangma White	SARS, Mokochung, Nagaland
12	Chahashye	SARS, Mokochung, Nagaland
13	Taposen Youli	SARS, Mokochung, Nagaland
14	Kedayishye	SARS, Mokochung, Nagaland
15	Shyekenyii	SARS, Mokochung, Nagaland
16	Amusu	SARS, Mokochung, Nagaland
17	Ongpangsuk	SARS, Mokochung, Nagaland
18	Moyatsuk	SARS, Mokochung, Nagaland
19	Sulijak	SARS, Mokochung, Nagaland
20	Moya Chali	SARS, Mokochung, Nagaland
21	Tsungmiki	SARS, Mokochung, Nagaland
22	Manen Red (SARS-5)	SARS, Mokochung, Nagaland
23	Pfukhi Lha	ICAR NEH Region, Nagaland
24	Rosho Lha	ICAR NEH Region, Nagaland
25	Tungo	ICAR NEH Region, Nagaland
26	Ngoni	ICAR NEH Region, Nagaland
27	Thupfu Lha	ICAR NEH Region, Nagaland
28	RCM-9	ICAR NEH Region, Nagaland

Environment	Nitrogen doses	N:P:K (Kg/ha)
E_1	zero nitrogen	0: 30: 30 kg/ha
E_2	low nitrogen	40: 30: 30 kg/ha
E_3	high nitrogen	60: 30: 30 kg/ha

Urea was applied in granular form and one half of the total requirements of urea were applied at the time of final land preparation as a basal dose in E_2 and E_3. The remaining urea was split in two equal halves and the first part was top dressed at tillering and second part at panicle initiation stage in both E_2 and E_3. Single super phosphate (SSP) and muriate of potash (MOP) along with compost @ 10,000 kg/ha was applied as basal at full dose at the time of final land preparation.

Design	RBD
Number of replication	3
Row to row distance	20cm
Plant to plant distance	10cm
Check variety	1
Genotypes	27
Season	*Kharif* 2021 and 2022

3.5 Intercultural operations:

Weeding was done twice at 25 and 55 days after transplanting in the main field and before application of split doses of urea. For disease and pest incidence, plant protection measures were followed as per recommendations from package and practices.

3.6 Observations for quantitative trait parameters:

Parameters were recorded on 5 plant samples at random. The various observations to be recorded are as under:

3.6.1 Germination percentage (%)

It is for estimating the viability of a population of seeds calculated as:

$$\text{Germination percentage} = \frac{\text{No.of seeds germinated}}{\text{Total no.of seeds}} \times 100$$

3.6.2 Days to 50% flowering

Days to 50% flowering was recorded as the number of days from planting to the day when 50% of the plants in the plot have matured.

3.6.3 Days to maturity

Days to maturity was measured as the number of days from planting to the day when 80% of the plants in the plot have flowered.

3.6.4 Plant height (cm)

Plant height of five selected plants was measured from the base of the plant above the ground up to the tip of the topmost spikelet (average of 5 plants).

3.6.5 Flag leaf length (cm)

Flag leaf length was measured as the length of the topmost leaf after panicle initiation on an average of 5 random plants.

3.6.6 Flag leaf breadth (cm)

Flag leaf breadth was measured as the width of the topmost leaf after panicle initiation on an average of 5 random plants.

3.6.7 Flag leaf area (cm^2)

The flag leaf area was calculated by following the formula (Palaniswamy and Gomez, 1972).

Flag leaf area = Flag leaf length x breadth x 0.75

3.6.8 Number of ear bearing tillers (EBT)

Number of ear bearing tillers was recorded as number of panicles having filled seeds from a plant.

3.6.9 Panicles/plant

Panicles/ plant were measured as the total number of panicles or tillers emerged from a plant.

3.6.10 Panicle length (cm)

Panicle length was measured from the neck to the tip of the mother tiller on an average of 5 random plants.

3.6.11 Panicle weight (g)

The weight of each panicle were weighed and recorded after harvesting on an average of random plants.

3.6.12 Spikelet fertility

The spikelet fertility was worked out using the following formula:

$$\text{Spikelet fertility (\%)} = \frac{\text{Number of filled spikelets/panicle}}{\text{Total number of spikelets (filed + unfilled)/panicle}} \times 100$$

3.6.13 Root length (cm)

Root length was recorded by separately measuring the length of root for each plant after harvesting.

3.6.14 Root dry weight (g)

Root dry weight was recorded as the weight of dry roots for each plant after harvesting.

3.6.15 Stem dry weight (g)

Stem dry weight was recorded as the weight of dry stem for each plant after harvesting.

3.6.16 Harvest Index (Donald, 1962)

Harvest index of each genotype was obtained as the ratio of grain yield to the biological yield at 14% moisture content.

$$\text{Harvest index} = \frac{\text{Economic yield}}{\text{Biological yield}}$$

3.6.17 Grain N%

Representative samples of grain were taken from each genotype from each plot at the time of harvesting of the crop for estimation of N in grain. The samples were oven dried at 60°C temperature up to constant weight and then powdered using grinder. The N content was determined with Micro-Kjeldahl method.

3.6.18 PNUE

Total N in a straw and grain at maturity was determined using Micro-Kjeldahl's apparatus and was used to analyze PNUE (Singh *et al*., 1998).

$$\text{PNUE} = \frac{\text{Total biomass production}}{\text{Amount of N in the plant at maturity}}$$

3.6.19 NUtE

The NUtE was derived using the following formula (Aynehband *et al*., 2014).

$$\text{NutE} = \frac{\text{Grain yield}}{\text{Amount of N in the plant at maturity}}$$

3.6.20 NHI

NHI was calculated as the ratio of grain N and N content in the above ground parts (straw and grain) at maturity as used by Dawson et al. (2008) and expressed as percent.

$$\text{NHI} = \frac{\text{Grain yield}}{\text{Amount of N in the plant at maturity}} \times 100$$

3.6.21 Biological Yield

The sampled plants of each plot were harvested by cutting at the ground level and weighed separately for each of the sampled plants and mean biological yield per plant was worked out.

3.6.22 100 grain weight (g)

100 grain weight was recorded as weight of hundred random seeds in grams on an average of 5 random plants.

3.6.23 Grain yield/ plant (g)

Grain yield/plant was recorded from the yield of each plant after harvesting on an average of 5 random plants.

3.6.24 Chlorophyll content estimation (Hiscox and Isrealstam, 1979)

The third fresh leaves from top of the plants will be collected. A known fresh weight of leaf sample was cut into small pieces and suspended in test tubes containing 7 ml of dimethyl sulphoxide (DMSO). Test tubes was incubated at 65^{o}C for 30 min in a water bath. The supernatant was decanted and another 3 ml of DMSO was added to the residue and incubated at 65^{o}C for 30 min. The supernatant was pooled and the volume has to be made up to 10 ml by adding DMSO. The absorbance of the extract was read at 663nm and 645nm using spectrophotometer. The chlorophyll content was determined by using the following formula (Arnon, 1949) and expressed as mg g^{-1} leaf fresh weight.

Chlorophyll a = $[12.7(A_{663}) - 2.69(A_{645})]$ (V/1000) x W x a

Chlorophyll b = $[22.9(A_{645}) – 4.68(A_{663})]$ (V/1000) x W x a

Total chlorophyll = $[20.2(A_{645}) + 8.02(A_{663})]$ (V/1000) x W x a

Where,

A = Absorbance at given wavelength (645 and 663 nm)

V = Volume of the DMSO used in extract (ml)

W = Fresh weight of the tissue extracted (g)

a = Path length of light (1cm)

3.6.25 Amylose content (Juliano, 1971)

The amylose content in each rice sample was determined by using spectrophotometrical technique. The procedures are the following:

1. Weigh 100mg well powdered milled rice into 100ml of volumetric flask.

2. Add 1ml of 95 per cent ethanol and 9ml of 1N NaOH.

3. Heat the sample for 10 min in boiling water bath, cool it and make up the volume to 100ml.

4. Pipette 5ml from the 100 ml into another 100 ml of volumetric flask.

5. Add 1ml 1N acetic acid and then 2ml iodide solution and make up the volume of 100 ml.

6. Shake, stand for 20min and determine the per cent transmittance at 620nm using a colorimeter.

7. Prepare a series of standard starch solution containing 0, 20, 40, 60, 80 and 100 per cent amylose as in the steps 1 to 5.

8. Read the transmittance of the standards at 620nm and plot a standard graph.

9. Amylose content of the sample was determined in reference to the standard curve and expressed on per cent basis.

10. Making of amylose standard-

a) Pipette out 1, 2, 3, 4, and 5 ml of the standard amylose into 100ml of volumetric flasks into three sections.

b) Keep one flask as blank without adding anything.

c) Add 1.0 ml 1N acetic acid and 2.0 ml K-I solution to all the flasks including blank.

d) Make up all the flasks to100 ml using distilled water and cover all the flasks with a blank cloth or aluminium foil to prevent direct light.

e) Keep for 20 min and reading was taken at 620nm in a spectrophotometer.

f) The standards including blank, correspond to 0, 4, 8, 12, 16 and 20 per cent of amylose.

g) Draw a standard curve using the absorbance reading.

Based on the amylose percentage varieties can be grouped a follows:

Category	Amylose content (%)
Waxy	1-2
Very low amylose	2-9
Low	9-20
Intermediate	20-25
High	25-33

Amylose content is calculated as = Optical density x slope of the curve x dilution factor.

3.6.26 Total nitrogen and crude protein estimation using Micro-Kjeldahl method

The soil sample from a definite depth was randomly collected from the field. Samples was taken to the laboratory and air dried in the shade and sieved through 2mm stainless steel sieve and stored in polythene bags and used for chemical assay. For plant analysis, the whole plant will also be dried in open air for few days, after that it was dried in hot air oven at about 60^{o}C for eight to ten hours to achieve complete drying. After drying, whole plant was powdered with the help of a grinder, passed through 2mm stainless steel sieve and used for chemical assay. The procedures are the following:

1. **Digestion**

1) Weigh 0.5g of prepared plant sample or 1g of soil sample and transfer it to the digestion tube.

2) Add 10ml of concentrated sulphuric acid and 5g of catalyst mixture to the sample.

3) Load the digestion tubes in to the digester and heat the digestion block.

4) Switch on the digestion unit and set the initial temperature 100^{o}C till frothing was over.

5) The block temperature was raised to 400^{o}C. The effective digestion starts only at 360^{o}C and beyond 410^{o}C.

6) The sample turns light green colour or colourless at the end of the digestion process.

2. Distillation

1) After cooling the digestion tube, load the tube in distillation unit and other side of hose keep 20ml of 4% boric acid with mixed indicator in 250ml conical flask.

2) 40ml NaOH (40%) was automatically added by distillation unit programme.

3) The digested sample was heated by passing steam at a steady rate and the liberated ammonia absorbed in 20ml of 4 % boric acid containing mixed indicator solution was kept in a 250ml conical flask.

4) With the absorption of ammonia, the pinkish colour turns to green.

5) Nearly 150ml of distillate was collected in about 8 minutes.

6) Simultaneously blank sample (without plant/soil) was run too.

3. Titration

1) The green colour distillate was titrated with 0.02N sulphuric acid and the colour will change to original shade (pinkish colour).

2) Note the blank and sample tier reading (1ml) and calculate the total nitrogen content present in plant/soil samples.

Calculations:

$$\text{Nitrogen content in plant (\%)} = \frac{\text{R (sample tier – blank tier) x Normality of acid x atomic weight of nitrogen x 100}}{\text{Sample weight (g) x 1000}}$$

$$\text{Nitrogen content in soil (\%)} = \frac{\text{R (sample tier – blank tier) x Normality of acid x atomic weight of nitrogen x 100}}{\text{Sample weight (g) x 1000}}$$

Crude protein content:

The total nitrogen was estimated by micro-kjeldahl method as per procedure suggested by AOAC (1995) and the crude protein was calculated by the following formula:

Crude protein content (%) = micro-kjeldahl nitrogen content (%) x 6.25 (based on the assumptions that nitrogen constitutes 16% of protein).

3.7 Observations for qualitative trait parameters:

Observations was recorded as per the Minimal Descriptor (for characterization and evaluation) of Agri-Horticultural Crops, National Bureau of Plant Genetics Resources (Mahajan *et al.*, 2000) and the traits was evaluated by visual observation of the individual plant or parts of the plant as shown in Table 3.2.

3.7.1 Early plant vigour

Early plant vigour was recorded after 25 days of transplanting.

3.7.2 Basal leaf sheath colour

Basal leaf sheath was recorded on the outer surface of the basal leaf sheath at late vegetative stage.

3.7.3 Leaf blade colour

Leaf blade colour was recorded at vegetative stage

3.7.4 Leaf pubescence

Leaf pubescence was recorded at vegetative stage

3.7.5 Panicle exsertion

Panicle exsertion was recorded at the hard dough stage (20 days after flowering).

3.7.6 Stigma colour

Stigma colour was recorded on spikelets at 50% flowering stage

3.7.7 Apiculus colour

Apiculus colour was recorded on spikelets at dough stage.

3.7.8 Panicle type

Panicle type was recorded near maturity (30 days after 50% flowering).

3.7.9 Awning

Awning was recorded 30 days after 50% flowering.

3.7.10 Seed coat colour (Kernel colour)

Seed coat colour was recorded when the seed was fully dried.

3.7.11 Hull colour (husk colur)

Hull colour was recorded at maturity stage.

3.8 Statistical analyses

3.8.1 ANOVA for Randomized Block Design

Analysis of variance for Randomized block design

Source	Df	SS	MS	F-value
Genotype	g-1	GSS	GMS= GSS/g-1	GMS/EMS
Replication	r-1	RSS	RMS= RSS/r-1	RMS/EMS
Error	(g-1)(r-1)	ESS	EMS= ESS/(g-1)(r-1)	

Where,

$$GMS = \sigma^2 e + r\sigma^2 g$$

$$RMS = \sigma^2 e + g\sigma^2 r$$

$$EMS = \sigma^2 e$$

Table 3.2: Descriptors and score code for 11 qualitative traits under study

S.No.	Trait	Score code	Descriptors
1	Early plant vigour	1	Poor
		2	Good
		3	Very Good
2	Basal leaf sheath colour	1	Green
		2	Purple lines
		3	Light purple
		3	Purple
		99	Others
3	Leaf Blade Colour	1	Light Green
		2	Green
		3	Dark Green
		4	Purple
		5	Purple margin
		6	Purple Blotch
		7	Purple
		99	Others
4	Leaf pubescence	1	Glabrous
		2	Intermediate
		3	Pubescent
		99	Others
5	Panicle exsertion	1	Well exserted
		3	Moderate
		5	Just
		7	Partly
		9	Enclosed
		99	Others
6	Stigma Colour	1	White
		2	Light Green
		3	Yellow
		4	Light purple
		5	Purple
		99	Others

Table 3.2: Descriptors and score code for 11 qualitative traits under study (*contd..)*

S.No.	Trait	Score code	Descriptors
7	Apicuclus colour	1	White
		2	Straw
		3	Brown
		4	Red
		5	Red apex
		6	Purple
		7	Purple apex
		99	Others
8	Panicle Type	0	Absent
		1	Compact
		5	Intermediate
		9	Open
		99	Others
9	Awning	1	Short and partly awned
		5	Short and full
		7	Long
		9	Long and full
		99	Others
10	Seed coat colour	1	White
		2	Light Brown
		3	Speckled Brown
		4	Brown
		5	Red
		6	Variable
		7	Purple
		99	Others
11	Hull Colour (Husk Colour)	1	Straw
		2	Golden
		3	Golden Brown
		4	Brown furrows on straw
		5	Purple
		6	Purple furrows om straw
		7	Brown
		8	Black
		99	Others

3.8.2 Genotypic and Phenotypic coefficient of variation

The coefficient of genotypic and phenotypic variation was calculated using formula suggested by Burton and Devane (1953).

$$GCV = \frac{\sqrt{Genotypic\ variance}}{X} \times 100$$

$$PCV = \frac{\sqrt{Phenotypic\ variance}}{X} \times 100$$

Where,

X= General mean of the character

Genotypic variance = $\sigma^2 g$

Phenotypic variance = $\sigma^2 g + \sigma^2 e$

The GCV and PCV are classified as proposed by Sivasubramanian and Madhavamenon (1973).

Low: Less than 10%

Moderate: 10-20%

High: More than 20%

3.8.3 Heritability percentage (Broad sense)

Heritability in broad sense was calculated by formula given by Allard (1960).

$$h^2_{bs} = \frac{Genotypic\ variance}{Phenotypic\ variance} \times 100$$

$$h^2_{bs} = \frac{\sigma g^2}{\sigma g^2 + \sigma e^2} \times 100$$

The heritability values are categorized as follows as given by Johnson *et al.* (1955).

Low: Less than 30%

Moderate: 30-60%

High: More than 60%

3.8.4 Genetic Advance (GA)

Genetic Advance was calculated by formula used by Miller *et al.* (1958). Thus

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

Where,

h^2 = Heritability in broad sense

σ_p = Phenotypic standard deviation of the original population

k = Selection differential at 5% selection intensity = 2.06

GA as % of mean was:

$$GA\% = \frac{Genetic\ Advance}{Mean} \times 100$$

The range of genetic advance as percent of mean was categorized as proposed by Johnson *et al.* (1955).

Low: Less than 10%

Moderate: 10-20%

High: More than 20%

3.8.5 Correlation studies

Phenotypic and genotypic correlation coefficient was computed as suggested by Al-Jibouri *et al.* (1958).

Phenotypic correlation coefficient (r_p)

$$r_p = \frac{\sigma_{pxy}}{\sqrt{\sigma_{px}^2 \times \sigma_{py}^2}}$$

Where,

σ_{pxy} = Phenotypic covariance between two characters

σ^2_{px} = Phenotypic variance of the x character

σ^2_{py} = Phenotypic variance of the y character

Genotypic correlation coefficient (r_g)

$$r_g = \frac{\sigma_{gxy}}{\sqrt{\sigma_{gx}^2 \times \sigma_{gy}^2}}$$

Where,

σ_{gxy} = Genotypic covariance between two characters

σ^2_{gx} = Genotypic variance of the x character

σ^2_{gy} = Genotypic variance of the y character

3.8.6 Path coefficient analysis given (Dewey and Lu, 1959)

Path analysis was done using the procedure by Dewey and Lu (1959). Path coefficient is simply a standard partial regression coefficient which permits separation of correlation coefficients into direct and indirect effects and measures the direct and indirect contribution of various independent characters on a dependent character. It thus, helps in understanding the cause and effect of relationship.

The correlation coefficient between i^{th} independent variable X_i and dependent variable Y is linearly related with correlation coefficients of the dependent variable with the remaining independent variables. This relation was denoted by:

$$r_{1y} = P_{1y} + P_{2y}.r_{12} + P_{3y}.r_{13} + \ldots\ldots\ldots\ldots + P_{ky}.r_{1k}$$

$$r_{2y} = P_{1y}.r_{21} + P_{2y} + P_{3y}.r_{23} + \ldots\ldots\ldots\ldots + P_{ky}.r_{2k}$$

$$\ldots\ldots \quad \ldots\ldots\ldots \quad \ldots\ldots \quad \ldots\ldots \quad \ldots\ldots\ldots \quad \ldots\ldots\ldots$$

$$r_{ky} = P_{1y}.r_{k1} + P_{2y}.r_{k2} + P_{3y}.r_{k3} + \ldots\ldots\ldots\ldots + P_{ky}$$

Where P_{1y} , P_{2y} , ……., P_{ky} are the coefficients in the linear relation and are known as path coefficients; r_{k1}, r_{k2}, ……., r_{ki} are the correlation coefficients among k independent variables and riy is the correlation coefficient between i^{th} independent variable X_i and the dependent variable Y. P_{iy} is called the direct effect of X_i on Y and = $P_{1y}.r_1$, $P_{2y}.r_{12}$, ……, $P_{ky}.r_{1k}$ are called the indirect effects if X_i on Y through X_1, X_2, ……, X_k, respectively. Therefore, the correlation coefficients (total effect) between X_i and T are the sum of direct and indirect effects of X_i on Y. The linear relations are represented by matrix notation as:

$$\begin{bmatrix} r1y \\ r2y \\ rky \end{bmatrix} = \begin{bmatrix} r11 & \cdots & r1k \\ \vdots & \ddots & \vdots \\ rk1 & \cdots & rkk \end{bmatrix} \begin{bmatrix} P1y \\ P2y \\ Pky \end{bmatrix}$$

Therefore, the path coefficients are obtained by simultaneous solution of the above equations which express the basic relationship between correlations and path coefficients.

The R variables consist of residual factors that influence dependent variable Y. The residual effect is obtained by the relations:

$$Rry = \sqrt{1 - (P1yr1y + P2yr2y + \cdots + Pkyrky}$$

3.8.7 D^2 statistics (Mahalanobis, 1936; Rao 1952)

Replicated data recorded on characters were used for Mahalanobis D^2 statistics (Mahalanobis, 1936) as explained by Rao (1952) to group the genotypes into different clusters.

Mahalanobis D^2 analysis between two genotypes estimated on the basis of the 'p' characters is given by the equation:

$$D^2 = \sum_{i=1}^{p} \sum_{j=1}^{p} wij(Xi1 - Xi2)(Xj1 - Xj2)$$

Where,

w_{ij} = variance-covariance matrix

w_{ij} = reciprocal of (w_{ij}), (ij = 1,2……, p).

X_{i1} = sample mean for i^{th} character for first sample

X_{i2} = sample mean for i^{th} character for second sample

3.8.8 Analysis of stability (Eberhart and Russell, 1966)

The mean data of each environment was subjected to pooled analysis of variance over environments to study GE interaction and phenotypic stability by the following model given by Eberhart and Russell (1966).

$Y_{ij} = m_i + b_iI_j + \delta_{ij}$ (i= 1, 2, 3,…… t and j = 1, 2, 3,….. s)

Where,

Y_{ij} = Mean of i^{th} genotype in the j^{th} environment

m_i = i^{th} genotypic mean over environment

b_i = Regression coefficient of the i^{th} genotype on environmental index which measure the response of this genotype to varying environments

I_j = Environmental index which is defined as the deviation of j^{th} environmental mean from the mean over all the environments and is calculated as

$$Ij = \left(\frac{\Sigma i\, Yij}{t}\right) - \left(\frac{\Sigma i \Sigma j Yij}{ts}\right) \text{ with } \Sigma_j I_j = 0$$

δ_{ij} = The deviation from regression of the i^{th} genotype at j^{th} environment

Pooled analysis of variance

Source of variations	**d.f.**	**MS**
Genotype	t-1	MS1
Env. + (genotype x Env.)	t(s-1)	
Environment (linear)	1	
Genotype x Env. (linear)	(t-1)	MS2
Pooled deviation	t(s-2)	MS3
Genotype 1	(s-2)	
Genotype 2	(s-2)	
Genotype t	(s-2)	
Pooled error	s(r-1) (t-1)	MS_4

Calculation of pooled error

Pool error was calculated as

$$\text{Pooled error} = \frac{(n1-1)(MS\ error\ \text{E1}) + \ldots\ldots\ldots\ldots\ldots + (n1-1)(MS\ error\ Es)}{(n1-1) + \ldots\ldots\ldots\ldots + (ns-1)}$$

Where,

(n1-1) = d.f. for error in environment 1

(ns-1) = d.f. for error in environemnt s

MS error E1 = mean sum of square due to error in environment 1 and

MS error Es = mean sum of square due to error in environment s

Pooled error MS was calculated as

$$\text{Pooled error MS} = \frac{Pooled\ error}{r}$$

Where, *r* = number of replication

Testing of significance

In order to compare genotypic means of each environment, standard error of difference (SE_d) and critical difference (CD) was calculated as follows:

$$SE_d = \sqrt{\frac{2MSe}{r}}$$

Where,

r = the number of replication

CD = SE_d x t for error *d.f.* at 5% probability level

The standard errors for the population means (SE_m) was calculated as follows:

$$SE_m = \sqrt{\frac{MS3}{s-1}}$$

Where, s = the number of environments

3.8.9 Stability parameters

The three stability parameters were calculated to compare the genotypes over environments.

1. Mean (m) = Mean of the i^{th} genotype over environment. Ideal genotype should have high mean over environments.
2. Regression coefficient (bi) = $\frac{\Sigma jYijIj}{\Sigma jI2j}$

Where,

$\Sigma_j Y_{ij} I_j$ = Sum of products of value of i^{th} genotype at j^{th} environment and environment index and

$\Sigma_j I^2_j$ = Sum of squares of environmental index

The ideal genotypes should have regression coefficient equal to 1 ($b_i = 1$).

3. Deviation mean square (s^2d_i) = $\left(\frac{\Sigma i\delta i2j}{s-2}\right) - \left(\frac{s2e}{r}\right)$

Where,

$\Sigma_i\delta_i 2_j = \left[\Sigma jY2ij - \frac{Y2i}{t}\right] - \frac{(\Sigma jYijIj)2}{\Sigma jI1j}$

s^2e = Estimates of pooled error

The ideal genotype should have deviation mean square from linear regression equal to zero ($s^2d_i = 0$).

Testing of significance of stability parameters:

To test the significance of difference of bi values from unity the procedure given by Gomez (1968) as follows:

$t = \frac{bi-1}{sb}$

where,

b_i = Regression coefficient

sb = Standard error of bi; calculated as $\sqrt{\frac{MS3}{\Sigma jI2j}}$

To test the significance of deviation mean square (s^2d_i) of each genotype from its regression, the appropriate formula as follows;

$F = \frac{s2di}{Pooled\ error\ MS}$

3.8.10 Correlation coefficient based on stability parameters

Simple correlation coefficients may be estimated among seed yield and its components trait based on regression coefficient (bi) values as well as mean square deviations (s^2d_i).

Correlation coefficient, $r_{(xy)} = \frac{\Sigma(xi-xi)(yi-yi)}{[\Sigma(xi-xi)2\ \Sigma(yi-yi)2]1/2}$

CHAPTER - IV

RESULTS AND DISCUSSIONS

RESULTS AND DISCUSSIONS

Observations on data recorded and analysed are presented as results and discussed under the following heads.

4.1 Studies on qualitative traits

Observations were recorded as per the Minimal Descriptor (for characterization and evaluation) of Agri-Horticultural Crops, National Bureau of Plant Genetics Resources (Mahajan *et al.,* 2000). The results are interpreted according to the descriptor given in Table 4.1 and graphs are illustrated for each of the 11 qualitative traits studied in Fig 4.1.

4.1.1 Early plant vigour

Among the 28 genotypes, 7 genotypes (28.5%) viz., Sungmangtsuk (SARS-1), Kezie (SASRS-94), Korea Tsuk, Longkhum Tsuk (SASRS-2), Yarba (SARS-3), Chishoghi and Thupfu Lha showed poor plant vigour genotypes revealed good plant vigour with 25% frequency such as Chali, Thangmo Red, Thangma White, Shyekenyii, Tsungmiki, Manen Red (SARS-5), Pfukhi Lha and Tungo. Plants with very good plant vigour have highest frequency (46.43%) with 13 genotypes viz., Apuapa (SARS-61), Tsushvuri, Chahashye, Taposen Youli, Kedayishye, Amusu, Ongpangsuk, Moyatsuk, Sulijak, Moya Chali, Rosho Lha, Ngoni and RCM-9.

4.1.2 Basal Leaf sheath colour

Among the 28 genotypes studied, the genotypes having green basal leaf sheath colour are having highest frequency (75%) with 21 no. of genotypes namely Sungmangtsuk (SARS-1), Apuapa (SARS-61), Kezie (SASRS-94), Korea Tsuk, Longkhum Tsuk (SASRS-2), Yarba (SARS-3), Thangma White, Chahashye, Taposen Youli, Shyekenyii, Amusu, Ongpangsuk, Moya Chali, Tsungmiki, Manen Red (SARS-5), Pfukhi Lha, Rosho Lha, Tungo, Ngoni, Thupfu Lha and RCM-9 whereas 7 genotypes are having purple lines with a

low frequency (25%) viz., Tsushvuri, Chali, Chishoghi, Thangmo Red, Kedayishye, Moyatsuk and Sulijak.

4.1.3 Leaf blade colour

Among all the genotypes studied, 12 genotypes are having green leaf balde colour with highest frequency (42.86%) viz., Sungmangtsuk (SARS-1), Apuapa (SARS-61), Kezie (SASRS-94), Korea Tsuk, Thangmo Red, Kedayishye, Shyekenyii, Ongpangsuk, Sulijak, Pfukhi Lha and Tungo while light green leaf blade colour are having second highest frequency (35.71%) with 10 no. of genotypes viz., Yarba (SARS-3), Tsushvuri, Chali, Chishoghi, Thangma White, Taposen Youli, Moya Chali, Tsungmiki, Manen Red (SARS-5) and Rosho Lha and remaining 6 genotypes are having lowest frequency (21.43%) viz., Chahashye, Amusu, Moyatsuk, Ngoni, Thupfu Lha and RCM-9.

4.1.4 Leaf pubescence

All the 28 genotypes viz., Sungmangtsuk (SARS-1), Apuapa (SARS-61), Kezie (SASRS-94), Korea Tsuk, Longkhum Tsuk (SASRS-2), Yarba (SARS-3), Tsushvuri, Chali, Chishoghi, Thangmo Red, Thangma White, Chahashye, Taposen Youli, Kedayishye, Shyekenyii, Amusu, Ongpangsuk, Moyatsuk, Sulijak, Moya Chali, Tsungmiki, Manen Red (SARS-5), Pfukhi Lha, Rosho Lha, Tungo, Ngoni, Thupfu Lha and RCM-9 are having glabrous leaf pubescence with a frequency of 100%.

4.1.5 Panicle exertion

Among the 28 genotypes, 16 genotypes are well exserted viz., Sungmangtsuk (SARS-1), Kezie (SASRS-94), Korea Tsuk, Chali, Chishoghi, Thangma White, Chahashye, Taposen Youli, Moyatsuk, Sulijak, Tsungmiki, Manen Red (SARS-5), Pfukhi Lha, Rosho Lha, Thupfu Lha and RCM-9 with highest frequency of 57.14%. Moderate panicle exsertion are having 11 genotypes namely, Longkhum Tsuk (SASRS-2), Yarba (SARS-3), Tsushvuri, Thangmo Red, Kedayishye, Shyekenyii, Amusu, Ongpangsuk, Moya Chali,

Tungo and Ngoni with a frequency of 39.29% and remaining one genotype possrsses partly panicle exsertion with a frequency of 3.51%.

4.1.6 Stigma colour

Among all the genotypes, yellow stigma colour has the highest frequency of 53.57% with 15 no. of genotypes viz., Longkhum Tsuk (SASRS-2), Chali, Chishoghi, Thangmo Red, Thangma White, Taposen Youli, Kedayishye, Shyekenyii, Amusu, Sulijak, Tsungmiki, Ngoni, Thupfu Lha, RCM-9 and Manen Red (SARS-5). Light green stigma colour has the second highest frequency (25%) with 7 genotypes viz., Yarba (SARS-3), Tsushvuri, Chahashye, Ongpangsuk, Moyatsuk, Moya Chali and Pfukhi Lha and remaining 6 no. of genotypes have white stigma colour viz., Sungmangtsuk (SARS-1), Apuapa (SARS-61), Kezie (SASRS-94), Korea Tsuk, Rosho Lha and Tungo with a frequency of 21.43%.

4.1.7 Apiculus colour

All the 28 genotypes viz., Sungmangtsuk (SARS-1), Apuapa (SARS-61), Kezie (SASRS-94), Korea Tsuk, Longkhum Tsuk (SASRS-2), Yarba (SARS-3), Tsushvuri, Chali, Chishoghi, Thangmo Red, Thangma White, Chahashye, Taposen Youli, Kedayishye, Shyekenyii, Amusu, Ongpangsuk, Moyatsuk, Sulijak, Moya Chali, Tsungmiki, Manen Red (SARS-5), Pfukhi Lha, Rosho Lha, Tungo, Ngoni, Thupfu Lha and RCM-9 are having straw apiculus colour with a frequency of 100%.

4.1.8 Panicle type

Compact panicle type has the highest frequency (64.29%) consisting of 18 genotypes viz., Apuapa (SARS-61), Kezie (SASRS-94), Yarba (SARS-3), Tsushvuri, Chali, Chishoghi, Chahashye, Amusu, Ongpangsuk, Moyatsuk, Sulijak, Moya Chali, Tsungmiki, Manen Red (SARS-5), Rosho Lha, Tungo, Thupfu Lha and RCM-9 while intermediate panicle type is having a frequency of 35.71% consisting of 10 genotypes viz., Sungmangtsuk (SARS-1), Korea

Tsuk, Longkhum Tsuk (SASRS-2), Thangmo Red, Thangma White, Taposen Youli, Kedayishye, Shyekenyii, Pfukhi Lha and Ngoni.

4.1.9 Awning

All the 28 genotypes viz., Sungmangtsuk (SARS-1), Apuapa (SARS-61), Kezie (SASRS-94), Korea Tsuk, Longkhum Tsuk (SASRS-2), Yarba (SARS-3), Tsushvuri, Chali, Chishoghi, Thangmo Red, Thangma White, Chahashye, Taposen Youli, Kedayishye, Shyekenyii, Amusu, Ongpangsuk, Moyatsuk, Sulijak, Moya Chali, Tsungmiki, Manen Red (SARS-5), Pfukhi Lha, Rosho Lha, Tungo, Ngoni, Thupfu Lha and RCM-9 are having shortly and partly awned with a frequency of 100%.

4.1.10 Seed coat colour

Among all the genotypes, white seed coat colour has the highest frequency (50%) with 14 no. of genotypes viz., Apuapa (SARS-61), Kezie (SASRS-94), Longkhum Tsuk (SASRS-2), Yarba (SARS-3), Tsushvuri, Chali, Chishoghi, Thangmo Red, Moyatsuk, Sulijak, Tsungmiki, Pfukhi Lha, Tungo and Thupfu Lha. Light brown colour has the second highest frequency (28.57%) with 8 genotypes viz., Thangma White, Kedayishye, Shyekenyii, Amusu, Ongpangsuk, Moya Chali, Ngoni and RCM-9 while red seed coat colour has lowest frequency (21.43%) with 6 no, of genotpyes viz., Sungmangtsuk (SARS-1), Korea Tsuk, Chahashye, Taposen Youli, Manen Red (SARS-5) and Rosho Lha.

4.1.11 Hull colour (Husk colour)

Among all the genotypes, golden hull colour has the highest frequency (64.29%) consisting of 18 genotypes viz., Apuapa (SARS-61), Kezie (SASRS-94), Longkhum Tsuk (SASRS-2), Yarba (SARS-3), Tsushvuri, Chali, Chishoghi, Taposen Youli, Amusu, Ongpangsuk, Moyatsuk, Sulijak, Moya Chali, Tsungmiki, Rosho Lha, Tungo, Ngoni and Thupfu Lha. Golden brown hull colour has the second highest frequency (21.43%) with 6 no. of genotypes

viz., Thangmo Red, Thangma White, Kedayishye, Shyekenyii, Manen Red (SARS-5) and Pfukhi Lha followed by black hull colour with frequency of 10.71% with 3 genotypes viz., Sungmangtsuk (SARS-1), Korea Tsuk and Chahashye. Only one genotype viz. RCM-9 has straw husk colour with a frequency of 3.57%.

Qualitative characters are less influenced by the environmental changes therefore, it is an important criterion for evaluating phenotypic diversity within the genotypes. In the present study, genetic variability was found in early plant vigour, basal leaf sheath, panicle exsertion, stigma colour, panicle type, seed coat colour, and hull colour whereas leaf pubescence, apiculus colour, and awning shows no variability. Among 28 genotypes, 13 genotypes like Apuapa (SARS-61), Tsushvuri, Chahashye, Taposen Youli, Kedayishye, Amusu, Ongpangsuk, Moyatsuk, Sulijak, Moya Chali, Rosho Lha, Ngoni and RCM-9 have good plant vigour therefore these genotypes have good germination. All the genotypes are also having glabrous leaves which is also a favourable agronomic trait for post harvesting for packaging and produce less dust causing itching effect on farmers. Panicle exsertion has also direct influence on natural outcrossing and results in good seed setting and 16 genotypes are having well exserted panicles which mean these genotypes will have high seed set.

Table 4.1: Characterization of genotypes based on 11 qualitative traits

Sl. No.	Qualitative traits	Score code	Frequency (%)	Number and name of genotypes
1	Early plant vigour	1.Poor	25	1.Sungmangtsuk (SARS-1) 2. Kezie (SASRS-94)3.Korea Tsuk 4. Longkhum Tsuk (SASRS-2) 5. Yarba (SARS-3) 6. Chishoghi 7. Thupfu Lha
		2.Good	28.57	1. Chali 2. Thangmo Red 3. Thangma White 4. Shyekenyii 5. Tsungmiki 6. Manen Red (SARS-5) 7. Pfukhi Lha 8. Tungo
		3.Very Good	46.43	1. Apuapa (SARS-61) 2.Tsushvuri 3. Chahashye 4. Taposen Youli 5. Kedayishye 6. Amusu 7. Ongpangsuk 8. Moyatsuk 9. Sulijak 10. Moya Chali 11. Rosho Lha 12. Ngoni 13. RCM-9
2	Basal Leaf sheath colour	Green	75	1. Sungmangtsuk (SARS-1) 2. Apuapa (SARS-61) 3. Kezie (SASRS-94) 4. Korea Tsuk 5. Longkhum Tsuk (SASRS-2) 6. Yarba (SARS-3) 7. Thangma White 8. Chahashye 9. Taposen Youli 10. Shyekenyii 11. Amusu 12. Ongpangsuk 13. Moya Chali 14. Tsungmiki 15. Manen Red (SARS-5) 16. Pfukhi Lha 17. Rosho Lha 18. Tungo 19. Ngoni 20. Thupfu Lha 21. RCM-9
		Purple lines	25	1. Tsushvuri 2. Chali 3. Chishoghi 4. Thangmo Red 5. Kedayishye 6. Moyatsuk 7. Sulijak
3	Leaf balde colour	Light Green	35.71	1. Yarba (SARS-3) 2. Tsushvuri 3. Chali 4. Chishoghi 5. Thangma White 6. Taposen Youli 7. Moya Chali 8. Tsungmiki 9. Manen Red (SARS-5) 10. Rosho Lha
		Green	42.86	1. Sungmangtsuk (SARS-1) 2. Apuapa (SARS-61) 3. Kezie (SASRS-94) 4. Korea Tsuk 5. Thangmo Red 6. Kedayishye 7. Shyekenyii 8. Ongpangsuk 9. Sulijak 10. Pfukhi Lha 11. Tungo 12. Longkhum Tsuk (SARS-2)
		Dark Green	21.43	1. Chahashye 2. Amusu 3. Moyatsuk 4. Ngoni 5. Thupfu Lha 6. RCM-9

Table 4.1: Characterization of genotypes based on 11 qualitative traits (*contd*…)

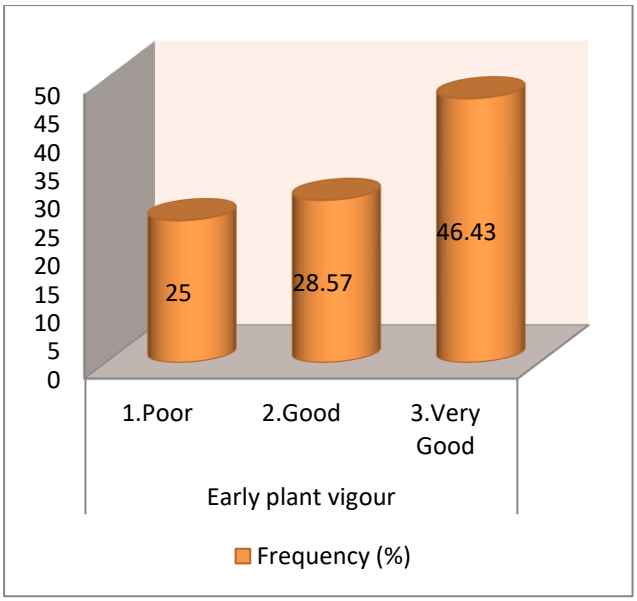
Sl. No.	Qualitative traits	Score code	Frequency (%)	Number and name of genotypes
4	Leaf pubescence	Glabrous	100	1. Sungmangtsuk (SARS-1) 2. Apuapa (SARS-61) 3. Kezie (SASRS-94) 4. Korea Tsuk 5. Longkhum Tsuk (SASRS-2) 6. Yarba (SARS-3) 7. Tsushvuri 8. Chali 9. Chishoghi 10. Thangmo Red 11. Thangma White 12. Chahashye 13. Taposen Youli 14. Kedayishye 15. Shyekenyii 16. Amusu 17. Ongpangsuk 18. Moyatsuk 19. Sulijak 20. Moya Chali 21. Tsungmiki 22. Manen Red (SARS-5) 23. Pfukhi Lha 24. Rosho Lha 25. Tungo 26. Ngoni 27. Thupfu Lha 28. RCM-9
5	Panicle exsertion	Well exserted	57.14	1. Sungmangtsuk (SARS-1) 2. Kezie (SASRS-94) 3. Korea Tsuk 4. Chali 5. Chishoghi 6. Thangma White 7. Chahashye 8. Taposen Youli 9. Moyatsuk 10. Sulijak 11. Tsungmiki 12. Manen Red (SARS-5) 13. Pfukhi Lha 14. Rosho Lha 15. Thupfu Lha 16. RCM-9
		Moderate	39.29	1. Longkhum Tsuk (SASRS-2) 2. Yarba (SARS-3) 3. Tsushvuri 4.Thangmo Red 5.Kedayishye 6. Shyekenyii 7. Amusu 8. Ongpangsuk 9. Moya Chali 10. Tungo 11. Ngoni
		Partly	3.57	1. Apuapa (SARS-61)
6	Stigma colour	White	21.43	1. Sungmangtsuk (SARS-1) 2. Apuapa (SARS-61) 3. Kezie (SASRS-94) 4. Korea Tsuk 5. Rosho Lha 6. Tungo
		Light Green	25	1. Yarba (SARS-3) 2. Tsushvuri 3. Chahashye 4. Ongpangsuk 5. Moyatsuk 6. Moya Chali 7. Pfukhi Lha
		Yellow	53.57	1. Longkhum Tsuk (SASRS-2) 2. Chali 3. Chishoghi 4. Thangmo Red 5. Thangma White 6. Taposen Youli 7. Kedayishye 8. Shyekenyii 9. Amusu 10. Sulijak 11. Tsungmiki 12. Ngoni 13. Thupfu Lha 14. RCM-9 15. Manen Red (SARS-5)

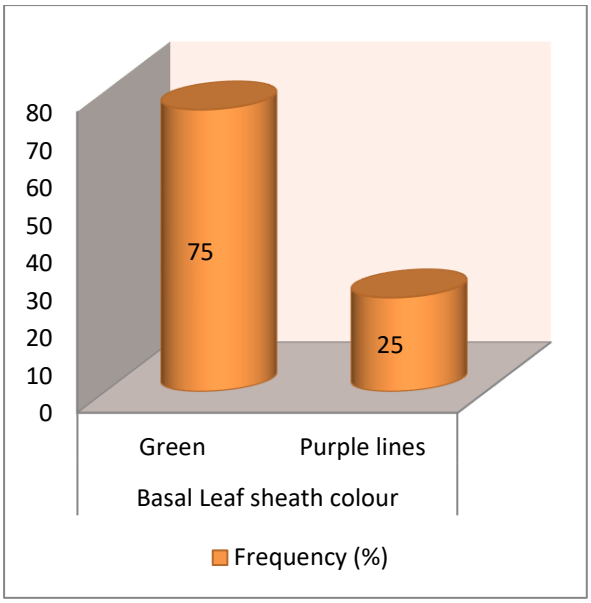
Table 4.1: Characterization of genotypes based on 11 qualitative traits (*contd*…)

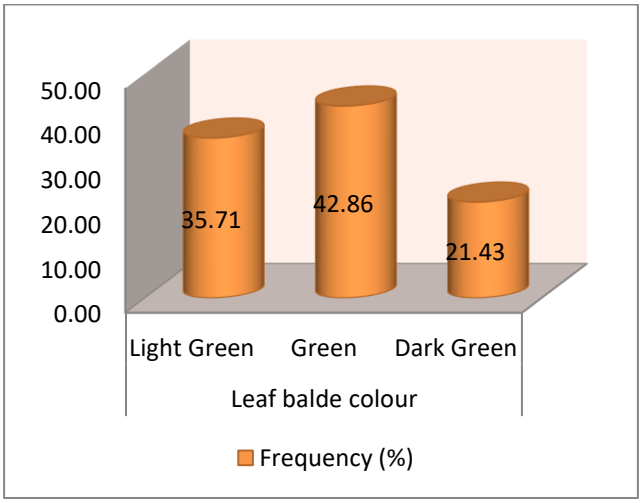
Sl.No.	Qualitative traits	Score code	Frequency (%)	Number and name of genotypes
7	Apiculus colour	Straw	100	1. Sungmangtsuk (SARS-1) 2. Apuapa (SARS-61) 3. Kezie (SASRS-94) 4. Korea Tsuk 5. Longkhum Tsuk (SASRS-2) 6. Yarba (SARS-3) 7. Tsushvuri 8. Chali 9. Chishoghi 10. Thangmo Red 11. Thangma White 12. Chahashye 13. Taposen Youli 14. Kedayishye 15. Shyekenyii 16. Amusu 17. Ongpangsuk 18. Moyatsuk 19. Sulijak 20. Moya Chali 21. Tsungmiki 22. Manen Red (SARS-5) 23. Pfukhi Lha 24. Rosho Lha 25. Tungo 26. Ngoni 27. Thupfu Lha 28. RCM-9
8	Panicle type	Compact	64.29	1. Apuapa (SARS-61) 2. Kezie (SASRS-94) 3. Yarba (SARS-3) 4. Tsushvuri 5. Chali 6. Chishoghi 7. Chahashye 8. Amusu 9. Ongpangsuk 10. Moyatsuk 11. Sulijak 12. Moya Chali 13. Tsungmiki 14. Manen Red (SARS-5) 15. Rosho Lha 16. Tungo 17. Thupfu Lha 18. RCM-9
		Intermediate	35.71	1. Sungmangtsuk (SARS-1) 2. Korea Tsuk 3. Longkhum Tsuk (SASRS-2) 4. Thangmo Red 5. Thangma White 6. Taposen Youli 7. Kedayishye 8. Shyekenyii 9. Pfukhi Lha 10. Ngoni
9	Awning	Short and partly awned	100	1. Sungmangtsuk (SARS-1) 2. Apuapa (SARS-61) 3. Kezie (SASRS-94) 4. Korea Tsuk 5. Longkhum Tsuk (SASRS-2) 6. Yarba (SARS-3) 7. Tsushvuri 8. Chali 9. Chishoghi 10. Thangmo Red 11. Thangma White 12. Chahashye 13. Taposen Youli 14. Kedayishye 15. Shyekenyii 16. Amusu 17. Ongpangsuk 18. Moyatsuk 19. Sulijak 20. Moya Chali 21. Tsungmiki 22. Manen Red (SARS-5) 23. Pfukhi Lha 24. Rosho Lha 25. Tungo 26. Ngoni 27. Thupfu Lha 28. RCM-9

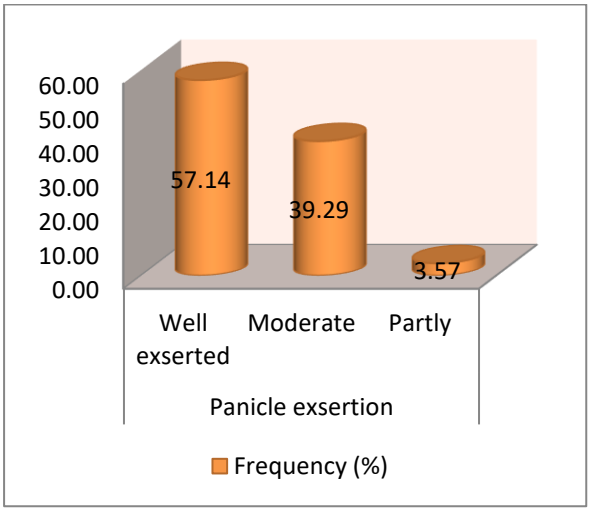
Table 4.1: Characterization of genotypes based on 11 qualitative traits (*contd*…)

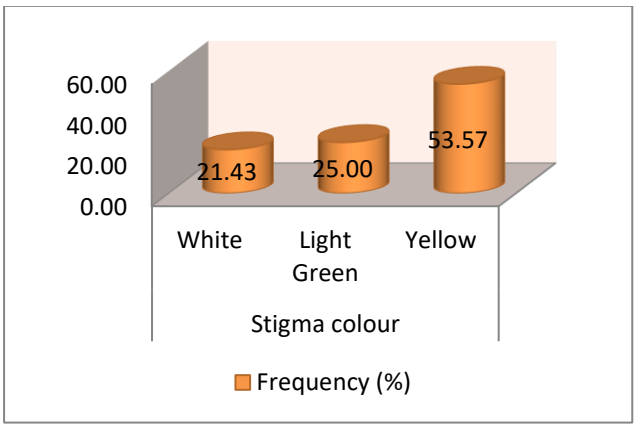
Sl.No.	Qualitative traits	Score code	Frequency (%)	Number and name of genotypes
10	Seed coat colour	White	50	1. Apuapa (SARS-61) 2. Kezie (SASRS-94) 3. Longkhum Tsuk (SASRS-2) 4. Yarba (SARS-3) 5. Tsushvuri 6. Chali 7. Chishoghi 8. Thangmo Red 9. Moyatsuk 10. Sulijak 11. Tsungmiki 12. Pfukhi Lha 13. Tungo 14. Thupfu Lha
		Light Brown	28.57	1. Thangma White 2. Kedayishye 3. Shyekenyii 4. Amusu 5. Ongpangsuk 6. Moya Chali 7. Ngoni 8. RCM-9
		Red	21.43	1. Sungmangtsuk (SARS-1) 2. Korea Tsuk 3. Chahashye 4. Taposen Youli 5. Manen Red (SARS-5) 6. Rosho Lha
11	Hull colour(Husk colour)	Straw	3.57	1. RCM-9
		Golden	64.29	1. Apuapa (SARS-61) 2. Kezie (SASRS-94) 3. Longkhum Tsuk (SASRS-2) 4. Yarba (SARS-3) 5. Tsushvuri 6. Chali 7. Chishoghi 8. Taposen Youli 9. Amusu 10. Ongpangsuk 11. Moyatsuk 12. Sulijak 13. Moya Chali 14. Tsungmiki 15. Rosho Lha 16. Tungo 17. Ngoni 18. Thupfu Lha
		Golden Brown	21.43	1. Thangmo Red 2. Thangma White 3. Kedayishye 4. Shyekenyii 5. Manen Red (SARS-5) 6. Pfukhi Lha
		Black	10.71	1. Sungmangtsuk (SARS-1) 2. Korea Tsuk 3. Chahashye











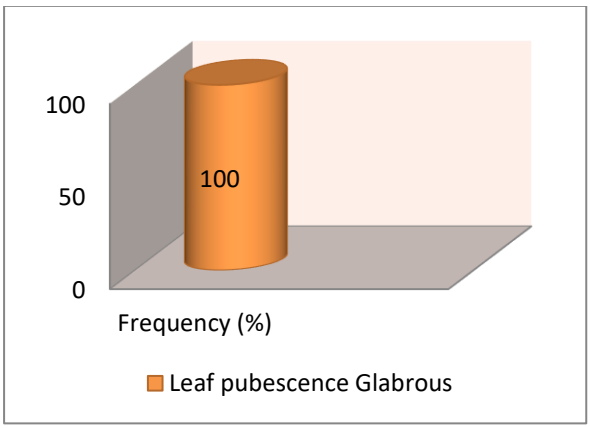


Fig 4.1: Graph representing frequency of variability found in 11 qualitative traits

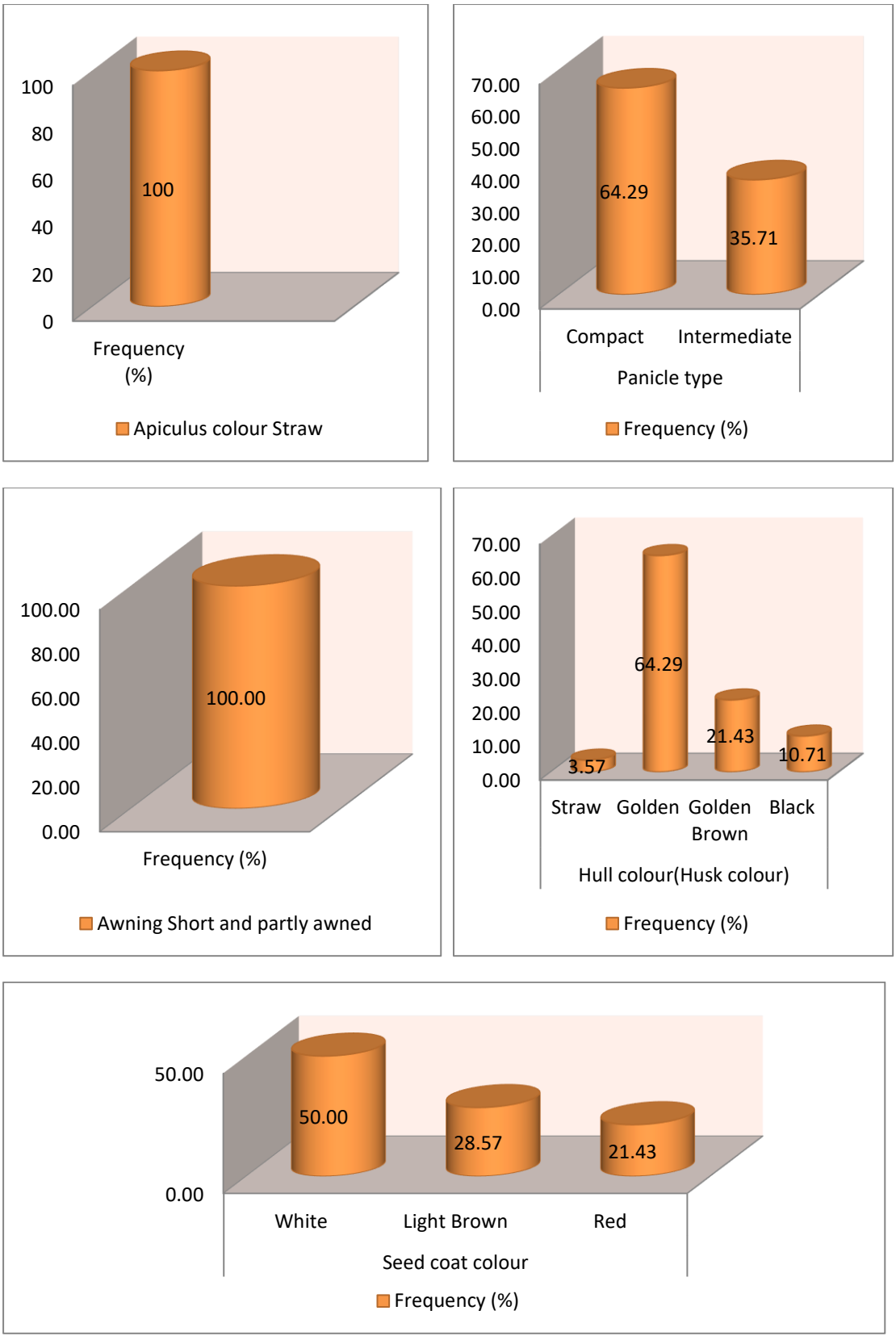


Fig 4.1: Graph representing frequency of variability found in 11 qualitative traits

4.2 Analysis of variance

Pooled analysis of variance revealed that all the 29 quantitative characters studied under 6 environments were showing significant differences as shown in table 4.2. Significantly diverse genotypes can be used for selecting diverse genotypes for NUE for yield and yield attributing traits. This suggests that there was sufficient scope in the current gene pool to choose promising lines for yield and its components. A large number of qualities in the genotypes were found to have high genetic diversity, which ensures the viability of these genotypes for use in breeding to increase grain yield and its associated characteristics. These findings are consistent with those previously reported by Mamata *et al.* (2017) and Longjam and Singh (2019), who also reported on related research.

4.3 Mean performance of genotypes

Mean performance of the genotypes over 6 environments for various characters along with standard error of mean (SEm) and critical difference at 5% level of significance (CD, 0.05) are presented in Table 4.3.

Germination percentage

Germination percentage was found to be highest in Amusu (100%), followed by Korea Tsuk, Tsushvuri, Moyatsuk and Rosho Lha, Longkhum Tsuk (SARS-2), RCM-9, Chali, Thangma White, Moya Chali and Pfukhi Lha which have values >90% whereas, it was found to be lowest in case of Apuapa (SARS-61) (26.67%) and Shyekenyii (26.67%) followed by Ngoni and Tungo. The average mean of germination percentage recorded was 71.17%.

Days to 50% flowering

Days to 50% flowering was recorded to be longest in RCM-9 (150.13) followed by Thupfu Lha, Moyatsuk and Rosho Lha, whereas, Moya Chali (98.58) was recorded to have shortest days to 50% flowering followed by Amusu, Tsungmiki and Ongpangsuk. The average mean of days to 50%

flowering recorded was 112.45. The short duration genotypes are essential for different cropping systems and in certain stress avoidance.

Days to maturity

RCM-9 (170.06) was found to have longest duration in days for maturity followed by Thupfu Lha, Ngono and Yarba (SARS-3) whereas it was the shortest in Chishoghi (133.89) followed by Thangma white, Moyatsuk and Chahashye. The average mean of days to maturity was recorded as 137.80.

Due to variations in early plant vigour, flowering and maturity days may vary. The earliest-emerging genotype may also have the earliest blossoming and the fastest maturation period. However, this mostly depends on environmental factors and genotype genetic behaviour (some genotypes required up to 40 days to mature after heading, while others took as little as 30 days) (Harrell *et al.*, 2021). In Nagaland conditions, genotypes with medium flowering and maturation dates may be acceptable for future breeding and production in order to shorten the growing season of genotypes with high yielding capacity and the longest maturation date and to reduce yield loss as a result of environmental stress. In contrast, late maturing genotypes can be employed in agro-ecologies with water shortages to promote high yield genotypes.

Plant height

Higher panicle length, the higher plant height, lower panicle number, lower filled grain and grain yield. However, this depends on the rice subspecies type (Indica, Japonica, Javanica). Plant height was found to be highest in Amusu (148.84cm) followed by Tsungmiki, Sulijak and Moyatsuk whereas it was found to be lowest in RCM-9 (82.03cm) which is the check variety followed by Thupfa Lha, Ngoni and Rosho Lha. The average mean of plant height recorded was 123.44cm.

Since shorter genotypes of rice are more likely to succumb to flooding while taller genotypes are more likely to lodge, genotypes with intermediate

plant height may be acceptable for breeding and production in the research area.

Flag leaf length

Flag leaf length was found to be longest in Kezie (SASRS-94) (45.02) followed by Kedayishye, Ngoni and Apuapa (SARS-61) whereas it was found to be shortest in case of Shyekenyii (16.93cm) followed by Yarba (SARS-3), Thangma White and Tsungmiki. The average mean of flag leaf length was recorded as 34.05cm. Flag leaf length of RCM-9 was 27.91cm in which it has short flag leaf length than most of the varieties.

Flag leaf breadth

Flag leaf breadth was found to be widest in Korea Tsuk (2.29cm) followed by Ngoni, Kezie (SASRS-94) and Thangmo Red whereas it was found be narrowest in RCM-9 (1.38cm) followed by Sulijak, Rosho Lha and Ongpangsuk. The average mean of flag leaf breadth was 2.02cm.

Flag leaf area

The flag leaf area was found to highest in Kezie (SASRS-94) (76.04 cm^2) followed by Ngoni, Korea Tsuk and Apuapa (SARS-61) whereas it was lowest in Shyekenyii (26.04cm^2) followed by RCM-9, Yarba (SARS-3) and Rosho Lha. The average mean of flag leaf area was recorded as 52.59cm^2.

Genotypes such as Kezie Tsuk (SARS-94), Korea Tsuk and Apuapa (SARS-61) were found superior for flag leaf length, flag leaf breadth and flag area respectively. However, considering the flag leaf component characters together, Kezie (SASRS-94), Kedayishye, Ngoni and Apuapa (SARS-61) were identified as promising genotypes. The genotypes Korea Tsuk, Ngoni, Kezie (SASRS-94) and Thangmo Red also possessed desirable flag leaf characteristics. The top three leaves of rice, especially the flag leaf, are the primary source of carbohydrates production, hence they play a significant role in better grain yield of rice genotypes (Abrol *et al*., 1993; Foyer, 1987).

Table 4.2: ANOVA for qualitative and quantitative traits of rice

Source	df	GER	DF	DM	PH	FLL	FLB	FLA	NEBT	PPP	PL
Rep	2	139.12	385.33	0.84	17.03	2.41	0.00	11.34	0.02	0.00	0.57
Genotype	27	1777.73**	728.65 *	198.63**	777.04**	148.96**	0.14**	569.25**	1.82**	0.27**	17.63**
Residuals	54	180.86	392.07	0.19	8.88	2.25	0.00	5.12	0.05	0.04	0.70

Source	df	PW	SF	RL	RDW	SDW	HI	TN	CP	CHL A	CHLB
Rep	2	0.01	1.66	1.00	0.02	0.20	26.75	0.01	0.00	482.33	2744.30
Genotype	27	1.75**	192.38**	2.47**	0.63**	4.69**	147.70**	0.27**	0.21**	87.93**	99.21**
Residuals	54	0.03	41.94	0.12	0.02	0.06	5.26	0.00	0.01	11.58	10.47

Source	df	TCHL	AC	GN%	PNUE	NUtE	BY	NHI	HSW	GYPP
Rep	2	2145.67	17.34	0.01	0.14	0.03	379.22	9.14	1.26	0.00
Genotype	27	86.3**	10.08*	0.10**	1.44**	1.75**	413.02	91.22**	2.57 *	2.14**
Residuals	54	7.84	4.57	0.00	0.03	0.04	362.64	3.27	1.22	0.00

Signifcance at 1% level of probability-**, Signifcance at 5% level of probability-*

No. of ear bearing tillers

The number of ear bearing tillers was found to be highest in Longkhum Tsuk (SASRS-2) (15.72) and Sulijak (15.72) followed by Thupfu Lha, RCM-9 and Ongpangsuk whereas it was found to be lowest in Sungmangtsuk (SARS-1) (12.78) followed by Moya Chali, Thangmo Red, Kedayishye and Ngoni. The average mean of number of ear bearing tillers was 14.44.

The grain yield will increase as the more number of productive tillers rises (Shankar *et al*., 2021). Due to competition for nutrients during stem extension, there may be a low number of productive tillers (Ambavaram *et al*., 2014). According to IRRI's classification from 2013, Longkhum Tsuk (SARS-2), Sulijak, Thupfu Lha, RCM-9, and Ongpangsuk had moderate tillering ability (15 tillers per plant). According to Kusutani *et al.* (2000), rice genotypes with more panicle-bearing tillers had better grain yields. Both low and high NUE cultivars had comparable tillering abilities, according to Zhang *et al*. (2009); the latter, however, had a higher proportion of productive tillers.

Panicles per plant

Panicles per plant was found to be highest in Thupfu Lha (10.81) followed by Sulijak, Chahashye and Longkhum Tsuk (SASRS-2) whereas it was found to be lowest in Sungmangtsuk (SARS-1) (9.11) followed by Thangmo Red, Manen Red (SASRS-5), Ngoni and Kedayishye. The average mean of panicles per plant was recorded as 5.42 and RCM-9 has panicles per plant of 10.25 which shows that it has less panicle per plant as compared to Thupfu Lha, Sulijak, Chahashye, Longkhum Tsuk, and Tsushvuri.

According to Ambvaram *et al*. (2014), assimilates created during photosynthetic activity and carbohydrates transported from vegetative tissues to the grain during pre-anthesis are the two main sources of carbon used in the filling process of rice grains. Carbohydrates produced during photosynthesis may be to blame for the rise in the amount of grains that are filled (Zing and Zang, 2010).

Panicle length

Panicle length was found to be highest in Kezie (SASRS-94) (31.09cmm) followed by Tsungmiki, Taposen Youli and Moyatsuk whereas it was found to be lowest in RCM-9 (22.25c) followed by Thupfu Lha, Thangmo Red and Apuapa (SARS-61). The average mean of panicle length was recorded as 27.10cm.

One of the crucial yield features with a strong positive correlation to grain production is panicle length (Habib *et al*., 2007). Therefore, choosing genotypes with lengthy panicles is a crucial breeding strategy. The genotypes Moyatsuk, Tsungmiki, Taposen Youli, and Kezie (SASRS-94) exhibited long (30–31 cm) panicles, while the others had medium (22-25cm) panicles. Similar findings were found by Pachauri *et al*. (2017), where the average panicle length was 25.58 cm and the majority of the accessions fall within the range of 26–30 cm.

Panicle weight

Panicle weight was recorded to be highest in Moya Chali (5.02g) followed by Apuapa (SARS-61), Amusu and Kezie (SARS-94) whereas it was found to be lowest in Thangma white (2.45g) followed by Thangmo Red, Sungmangtsuk (SARS-1) and Taposen Youli. The average mean of panicle was recorded as 3.94g and RCM-9 has a panicle weight of 3.59g which shows it has lower panicle weight as compared to Moyal Chali, Apuapa (SARS-61), Amusu, Kezie (SARS-94), Tsushvuri, Chali, Ongpangsuk, Moyatsuk, Tsungmiki and Thupfu Lha.

Spikelet fertility

Spikelet fertility was observed to be highest in Thangma white (87.87%) followed by Tsushvuri, Yarba (SARS-3) and Kezie (SARS-94) whereas it was found to be lowest in Nogni (55.07%) followed by Korea Tsuk, Tsungmiki, Thangmo Red, Chali, and RCM-9. The average mean of spikelet fertility was recorded as 76.89%.

As a result, it was discovered that the genotype Thangma white is extremely fertile (more than 85%), while Tsushvuri, Yarba (SARS-3) and Kezie (SARS-94) have fertile spikelets (more than 80%), and all other genotypes fall into the partial fertile (50–74%) group. It is possible that incorrect grain filling and unbalanced nutrition are to blame for the partial sterility. Due to its significant impact on yield, spikelet fertility requires prior attention in rice development programmes (Hasan *et al*., 2011).

Root length

Root length was observed to be the longest in Amusu (29.97cm) followed by Taposen Youli, Ngoni and Thangma white, Thangmo Red, Sulijak and RCM-9 whereas it was found to be shortest in Manen Red (SARS-5) (26.20cm) followed by Sungmangtsuk (SARS-1), Thupfu Lha and Apuapa (SARS-61). The average mean of root length was recorded as 27.43cm.

Root dry weight

Root dry weight was found to be highest in Taposen Youli (7.96g) followed by Chahashye, Tsushvuri, Yarba (SARS-3) and Thangmo Red whereas it was found to lowest in RCM-9 (5.77g) followed by Pfukhi Lha, Shyekenyii and Sungmangtsuk. The average mean of root dry weight was recorded as 6.81g.

Root density and its distribution in the soil are the primary factors in rice plants' ability to absorb N, especially during the vegetative stage (Youngdahl *et al*., 1982). Rice grain yields and N uptake can both be impacted by root morpho-physiology (Fan, 2010). The Taposen Youli and Thangmo Red genotype has long roots and a lot of dry weight in the roots. Desirable root architecture characteristics were present in the genotypes Amusu, Ngoni, Thangma white, Thangmo Red, Sulijak, and RCM-9 as well. By improving water and N acquisition efficiency, these genotypes enhanced root systems may improve agronomic performance. A high yielding rice cultivar has greater root

physiological activity than a low yielding cultivar, according to Jiang *et al*. (1988).

Stem dry weight

Stem dry weight was observed to be highest in Thangmo red (17.14g) followed by Amusu, Thupfu Lha, Thangma White, Tsungmiki, Shyekenyii and RCM-9 whereas it was found to be lowest in Tungo (11.87g) followed by Sungmangtsuk, Apuapa (SARS-61) and Pfukhi Lha. The average mean of stem dry weight was recorded as 14.38g.

Harvest index

Harvest index is a measure of reproductive efficiency. It was recorded to be highest in Manen Red (SARS-5) (43.63%) followed by Thupfu Lha, Ngoni, Amusu, Pfukhi Lha, Moya Chali and RCM-9 whereas it was found to be lowest in Ongpangsuk (19.20%) followed by Sungmangtsuk (SARS -1), Thangmo Red and Sulijak. The average mean of harvest index was recorded as 30.36%.

The harvest index, a crucial trait of physiological significance, shows the effectiveness of a specific genotype's dry matter partitioning to the economic portion (Das *et al*., 2013). Among the genotypes, Manen (SARS-5) and Taposen Youli had the highest yielding capacities along with corresponding high harvest indices and biological yields, which suggested the presence of tall traditional cultivars with improved translocation efficiency. Six upland rice varieties showed a substantial variation, with a range of 31.7 to 33, according to Osundare *et al*. (2017). The harvest index% ranged from G44's lowest reading of 22.54% to G49's highest reading of 56.35%. 34 genotypes showed the maximum value higher than both Azemera (37%) and Pawe-1 (27.3%) (Demeke *et al*., 2023). Indirect selection of this feature is an option for increasing grain output, and harvest index is also crucial for variety breeding.

Total nitrogen

Total nitrogen was recorded to be highest in Ongpangsuk (2.55%) followed by Kedayishye, Moya Chali and Moyatsuk whereas it was found to be

lowest in Apuapa (SARS-61) (1.51%) followed by Thangma white, Sungmangtsuk (SARS-1), Tsushvuri and RCM-9. The average mean of total nitrogen was recorded as 2.12%.

Crude protein

According to Kawakatsu and Takaiwa (2019), rice has a protein level of roughly 7%. Juliano (2016) divided the crude protein content of rice into three categories: brown rice (7.1–8.3 g), milled rice (6.3–7.1 g), and rice bran (11.3–14.9 g). Crude protein was observed to be highest in Moyatsuk (6.54%) followed by Kedayishye, Moya Chali and Pfukhi Lha whereas it was found to be lowest in Yarba (SARS-3) (5.62%) followed by Rosho Lha, Shyekenyii and Taposen Youli, Tsungmiki, Tungo, Apuapa (SARS-61), Chahashye and RCM-9. The average mean of crude protein was found as 6.26%. Genotypes with high crude protein content could be employed for conventional breeding methods to increase protein content, as demonstrated by Demeke *et al*. (2023), who found that grain crude protein concentration ranged from 5.95% to 8.45% while their means were 7.07%.

Chlorophyll content

Increased photosynthetic rate is supported by leaf chlorophyll concentration in leaf blades and is influenced by different degrees of soil N status (Miah *et al*., 1997). Up to a particular threshold of soil N concentration, the amount of chlorophyll a, chlorophyll b, and total chlorophyll in leaves increased (Vijayalakshmi *et al*., 2015). All of the genotypes in the current investigation displayed significant genotypic variability for leaf chlorophyll concentration.

Cholorophyll a

Chlorophyll a was found to be highest in Pfukhi Lha (25.06 mg/g) followed by Manen red (SARS-5), RCM-9 and Thupfu Lha whereas it was found to be lowest in Kezie (SARS-94) (10.44 mg/g) followed by Shyekenyii,

Korea Tsuk and Chali. The average mean of chlorophyll a was recorded as 15.51 mg/g.

Chlorophyll b

Chlorophyll b was observed to be highest in Pfukhi Lha (36.08 mg/g) followed by Rosho Lha, Ngoni, Manen Red (SARS-5), Tungo, Thupfu Lha and RCM-9 whereas it was found to be lowest in Kezie (SARS-94) (19.38 mg/g) followed by Longkhum Tsuk (SARS-2), Yarba (SARS-3) and Thangma white. The average mean of chlorophyll b was recorded as 24.74 mg/g.

Total chlorophyll

Total chlorophyll was recorded to be highest in Pfukhi Lha (32.07 mg/g) followed by Rosho Lha, Ngoni and RCM-9 whereas it was lowest in Kezie (SARS-94) (17.17 mg/g) followed by Yarba (SARS-3), Longkhum Tsuk and Korea Tsuk. The average mean of total chlorophyll was recorded as 22.14 mg/g.

Pfukhi Lha, Rosho Lha, Ngoni, and RCM-9 had significantly higher chlorophyll contents than the other genotypes. These genotypes could be viewed as possible donors for the capacity to produce increased biomass and photosynthetic capacity if they retain higher leaf chlorophyll a and chlorophyll b levels during the growth phase (Hassan *et al*., 2009).

Amylose content

Amylose content was recorded to be highest in Taposen Youli (14.70%) followed by Korea Tsuk, Chahashye and Thangma white whereas it was lowest in Chishoghi (6.19%) and Kezie (SARS-64) (6.19%) followed by Manen Red (SARS-5), Amusu, Sulijak, Chali, Apuapa (SARS-61), Rosho Lha, Thupfu Lha, Sungmangtsuk (SARS-1) and RCM-9. The average mean of amylose content was recorded as 8.42.

Because of their greater amylose content, genotypes including Taposen Youli, Korea Tsuk, Chahashye, and Thangma white were recognised as desirable cultivars. This is crucial for grain filling, which mobilises during the

grain filling stage to become a significant source of nutrients for rice grain yield and has a strong link with grain yield (Wang *et al*., 2016). High amylose concentration is therefore viewed as a feature that could be advantageous for increasing rice yield.

Grain N%

Grain N% was recorded to be highest in Thangmo red (3.98) followed by Chahashye and Ngoni whereas it was lowest in Shyekenyii (3.17) followed by Ongpangsuk and Manen Red (SARS-5). The average mean of grain N% was recorded as 1.7.

The grain N content is a crucial measure of NUE and grain nutritional quality (Masclaux-Daubresse *et al*., 2010). Vijaylaskshmi *et al*., (2013) reported that grain N concentration is due to genetic control but can be managed by N supply.

Physiological Nitrogen Use Effiicency (PNUE)

PNUE was recorded to be highest in Taposen Youli (14.04) followed by Thangmo Red and Thangma White whereas it was lowest in case of Pfukhi Lha (10.98) followed by Sungmangtsuk (SARS-1) and Tungo. The average mean of PNUE was recorded as 12.44.

Among all the genotypes, 16 genotypes namely Kezie (SARS-94), Longkhum Tsuk (SARS-2), Tsushvuri, Chali, Chishoghi, Chahashye, Kedayishye, Shyekenyii, Amusu, Ongpangsuk, Sulijak, Moya Chali, Manen Red (SARS-5), Rosho Lha, Ngoni and Thupfu Lha are in par with average mean indicating the ability to utilise accumulated N for biomass production. The accumulation and redistribution of biomass and N in rice are thus connected, and PNUE is a crucial measure for measuring NUE in rice (De Datta, 1986; Peng *et al*., 2002).

Nitrogen Uptake Efficiency (NutE)

NUtE was recorded to be highest in Yarba (SARS-3) (9.90) followed by Amusu and Tsushvuri whereas it was lowest in Sulijak (6.95), Ngoni and Taposen Youli and the overall mean was 7.98.

Amusu and Tsushvuri were on par with Yarba (SARS-3) among all genotypes. Because N has a major impact on grain yield by influencing both the source and sink, both total N uptake and NutE considerably boosted grain yield (Zhu *et al*., 2016). Accordingly, rice genetic improvement is linked to high NUE, which increases the number of spikelets/sqm and grain yield (Ju *et al*., 2015).

Biological yield

Biological yield was recorded to be highest in Taposen Youli (83.25 g/plant) followed by Sungmangtsuk (SARS-1) and Tsungmiki whereas it was lowest in Chali (19.42 g/plant) followed by Chishoghi and Tsushvuri. The average mean was 25.63 g/plant.

According to Abebe *et al*. (2017), biomass ranged from 5.28 t/ha to 11.15 t/ha where variations in plant height, panicle length, or tiller count may be the cause of variations in biomass yield. The distribution of rainfall, solar radiation, temperature, and relative humidity all have a significant impact on the aforementioned features and also have a direct impact on biomass yield. According to research from many academics, including Abebe *et al*. (2019) and Fentie *et al*. (2021), biomass yield has a significant favourable impact on grain yield. So choosing genotypes with the best biomass yield could indirectly increase grain yield.

Nitrogen Harvest Index (NHI)

As a trait of the genotypes, variation in the NHI may be helpful for choosing rice genotypes with higher grain production (Fageria and Baligar, 2003). Ngoni (65.17) had the highest mean nitrogen harvest index, followed by Kedayishye, Sulijak, and Moyatsuk, while Yarba (SARS-3) had the lowest

mean nitrogen harvest index, followed by Rosho Lha, Shyekenyii, and Amusu. It was noted that the average mean was 52.32.

According to Fageria (2014), the NHI is a crucial statistic for determining how well absorbed N is transferred from vegetative plant parts to grain. This shows that Ngoni, Kedayishye, and Sulijak had relatively high retranslocation efficiency of absorbed N. According to Fageria and Baligar (2003), nitrogen partitioning in crop plants reveals how effectively the plant uses ingested nitrogen to produce grains. The existence of an extremely substantial link between NHI and grain yield (Fageria and Baligar, 1996) serves as additional confirmation of this. Therefore, NHI should be regarded as a crucial selection criterion in breeding to create genotypes that utilise N effectively and produce a significant amount of harvest.

100 grain weight

The measurement of seed size that has the most direct impact on grain yield is 100 grain weight. It was observed to be highest in Tsushvuri (7.55g), Apuapa (SARS-61), Moya Chali, and Tsungmiki, while Sungmangtsuk (SARS-1) (2.55g), Thangmo Red, Thagma White, Taposen Youli and RCM-9 had the lowest 100 grain weights. 100 grains had an average mean weight of 4.19g.

Nearly all genotypes have extremely low grain weight (less than 15g) and according to Habib *et al*. (2007) and Akhtar *et al*. (2011), there is a significant correlation between yield and thousand grain weights. For variety breeding, grain weight is also crucial, and indirect selection of this characteristic is a potential approach to increase grain production.

Grain yield per plant

It is a complicated trait that is affected in multiple ways, including the nature of genes, the environment, and the way that genotype and environment interact and the number of panicles (productive tillers), number of grains per panicle, and grain weight are its main determinants (Ambavaram *et al*., 2014).

Grain yield per plant was recorded to be highest in Tsushvuri (6.64g) followed by Amusu, Thupfu Lha and Yarba (SARS-3) whereas it was lowest in Taposen Youli (3.26g) followed by Sungmangtsuk (SARS-1), Thangma white, Sulijak, Longkhum Tsuk (SARS-2) and Thangmo Red. The average mean of grain yield per plant was recorded as 4.67g. RCM-9 has mean of 4.19g in which varieties it peformed better than varieties like Taposen Youli (3.26g), Sungmangtsuk (SARS-1) (3.56)g, Thangma white (3.72g), Sulijak (3.73g), Longkhum Tsuk (SARS-2) (3.83g), Thangmo Red (3.83g) and Korea Tsuk (4.18g).

From the result, some of the varieties like Tsushvuri, Amusu, Thupfu Lha, Yarba (SARS-3), Apuapa (SARS-61), Moya Chali, Tsungmiki, Taposen Youli, Rosho Lha, Ngoni, Manen red (SARS-5), Ongpangsuk, Kedayishye, Thangma white, Thangmo Red Kezie (SARS-64), Sulijak, Chahashye and Longkhum Tsuk (SASRS-2) performed better than the check variety RCM-9 for yield attributing traits like grain yield per plant, 100 grain weight, panicle length, panicle weight, number of ear bearing tillers, spikelet fertility, total nitrogen, crude protein, harvest index, chlorophyll a, chlorophyll b and total chlorophyll whereas for yield RCM-9 performed better than varieties like Taposen Youli, Sungmangtsuk (SARS-1), Thangma white, Sulijak, Longkhum Tsuk (SARS-2), Thangmo Red and Korea Tsuk (Table 4.4).

In case of NUE traits like grain N%, PNUE, NUtE, NHI, BY and amylose content, varieties like Taposen Youli, Korea Tsuk, Chahashye. Thangma white, Thangmo Red, Chahashye, Ngoni, Yarba (SARS-3), Amusu and Tsushvuri, Sungmangtsuk (SARS-1), Tsungmiki, Kedayishye, Sulijak and Moyatsuk performed better than the check variety RCM-9 whereas Chishoghi, Kezie (SARS-64), Chali, Apuapa (SARS-61), Rosho Lha, Thupfu Lha, Shyekenyii, Ongpangsuk, Manen Red (SARS-5) and Tungo performed lower than RCM-9 (Table 4.4).

Table 4.3: Mean performance of 28 upland rice genotypes

S.No	Genotype	GER (%)	DF50 (days)	DM (days)	PH (cm)	FLL (cm)	FLB (cm)	FLA (cm2)	NEBT	PPP	PL (cm)	PW (g)	SF (%)	RL (cm)	RDW (g)	SDW (g)	HI (%)	TN (%)	CP (%)	CHL A (mg/g)	CHLB (mg/g)	TCHL (mg/g)	AC (%)	GN (%)	PNUE (%)	NUtE	BY	NHI (%)	HSW (g)	GYPP (g)
1	Sungmangtsuk (SARS-1)	70.00	106.03	140.61	108.92	34.82	2.08	53.81	12.78	9.11	26.86	2.67	77.96	26.58	6.29	12.33	20.66	1.65	6.12	16.82	23.70	21.36	7.24	3.37	11.46	7.13	30.22	50.91	2.55	3.56
2	Apuapa (SARS-61)	26.67	109.13	142.33	112.79	43.61	2.13	69.97	13.78	9.72	23.66	4.99	76.96	26.76	6.96	12.47	27.77	1.51	6.09	12.59	21.04	18.65	6.97	3.33	11.94	8.20	20.52	53.57	4.67	5.42
3	Kezie (SASRS-94)	71.67	110.03	139.50	112.49	45.02	2.25	76.04	14.06	9.97	31.09	4.74	84.00	27.04	7.12	15.18	31.34	1.87	6.30	10.44	19.38	17.17	6.19	3.47	12.76	7.79	20.96	50.58	4.34	4.66
4	Korea Tsuk	96.67	110.14	139.72	113.71	42.97	2.29	73.97	14.39	10.03	28.27	3.16	61.25	25.92	6.43	13.97	25.50	2.35	6.41	11.04	19.96	17.78	10.74	3.47	11.75	7.59	22.42	50.58	3.87	4.18
5	Longkhum Tsuk (SASRS-2)	92.22	105.71	140.78	122.78	38.50	2.06	59.35	15.72	10.69	27.92	3.49	75.68	27.64	6.94	13.34	26.90	2.03	6.19	11.93	19.49	17.44	9.19	3.50	12.51	7.22	26.99	55.22	3.77	3.83
6	Yarba (SARS-3)	36.67	112.99	143.56	110.03	23.41	2.00	35.10	15.11	10.06	27.66	4.66	84.05	26.78	7.25	14.93	23.83	2.11	5.62	11.23	19.57	17.38	10.10	3.19	13.38	9.90	21.71	38.97	4.17	5.49
7	Tsushvuri	93.33	106.04	140.22	115.18	30.77	2.08	48.08	15.06	10.42	26.33	4.57	85.50	27.69	7.38	14.01	26.64	1.72	6.18	12.34	21.64	19.34	8.95	3.46	12.61	9.34	19.66	49.59	7.55	6.64
8	Chali	90.00	108.24	140.56	121.12	33.01	2.17	53.64	14.11	9.83	24.96	4.30	72.48	26.82	6.85	13.84	27.88	1.86	6.32	11.08	20.56	18.09	6.85	3.44	12.21	7.79	19.42	54.56	4.33	4.85
9	Chishoghi	73.33	107.69	138.89	126.76	34.78	2.18	56.71	13.78	9.72	25.13	3.33	78.44	26.81	6.90	14.01	25.45	2.43	6.24	13.21	23.26	20.63	6.19	3.31	12.43	7.71	19.56	49.25	3.58	4.21
10	Thangmo Red	66.67	106.39	142.50	134.03	39.09	2.21	64.67	13.67	9.17	23.26	2.66	66.17	28.37	7.25	17.14	20.78	2.19	6.43	11.86	20.57	18.21	8.78	3.98	13.79	7.36	20.30	52.57	2.77	3.83
11	Thangma White	90.00	110.28	138.94	125.67	25.51	2.02	38.59	14.78	10.00	24.73	2.45	87.87	28.59	6.98	16.09	28.38	1.59	6.29	11.53	20.10	17.85	10.34	3.77	13.57	8.19	22.57	55.56	2.83	3.72
12	Chahashye	31.11	110.83	139.22	139.84	36.00	2.08	56.16	15.11	10.72	26.77	3.59	78.81	27.14	7.51	13.66	26.79	1.93	6.10	12.84	22.61	20.05	10.53	3.94	12.84	8.53	22.45	49.92	4.32	4.48
13	Taposen Youli	76.11	103.86	140.22	122.04	28.61	1.72	36.57	15.06	10.42	30.39	3.05	77.51	28.86	7.96	14.63	24.17	2.12	5.99	12.93	22.38	19.87	14.70	3.69	14.04	7.02	33.25	48.59	3.16	3.26
14	Kedayishye	66.67	106.47	140.78	125.76	44.18	2.02	66.61	13.67	9.33	30.20	4.73	81.24	27.84	6.43	14.02	31.69	2.54	6.51	13.22	23.18	20.52	7.83	3.46	12.10	7.18	20.61	63.18	4.18	4.34
15	Shyekenyii	26.67	105.53	141.28	138.52	16.93	2.06	26.04	14.44	9.56	27.74	3.39	76.26	26.79	6.27	14.91	30.33	2.16	5.96	11.02	20.35	18.03	9.06	3.17	12.23	8.19	22.59	45.27	4.15	4.58
16	Amusu	100.00	99.36	141.28	148.84	41.32	2.03	62.72	14.06	9.58	26.76	4.87	83.46	29.97	6.40	16.54	40.76	1.94	6.26	12.11	21.37	18.88	6.80	3.40	12.64	9.70	28.65	48.26	4.62	6.30
17	Ongpangsuk	67.78	103.42	140.17	134.00	31.57	1.69	40.52	15.17	10.14	25.49	4.54	80.32	27.19	6.72	14.67	19.20	2.55	6.38	12.64	23.05	20.46	8.61	3.27	12.29	8.18	25.39	49.92	4.61	4.95
18	Moyatsuk	93.33	115.72	139.00	141.07	39.20	2.09	61.59	14.56	9.89	30.27	4.61	80.37	27.02	6.88	13.93	30.86	2.48	6.54	11.43	20.60	18.28	8.84	3.30	11.84	7.81	24.73	57.55	5.34	5.10
19	Sulijak	73.33	112.88	139.78	143.87	35.58	1.63	45.86	15.72	10.75	26.90	3.71	84.43	28.27	6.66	14.24	20.92	2.40	6.46	12.82	22.43	19.90	6.81	3.50	12.20	6.95	28.97	60.86	4.16	3.73
20	Moya Chali	90.00	98.58	140.11	139.33	36.61	2.18	59.83	13.39	9.25	26.96	5.02	81.25	27.41	6.81	14.64	38.42	2.52	6.44	11.67	20.69	18.36	8.06	3.82	12.40	8.32	23.48	56.88	4.65	5.57
21	Tsungmiki	76.67	100.07	139.89	146.95	26.77	2.08	41.62	14.06	9.58	30.61	4.13	64.47	26.83	7.04	15.76	32.14	2.06	6.02	22.55	30.72	27.31	10.08	3.55	13.02	8.71	29.23	49.92	4.64	5.07
22	Manen Red (SARS-5)	86.67	111.93	139.44	123.49	34.33	1.92	49.70	13.94	9.31	27.55	3.40	82.59	26.20	6.64	14.60	43.63	2.31	6.39	24.58	34.06	30.27	6.64	3.27	12.30	7.80	26.67	49.92	3.60	4.28
23	Pfukhi Lha	90.00	115.14	140.33	118.98	28.27	2.08	44.04	14.06	9.69	27.83	4.63	84.72	27.16	6.08	12.73	39.93	2.11	6.44	25.06	36.08	32.07	9.05	3.42	10.98	7.91	23.25	51.24	4.54	4.79
24	Rosho Lha	93.33	115.17	140.22	106.90	27.98	1.69	35.32	14.06	9.36	30.19	3.63	67.56	27.61	6.94	13.65	32.73	2.47	5.90	22.68	35.65	31.66	7.07	3.44	12.29	8.05	20.78	44.61	4.16	4.47
25	Tungo	28.89	106.49	139.94	139.37	28.83	2.17	46.31	15.00	9.83	27.40	4.00	70.50	27.33	6.91	11.87	34.42	2.26	6.08	23.11	32.86	29.17	8.00	3.63	11.69	8.03	24.30	52.24	4.55	4.63
26	Ngoni	27.78	108.03	147.83	101.65	43.68	2.26	74.83	13.67	9.33	28.69	3.73	55.07	28.85	6.97	14.54	40.95	2.25	6.81	23.58	34.13	31.23	7.55	3.92	12.72	6.98	21.13	65.17	3.87	4.24
27	Thupfu Lha	66.67	133.98	166.11	100.14	34.20	1.96	59.25	15.61	10.81	23.02	4.66	81.04	26.59	6.45	16.19	41.81	1.99	6.39	23.97	32.13	29.22	7.15	3.75	12.72	8.45	21.71	57.21	4.64	6.28
28	RCM-9	90.00	150.13	180.06	82.03	27.91	1.38	32.38	15.50	10.25	22.25	3.59	72.99	27.97	5.77	14.85	36.11	1.83	6.10	24.09	31.08	30.75	7.37	3.53	11.74	7.44	26.14	52.90	3.74	4.19
	Grand Mean	71.17	112.45	142.97	123.44	34.05	2.02	52.59	14.44	5.42	27.10	3.94	76.89	27.43	6.81	14.38	30.36	2.12	6.26	15.51	24.74	22.14	8.42	1.75	12.44	7.98	25.63	52.32	4.19	4.67
	Sem	7.76	11.43	0.28	1.72	0.87	0.02	1.31	0.13	0.12	0.48	0.10	3.74	0.20	0.08	0.14	1.32	0.03	0.06	1.96	1.87	1.62	1.23	0.04	0.10	0.11	10.99	1.04	0.64	0.03
	CD (5%)	22.01	32.41	0.75	4.88	2.45	0.07	3.71	0.38	0.33	1.37	0.28	10.60	0.56	0.24	0.39	3.75	0.08	0.17	5.57	5.30	4.58	3.50	0.10	0.28	0.31	31.17	2.96	1.81	0.09
	CD (1%)	29.32	43.17	1.20	6.50	3.27	0.09	4.93	0.51	0.44	1.82	0.38	14.12	0.74	0.31	0.52	5.00	0.11	0.23	7.42	7.05	6.11	4.66	0.13	0.37	0.41	41.51	3.94	2.41	0.11
	Environmental Variance	180.86	392.07	0.25	8.88	2.25	0.00	5.12	0.05	0.04	0.70	0.03	41.94	0.12	0.02	0.06	5.26	0.00	0.01	11.58	10.47	7.84	4.57	3.45	1.38	0.04	74.30	3.27	1.22	0.00

Table 4.4: Comparison of mean performance with check variety RCM-9

Character	Highest	Lowest	Performance of check variety RCM-9	Remarks Better performance over check
Germination percentage (%)	Amusu (100%)	Shyekenyii and Apuapa (SARS-61) (26.67)	90%	Amusu
Days to 50% flowering (days)	RCM-9 (150.13)	Amusu (99.36)	150.13	Amusu
Days to maturity (days)	RCM-9 (180.06)	Chishoghi (138.89)	180.06	Chishoghi
Plant height (cm)	Amusu (148.84)	RCM-9 (82.03)	82.03	-
Flag leaf length (cm)	Kezie (SARS-94) (45.02)	Shyekenyii (16.93)	27.91	-
Flag leaf breadth (cm)	Korea Tsuk (2.29)	RCM-9 (1.38)	1.38	-
Flag leaf area (cm^2)	Kezie (SARS-94) (76.04)	Shyekenyii (26.04)	32.38	Kezie (SARS-94)
No. of ear bearing tillers	Longkhum Tsuk (SASRS-2) and Sulijak (15.72)	Sungmangtsuk (SARS-1) (12.78)	15.50	At par
Panicles per plant	Thupfu Lha (10.81)	Sungmangtsuk (SARS-1) (9.11)	10.25	At par
Panicle Length (cm)	Kezie (SASRS-94) (31.09)	RCM-9 (22.25)	22.25	Kezie (SASRS-94)
Panicle weight (g)	Moya Chali (5.02)	Thangma White (2.45)	3.59	Moya Chali
Spikelet fertility (%)	Thangma White (87.87)	Ngoni (55.07)	72.99	Thangma White
Root length (cm)	Amusu (29.97)	Manen Red (SARS-5) (26.20)	27.97	Amusu
Root dry weight (g)	Taposen Youli (7.96)	RCM-9 (5.77)	5.77	Taposen Youli

Stem dry weight (g)	Thangmo Red (17.14)	Tungo (11.87)	14.85	Thangmo Red
Harvest Index (%)	Manen Red (SARS-5) (43.63)	Ongpangsuk (19.20)	36.11	Manen Red
Total Nitrogen (%)	Ongpangsuk (2.55)	Apuapa (SARS-61) (1.51)	1.83	Ongpangsuk
Crude Protein (%)	Moyatsuk (6.54)	Yarba (SARS-3) (5.62)	6.10	Moyatsuk
Chlorophyll a (mg/g)	Pfukhi Lha (25.06)	Kezie (SASRS-94) (10.44)	24.09	Pfukhi Lha
Chlorophyll b (mg/g)	Pfukhi Lha (36.08)	Kezie (SASRS-94) (19.38)	31.08	Pfukhi Lha
Total chlorophyll (mg/g)	Pfukhi Lha (32.07)	Kezie (SASRS-94) (17.17)	30.75	Pfukhi Lha
Amylose content (%)	Taposen Youli (14.70)	Chishoghi (6.19)	7.37	Taposen Youli
Grain N%	Thangmo Red (3.98)	Shyekenyii (3.17)	3.53	Thangmo Red
PNUE	Taposen Youli (14.04)	Pfukhi Lha (10.98)	11.74	Taposen Youli
NUtE	Yarba (SARS-3) (9.90)	Sulijak (6.95)	7.44	Yarba (SARS-3)
Biological yield (g/plant)	Sungmangtsuk (SARS-1) (30.22)	Chali (19.42)	26.14	Sungmangtsuk (SARS-1)
NHI (%)	Ngoni (65.17)	Yarba (SARS-3) (38.97)	52.90	Ngoni
100 grain weight (g)	Tsushvuri (7.55)	Sungmangtsuk (SARS-1) (2.55)	3.74	Tsushvuri
Grain yield per plant (g)	Tsushvuri (6.64)	Taposen Youli (3.26)	4.19	Tsushvuri

4.4 Coefficient of variation

It was found that the phenotypic coefficient of variation had greater values than the genotypic coefficient of variation, indicating that the environment had an impact on the performance of the genotype (Table 4.6 and

Table 4.7). Days to maturity, flag leaf length, breadth, area, number of ear bearing tillers, total nitrogen, crude protein, 100 grain weight and grain yield per plant had minor differences between genotypic and phenotypic characters that suggested less environmental influence on the expression of these traits. The genotypic and phenotypic coefficient of variation showed that there were not many significant differences for the number of ear-bearing tillers and grain yield per plant, indicating that genetic factors primarily determined the expression of these traits. As a result, any selection pressure applied to these characters may help to realise improvement in the early generations. However, there were significant differences in case of grain weight, panicle length, panicle weight, spikelet fertility, amylose content, grain N%, PNUE and NUtE.

The chlorphyll a (6.71), germination percentage (5.1), chlorophyll b (3.59), spikelet fertility (3.27) and total chlorophyll (3.23) showed the largest differences between genotypic and phenotypic coefficient of variation, while the days to maturity (0.01) showed the least differences. For the majority of these features, numerous researchers reported similar findings (Dhurai *et al*., 2014; Rashmi *et al.*, 2017; Harsha *et al*., 2017) Low GCV and PCV were also noted in days to maturity, number of ear-bearing tillers, panicles per plant, panicle length, root length, root dry weight, stem dry weight, crude protein, and PNUE, indicating that these characteristics were less variable.

As indicated by Shivasubramanian and Menon (1973) for GCV and PCV; Robinson *et al*. (1949) for heritability; and Johnson *et al*. (1955) for GA, the estimates of genetic parameters were divided into low, moderate, and high categories as follows.

	GCV(%)	**PCV(%)**	**h^2_{bs} (%)**	**GA% of mean**
High	>20	>20	>60	>20
Moderate	10-20	10-20	30-60	10-20
Low	<10	<10	<30	<10

The genotypic coefficient of variation was observed to be highest for chlorophyll a (32.52) followed by germination percentage, flag leaf area, total chlorophyll, harvest index, chlorophyll b and flag leaf length. Characters like biological yield, 100 grain weight and grain yield per plant showed moderate genotypic coefficient of variation along with plant height, flag leaf breadth, grain N%, panicle weight (19.22), total nitrogen (14.09) and amylose content (24.70). Remaining characters like days to 50% flowering, days to maturity, number of ear bearing tillers, panicles per plant, panicle length, spikelet fertility, NutE, root length, root dry weight, stem dry weight and crude protein were showing low genotypic coefficient of variation and root length was showing lowest values for genotypic coefficient of variation (Table 4.3).

Similarly, phenotypic coefficient of variation was observed to be highest for chlorophyll a (39.23) and lowest for root length (3.46) as shown in the Table 4.7. Characters showing high phenotypic coefficient of variation were germination percentage, amylose content, harvest index, flag leaf area, chlorophyll b, total chlorophyll and flag leaf length. Characters showing moderate coefficient of variation were panicle weight, grain yield per plant, total nitrogen, plant height, spikelet fertility, grain N%, biological yield, 100 grain weight and flag leaf breadth whereas characters showing low phenotypic coefficient of variation were days to 50% flowering, NUtE, panicle length, stem dry weight, root dry weight, panicles per plant, days to maturity, PNUE, number of ear bearing tillers, crude protein and root length. Moderate GCV and PCV for grain yield per plant had earlier been reported by Rahman *et al*. (2012).

The genetic variability that is present in distinct quantitative traits can be compared using the GCV. Chlorophyll a, germination %, flag leaf area, and harvest index also had high magnitudes of GCV and PCV estimates, which indicated that there was a lot of variation across the 28 genotypes for these traits. Low GCV and PCV values were found for panicle length and crude

protein content, indicating that a greater degree of genetic variation was needed for these traits to be used as selection criteria for yield improvement (Srivastava *et al*., 2017). These variations must then be created through techniques like mutation and recombination, followed by selection. Similar results have been reported by Tadesse Girma *et al*. (2018), Sandeep *et al*. (2018), Hasan *et al*. (2019) for maturity and panicle length and Demeke *et al*. (2023) for crude protein and panicle length.

Plant height, spikelet fertility, grain N%, and flag leaf breadth showed moderate GCV and PCV. These showed that the genotypes had enough genetic diversity to allow for improvement through selection. Ayenew *et al*. (2019) and Demeke *et al*. (2023) also reported on plant height among 36 and 70 upland rice varieties, respectively, in agreement with this finding.

Chlorophyll a, germination rate, harvest index, and flag leaf length were having high GCV and PCV and high GCV and PCV values indicated that the genotypes in this study had a wide genetic base and high variability, enabling effective genetic improvement through selection based on phenotypic expression of these traits. On the other hand, according to a study conducted by Demeke *et al*. (2023), the harvest index also has a moderate GCV and a high PCV.

4.5 Heritability in broad sense and genetic advance (% mean)

The estimate of heritability can be used for genetic gain and its predictive role can be used to show the dependability of the phenotypic value as a reference to breeding value (Lipi *et al*., 2020). Heritability is a good indicator of character transfer from parents to offspring. The broad sense heritability for this study ranged from low to high for all studied quantitative characteristics i.e., from 54% for spikelet fertility to 99.76% for 100 grain weight, suggesting that the genotypic differences mostly determined the manifestation of the phenotype with little influence from environmental factors. As a result, mass selection and progeny testing have a good chance of changing

how these traits present themselves. Mulugeta Bitew *et al*. (2016) also reported for days to maturity, thousand grain weight, and protein content, which supports this conclusion. Similarly, Roy and Shil (2020) reported on panicle length and plant height, and Prasad *et al*. (2017) reported on grain yield.

Low environmental influences on trait expression are indicated by high heritability, which enables breeders to pick a genotype with confidence based on phenotypic performance. The estimation of heritability is crucial in plant breeding because of this and nearly all of the studied traits were found to have strong heritability, as seen in the Table 4.7. Heritability was high for many important characters associated with NUE for yield and yield attributes like grain yield per plant, 100 grain weight, biological yield, days to 50% flowering, total nitrogen, PNUE, NUtE, number of ear bearing tillers, grain N%, NHI which consist of >90% heritlability. Remaining characters having high heritability were panicle length, panicle weight, crude protein, amylose content and panicles per plant. High heritability for grain yield per plant was also reported by Nithya *et al*. (2020) and Akshay *et al*. (2022). Similarly, heritability was high for other characters like days to maturity, plant height, flag leaf area, flag leaf length, flag leaf breadth, stem dry weight, root dry weight, harvest index, root length, total chlorophyll, germination percentage, chlorophyll b and chlorophyll a indicating usefulness of phenotypic selection for these traits. Moderate heritability was found only in spikelet fertility.

A useful indicator of improvements that might be made as a result of selecting a suitable population is genetic advance (Islam *et al*., 2015). The traits investigated in this study included those with high genetic progress at 5% selection intensity expressed as a percentage of the mean (Table 4.7). High GAM results revealed the potential for exploiting this feature for genetic improvement through selection and the maximal control of characters through additive gene action. In this study, high GAM was recorded for germination percentage (57.69%) followed by chlorophyll a, flag leaf area, harvest index,

total chlorophyll, flag leaf length, chlorophyll b, panicle weight, amylose content, biological yield, 100 grain weight, grain yield per plant, total nitrogen, plant height, flag leaf breadth, NHI and grain N%. Ajmera *et al*. (2017) and Abebe *et al*. (2017) reported similar result for the above-mentioned traits.

Similarly, characters showing moderate genetic advance as percent of mean were NUtE, PNUE, days to 50% flowering, stem dry weight, panicle length, spikelet fertility, root dry weight, days to maturity and number of ear bearing tillers. Moderate GAM suggested that both additive and non-additive genes had a moderate influence on these characteristics. For panicle length, similar results were reported by Prasad *et al*. (2017), Roy and Shil (2020), and Demeki *et al*. (2023). Panicles per plant, crude protein, and root length were traits with poor genetic advance as a percentage of mean.

In determining the efficacy of selection for a given trait, heritability coupled with GA is more informative than heritability alone (Johnson *et al*., 1955). Understanding the type of gene action involved in the expression of different polygenic traits is made easier with the use of GA estimation. Days to maturity, number of ear-bearing tillers, panicle length, root dry weight, stem dry weight, amylose content, biological yield, 100 grain weight and NHI all showed high heritability and high to moderate genetic advance as a percent of mean, indicating that genetic factors significantly influenced the expressivity of these traits and had little to no influence from the environment. Multi-environment selection methods would be appropriate for bringing about the necessary improvement in these characters, according to the moderate environmental influence on these characters.

Germination percentage, plant height, flag leaf length, breadth, and area, panicle weight, harvest index, total nitrogen, chlorophyll a, chlorophyll b, and total chlorophyll, NHI, and grain yield per plant all showed high heritability along with high genetic advance as a percentage of mean, demonstrating the role of additive gene effect and indicating that improvement in these characters

would be possible through direct selection. PNUE and NUtE also exhibit high heritability and low genetic advance for NUE yield and yield-attributing traits such as panicle length, which also suggests preponderance of non-additive gene action on the expression of the character.

The presence of both additive and non-additive gene action on the development of these traits is indicated by low heritability in combination with moderate GA for spikelet fertility. In terms of panicles per plant, root length, and crude protein, high heritability and low GA were found, indicating that non-additive gene action predominates in the expression of the traits and that direct selection is not conceivable due to environmental factors.

4.6 Average mean of 29 quantitative characters in each environment

From the Table 4.5 it was shown that among NUE yield and yield attributing traits the average performance of each trait varies in each enivronment. The characters viz., panicle length, spikelet fertility, harvest index and grain yield per plant environment had higher values in E_3 as compared to other two environments. In case of E_2, amylose content, grain N%, PNUE, biological yield and NHI had maximum values and in E_1 environment, grain N%, NUtE and 100 grain weight had maximum values.

Table 4.5: Comparison of average mean of 29 quantitative characters in each environment

ENV	GER	DF	DM	PH	FLL	FLB	FLA	NEBT	PPP	PL
1	71.19	110.22	137.92	120.33	33.72	2.02	52.62	14.52	26.68	26.68
2	71.07	117.21	137.73	125.00	34.69	2.01	53.01	14.09	5.37	27.13
3	71.25	109.92	137.74	124.99	33.74	2.03	52.13	14.71	5.67	27.64

ENV	PW	SF	RL	RDW	SDW	HI	TN	CP	CHL A	CHLB
1	4.09	76.96	27.02	6.47	14.31	29.82	2.35	5.82	15.50	24.59
2	4.02	76.37	27.68	7.02	14.61	30.25	2.31	6.03	15.99	24.91
3	3.71	77.35	27.58	6.96	14.23	31.00	2.15	6.92	16.57	24.71

ENV	TCHL	AC	GN%	PNUE	NUtE	BY	NHI	HSW	GYPP
1	22.15	8.43	1.82	12.58	8.32	25.61	51.28	4.45	4.61
2	22.22	8.47	1.82	13.36	7.67	25.68	54.34	2.54	4.67
3	22.05	8.35	1.72	11.39	7.96	25.61	51.35	4.06	4.71

GER-Germinatin percentage
DF-Days to flowering
DM-Days to maturity
PH-Plant height
FLL-Flag leaf length
FLB-Flag leaf breadth
FLA-Flag leaf area
NEBT-No. of ear bearing tillers
PPP-Panicles per plant
PL-Panicle length
PW-Panicle weight
SF-Spikelet fertility
RL-Root length
RDW-Root dry weight
SDW-Stem dry weight
HI-Harvest Index
TN-Total Nitrogen
CP-Crude protein
CHL A-Chlorophyll a
CHL B-Chlorophyll b
TCHL-Total chlorophyll
AC-Amylose content
GN%-Grain nitrogen%
PNUE-Physiological nitrogen use efficiency
NutE-Nitrogen uptake efficiency
BY-Biological Yield
NHI-Nitrogen Harvest Idex
HSW-100 grain weight
GYPP-Grain yield per plant

Table 4.6: Comparison of GCV, PCV, h^2_{bs} and GAM among 29 quantitative traits studied

Character	GCV	PCV	h^2_{bs}	GAM	Remarks
Germination percentage	High	High	High	High	High h^2_{bs} and High GAM
Days to 50% flowering	Low	Low	High	Moderate	High h^2_{bs} and moderate GAM
Days to maturity	Low	Low	High	Moderate	High h^2_{bs} and moderate GAM
Plant height	Moderate	Moderate	High	High	High h^2_{bs} and High GAM
Flag leaf length	High	High	High	High	High h^2_{bs} and High GAM
Flag leaf breadth	Moderate	Moderate	High	High	High h^2_{bs} and High GAM
Flag leaf area	High	High	High	High	High h^2_{bs} and High GAM
No. of ear bearing tillers	Low	Low	High	Moderate	High h^2_{bs} and moderate GAM
Panicles per plant	Low	Low	High	Low	High h^2_{bs} and low GAM
Panicle Length	Low	Low	High	Moderate	High h^2_{bs} and moderate GAM
Panicle weight	Moderate	Moderate	High	High	High h^2_{bs} and High GAM
Spikelet fertility	Low	Moderate	Moderate	Moderate	Moderate h^2_{bs} and Moderate GAM
Root length	Low	Low	High	Low	Nil
Root dry weight	Low	Low	High	Moderate	High h^2_{bs} and moderate GAM
Stem dry weight	Low	Low	High	Moderate	High h^2_{bs} and moderate GAM
Harvest Index	High	High	High	High	High h^2_{bs} and High GAM
Total Nitrogen	Moderate	Moderate	High	High	High h^2_{bs} and High GAM
Crude Protein	Low	Low	High	Low	Nil
Chlorophyll a	High	High	High	High	High h^2_{bs} and High GAM
Chlorophyll b	High	High	High	High	High h^2_{bs} and High GAM
Total chlorophyll	High	High	High	High	High h^2_{bs} and High GAM
Amylose content	High	High	High	High	High h^2_{bs} and High GAM
Grain N%	Moderate	Moderate	High	High	High h^2_{bs} and High GAM
PNUE	Moderate	Low	High	Moderate	High h^2_{bs} and moderate GAM
NUtE	Moderate	Low	High	Moderate	High h^2_{bs} and moderate GAM
Biological yield	Moderate	Moderate	high	High	High h^2_{bs} and High GAM
NHI	High	Moderate	High	High	High h^2_{bs} and High GAM
100 grain weight	Moderate	Moderate	High	High	High h^2_{bs} and High GAM
Grain yield per plant	Moderate	Moderate	High	High	High h^2_{bs} and High GAM

Table 4.7: Estimation of GCV, PCV, heritability and genetic advance at 5% of mean for 29 characters in 28 rice genotypes

S.No	Character	Range	GCV	PCV	Heritability (bs) %	Genetic advance as % of mean
1	GER	10 - 100	32.42	37.52	74.64	57.69
2	DF50	96 - 93	9.42	9.37	95.73	18.47
3	DM	133.83 - 137.76	5.90	5.91	98.00	12.14
4	PH	80.07 - 151.75	12.96	13.19	97.00	26.25
5	FLL	15.98 - 48.42	20.54	21.00	96.00	41.37
6	FLB	1.35 - 2.32	10.53	10.75	96.00	21.24
7	FLA	25.23 - 77.99	26.08	26.43	97.00	53.00
8	NEBT	12.50 - 16	5.31	5.55	92.00	10.46
9	PPP	4.33 - 6.17	5.08	6.31	65.00	8.43
10	PL	21.6 - 31.7	8.77	9.29	89.00	17.03
11	PW	2.36 - 5.12	19.22	19.72	95.00	38.59
12	SF	41.82 - 92.42	9.21	12.48	54.00	14.00
13	RL	25.53 - 30.27	3.23	3.46	87.00	6.21
14	RDW	5.73 - 8.12	6.60	6.93	91.00	12.96
15	SDW	11.77 - 17.31	8.64	8.79	96.00	17.48
16	HI	16.95 - 44.07	22.70	23.92	90.00	44.37
17	TN	1.46 - 2.61	14.09	14.29	97.00	28.61
18	CP	5.52 - 7.31	4.02	4.35	85.00	7.64
19	CHL A	4.76 - 26.1	32.52	39.23	69.00	55.54
20	CHLB	7.98 - 43.38	21.99	25.58	74.00	38.92
21	TCHL	7.19 - 38.50	23.10	26.33	77.00	41.73
22	AC	5.36 - 20.79	24.70	26.43	87.33	47.55
23	GN%	1.28 - 2.25	10.35	10.91	90.00	20.21
24	PNUE	10.80 - 14.19	5.51	5.68	94.00	11.01
25	NUtE	6.86 - 10.24	13.49	13.71	96.91	27.37
26	BY	19.17 - 199.65	13.49	13.71	96.91	6.93
27	NHI	38.31 - 67.16	10.35	10.91	90.00	20.22
28	HSW	2.54 - 14.31	15.94	15.96	99.76	32.81
29	GYPP	3.255 - 6.6433	18.09	18.12	98.00	37.19

4.7 Correlation studies

The main goal of any breeding is to increase productivity. The most significant characteristic that results from the multiplicative impacts of numerous component traits is grain yield. Grain yield is an interaction phenotype—a harmonic understanding, mutual adjustment, and presentation of its component characters—rather than a gene per se. Since yield generally has low heritability, hence, direct selection of yield is unlikely to be successful. When creating a breeding strategy to boost yield, knowledge of the intensity and direction of the relationships between the grain yield and the component traits as well as between those relationships will be very helpful.

Table 4.9 and 4.10 shows the genotypic and phenotypic connections between grain yield and yield attributing characters. For the majority of the traits under investigation, phenotypic correlation coefficients were larger than their corresponding genotypic correlation coefficients (Ajdah *et al*., 2020).

4.8 Association of yield with its attributing characters

From the Table 4.9 and 4.10, at genotypic level grain yield per plant showed significant positive correlation with panicle weight (0.7966), harvest index (0.3811), NUtE (0.8055) and 100 grain weight (0.69). Grain yield per plant also showed negative significant correlation with biological yield (-0.9469).

Similarly, at phenotypic level grain yield per pant showed significant positive correlation with panicle weight (0.7729), spikelet fertility (0.2218), harvest index (0.3524), NUtE (0.7837) and 100 grain weight (0.5693). Negative significant correlation with grain yield was also found with biological yield (-0.2163).

4.9 Association amongst yield attributing characters

Association among yield attributing characters has been shown in Table 4.9 and 4.10 and discussed as shown below.

Germination percentage

Germination percentage has no positive and negative significant correlation with yield attributing characters at genotypic level but at phenotypic level it has significant positive association with total nitrogen (0.3476) and crude protein (0.2369).

Days to 50% flowering

At genotypic level, days to 50% flowering has positive significant association with days to maturity (0.7445), number of ear bearing tillers (0.446), toal nitrogen (0.7431) and crude protein (0.5136) whereas it has negative significant association with plant height (-0.42), flag leaf breadth (-0.443), root dry weight (-0.4034), physiological nitrogen use efficiency (-0.4483) and biological yield (-0.467). In case of phenotypic level, it has only significant positive association with days to maturity (0.3532).

Days to maturity

At genotypic level, days to maturity has positive significant association with chlorophyll a (0.4983), chlorophyll b (0.3759) and total chlorophyll (0.463) and negative significant association with plant height (-0.6467), flag leaf breadth (-0.4601), panicle length (-0.532) and root dry weight (-0.4496). At phenotypic level, it has significant positive association with plant height (0.6467), number of ear bearing tillers (0.3306), stem dry weight (0.2452), harvest index (0.3374), chlorophyll a (0.41), chlorophyll b (0.3211) and total chlorophyll (0.4051) but it has negative significant association with plant height (-0.6359), flag leaf breadth (-0.45) panicle length (-0.5031) and root dry weight (-0.4267).

Plant height

Plant height has negative significant association with chlorophyll a (-0.4055) and total chlorophyll (-0.3972) at genotypic level. At phenotypic level, it has significant positive association with flag leaf breadth (0.2181), panicle length (0.2369), root dry weight (0.2156) and total nitrogen (0.2301) and also showed negative significant association with chlorophyll a (-0.3129), chlorophyll b (-0.2762) and total chlorophyll (-0.3334).

Flag leaf length

At genotypic level, flag leaf length has positive significant association with flag leaf breadth (0.4027), flag leaf area (0.9491), crude protein (0.6314), grain nitrogen % (0.5599) and NHI (0.5599) but it has negative significant association with amylose content (-0.4625) and biological yield (-0.5076). Whereas at phenotypic level, it has positive significant association with flag leaf breadth (0.3777), flag leaf area (0.9456), panicles per plant (0.2429), panicle weight (0.2206), total nitrogen (0.2542), crude protein (0.5827), grain N% (0.5263) and nitrogen harvest index (0.5263) but it has negative significant association with no. of ear bearing tillers (-0.3022), amylose content (-0.2379) and NUtE (-0.2992).

Flag leaf breadth

Flag leaf breadth has positive significant association with flag leaf area (0.6426) but it has negative significant association with number of ear bearing tillers (-0.5171) and biological yield (-0.3825) at genotypic level. In case of phenotypic level, It has positive significant association with flag leaf area (0.6278) and crude protein (0.253) but has negative significant association with number of ear bearing tillers (-0.4866), root length (-0.2498), chlorophyll a (-0.2241), chlorophyll b (-0.2227) and total chlorophyll (-0.2698).

Flag leaf area

At genotypic level, flag leaf area has positive significant association with crude protein (0.6246), grain nitrogen % (0.5179) and NHI (0.5179) but it has negative significant association with number of ear bearing tillers (-0.4012), amylose content (-0.4339) and biological yield (-0.8215). Similarly, at phenotypic level it has positive significant association with panicles per plant (0.2925), panicle weight (0.218), total nitrogen (0.2752), crude protein (0.5751), grain N% (0.4905) and NHI (0.4905) but it has negative significant association with number of ear bearing tillers (-0.3729) and amylose content (-0.2214).

Number of ear bearing tillers

At genotypic level, number of ear bearing tillers have only positive significant association with panicles per plant (0.4243), amylose content (0.4209) and biological yield (0.5376). Similarly, at phenotypic level it has also significant positive association with panicles per plant (0.324) and spikelet fertility (0.2146).

Panicles per plant

Panicles per plant has positive significant association with root dry weight (0.4524) and 100 grain weight (0.4006) at genotypic level whereas at phenotypic level, it has positive significant association with root dry weight (0.3441), grain N% (0.2249), PNUE (0.2326) and NHI (0.2249).

Panicle length

At genotypic level, panicle length has positive significant association with amylose content (0.394) and biological yield (0.8015). Similarly at phenotypic level, it has positive significant association with root dry weight (0.2644).

Panicle weight

At genotypic level, panicle weight has positive significant association with NutE (0.4955), 100 grain weight (0.991) and grain yield per plant (0.7966) but it has negative significant association with amylose content (-0.4179) and biological yield (-0.7307). Whereas at phenotypic level, it has positive significant association with spikelet fertility (0.2602), harvest index (0.3338), NUtE (0.4659), 100 grain weight (0.5008) and grain yield per plant (0.7729) and negative significant association with PNUE (-0.2373).

Spikelet fertility

At genotypic level, spikelet fertility has positive significant association with NutE (0.3849) but negative significant association with chlorophyll a (-0.3982), chlorophyll b (-0.3904) and total chlorophyll (-0.3986). Whereas at phenotypic level, it has positive significant association with NUtE (0.2796) and

grain yield per plant (0.2218) but has negative significant association with total chlorophyll (-0.2198).

Root length

Root length has positive significant association with stem dry weight (0.391) and physiological nitrogen use efficiency (0.4354) at genotypic level whereas it has positive significant association with stem dry weight (0.3711), grain N% (0.2268), PNUE (0.3824) and NHI (0.2268) at phenotypic level.

Root dry weight

At genotypic level, root dry weight has positive significant association with amylose content (0.6773) and physiological nitrogen use efficiency (0.7244) whereas it has negative significant association with harvest index (-0.3846), chlorophyll a (-0.3909). In case of phenotypic level, it has positive significant association with amylose content (0.3406), PNUE (0.7271) and biological yield (0.2547) but it has negative significant with harvest index (-0.3489), chlorophyll a (-0.292), chlorophyll b (-0.2579) and total chlorophyll (-0.2976).

Stem dry weight

Stem dry weight has positive significant association with any PNUE (0.6862) at genotypic level but in case of phenotypic level, it has positive significant association with total nitrogen (0.2759), PNUE (0.6651) and NUtE (0.2587).

Harvest index

At genotypic level, harvest index has positive significant association with chlorophyll a (0.6766), chlorophyll b (0.6662), total chlorophyll (0.6635) and grain yield per plant (0.3811) whereas it has negative significant association with amylose content (-0.4685) and biological yield (-0.4492). At phenotypic level, it has positive significant association with chlorophyll a (0.5559), chlorophyll b (0.5606), total chlorophyll (0.5688) and grain yield per plant (0.3524) but negative significant aasociation with PNUE (-0.2182).

Total nitrogen

At genotypic level, it has positive significant association with crude protein (0.6325) and 100 grain weight (0.45) and negative significant association with biological yield (-0.4563). In case of phenotypic level, it has positive significant association with crude protein (0.6579).

Crude protein

It has positive significant association with grain N% (0.7936) and NHI (0.7936) but negative significant association with NUtE (-0.4333) and biological yield (-0.648) at genotypic level. Similarly, at phenotypic level it has positive significant association with grain N% (0.7373) and nitrogen harvest index (0.7373) and negative significant association with NUtE (-0.4105).

Chlorophyll a

It has positive significant association with chlorophyll b (0.99, 0.9607) and total chlorophyll (0.9947, 0.9723) at both genotypic and phenotypic level. It has also negative significant association with PNUE (-0.2616) at phenotypic level.

Chlorophyll b

It has positive significant association with total chlorophyll (0.9977, 0.9886) at both genotypic and phenotypic level. But it has negative significant association with PNUE (-0.2713) at phenotypic level.

Total chlorophyll

It has no significant association with any traits studied at genotypic level but it has negative significant association with PNUE (-0.2823) at phenotypic level.

Amylose content

It has positive significant association with PNUE (0.635) at genotypic level. Similarly, it has positive significant association with PNUE (0.3371) in case of phenotypic level.

Grain N%

It has positive significant association with biological yield (0.9921, 0.9982) at both genotypic and phenotypic level but also negative significant association with NUtE (-0.5628, -0.5697.) at both genotypic and phenotypic level and negative significant association with biological yield (-0.3854) at genotypic level.

PNUE

It has no significant association at genotypic level but positive significant association with biological yield (0.2372) at phenotypic level.

NUtE

It has positive significant association with 100 grain weight (0.7353, 0.3912) and grain yield per plant (0.8055, 0.7837) at genotypic and phenotypic level but it has also negative significant association with biological yield (-0.7309) and nitrogen harvest index (-0.5697) at genotypic level and negative significant association with NHI (-0.567) at phenotypic level.

Biological yield

It has negative significant association with 100 grain weight (-0.9469) at genotypic level while it has negative significant association with grain yield per plant (-0.2163) at phenotypic level.

NHI

It has no significant association with the traits studied at genotypic and phenotypic level.

100 grain weight

It has positive significant association with grain yield per plant (0.69, 0.5693) at genotypic and phenotypic level.

The correlation analysis revealed that grain yield has moderate to strong positive correlation with panicle weight (0.7966), harvest index (0.3811), NUtE (0.8055) and 100 grain weight (0.69) at genotypic level whereas grain yield has low to strong positive correlation with panicle weight (0.7729), spikelet fertility (0.2218), harvest index (0.3524), NUtE (0.7837) and 100 grain

weight (0.5693) at phenotypic level. Significant association of grain yield with NUtE (Fageria *et al*., 2010 and Samont *et al*., 2006), 100 grain weight (Padmaja *et al*., 2011 and Shrestha *et al*. 2018), harvest index (Singh *et al*., 2018) were found from earlier studies. Similar result for NUtE was found by Ashan *et al*. (2014); Ifltekharuddaula *et al*. (2002); Madhavilatha *et al*. (2005); Abarshahr *et al*. (2011). Further it was also supported by Wattoo *et al*. (2010) and Zahid *et al*. (2014). While this conclusion was found contrary to that of Minnie *et al*. (2013), who observed a negative connection with 1000 grain weight.

From the correlation, it can be inferred that the traits that are economically valuable to enhance the production of rice per hectare are those that are positively correlated with one another and with grain yield. Thus, it can be concluded that grain yield increases anytime there is an increase in features that are positively correlated (Minnie *et al*., 2013), whereas negative correlation between traits and grain yield also plays a significant role in improving yield per hectare of rice cultivation. The negative correlation indicates that an increase in one will lead to a decrease in another, hence it might be crucial in breeding selection.

Flag leaf is more significant in cereals like rice because it offers the greatest assimilation of photosynthates for storage in the grains. By increasing the amount of photosynthesis produced, which is then transported or translocated into grains, a larger flag leaf area will eventually contribute to an increase in photosynthetic efficiency. This will improve grain weight and ultimately yield. As a result, flag leaf area and grain yield are directly related (Riaz and Chowdhry, 2003). Cook and Evans (1983), who claimed that flag leaf is the most significant site of photosynthesis for feeding carbon to grains, provided more evidence in support of this. While some research (Ashan *et al*., 2014) showed a negative connection with flag leaf area.

Days to 50% flowering and days to maturity had a high genotypic correlation but a moderate phenotypic correlation. Days to maturity also

showed moderate to strong genotypic and phenotypic correlations with chlorophyll a, chlorophyll b, and total chlorophyll. Days to 50% flowering also showed a negative, non-significant correlation to grain yield. Additionally, a negative non-significant connection between this feature and plant height was attained. Positive and highly significant correlation was seen between plant height and panicle length. Both Singh *et al*. 2018 and Kishore et al. 2007 produced results with comparable patterns. This suggests that a longer panicle can retain more grains than a panicle that is very short. Breeders should therefore use panicle length as a selection factor in addition to other features if the goal is to increase yield. The findings of rice researchers, including Rathod *et al*. (2016), Akinwale *et al*. (2011), and Bekele *et al*. (2013), are in agreement with this one.

There was a negative association between plant height and grain yield, demonstrating that growing plants do not always result in more rice being produced. Days to maturity had also a negative, non-significant connection with grain yield. This result concurs with Jeke *et al*. (2021) because there is a genetic capability for an early maturing genotype to produce better yield than a late maturing crop and vice versa, grain production is not mostly dependent on growth time. According to Li *et al*. (2019), selection of genotypes for advancement cannot focus solely on days to maturity as a direct feature for selection.

Amylose content having high genotypic and phenotypic association with PNUE and biological yield demonstrated a source-sink relationship in which stem reserves may act as a source of grain filling. The substantial interrelationships between chlorophyll features at both levels and their negative significant phenotypic associations with PNUE suggest that high chlorophyll content throughout the growth period greatly increased photosynthetic capability, which in turn increased physiological NUE. Leaf chlorophyll concentration in leaf blades supports higher photosynthesis rates.

At both genotypic and phenotypic levels, spikelet fertility (%), harvest index, and 100 grain weight were all positively correlated with grain yield per plant. A similar correlation between spikelet fertility and single plant yield was found by Borkakati *et al*. (2005) and was both positive and significant. According to Padmaja *et al*. (2011), 100 grain weight showed a favourable and substantial correlation with single plant production. Previous studies, including those on harvest index and spikelet fertility (Sravan *et al*., 2012; Singh *et al*., 2018) and on both harvest index and 100 grain weight. Patel *et al*. (2014) supported the found positive connection of grain production with a wide range of traits. For upland rice, these traits could be used as selection criteria to increase grain yield. According to Padmaja *et al*. (2011) investigation, the single plant yield exhibited a significant positive correlation with 100-seed weight, productive tillers per plant, spikelet fertility, total tillers per plant, grains per panicle and panicle length.

Both genotypically and phenotypically, there is a positive association between crude protein and grain N%. Grain protein variations assessed from multi-environment experiments have been proposed as a feasible breeding target since they appear to be rather resilient across multiple environments and would be helpful in boosting total N intake by maturity, according to Bogard *et al*. (2010).

Additionally, it was discovered that the component characters were related to one another. At both the genotypic and phenotypic levels, there was a moderatlysignificant positive relationship between the characteristics grain N, NUtE, and NHI. The genetic and phenotypic relationships between yield-related traits such panicle length, spikelet fertility, 100 grain weight, and biological yield were low to moderate. The yield-contributing characters like biological yield, 100 grain weight, and grain yield per plant were significantly positively correlated with NUE-related traits, PNUE and NUtE at both the genotypic and phenotypic levels. Furthermore, moderate to strong magnitudes of correlations suggested that the genotypes with improved yields may be the

result of their effective uptake and utilization of the available N from the soil. Therefore, improving rice production with high NUE could be achieved through indirect selection for traits with moderate to high heritability. Both at the genotypic and phenotypic levels, there were substantial and moderately positive associations between panicle weight, NUtE, panicles per plant, and total nitrogen. A rise in dry matter production and nitrogen uptake throughout the lengthy vegetative stage may have contributed to the genotypes ability to fill their grains, as indicated by the positive correlation between panicles per plant and root dry weight, grain N%, PNUE, NHI, and 100 grain weight.

One of the main goals of the present study is to identify high yielding N use efficient genotypes. To meet these goals, it is important to select plant features that are both related with high grain yield and high NUE. These strong associations could be used by plant breeders to choose high yielding genotypes that use nitrogen more effectively and yield grains with higher protein content.

4.10 Path coefficient analysis

Although correlation coefficients measure the relationship between two characters, they do not provide the unofficial grounds for their association. In order to identify the crucial traits for improvement, a plant breeder must have knowledge of the direct and indirect effects of each component on the grain production. In this study, path coefficient analysis was only conducted for the characters that had a moderate to strong positive correlation with grain yield at both the phenotypic and genotypic levels. Wright (1921) developed this method as a biometric tool for understanding the direct and indirect effects of the component characters on grain yield. The direct and indirect effects were classified on scale given by Lenka and Misha (1973) (Table 4.8) respectively.

Table 4.8: The scale of direct and indirect effects values and their rate of scale according to Lenka and Mishra (1973)

Values of direct and indirect effects	Rate of scale
0.00-0.09	Negligible
0.10-0.19	Low
0.20-0.29	Moderate
0.30-0.99	High
More than 1.00	Very high

Table 4.9: Genotypic correlation coefficients among all the characters in 28 rice genotypes

	GER	DF50	DM	PH	FLL	FLB	FLA	NEBT	PPP	PL	PW	SF	RL	RDW	SDW
GER	1**	0.3437	-0.0062	-0.0162	0.0899	-0.2263	-0.0119	0.01	-0.0271	0.0772	-0.0364	0.2602	0.1321	-0.2196	0.2149
DF50		1**	0.7445**	-0.42*	0.0166	-0.443*	-0.0588	0.446*	-0.0769	-0.1842	0.1582	0.1075	-0.1993	-0.4034*	-0.0498
DM			1**	-0.6467**	-0.0986	-0.4601*	-0.1184	0.3468	-0.0377	-0.532**	0.0553	-0.1306	0.0535	-0.4496*	0.2515
PH				1**	-0.0251	0.2256	-0.0281	-0.0389	-0.0403	0.2537	0.0762	0.1877	0.1597	0.2272	0.1262
FLL					1**	0.4027*	0.9491**	-0.3324	0.2778	0.0787	0.2364	-0.1556	0.1026	0.0315	-0.0463
FLB						1**	0.6426**	-0.5171**	0.1996	0.1655	0.1029	-0.2395	-0.2514	0.2036	-0.0854
FLA							1**	-0.4012*	0.3295	0.0595	0.2309	-0.2327	-0.0219	0.054	-0.0162
NEBT								1**	0.4243*	-0.1914	0.0062	0.2392	0.0805	0.1238	0.0763
PPP									1**	0.0838	0.1511	0.2421	0.125	0.4524*	-0.02
PL										1**	0.1183	-0.1339	-0.0137	0.2656	-0.1875
PW											1**	0.3374	-0.0814	-0.0978	-0.0792
SF												1**	0.0127	-0.0215	0.0397
RL													1**	0.1872	0.391*
RDW														1**	0.332
SDW															1**
HI															
TN															
CP															
CHL A															
CHLB															
TCHL															
AC															
GN%															
PNUE															
NUtE															
BY															
NHI															
HSW															
GYPP															

Signifcance at 1% level of probability-**, Signifcance at 5% level of probability-*

Table 4.9: Genotypic correlation coefficients among all the characters in 28 rice genotypes (*contd*….)

	HI	TN	CP	CHL A	CHLB	TCHL	AC	GN%	PNUE	NUtE	BY	NHI	HSW	GYPP
GER	0.1091	0.4344*	0.2875	-0.0151	-0.0298	-0.0157	0.0015	0.0294	-0.0876	-0.0407	0.2938	0.0294	0.0907	0.0291
DF50	0.3581	0.7431**	0.5136**	0.2638	0.1968	0.2711	-0.1626	0.2464	-0.4483*	-0.1589	-0.467*	0.2464	0.2676	0.0935
DM	0.3577	-0.177	-0.0327	0.4983**	0.3759*	0.463*	-0.2494	0.1639	-0.0797	-0.0474	-0.16	0.1639	-0.0524	0.1468
PH	-0.1594	0.3004	0.1424	-0.4055*	-0.3352	-0.3972*	0.2003	-0.0013	0.1379	0.1875	0.1517	-0.0013	0.1739	0.0565
FLL	0.0736	0.292	0.6314**	-0.2345	-0.2268	-0.2256	-0.4625*	0.5599**	-0.1128	-0.3062	-0.5076**	0.5599**	0.0156	0.0192
FLB	0.0689	0.2695	0.2847	-0.2901	-0.2789	-0.3243	-0.0877	0.1109	-0.0018	0.1148	-0.3825 *	0.1109	0.1052	0.1791
FLA	0.1284	0.3338	0.6246**	-0.2336	-0.2353	-0.2422	-0.4339*	0.5179**	-0.0851	-0.2154	-0.8215**	0.5179**	0.0339	0.1003
NEBT	-0.146	-0.1332	-0.2339	-0.0217	-0.0479	-0.0156	0.4209*	-0.0802	0.1737	0.1419	0.5376**	-0.0802	0.3337	0.065
PPP	-0.0689	0.0267	0.125	-0.3025	-0.3012	-0.2885	0.3717	0.2787	0.2794	0.0305	0.2657	0.2787	0.4006*	0.1323
PL	0.0843	0.1979	0.0262	-0.0273	0.0579	0.0063	0.394*	-0.0756	0.0081	-0.0946	0.8015**	-0.0756	0.1601	-0.1524
PW	0.3678	0.0933	0.1165	-0.0242	0.0067	-0.0055	-0.4179*	0.0771	-0.2668	0.4955**	-0.7307**	0.0771	0.991**	0.7966**
SF	-0.0483	-0.1582	-0.1301	-0.3982*	-0.3904*	-0.3986*	-0.0892	-0.1486	0.0119	0.3849*	0.0805	-0.1486	0.2741	0.3018
RL	0.0948	-0.0192	0.146	-0.0935	-0.0475	-0.0323	0.1688	0.2681	0.4354*	-0.0403	0.1407	0.2681	-0.1218	-0.0841
RDW	-0.3846*	0.1057	-0.1809	-0.3909*	-0.324	-0.3614	0.6773**	-0.188	0.7244**	0.1392	-0.2938	-0.188	0.1194	-0.0511
SDW	0.1338	0.3105	0.1254	-0.1451	-0.1726	-0.1529	0.1371	-0.0401	0.6862**	0.2596	0.1176	-0.0401	-0.2046	0.157
HI	1**	0.1699	0.2844	0.6766**	0.6662**	0.6635**	-0.4685*	0.228	-0.2306	0.1625	-0.4492*	0.228	0.2655	0.3811*
TN		1**	0.6325**	-0.0188	0.0479	0.0249	0.047	0.1409	0.031	-0.0299	-0.4563*	0.1409	0.45*	0.1438
CP			1**	0.0505	0.0863	0.0795	-0.3118	0.7936**	-0.192	-0.4333*	-0.648**	0.7936**	0.1722	-0.0285
CHL A				1**	0.99**	0.9947**	-0.3674	0.1085	-0.3433	-0.1444	-0.096	0.1085	-0.0667	-0.1218
CHLB					1**	0.9977**	-0.3578	0.0907	-0.3381	-0.1357	-0.14	0.0907	-0.0046	0.004
TCHL						1**	-0.3594	0.108	-0.3412	-0.1534	-0.1294	0.108	-0.0185	-0.0062
AC							1**	-0.3341	0.635**	0.0506	0.0557	-0.3341	-0.2986	-0.328
GN%								1**	-0.1766	-0.5628**	-0.3854*	0.9921**	0.0691	-0.158
PNUE									1**	0.1937	-0.1696	-0.1766	-0.3163	-0.0823
NUtE										1**	-0.7309**	-0.5628**	0.7353**	0.8055**
BY											1**	-0.3854*	-0.9469**	-0.1995
NHI												1**	0.069	-0.158
HSW													1**	0.69**
GYPP														1**

Signifcance at 1% level of probability-**, Signifcance at 5% level of probability-*

Table 4.10: Phenotypic correlation coefficients among all the characters in 28 rice genotypes

	GER	DF50	DM	PH	FLL	FLB	FLA	NEBT	PPP	PL	PW	SF	RL	RDW	SDW
GER	1**	0.0632	-0.0105	-0.0179	0.0796	-0.1698	-0.0028	-0.0054	-0.029	0.0369	-0.0274	0.1308	0.1124	-0.1839	0.1737
DF50		1**	0.3532**	-0.2037	-0.0063	-0.1909	-0.0258	0.1923	-0.0587	-0.0456	0.0618	0.051	-0.1069	-0.1843	0.0379
DM			1**	-0.6359**	-0.0963	-0.45**	-0.1168	0.3306**	-0.0343	-0.5031**	0.056	-0.1052	0.0463	-0.4267**	0.2452*
PH				1**	-0.0233	0.2181*	-0.0263	-0.0337	-0.0248	0.2369*	0.0694	0.1568	0.1517	0.2156*	0.1219
FLL					1**	0.3777**	0.9456**	-0.3022**	0.2429*	0.0815	0.2206*	-0.1408	0.0994	0.0338	-0.0444
FLB						1**	0.6278**	-0.4866**	0.2033	0.1511	0.0989	-0.1639	-0.2498*	0.1979	-0.0811
FLA							1**	-0.3729**	0.2925**	0.0614	0.218*	-0.1883	-0.016	0.0544	-0.0133
NEBT								1**	0.324**	-0.1644	0.0191	0.2146*	0.094	0.1051	0.0806
PPP									1**	0.1045	0.087	0.1703	0.0505	0.3441**	0.00
PL										1**	0.1131	-0.0693	-0.0018	0.2644*	-0.1504
PW											1**	0.2602*	-0.077	-0.0705	-0.0778
SF												1**	0.0494	-0.0414	0.0316
RL													1**	0.1453	0.3711**
RDW														1**	0.0782
SDW															1**
HI															
TN															
CP															
CHL A															
CHLB															
TCHL															
AC															
GN%															
PNUE															
NUtE															
BY															
NHI															
HSW															
GYPP															

Signifcance at 1% level of probability-**, Signifcance at 5% level of probability-*

Table 4.10: Phenotypic correlation coefficients among all the characters in 28 rice genotypes (*contd…*)

	HI	TN	CP	CHL A	CHLB	TCHL	AC	GN%	PNUE	NUtE	BY	NHI	HSW	GYPP
GER	0.0969	0.3476**	0.2369*	-0.0583	-0.0435	-0.0447	-0.048	0.0289	-0.0926	-0.0455	0.0585	0.0289	0.0633	0.0262
DF50	0.0463	0.0161	0.1012	0.1588	0.1291	0.1625	-0.0647	0.1478	-0.1292	-0.0742	-0.0295	0.1478	0.0753	0.0638
DM	0.3374**	-0.1461	-0.0311	0.41**	0.3211**	0.4051**	-0.1338	0.1579	-0.0764	-0.0473	-0.0297	0.1579	-0.0328	0.1461
PH	-0.1335	0.2301*	0.1275	-0.3129**	-0.2762*	-0.3334**	0.1097	-0.011	0.1361	0.1868	0.0519	-0.011	0.0808	0.0523
FLL	0.0563	0.2542*	0.5827**	-0.1685	-0.1683	-0.1737	-0.2379*	0.5263**	-0.1059	-0.2992**	-0.0945	0.5263**	0.0028	0.0157
FLB	0.0625	0.2003	0.253*	-0.2241*	-0.2227*	-0.2698*	-0.0307	0.1087	0.0062	0.1066	-0.2082	0.1087	0.0781	0.1762
FLA	0.1087	0.2752*	0.5751**	-0.1713	-0.1811	-0.1928	-0.2214*	0.4905**	-0.0776	-0.2131	-0.1624	0.4905**	0.0261	0.0965
NEBT	-0.1456	-0.0755	-0.1859	-0.0166	-0.0472	-0.0189	0.2107	-0.048	0.1576	0.1239	0.1005	-0.048	0.161	0.0608
PPP	-0.035	0.005	0.091	-0.1646	-0.1359	-0.1765	0.1667	0.2249*	0.2326*	0.0217	0.1465	0.2249*	0.1632	0.1036
PL	0.0549	0.1851	0.0559	-0.0158	0.05	0.0065	0.1714	-0.0392	0.0294	-0.091	0.1851	-0.0392	0.0604	-0.139
PW	0.3338**	0.0609	0.0997	-0.0287	0.0051	-0.009	-0.2127	0.0826	-0.2373*	0.4659**	-0.1602	0.0826	0.5008**	0.7729**
SF	-0.0163	-0.115	-0.1052	-0.1888	-0.2079	-0.2198*	-0.0545	-0.1186	-0.0037	0.2796*	0.0341	-0.1186	0.1857	0.2218*
RL	0.072	0.0176	0.1382	-0.0686	-0.0549	-0.0347	0.0901	0.2268*	0.3824**	-0.0252	0.1562	0.2268*	-0.0688	-0.0799
RDW	-0.3489**	0.0887	-0.1391	-0.292**	-0.2579*	-0.2976**	0.3406**	-0.1372	0.7271**	0.1121	0.2547*	-0.1372	0.0802	-0.0468
SDW	0.0893	0.2759*	0.1355	-0.1299	-0.1573	-0.1418	0.0438	-0.0347	0.6651**	0.2587*	0.0115	-0.0347	-0.0886	0.1587
HI	1**	0.06	0.2048	0.5559**	0.5606**	0.5688**	-0.1836	0.1931	-0.2182*	0.1477	-0.0963	0.1931	0.1121	0.3524**
TN		1**	0.6579**	-0.053	-0.0156	-0.0239	-0.0736	0.0904	-0.0331	-0.0072	-0.0555	0.0903	0.1656	0.1264
CP			1**	-0.0048	0.0193	0.0191	-0.209	0.7373**	-0.1899	-0.4105**	-0.0996	0.7373**	0.0336	-0.0207
CHL A				1**	0.9607**	0.9723**	-0.0871	0.0746	-0.2616*	-0.0837	-0.0199	0.0746	-0.0281	0.00
CHLB					1**	0.9886**	-0.0997	0.0628	-0.2713*	-0.0851	-0.0243	0.0628	0.0034	0.0033
TCHL						1**	-0.1097	0.0765	-0.2823**	-0.1021	-0.0271	0.0765	-0.0079	-0.0054
AC							1**	-0.1732	0.3371**	0.0245	-0.1144	-0.1732	0.0042	-0.183
GN%								1**	-0.1363	-0.5697**	-0.065	0.9982**	-0.0407	-0.1504
PNUE									1**	0.1745	0.2372*	-0.1363	-0.128	-0.0803
NUtE										1**	-0.154	-0.5697**	0.3912**	0.7837**
BY											1**	-0.065	-0.1335	-0.2163*
NHI												1**	-0.0407	-0.1504
HSW													1**	0.5693**
GYPP														1**

Signifcance at 1% level of probability-**, Signifcance at 5% level of probability-*

Table 4.12: Direct (diagonal) and indirect effects of 10 characters on grain yield per plant at genotypic level

	PL	HI	AC	GN%	PNUE	NUtE	BY	NHI	HSW
PL	-0.09935	0.00552	-0.01566	-0.01877	-0.00052	-0.07376	-0.01507	0.00267	0.0625
HI	-0.00742	0.07391	0.01804	0.05562	0.0147	0.12391	-0.00173	-0.0081	0.10419
AC	-0.02833	-0.02427	-0.05492	-0.05961	-0.03396	-0.02118	-0.0057	0.00874	-0.07481
GN%	0.00751	0.01655	0.01318	0.24836	0.01133	-0.439	0.00017	-0.03623	0.02007
PNUE	-0.0008	-0.01694	-0.02908	-0.04387	-0.06414	0.1511	0.01733	0.00637	-0.10222
NUtE	0.00939	0.01174	0.00149	-0.13978	-0.01243	0.78	0.00948	0.02037	0.12523
BY	-0.01465	0.00125	-0.00306	-0.00041	0.01088	-0.07234	-0.10218	0.0001	-0.01904
NHI	0.00734	0.01653	0.01326	0.24862	0.01129	-0.43906	0.00028	-0.03619	0.02003
HSW	-0.02138	0.02652	0.01415	0.01716	0.02258	0.33639	0.0067	-0.0025	0.29038
Residual value		**0.1204**							

Table 4.11: Direct (diagonal) and indirect effects of 10 characters on grain yield per plant at genotypic level

	PL	HI	AC	GN%	PNUE	NUtE	BY	NHI	HSW
PL	-0.10272	0.00569	-0.01176	-0.0065	-0.00134	-0.06875	-0.01417	-0.0024	0.06305
HI	-0.00737	0.07927	0.01483	0.0329	0.01013	0.11644	-0.00142	0.01143	0.1108
AC	-0.02423	-0.02357	-0.04985	-0.03675	-0.02195	-0.02188	-0.00592	-0.01258	-0.07457
GN%	0.00405	0.01581	0.0111	0.16681	0.00612	-0.42985	0.00049	0.05694	0.02024
PNUE	-0.003	-0.01747	-0.0238	-0.02198	-0.04596	0.13146	0.01588	-0.00784	-0.10759
NUtE	0.00936	0.01223	0.00145	-0.09399	-0.00801	0.75413	0.00882	-0.03248	0.13221
BY	-0.01463	0.00113	-0.00297	-0.00081	0.00734	-0.06686	-0.09951	-0.00014	-0.02055
NHI	0.00432	0.01588	0.01099	0.16468	0.00631	-0.4297	0.00025	0.05705	0.01961
HSW	-0.02057	0.0279	0.01181	0.01061	0.01571	0.31695	0.0065	0.00355	0.31493
Residual value		**0.1451**							

Ten characteristics, including panicle length, harvest index, amylose content, grain N%, PNUE, NUtE, BY, NHI, 100 grain weight, grain yield per plant, and (R) residual factor, were included in the path diagram for coefficient analysis. In this study, panicle length, harvest index, amylose content, grain N%, PNUE, NutE, biological yield, 100 grain weight, and grain yield per plant were considered independent or causal variables, but grain yield was considered a resulting "dependent" variable. table 4.11 and 4.12 provides further explained the path coefficient results and discussions:

4.10.1 Path coefficient analysis at genotypic level

Direct and indirect effect of the component characters on grain yield at phenotypic level are presented in Table 4.12. The path coefficients revealed that in path coefficient analysis for the genotypic characters NUtE had the most positive direct influence (0.78) on grain yield out of all the characters, followed by Grain N% (0.24836) and 100 grain weight (0.29038), each of which also had highly favourable indirect effects via the other. Although biological yield showed the highest negative direct effect (-0.10218) on grain yield followed by panicle length, amylose content, PNUE and NHI, its indirect effect via PNUE (0.01733) was low and via NUtE (0.00948) was low. Similarly, high indirect effects via nitrogen harvest index resulted in significant positive yield correlation of NUtE which resulted in significant yield correlations. Low positive and negative indirect effects via harvest index and biological yield respectively resulted in negative yield correlation of NHI which registered high direct effect on grain yield. Regardless of the direct effects, most characters show minimal to modestly beneficial indirect effects as measured by biological yield, grain N%, 100 grain weight, and NUtE. As a result, the observed yield correlations of biological yield, grain N%, 100 grain weight, and NUtE were consistent with their low to high direct effects on grain yield, indicating that selection for these traits was successful in achieving the desired yield

enhancement in rainfed upland rice. The residual effect, which was 0.1204, was acceptable.

4.10.2 Path coefficient analysis at phenotypic level

Similarly, Table 4.11 revealed that NutE had the most positive influence on grain yield (0.75413) followed by 100 grain weight, Grain N% and harvest index. Characters like Biological yield (0.16681) had high negative direct influence followed by panicle length, amylose content and PNUE. The effect of residual factor (0.145) on grain yield per plant was negligible, thereby, suggested that no other major yield contributing component is left over.

High positive direct effects of NUtE and 100 grain weight on grain yield were found by path coefficient analysis at genotypic and phenotypic levels. Previous studies also noted the strong positive direct impacts of grain N% and NutE on grain production (Mundim *et al*. 2013). These qualities were shown to have high heritability estimates. Therefore, in order to boost rice grain yield genetically, these two features should receive priority attention. In the rice yield development programme, panicle length, harvest index, PNUE, and NHI may also be taken into consideration as selection indices due to their high heredity.

From a physiological perspective, it is interesting to note that the nitrogen utilization is less pronounced under high N than under low N level. As the nitrogen from soil is not limiting under high N, it can be absorbed at any time and in greater quantities, so the need for remobilization of the nitrogen absorbed is less pronounced. On the other hand, as the nitrogen from soil is limiting under low N, it cannot be absorbed at all and must be mobilised. Because of this, the findings of the route analysis and the heritability estimates indicate that direct selection is still the most effective way to improve the selection efficiency for NUE under each individual situation of N availability.

4.11 Diversity analysis (Mahalanobis D^2 statistics)

With the knowledge that genetic variability is the basis for crop improvement, determining the extent and degree of germplasm diversity and genetic relationships among breeding materials is a crucial aid in crop improvement strategies (Abebaw, 2020). Genetic variability gives plant breeders the chance to develop new and improved cultivars with desirable characteristics, and it is the key to reliable and sustainable production of the food crops through breeding. In order to effectively evaluate and use germplasms to investigate their variability and discover desirable agronomic features, quantifying the diversity of crops that are now available is crucial.

In plant breeding, there is a continuous process of identifying diverse parents with high genetic variability for combining desirable characteristics, and similarly, the success of any programme to improve rice depends on the use of various germplasm from around the world. The implementation of any breeding programme aimed at crop improvement with examining the variability available in their germplasm for identification of desirable agronomic traits requires understanding of good genetic diversity.

4.11.1 Cluster constellation

Mahalanobis D^2 statistics (1936) was used in this study to access the genetic diversity of a group of 28 upland rice varieties. As seen in Table 4.13 and Fig 4.1, the 28 genotypes are divided into five clusters with varying numbers of entries, indicating the presence of a wide range of genetic variation both within and between the clusters. Ushakumari and Rangaswamy (1997), Nayak *et al*. (2004), and Krishnamurthy *et al.* (2015) all reported findings of a similar nature.

Among all the clusters, Cluster 5 being the largest having maximum number of genotypes consisting of 12 genotypes namely, Thangmo Red, Ongpangsuk, Sulijak, Thangma White, Longkhum Tsuk (SASRS−2), Chahashye, Apuapa (SARS−61), Kezie (SASRS−94), Sungmangtsuk

(SARS−1), Korea Tsuk, Chali and Chishoghi while Cluster 2 consist of 9 genotypes like Moyatsuk, Kedayishye, Moya Chali, Ngoni, Pfukhi Lha, Tungo, Tsungmik,i Manen Red (SARS−5) and Rosho Lha. There are 2 and 4 genotypes in Clusters 1 and 4, respectively, including Thupfu Lha and RCM-9, Yarba (SARS-3), Shyekenyii, Tsushvuri, and Amusu. The sole genotype in the remaining cluster 3 is Taposen Youli.

Genotypes which has high mean for NUE yield and yield attributes were under all the four clusters i.e., Cluster 2 consists of Ngoni and Manen Red (SARS-5) which had high values of NHI and harvest index, Cluster 3 consist of Taposen Youli (high value for amylose content, PNUE and biological yield), Cluster 4 consist of Yarba (SARS-3) and Tsushvuri (high value for NUtE, 100 grain weight and grain yield per plant), Cluster 5 consists of Thangmo Red, Thagma white, Kezie (SARS-94) and Sungmangtsuk (SARS-1) (high values for GN%, spikelet fertility, panicle length and biological yield) whereas check variety RCM-9 falls under Cluster 1 which have high values for days to 50% flowering and days to maturity.

Table 4.13: Grouping of genotypes into different clusters

Cluster	No. of genotypes	Name of genotypes
Cluster 1	2	Thupfu Lha and RCM-9
Cluster 2	9	Moyatsuk, Kedayishye, Moya Chali, Ngoni, Pfukhi Lha, Tungo, Tsungmik,i Manen Red (SARS−5) and Rosho Lha
Cluster 3	1	Taposen Youli
Cluster 4	4	Yarba (SARS−3), Shyekenyii, Tsushvuri and Amusu
Cluster 5	12	Thangmo Red, Ongpangsuk, Sulijak, Thangma White, Longkhum Tsuk (SASRS−2), Chahashye, Apuapa (SARS−61), Kezie (SASRS−94), Sungmangtsuk (SARS−1), Korea Tsuk, Chali and Chishoghi

4.11.2 Inter and intra cluster distances

The inter-cluster differences in the current study ranged from 6.48 to 10.00, indicating a significant level of genetic variation among the genotypes associated with various clusters as shown in the Table 4.14. The genotypes in clusters 2 (9.12) and 4 (7.53) were likewise very distinct from one another and this indicates the occurrence of high genetic diversity between the genotypes diverged into different clusters. Parents should be chosen from two clusters with a greater inter-cluster distance, according to recommendations made by Chaturvedi and Maurya (2005), Yadav *et al*. (2011), Eswaran (2012), and Kumar *et al*. (2013).

The lack of variation in intra-cluster distances in comparison to inter-cluster differences suggests that there is little genetic diversity among the genotypes associated with different clusters. The genotypes inside the clusters are homogeneous, as evidenced by the fact that intra-cluster differences were significantly less than inter-cluster ones (Kumar *et al*., 2013). Therefore, to produce superior segregants and promote genetic advancement, the genotypes from the clusters with the greatest inter-cluster distances can be chosen. The

findings concurred with those of Priya *et al*. (2017), Ashok *et al*. (2017), and Priyanka *et al*. (2015). Cluster 3 (7.30) and Cluster 5 (5.24) had the maximum intra-cluster distance in the current analysis. The most differed nature of genotypes was revealed by Clusters 3 (7.30) and 4 (6.15), which both exhibit substantial intra-cluster distance. Additionally, it showed that the genotypes in this cluster such as Taposen Youli, Yarba (SARS-3), Shyekenyii, Tsushvuri and Amusu had the highest levels of variability for the characteristics being studied.

Table 4.14: Average intra and inter-cluster distances among 28 genotypes

	Cluster 1	**Cluster 2**	**Cluster 3**	**Cluster 4**	**Cluster 5**
Cluster 1	**6.46**	9.12	7.96	7.53	6.48
Cluster 2		**6.45**	10.00	8.45	9.03
Cluster 3			**7.30**	8.47	7.37
Cluster 4				**6.15**	7.08
Cluster 5					**5.24**

4.11.3 Cluster mean for different traits

The average performance of all the genotypes found within a given cluster is determined by cluster means where 29 quantitative traits were analysed and the results showed that there were distinct disparities between different clusters for each character. According to Table 4.15 and 4.16, the characters with the highest to lowest cluster mean values in relation to each cluster are detailed below.

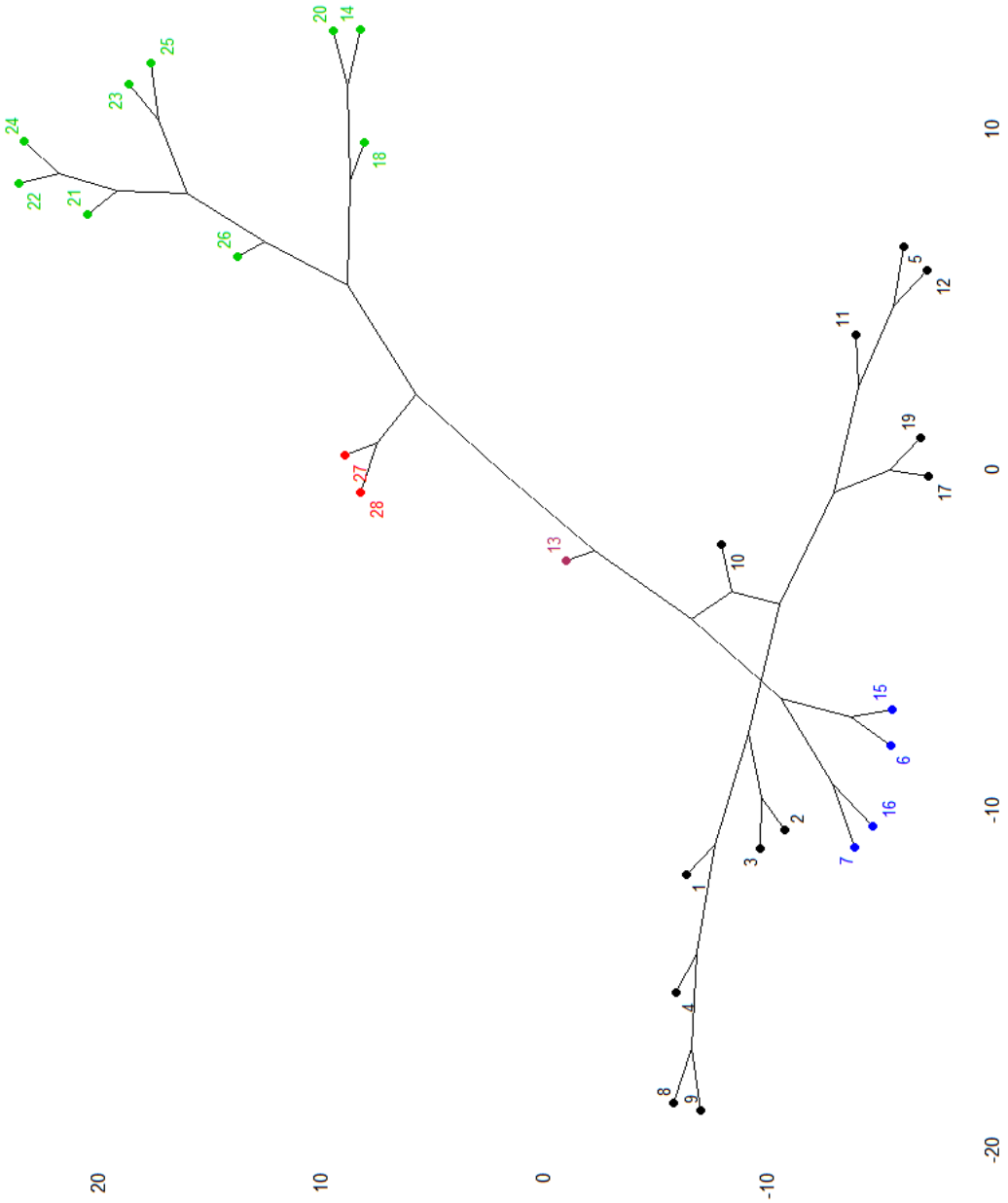


Fig 4.2: Cluster tree for 28 genotypes under study

Number of ear bearing tillers, panicles per plant, panicle length, panicle weight and spikelet fertility showed cluster means ranging from 14.087 to 15.556, 9.5185 to 10.528, 22.633 to 28.71, 3.3003 to 4.5779, and 70.818 to 82.365 respectively. Cluster mean for harvest index varied from 25.713 to 38.96. Amylose content showed cluster means ranging from 7.2591 to 10.584. NUE yield and yield attributes like GN%, PNUE, NUtE, BY, NHI, 100 grain weight and grain yield per plant showed cluster means ranging from 1.6241 to 1.8484, 12.151 to 13.31, 7.6334 to 8.213, 22.87 to 32.145, 12.041 to 13.812, 3.565 to 5.0171 and 4.226 to 5.2347. The divergence in quantitative characters were also reported by Subudhi et al. (2008), Parikh et al. (2011), Priyanka et al. (2015), Behera et al. (2018) and Singh et al. (2020). The highest means of the five clusters are found for traits like days to maturity, days to 50% flowering, plant height, germination percentage, and spikelet fertility, indicating that highly desirable genotypes may be recombined in the F_2 generation through selection of various traits from these clusters and hybridization. The generation of genotypes with high yields particular to a trait could additionally benefit from trait-specific selections. The lowest mean values across all clusters are found for the characteristics flag leaf breadth, panicle weight, total nitrogen, grain N%, and 100 grain weight, indicating that selection of these traits has a limited potential for use in breeding programmes.

Among the clusters, cluster 5 and cluster 1 had the lowest mean value for days to maturity and days to 50% flowering, and it may be used to choose genotypes for the development of high-yielding varieties. The goal of earliness can also be achieved by choosing parents from this cluster. Reddy et al. 2020 demonstrated a comparable outcome for days to maturity and days to 50% flowering. The highest mean value for panicles per plant, number of ear-bearing tillers, and grain yield per plant were all recorded in clusters 1 and 2, which suggests the potential for their use in breeding programmes. Clusters 1 and 2 also had the highest values for panicle weight and grain yield per plant.

The genotypes in Clusters 1 and 3 showed the highest values for grain N%, PNUE (physiological nitrogen uptake efficiency), NUtE, BY, and NHI, indicating that these genotypes can be used for breeding NUE for yield and yield-attributing traits like Thupfu Lha, RCM-9, and Taposen Youli. To obtain a wide range of diversity and to separate out acceptable recombinants, it is necessary to introgress the genotypes from clusters separated by moderate to large distances. In order to achieve the desired trait combinations in subsequent generations, genotypes from clusters with desirable characteristics such as Thupfu Lha, RCM-9, and Taposen Youli may be selected for intercrossing.

When fertilizers are applied, rice cultivars with a medium height (100 to 102 cm) are good for the majority of areas and are not prone to lodging. Short cultivars (less than 100 cm in height) respond well to fertilizers and are best suited for level fields, especially in irrigated areas. This shows that there is evidence for obtaining short upland rice genotypes, which may be best suited to level fields especially in irrigated areas and will be more responsive to fertilizers (Gebrie and Abebe, 2022). The majority of genotypes included under all clusters except cluster 2 had a plant height (PH) less than 100 cm.

No cluster had genotypes that could be directly chosen and used and possessed all the desirable features. There were clusters that were relatively far apart for both the minimum and maximum cluster mean values. However, the genotypes chosen from clusters 1 through 3 had high mean values for the attributes NUE, yield, and yield components, indicating their suitability for use in hybridization programmes that aim to increase these traits. To judiciously combine all the required features, it is therefore necessary to hybridize between chosen genotypes from divergent clusters. High mean genotype values may be employed directly for adaptation or as parents in a future breeding plan.

Table 4.15: Mean performance of different clusters among 29 quantitative traits

	GER	DF50	DM	PH	FLL	FLB	FLA	NEBT	PPP	PL
Cluster 1	83.49	114.21	135.19	135.43	37.03	1.96	55.03	14.52	9.91	27.56
Cluster 2	78.33	142.05	165.58	91.09	31.06	1.67	45.81	15.56	10.53	22.63
Cluster 3	54.54	108.31	135.95	128.36	28.26	2.01	42.86	14.69	9.99	26.76
Cluster 4	67.22	109.47	136.28	122.89	31.64	2.03	48.64	14.13	9.52	28.71
Cluster 5	74.37	108.14	135.34	116.94	38.96	2.17	63.36	14.09	9.87	26.84

	PW	SF	RL	RDW	SDW	HI	TN	CP	CHL A	CHLB
Cluster 1	4.58	82.37	27.91	6.75	14.58	29.78	2.31	6.40	12.32	21.85
Cluster 2	4.13	77.01	27.28	6.11	15.52	38.96	1.91	6.24	24.03	31.61
Cluster 3	3.30	78.45	27.75	7.20	15.23	25.71	2.02	6.07	11.90	20.93
Cluster 4	3.92	70.82	27.33	6.76	13.86	37.30	2.24	6.27	23.59	33.92
Cluster 5	3.81	75.25	26.80	6.78	13.59	26.50	1.96	6.24	12.44	21.06

	TCHL	AC	GN%	PNUE	NUtE	BY	NHI	HSW	GYPP
Cluster 1	19.39	7.99	1.85	12.30	8.21	24.50	12.38	5.02	5.23
Cluster 2	29.98	7.26	1.84	12.23	7.94	23.92	12.54	4.19	5.23
Cluster 3	18.57	10.58	1.62	13.31	8.20	32.15	13.81	3.57	4.23
Cluster 4	30.29	8.07	1.75	12.17	7.91	24.23	12.04	4.23	4.58
Cluster 5	18.73	7.62	1.75	12.15	7.63	22.87	12.21	3.87	4.39

Table 4.16: Performance of 29 quantitative characters in each cluster

Cluster	High Mean Value	Lower Mean Value
Cluster 1	Germination percentage, plant height, panicle weight, spikelet fertility, root length, total nitrogen, crude protein, grain N%, NutE, 100 grain weight and grain yield per plant	Days to maturity and panicles per plant
Cluster 2	Days to 50% flowering, days to maturity, panicles per plant, stem dry weight, harvest index, chlorophyll a and grain yield per plant	Plant height, flag leag breadth, flag leaf area, panicle length, root length, root dry weight, total nitrogen and amylose content
Cluster 3	No. of ear bearing tillers, root dry weight, amylose content, PNUE, biological yield and NHI	Germination percentage, flag leaf length, panicle weight, harvest index, crude protein, chlorophyll a, chlorophyll b, total chlorophyll, grain N%, 100 grain weight and grain yield per plant
Cluster 4	Panicle length, chlorophyll b and total chlorophyll	Spikelet fertility and NHI
Cluster 5	Flag leaf length, flag leaf breadth and flag leaf area	Days to 50% flowering, No. of ear bearing tillers, stem dry weight, PNUE, NUtE and biological yield

4.11.4 Euclidean Distance

According to the findings, there is enough genetic diversity among the 28 upland rice genotypes under study, with distances between genotypes 9 and 8 (Chishoghi and Chali) and 28 and 13 (RCM-9 and Taposen Youli) ranging from 12.08 and 3.18, respectively (Fig 4.3). The dendogram in Fig 4.4 and Fig 4.5 is used to display a number of genotypes grouped into three distinct categories. The genetic differences between and within the clusters were further revealed using the dendogram. The Euclidean distances in the dendogram also showed the differences between the clusters that formed, as seen in the figure.

Euclidean Distance	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27
2	6.21																										
3	6.90	5.06																									
4	6.18	6.73	5.72																								
5	6.54	6.31	5.15	4.66																							
6	9.22	7.60	7.59	8.71	7.53																						
7	9.61	6.59	6.73	8.28	6.86	6.28																					
8	5.40	4.21	4.39	4.73	4.18	7.05	5.77																				
9	4.86	5.43	4.84	4.79	4.66	7.07	7.27	3.18																			
10	8.03	8.50	7.62	7.05	7.09	9.00	9.60	6.50	5.83																		
11	7.44	8.26	7.33	7.75	5.49	7.32	7.75	5.88	6.06	5.84																	
12	7.68	5.83	5.96	6.31	4.41	5.45	5.94	5.17	5.22	6.82	5.74																
13	10.42	11.39	10.26	10.02	7.88	9.17	10.52	9.88	9.64	9.21	7.78	7.91															
14	6.62	6.24	4.82	5.74	5.64	9.31	8.28	5.00	4.93	7.46	7.82	7.00	10.45														
15	6.74	7.21	7.36	7.18	6.59	5.50	7.63	5.62	5.29	8.07	6.43	5.84	9.47	7.42													
16	9.46	7.57	6.47	8.62	7.71	8.18	6.70	6.49	7.13	8.22	7.54	7.60	11.04	7.01	7.98												
17	7.41	6.54	6.34	6.30	4.98	6.22	6.09	4.64	4.48	7.57	6.53	5.16	8.94	5.74	5.22	6.95											
18	8.62	7.47	6.08	6.55	6.49	9.24	7.70	6.05	6.48	9.47	8.75	7.37	11.08	5.65	8.08	8.14	6.44										
19	7.77	7.78	6.93	7.27	4.37	9.10	8.16	5.89	5.70	8.43	6.71	6.40	9.18	5.77	7.20	8.33	4.23	6.53									
20	7.57	6.08	5.06	6.17	6.29	7.92	6.59	4.21	4.66	7.11	7.32	6.52	10.46	3.87	6.65	5.05	5.36	6.03	7.07								
21	7.82	7.71	6.99	7.01	6.80	6.67	7.02	5.90	6.00	7.60	7.15	5.83	8.74	7.06	5.60	7.07	6.00	7.90	8.02	5.97							
22	6.32	7.55	6.72	6.98	6.91	8.75	8.59	5.86	4.91	8.18	7.51	7.27	10.34	5.94	6.84	7.75	6.37	7.48	7.32	5.88	5.47						
23	6.98	7.55	7.77	7.79	7.64	9.60	8.36	6.56	6.68	10.80	9.04	8.41	11.74	6.63	7.43	8.48	6.89	7.30	7.73	6.88	6.78	4.67					
24	7.05	8.35	7.88	7.74	7.33	7.78	8.38	6.72	5.97	9.06	8.38	7.66	9.78	7.34	6.71	8.60	6.40	8.31	7.88	7.44	5.15	4.64	5.82				
25	6.86	6.24	7.32	7.18	6.29	7.91	7.74	5.83	5.46	9.27	8.41	5.85	10.30	6.54	5.81	8.50	5.90	7.45	6.81	6.72	5.36	5.39	4.88	5.37			
26	8.65	8.32	7.97	7.99	8.36	11.75	10.72	7.78	7.72	8.26	9.75	8.98	11.80	6.28	9.95	9.64	9.20	9.08	9.04	7.83	8.09	7.14	8.14	8.19	7.24		
27	10.03	7.93	8.18	8.98	8.06	8.89	7.79	7.30	8.02	9.93	8.83	7.95	12.02	8.47	9.02	8.42	7.54	8.52	8.48	8.05	8.05	7.02	7.57	8.42	7.85	8.61	
28	9.41	10.01	10.74	10.31	9.13	10.60	10.63	9.00	9.39	11.33	9.53	10.27	12.08	10.15	9.54	10.86	8.84	10.28	8.92	10.76	9.94	8.31	8.25	7.99	9.10	10.29	6.45

Fig.4.3: Euclidean Distance between 28 genotypes under study

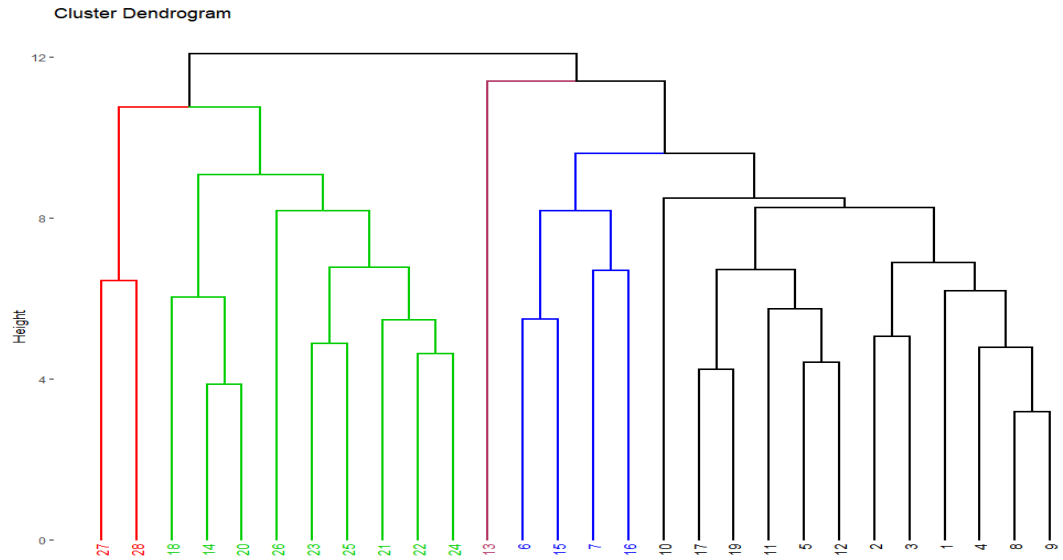


Fig 4.4: Dendogram showing eclucidean distances based on 29 quantitative traits among 28 genotypes under study

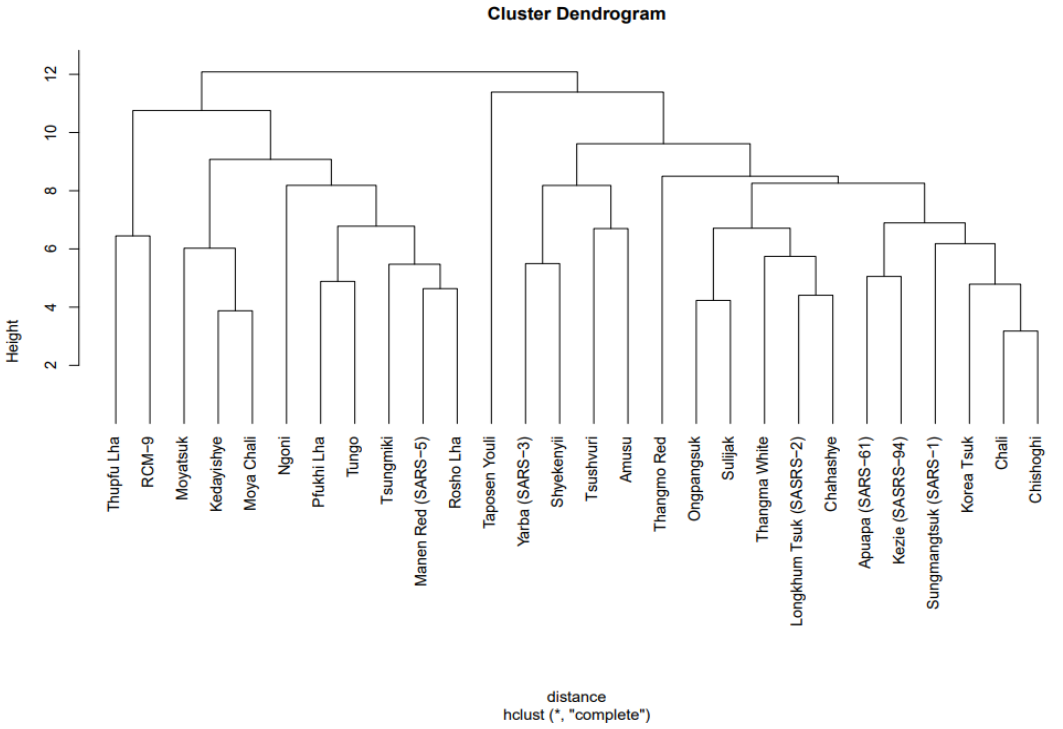


Fig 4.5: Dendogram showing distances among 28 genotypes under study

4.11.5 Trait-wise contribution towards genetic divergence

Among the 29 quantitative traits under investigation, chlorophyll a and total chlorophyll (7.41%) contributed maximum towards the observed diversity (Table 4.17) followed by flag leaf area, chlorophyll b, flag leaf length, PNUE, flag leaf breadth, crude protein, NHI, days to maturity, amylose content, root dry weight, number of ear bearing tillers, harvest index and grain N %. Therefore, these traits should be emphasised during hybridization and selection in the population that is segregating. Plant height, panicles per plant, days to 50% flowering, panicle weight, stem dry weight, NUtE, panicle length, spikelet fertility, root length, total nitrogen, grain yield per plant, and 100 grain weight are the traits that contribute to less divergence. According to Reddy *et al*. 2020, the least genetic diversity was contributed by grain yield per plant, plant height, panicles per plant, and panicle length. Singh and Singh (2003) also noted that among all characters, the minimum contribution of days to 50% flowering and grain yield. During selection, the qualities that cause divergence should be taken into account.

Table 4.17: Contribution of individual quantitative trait towards divergence

Sl. No.	Characters	% Contribution
1	Germination %	0.08
2	Days to 50% flowering	2.23
3	Days to maturity	4.88
4	Plant height (cm)	2.66
5	Flag leaf length (cm)	6.28
6	Flag leaf breadth (cm)	5.45
7	Flag leaf area (cm2)	7.15
8	No. of ear bearing tillers (EBT)	4.78
9	Panicles/plant	2.38
10	Panicle length (cm)	0.62
11	Panicle weight (g)	1.21
12	Spikelet fertility	0.58
13	Root length (cm)	0.58
14	Root dry weight (g)	4.81
15	Stem dry weight (g)	1.12
16	Harvest Index	4.46
17	Total nitrogen	0.58
18	Crude protein	5.08
19	Chlorophyll a	7.41
20	Chlorophyll b	7.08
21	Total chlorophyll	7.41
22	Amylose content	4.85
23	Grain N%	3.41
24	PNUE	5.55
25	NUtE	0.89
26	Biological Yield	2.81
27	NHI	5.06
28	100 grain weight (g)	0.28
29	Grain yield/ plant (g)	0.32

4.12 Assessment of the environments

The erratic weather during the 2021–2022 growing season was mostly brought on by variations in rainfall volume and ASSH (Average Sunshine Hour). During the crop time, the annual fluctuations in climatic factors like maximum and minimum temperatures and relative humidity were minimal. The total rainfall received during the vegetative and reproductive period was 138.8 mm and 116.2mm, respectively in 2021 while the same was 261.8 mm and 161.2 mm in 2022. Likewise the crop in 2021 received ASSH of 3.2 and 5.9 during vegetative and reproductive period respectively as against 4.8 and 5.2 hrs of ASSH during the same period of 2022. The final grain yield was not primarily influenced by high rainfall and due to aerobic rice's suitability for water-scarce areas; upland rice crops need less water than lowland rice (Bouman *et al*. 2005). This was demonstrated in the breeding approach for places with a shortage of water (Courtois *et al*. 2000; Bernier *et al.* 2007, 2008), and it is also frequently used in water-saving systems (Tuong and Bouman 2003).

It is crucial to assess the genotype at various N concentrations in order to identify the variations in genotypic response to NUE. Regression lines were fitted using the N levels as independent variables such as the NUE-related characteristics and grain yield per plant as the dependent variables in order to predict the environmental changes under study. In Figure 4.6, there was evidence of a positive linear association between N levels with Chl b and NUtE. Although an increase in N levels often corresponds to a drop in these variables, the slope of regression was negative for Chlorophyll a (chl a), Total Chlorophyll (Tchl), Amylose Content (AC), Grain N% (GN%), PNUE, and NHI. These results showed that the characteristics responded differently to varied N levels. As a result, these environments produced by the application of graded N levels were successful in causing environmental variations for screening NUE in rice.

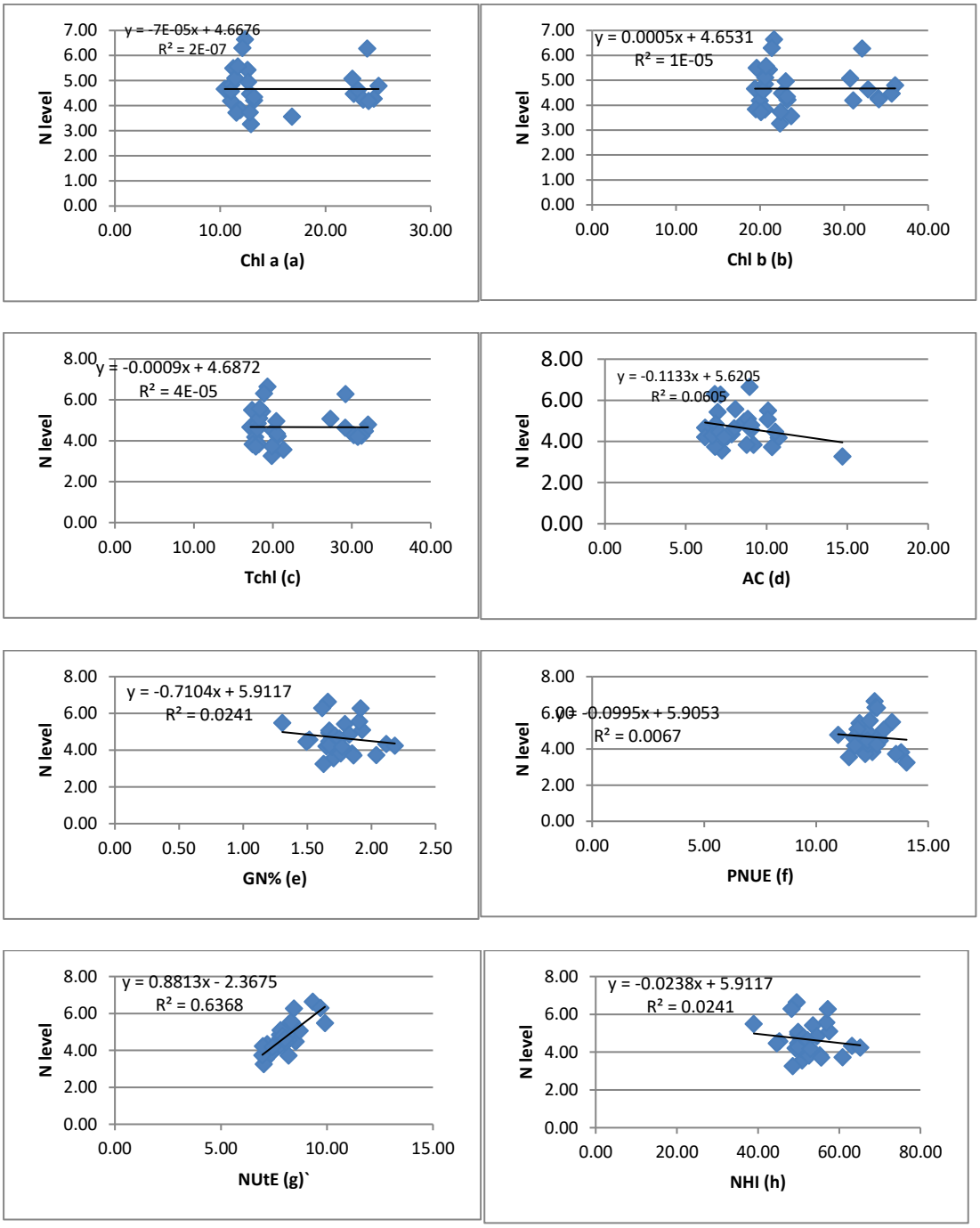


Fig 4.6. Relationship of N level with chl a (a), chl b (b), Tchl (c), AC (d), GN% (e), PNUE (f), NUtE (g) and NHI (h).

4.13 GxE interaction and phenotypic stability

The term "GxE interaction" refers to the interaction between the impacts of genetic and non-genetic characteristics on development of genotypes (Comstock and Moll, 1963). Any character's level of performance is determined by three factors: genotype (G), environment in which it is grown (E), and the interaction between G and E (GEI). Identification of genotypes appropriate for particular environment is made possible by the interaction between these two explicating factors. According to Blanche *et al.* (2009), the environmental influence often makes up a significant amount of the total variation. Additionally, G x E interactions have a significant impact on a variety's phenotype, making stability analysis necessary to characterise a variety's performance in different environments and aid plant breeders in choosing desirable varieties. Significant yield variations were detected by Mosavi (2013) among rice genotypes, environments, and genotype by environment interactions. Therefore, the main goal of the current study was to assess and choose rice varieties that may perform well at various N levels as well as to discover acceptable genotypes for Nagaland's highland ecology.

4.14 Analysis of variance for stability

The phenology, crop variety, and growth stage of the crop species will all affect how the crops react to different surroundings. Plant breeders' biggest obstacle is the variation in genotype responses across environments known as genotype-environment interaction (Comestock & Moll, 1963). Significant GxE interaction suggests that not all genotypes exhibit the same phenotypic responses to different agro-ecological situations. These would result from the genotypes' rank changing from one site or year to the next. Thus, GxE interactions are more significant in plant breeding because they decrease the genotypic values' stability in a wide range of environments.

A pooled analysis of variance for stability was performed for yield, yield-attributing variables, and NUE-related traits according to Eberhart and

Russell (1966). The results are shown in Table 4.18. Environment plus GxE interaction components were further divided into environment (linear), GxE (linear), and pooled deviations from regression in the stability analysis. The pool analysis of variance showed that genotypes varied significantly across environments for all the characters. The highly significant linear environmental variation for each character indicated that there were large differences between their environments and that these differences had an unfavourable effect on the traits. Among the studied characteristics, with the exception of chlorophyll a, chlorophyll b, total chlorophyll, amylose concentration, and biological yield were significantly influenced by the linear environment (linear). The characters panicle length, spikelet fertility, PNUE, NUtE, NHI, GN%, 100 grain weight, and grain yield per plant were also found to have strong linear GxE interactions.

As a result, the highly substantial GxE effects imply that the genotypes may have been chosen for their ability to adapt to particular environments. The results of Aina *et al.* (2009) and XuFei-fei *et al*. (2014) in the GxE interaction effects of cassava genotypes are aligned with this. This further demonstrates the challenges faced by breeders when deciding which novel varieties to introduce and significant differences between genotypic means explained the majority of the variation in grain yield, according to the sum of squares for genotypes, which is consistent with the findings of Misra *et al*. (2009) and Fentie *et al*. (2013) in rice production.

4.15 Stability parameter

According to Eberhart and Russell (1966) a stable genotype means a high trait mean, unit regression (bi=1) and least deviation from regression (S^2_{di}=0). If regression coefficient is greater than unity (b >1) it is considered to below average stable and if regression coefficient is less than unity (b<1) it is considered to above average stable. Sometimes desirably important traits show low GxE but high on other traits such that they adjust in

Table 4.18: Pooled analysis of variance for stability for 28 upland rice genotypes

Source	df	GER	DF	DM	PH	FLL	FLB	FLA	NEBT	PPP	PL
Replication within environment	6	137.60**	1131.45**	0.90**	25.20**	3.53**	0.005**	26.96**	0.07	0.25**	1.73**
Environments	2	0.69	1431.70**	1.02**	608.85**	25.87**	0.01**	18.48**	8.54**	3.87**	19.73**
Genotypes	27	5325.29**	2185.964**	595.88**	2331.12**	446.87**	0.41**	1708.96**	5.35**	0.75**	52.89**
Env x Gen.	54	1.83	1367.45**	1.83**	49.80**	5.89**	0.03**	35.29**	1.01**	0.35	5.15
Pooled Error	162	181.84	1192.02	0.47	15.09	3.50	0.005	10.58	0.15	0.16	2.10
Total	251	71.15	112.45	137.80	123.44	34.05	2.02	52.47	14.44	5.43	5.34
ECV%		18.95	30.70	0.50	3.15	5.50	3.40	6.20	2.65	7.31	27.10

Source	df	PW	SF	RL	RDW	SDW	HI	TN	CP	CHL A	CHLB
Replication within environment	6	0.06	20.52	1.54**	0.05**	0.45**	35.98**	0.01**	0.06**	482.42**	2744.40**
Environments	2	3.34**	20.50	10.79**	7.53**	3.49**	29.63**	0.16**	28.42**	0.15	2.18
Genotypes	27	5.25**	577.14**	7.40**	1.89**	14.07**	443.11**	0.81**	0.60**	263.79**	297.62**
Env x Gen.	54	0.58**	28.46	9.50**	1.09**	1.02**	18.95**	0.37**	0.43**	0.06	0.30
Pooled Error	162	0.10	60.50	0.34	0.06	0.17	15.16	0.01	0.04	11.60	10.54
Total	251	3.94	76.89	27.43	6.81	14.38	30.36	2.12	6.26	15.51	24.74
ECV%		8.10	10.12	2.14	3.63	2.86	12.83	3.80	3.09	21.96	13.12

Table 4.18: Pooled analysis of variance for stability for 28 upland rice genotypes (*contd*..)

Source	df	TCHL	AC	GN%	PNUE	NUtE	BY	NHI	HSW	GYPP
Replication within environment	6	2145.80**	17.36**	0.01	0.26**	0.08**	379.28**	9.99**	3.72**	0.003
Environments	2	0.68	0.30	0.28**	83.20**	12.26**	0.13	255.58**	4.37**	0.20**
Genotypes	27	258.90**	30.25**	0.40**	4.32**	1.98**	1239.05	273.67**	7.70**	6.42**
Env x Gen.	54	0.13	0.02	0.13**	1.43**	0.99**	0.23	112.51**	3.66**	0.21**
Pooled Error	162	7.89	4.58	0.01	0.10	0.03	362.70	7.18	3.67	0.01
Total	251	22.14	8.42	1.79	12.44	7.61	25.63	52.32	4.19	4.67
ECV%		12.68	25.42	5.85	2.53	2.36	74.30	5.12	45.71	1.94

Signifcance at 1% level of probability-**, Signifcance at 5% level of probability-*

response to changing environment. Therefore, stability in certain yields components and other yield components can result in stability in yielding ability as they compensate each other.

The varieties having the lowest mean for all the varieties studied as compared to the population mean and when regression coefficient is below unity and less deviation from regression indicates that these varieties are not having stable performance but can adapt in diverse environments. So, these varieties cannot be used as stable lines. Varieties having highest mean value for yield among the varieties studied than population mean and when regression coefficient value is around unity and less deviation from regression indicates that those varieties had stable performance across the environments and less sensitive to environment it can adapt to the diverse environments. Hence, it can be used as stable line adopted across the environments and could be released for large scale trials. Similarly, varieties which have high mean value and regression coefficient more than unity and less deviation from regression identified that these varieties are stable lines across the environments and can adapt to diverse environments.

There are mean performance of the genotypes (m), linear coefficient of genotypic means on environmental indices (bi) and mean square due to deviation from regression (S^2_{di}) among all the characters studied (Table 4.19, Table 4.20 and Appendix III).

Germination percentage

Germination percentage revealed higher mean traits for Amusu, Korea Tsuk, Tsushvuri, Rosho Lha, Longkhum Tsuk (SASRS-2), Chali, Thangma White, Moya Chali, Pfukhi Lha and RCM-9 along with regression coefficient greater than unity (b>1) and no deviation from regression coefficient. So these genotypes are considered to be below average stable and adapted better to environments. Apuapa (SARS-61), Chahashye, Tungo and Ngoni have also

lower mean value along with regression coefficient greater than unity (b>1) and least deviation or non-significant from regression coefficient.

Days to 50% flowering

Days to 50% flowering revealed that Chali, Kezie (SASRS-94), Taposen Youli, Amusu, Tsungmiki, Pfukhi Lha, Ngoni and Thupfu Lha have higher mean value along with regression coefficient greater than unity (b>1) and least deviation from regression coefficient. Therefore, these genotypes were regarded as stable. Korea Tsuk, Moyatsuk, Sulijak and Tungo have also lower mean value along with regression coefficient greater than unity (b>1) and least deviation or non-significant from regression coefficient.

Days to maturity

Genotypes such as Moyatsuk, Manen Red (SARS-5), Ngoni and Ongpangsuk were considered to be stable genotypes for days to maturity as these genotypes have higher mean with regression coefficient greater than unity (b>1) and least deviation from regression coefficient.

Plant height

Manen Red (SARS-5), Pfukhi Lha and Sulijak were the genotypes that are stable for plant height for having a higher mean trait, regression coefficient greater than unity (b > 1), and least or non-significant deviation from zero ($s^2di = 0$).

Flag leaf length

Apuapa (SARS-61), Kezie (SASRS-94), Tsushvuri, Chali, Thangma White, Moyatsuk, Manen Red (SARS-5), Ngoni and Thupfu Lha were the genotypes that are stable for flag leaf length for having a higher mean trait, regression coefficient greater than unity (b > 1), and least or non-significant deviation from zero ($s^2di = 0$). Pfukhi Lha has also lower mean value along with regression coefficient greater than unity (b>1) and least deviation or non-significant from regression coefficient.

Flag leaf breadth

Flag leaf breadth revealed that Chishoghi, Kedayishye, Moya Chali, Amusu, Tsungmiki, Manen Red (SARS-5), Pfukhi Lha, Rosho Lha and Tungo have higher mean value along with regression coefficient greater than unity (b>1) and least deviation or non-significant from regression coefficient. Therefore, these genotypes were regarded as stable. RCM-9 has lower mean value along with regression coefficient greater than unity (b>1) and least deviation or non-significant from regression coefficient.

Flag leaf area

Flag leaf area revealed that Kezie (SASRS-94), Korea Tsuk, Moyatsuk and Ngoni have higher mean value along with regression coefficient greater than unity (b>1) and least deviation or non-significant from regression coefficient and these genotypes were regarded as stable. Thangma White, Pfukhi Lha, and RCM-9 have lower mean value along with regression coefficient greater than unity (b>1) and least deviation or non-significant from regression coefficient.

Number of ear bearing tillers

Kezie (SASRS-94), Longkhum Tsuk (SASRS-2), Thangmo Red, Rosho Lha and Tungo have higher mean value along with regression coefficient greater than unity (b>1) and least deviation or non-significant from regression coefficient. Therefore, these genotypes were regarded as stable. Kedayishye, Manen Red (SARS-5) and Ngoni also have lower mean value along with regression coefficient greater than unity (b>1) and least deviation or non-significant from regression coefficient.

Panicles per plant

Longkhum Tsuk (SASRS-2), Yarba (SARS-3), Chali, Chishoghi, Chahashye, Moya Chali, Tsungmiki, and Ngoni have higher mean value along with regression coefficient greater than unity (b>1) and least deviation or non-

significant from regression coefficient for panicles per plant. Therefore, these genotypes were regarded as stable. Shyekenyii, Manen Red (SARS-5) and Tungo have lower mean value along with regression coefficient greater than unity (b>1) and least deviation or non-significant from regression coefficient.

Panicle length

Chahashye, Shyekenyii and Amusu have higher mean value along with regression coefficient greater than unity (b>1) and least deviation or non-significant from regression coefficient for panicle length. Therefore, these genotypes were regarded as stable. Thupfu Lha and RCM-9 have lower mean value along with regression coefficient greater than unity (b>1) and least deviation or non-significant from regression coefficient.

Panicle weight

Yarba (SARS-3), Chahashye, Manen Red (SARS-5), Rosho Lha, Tungo, Ngoni and RCM-9 have higher mean value along with regression coefficient greater than unity (b>1) and least deviation or non-significant from regression coefficient for panicle weight. Therefore, these genotypes were regarded as stable. Thangmo Red and Thangma White have lower mean value along with regression coefficient greater than unity (b>1) and least deviation or non-significant from regression coefficient.

Spikelet fertility

Longkhum Tsuk (SASRS-2), Yarba (SARS-3), Tsushvuri, Chali, Kedayishye, Shyekenyii, Moyatsuk, Sulijak, Moya Chali, Thupfu Lha and RCM-9 have higher mean value along with regression coefficient greater than unity (b>1) and least deviation or non-significant from regression coefficient for spikelet fertility. Therefore, these genotypes were regarded as stable. Tsungmiki has also lower mean value along with regression coefficient greater than unity (b>1) and least deviation or non-significant from regression coefficient.

Root length

Root length revealed that, Tsushvuri, Kedayishye, Pfukhi Lha and Moya Chali have higher mean value along with regression coefficient greater than unity (b>1) and least deviation or non-significant from regression coefficient and these genotypes were regarded as stable. Apuapa (SARS-61), Korea Tsuk, Chali have lower mean value along with regression coefficient greater than unity (b>1) and least deviation or non-significant from regression coefficient.

Root dry weight

Root dry weight revealed that Yarba (SARS-3), Chishoghi, Tungo and Ngoni have higher mean value along with regression coefficient greater than unity (b>1) and least deviation or non-significant from regression coefficient and these genotypes were regarded as stable. Ongpangsuk has lower mean value along with regression coefficient greater than unity (b>1) and least deviation or non-significant from regression coefficient.

Stem dry weight

Yarba (SARS-3) and Amusu have higher mean value along with regression coefficient greater than unity (b>1) and least deviation or non-significant from regression coefficient for stem dry weight and these genotypes were regarded as stable while Chali and Pfukhi Lha has lower mean value along with regression coefficient greater than unity (b>1) and least deviation or non-significant from regression coefficient.

Harvest Index

For harvest index, Amusu, Kezie (SASRS-94), Moya Chali and Thupfu Lha showed higher mean value along with regression coefficient greater than unity (b>1) and least deviation or non-significant from regression coefficient whereas Korea Tsuk, Chali, Chishoghi, Thangmo Red, Taposen Youli, Kedayishye and Shyekenyii showed lower mean value along with regression

coefficient greater than unity (b>1) and least deviation or non-significant from regression coefficient.

Total nitrogen

The genotypes Moyatsuk and Rosho Lha were most suitable and stable for total nitrogen under better environmental conditions due to the presence of high mean value, bi value more than unity and non-significant deviation from regression. Genotypes Chali and Chahashye were having lower mean value along with regression coefficient greater than unity (b>1) and least deviation or non-significant from regression coefficient.

Crude protein

Genotypes such as Thangmo Red, Ongpangsuk and Thupfu Lha were most suitable and stable for crude protein under better environmental conditions due to the presence of high mean value, bi value more than unity and non-significant deviation from regression. Genotypes like Longkhum Tsuk (SASRS-2), Tsushvuri, Tsungmiki and Tungo have low mean value, bi value more than unity and non-significant deviation from regression. This indicates that these varieties are not having stable performance but can adapt in diverse environments. So, these varieties cannot be used as stable lines.

Chlorophyll a

Apuapa (SARS-61) was the most suitable and stable for chlorophyll a under better environmental conditions due to the presence of high mean value, bi value more than unity and non-significant deviation from regression.

Chlorophyll b

Manen Red (SARS-5), Rosho Lha, Tungo, Ngoni and Thupfu Lha have showed higher mean value along with regression coefficient greater than unity (b>1) and least deviation or non-significant from regression coefficient for chlororphyll b. Therefore, these genotypes are stable. Kezie (SASRS-94),

Korea Tsuk, Longkhum Tsuk (SASRS-2) and Yarba (SARS-3) have low mean value, bi value more than unity and non-significant deviation from regression.

Total chlorophyll

Total chlorophyll revealed that genotypes like Tsungmiki, Manen Red (SARS-5), Rosho Lha, Thupfu Lha and RCM-9 were most stable as they have higher mean value along with regression coefficient greater than unity (b>1) and least deviation or non-significant from regression coefficient. Kezie (SASRS-94), Korea Tsuk, Longkhum Tsuk (SASRS-2) and Yarba (SARS-3) also have low mean value, bi value more than unity and non-significant deviation from regression.

Amylose content

Yarba (SARS-3), Thangma White and Taposen Youli showed higher mean value along with regression coefficient greater than unity (b>1) and least deviation or non-significant from regression coefficient for amylose content. Therefore, these genotypes are stable. Apuapa (SARS-61), Kezie (SASRS-94), Sulijak and Amusu have low mean value, bi value more than unity and non-significant deviation from regression.

GN%

Thangma White, Chahashye, Moya Chali, Tsungmiki and Tungo showed higher mean value along with regression coefficient greater than unity (b>1) and least deviation or non-significant from regression coefficient for grain N% which shows that these genotypes are stable. Kezie (SARS-94), Chishoghi and Amusu also have lower mean value along with regression coefficient greater than unity (b>1) and least deviation or non-significant from regression coefficient.

PNUE

PNUE revealed that genotypes like Tsushvuri and Shyekenyii have higher mean value along with regression coefficient greater than unity (b>1)

and least deviation or non-significant from regression coefficient for PNUE which shows that these genotypes are stable.

NUtE

Kezie (SARS-94) showed higher mean value along with regression coefficient greater than unity (b>1) and least deviation or non-significant from regression coefficient for NUtE which shows that these genotypes are stable.

Biological Yield (BY)

Amusu, Ongpangsuk, Moyatsuk, Sulijak, Tsungmiki and Manen Red (SARS-5) have showed higher mean value along with regression coefficient greater than unity (b>1) and least deviation or non-significant from regression coefficient for biological yield. Therefore, these genotypes are stable. Whereas genotypes like Korea Tsuk, Thangmo Red, Thangma White, Chahashye, Pfukhi Lha, Rosho Lha and Ngoni have lower mean value along with regression coefficient greater than unity (b>1) and least deviation or non-significant from regression coefficient.

Nitrogen harvest index (NHI)

Kezie (SARS-94), Longkhum Tsuk (SARS-2), Thangma White, Moyatsuk, Sulijak, Moya Chali, Pfukhi Lha and Tungo have showed higher mean value along with regression coefficient greater than unity (b>1) and least deviation or non-significant from regression coefficient for nitrogen harvest index.

100 grain weight

100 grain weight revealed Tsushvuri has higher mean value along with regression coefficient greater than unity (b>1) and least deviation or non-significant from regression coefficient for 100 grain weight. Therefore, these genotypes are stable. Chali has low mean value, bi value more than unity and non-significant deviation from regression.

Grain yield per plant

Kezie (SASRS-94) and RCM-9 have higher mean value along with regression coefficient greater than unity (b>1) and least deviation or non-significant from regression coefficient for grain yield per plant. Therefore, these genotypes are stable and can adapt to different environments for higher yield.

4.16 Stability for NUE yield and yield attributing traits

Genotypes with higher grain yield along with stability for different characters are summarized in Table 4.20. Kezie (SARS-94) had above average stability for harvest index, grain N%, NUtE, grain yield per plant and NHI. Korea Tsuk and Manen Red (SARS-5) exhibited above average stability for panicle length. Longkhum Tsuk also showed above average stability for panicle length with NHI. Similarly, Yarba (SARS-3) exhibited above average stability for panicle length, spikelet fertility and amylose content and Shyekenyii also exhibited above average stability for panicle length, harvest index and grain N%. Tsushvuri, Kedayishye, Amusu, Moyatsuk and Thupfu Lha exhibited above average stability for spikelet fertility along with grain N%, 100 grain weight for Tsushvuri, harvest index for Kedayishye, harvest index and biological yield for Amusu and Moyatsuk. Taposen Youli and Rosho Lha registered for above average stability for amylose content. Thangma White also registered for above average stability for amylose content, NHI and grain N%. Similarly, Tsungmiki also showed above average stability for amylose content, biological yield and grain N%. Moya Chali showed above average stability for harvest index, biological yield, NHI and grain N%. Ongpangsuk exhibited above average stability only for biological yield whereas Sulijak and Pfukhi Lha both exhibited above average stability for biological yield and NHI. Similarly, Chahashye showed above average stability only for grain N% whereas Tungo showed above average stability for grain N% and NHI. Only Tsungmiki exhibited average stability for amylose content. Therefore, these genotypes

were most desirable for stable yield performance with greater adaptation at wide range of environments under study. High yielding Tsushvuri, Amusu, Thupfu Lha and Yarba (SARS-3) did not show stability for yield performance but had stability for other NUE and yield attributing traits. However, the genotype Kezie (SARS-94) possessed stability for grain yield per plant and NUtE suggesting that this genotype would be suitable for N non-limiting environment.

Given that the genotypes did not show uniform responses and stability patterns, it may be difficult to make any conclusions about the stability of a genotype for all the traits.

4.17 Winners of genotype in each environment for 100 grain weight and grain yield per plant

Among 28 genotypes, there are genotypes which performed better than some other varieties across each environment for 100 grain weight and grain yield per plant as shown in Table 4.21. Among 29 traits Tsushvuri showed best performance among all the three environments. Similarly, for 100 grain weight Tsushvuri performed best in environment 1 (zero doses of N Kg/ha) whereas Moytasuk performed performed best in environment 2 (40 kg/ha N) and environment 3 (60 kg/ha N). The genotypes which performed best in these three environments are stable across each environment which shows that these genotypes can be used for further improvement in breeding programmes.

Table 4.19: Characters showing AAS and BAS for NUE yield and yield attributing traits

Character	Above average stability (AAS)	Below average stability (BAS)
Panicle length (cm)	Korea Tsuk, Longkhum Tsuk (SARS-2), Yarba (SARS-3), Shyekenyii, Manen Red (SARS-5)	Kezie (SARS-94), Moyatsuk, Tsungmiki
Spikelet fertility	Yarba (SARS-3), Tsushvuri, Kedayishye, Amusu, Moyatsuk, Moya Chali, Thupfu Lha	Ongpangsuk, Manen Red (SARS-5), Pfukhi Lha, Thangma white, Kezie (SARS-94)
Harvest Index	Keizie (SARS-94), Kedayishye, Shyekenyii, Amusu, Moya Chali	Ngoni, RCM-9, Tsungmiki, Tungo
Amylose content	Yarba (SARS-3), Thangma white, Taposen Youli, Tsungmiki, Rosho Lha	Korea Tsuk, Longkhum Tsuk (SARS-2), Tsushvuri, Shyekenyii, Ongpangsuk, Pfukhi Lha, Tungo
Grain N%	Thangma white, Chahashye, Moya Chali, Tsungmiki, Tungo	Korea Tsuk, Yarba (SARS-3), Tsushvuri, Taposen Youli, Ongpangsuk
PNUE	Tsushvuri, Shyekenyii	Longkhum Tsuk, Chishoghi, Manen Red (SARS-5), Taposen Youli
NUtE	Kezie (SARS-94)	Thangmo Red
Biological yield	Amusu, Ongpangsuk, Sulijak, Moya Chali, Tsungmiki, Manen Red (SARS-5)	Taposen Youli, Sungmangtsuk (SARS-1)
Nitrogen harvest index	Kezie (SARS-94), Longkhum Tsuk (SARS-2), Thangma White, Moyatsuk, Sulijak, Moya Chali, Pfukhi Lha, Tungo	Kedayishye, Ngoni
100 grain weight (g)	Tsushvuri	Moyatsuk, Amusu, Apuapa (SARS-61), Thupfu Lha
Grain yield/ plant (g)	Kezie (SARS-94) and RCM-9	Thupfu Lha, Amusu, Tsushvuri

Table 4.20: Upland rice genotypes showing stability for different characters

Genotypes	Characters showing b>1 and $S^2di=0$	Characters showing b=1 and $S^2di=0$
Kezie (SARS-94)	HI, GN%, NUtE, GYPP, NHI	
Korea Tsuk	PL	
Longkhum Tsuk	PL, NHI	
Yarba (SARS-3)	PL, SF, AC	
Shyekenyii	PL, HI, GN%	
Manen red (SARS-5)	PL	
Tsushvuri	SF, GN%, HSW	
Kedayishye	SF, HI	
Amusu	SF, HI, BY	
Moyatsuk	SF, BY, NHI	
Thupfu Lha	SF	
Thangma White	AC, NHI, GN%	
Taposen Youli	AC	
Moya Chali	HI, BY, NHI, GN%	
Tsungmiki	AC, BY, GN%	AC
Rosho Lha	AC	
Ongpangsuk	BY	
Sulijak	BY, NHI	
Pfukhi Lha	BY, NHI	
Tungo	NHI, GN%	
Chahashye	GN%	

Table 4.21: Winners of genotype in each environment

ENV	E1	E2	E3
100 grain weight (g)	Tsushvuri	Moyatsuk	Moyatsuk
Grain yield/ plant (g)	Tsushvuri	Tsushvuri	Tsushvuri

4.18 Favourable environment

According to environmental index, among the three environments namely, E1, E2 and E3 they are classified into two classes and from those classes, environment 1 (E1) was considered unfavourable while environment 2 and 3 (E_2 and E_3) were considered favourable as shown in the table 4.22 and Fig 4.6.

Table 4.22: Environmental index for the three environments

S.No	ENV	Y (yield)	index	class
1	E_1	4.614	-0.052	unfavorable
2	E_2	4.674	0.008	favorable
3	E_3	4.712	0.045	favorable

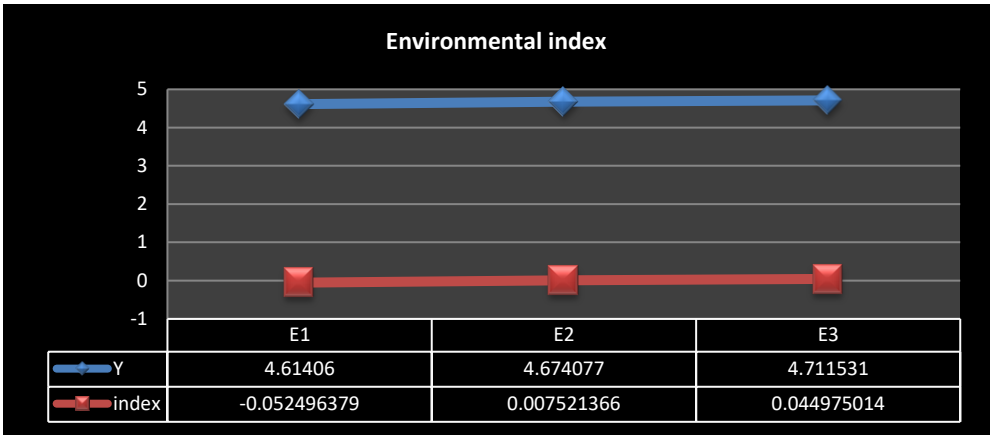


Fig 4.7: Graph representing environmental index

4.19 Correlation based on stability

According to Graphius (1956), the genetic explanation for yield stability may be simplified by the examination of specific grain yield components. Plant breeders may successfully choose grain yield stability by choosing these correlated traits if yield is associated with high yield stability. Table 4.23 to Table 4.25 shows the correlation based on stability characteristics that was done in order to determine the genetic relationship between grain yield and its component traits. Correlation studied based on mean values (Table 4.24) revealed among all the characters only 100 grain weight and NUtE had positive significant correlation with grain yield suggesting that stability for grain yield with NUtE and 100 grain weight could be improved. In case of b_i values all the characters show non-significant correlation with grain yield whereas NHI was positively correlated with spikelet fertility and grain N% (Table 4.24). Similarly, S^2_{di} values also show non-significant for all the characters studied (Table 4.25). These results revealed that the genotypes for different traits had separate mean performance, responses, and stability (Thiruknanakumar, 1991). Therefore, unpredictable environmental factors like seasonal or yearly

variations may have a significant impact on how the component traits are expressed, which in turn confers stability in genotype yield.

Table 4.23: Correlation for stability parameters based on mean values

	PL	SF	HI	AC	GN%	PNUE	NUtE	BY	NHI	HSW	GYPP
PL	1										
SF	-0.106^{NS}	1									
HI	0.074^{NS}	-0.035^{NS}	1								
AC	0.272^{NS}	-0.068^{NS}	-0.315^{NS}	1							
GN%	-0.003^{NS}	0.017^{NS}	0.207^{NS}	-0.146^{NS}	1						
PNUE	0.016^{NS}	0.005^{NS}	-0.225^{NS}	0.468*	-0.104^{NS}	1					
NUtE	-0.146^{NS}	0.294^{NS}	0.034^{NS}	0.095^{NS}	-0.440*	0.370^{NS}	1				
BY	0.289^{NS}	0.039^{NS}	-0.158^{NS}	0.647**	-0.110^{NS}	0.379*	-0.170^{NS}	1			
NHI	-0.063^{NS}	-0.135^{NS}	0.216^{NS}	-0.244^{NS}	0.829**	-0.161^{NS}	-0.554**	-0.125^{NS}	1		
HSW	0.10 4^{NS}	0.222^{NS}	0.180^{NS}	-0.104^{NS}	-0.011^{NS}	-0.212^{NS}	0.492**	-0.263^{NS}	-0.020^{NS}	1	
GYPP	-0.147^{NS}	0.266^{NS}	0.372^{NS}	-0.246^{NS}	-0.129^{NS}	-0.082^{NS}	0.771**	-0.361^{NS}	-0.156^{NS}	0.797**	1

Signifcance at 1% level of probability-**, Signifcance at 5% level of probability-*

Table 4.24: Correlation for stability parameters based on b_i values

	PL	SF	HI	AC	GN%	PNUE	NUtE	BY	NHI	HSW	GYPP
PL	1										
SF	0.182^{NS}	1									
HI	0.110^{NS}	0.006^{NS}	1								
AC	0.313^{NS}	-0.088^{NS}	0.082^{NS}	1							
GN%	0.038^{NS}	0.450^{*}	-0.064^{NS}	0.070^{NS}	1						
PNUE	0.109^{NS}	-0.015^{NS}	-0.118^{NS}	-0.195^{NS}	-0.037^{NS}	1					
NUtE	0.288^{NS}	0.219^{NS}	-0.257^{NS}	-0.213^{NS}	0.195^{NS}	0.230^{NS}	1				
BY	-0.195^{NS}	-0.208^{NS}	-0.257^{NS}	0.257^{NS}	0.210^{NS}	-0.000^{NS}	-0.029^{NS}	1			
NHI	0.026^{NS}	0.450^{*}	-0.064^{NS}	0.064^{NS}	1.000^{**}	-0.041^{NS}	0.193^{NS}	0.205^{NS}	1		
HSW	0.202^{NS}	0.188^{NS}	-0.088^{NS}	-0.164^{NS}	-0.236^{NS}	0.085^{NS}	0.265^{NS}	-0.183^{NS}	-0.237^{NS}	1	
GYPP	0.045^{NS}	0.165^{NS}	0.238^{NS}	-0.211^{NS}	0.025^{NS}	-0.176^{NS}	0.036^{NS}	-0.256^{NS}	0.024^{NS}	-0.019^{NS}	1

Signifcance at 1% level of probability-**, Signifcance at 5% level of probability-*

Table 4.25: Correlation for stability parameters based on S^2_{di} values

	PL	SF	HI	AC	PNUE	NUtE	BY	NHI	HSW	GYPP
PL	1									
SF	0.024 ^{NS}	1								
HI	0.1322 ^{NS}	-0.0878 ^{NS}	1							
AC	0.1661 ^{NS}	-0.196 ^{NS}	-0.0234 ^{NS}	1						
PNUE	-0.1007 ^{NS}	0.0359 ^{NS}	0.3491 **	0.1029 ^{NS}	1					
NUtE	-0.0953 ^{NS}	0.1304 ^{NS}	-0.1205 ^{NS}	-0.3227 *	-0.3125 *	1				
BY	0.1421 ^{NS}	0.0539 ^{NS}	0.3164 *	-0.0921 ^{NS}	0.2964 *	0.1385 ^{NS}	1.0002			
NHI	0.0691 ^{NS}	-0.2033 ^{NS}	-0.1488 ^{NS}	0.0303 ^{NS}	-0.1091^{NS}	0.0263 ^{NS}	-0.148 ^{NS}	1		
HSW	0.1922 ^{NS}	0.0382 ^{NS}	-0.0467 ^{NS}	0.6325 **	0.1806 ^{NS}	-0.4747 **	-0.0728 ^{NS}	-0.023 ^{NS}	1	
GYPP	0.259 ^{NS}	0.2149 ^{NS}	-0.0877 ^{NS}	-0.1241 ^{NS}	-0.1129 ^{NS}	0.0654 ^{NS}	-0.0523 ^{NS}	0.0464 ^{NS}	0.0423 ^{NS}	1

Signifcance at 1% level of probability-**, Signifcance at 5% level of probability-*

CHAPTER - V

SUMMARY AND CONCLUSION

SUMMARY AND CONCLUSION

In the present investigation, a set of 28 upland rice genotypes were evaluated under varying N regime with the objectives to study the performance of the genotypes in response to different N level, magnitude of genetic variation and diversity among the genotypes in respect of various morpho-physiological and biochemical traits, interrelationship of various characters, GxE interaction over N limiting and N non-limiting environments. Further, study on correlation of different characters with the stability of yield was also carried out.

The genotypes were evaluated in field experiments conducted during *Kharif* 2021 and *Kharif* 2022 under 3 different environments (N level) in RBD with 3 replications at the Experimental Farm, Department of Genetics and Plant Breeding, SAS, Medziphema. The observations were recorded on 29 different characters consisting of morpho-physiological and biochemical traits.

The salient findings of the present investigation are summarized as follows:

1. The pooled analysis of variance revealed existence of significant genetic variation among the genotypes for all the traits.
2. The genotypes namely Yarba (SARS-3), Amusu, Tsushvuri and Thupfu Lha were found to be superior for grain yield and NUtE, as revealed from their high mean performance.
3. The GCV was found to be high for chlorophyll a, germination percentage, flag leaf area, total chlorophyll, harvest index, chlorophyll b and flag leaf length. High heritability coupled with high GA was recorded for germination percentage, plant height, flag leaf length, breadth, and area, panicle weight, harvest index, total nitrogen, chlorophyll a, chlorophyll b, and total chlorophyll, NHI, and grain yield per plant indicating selection for these traits would be effective.

4. In case of qualitative traits, genetic variability was found in early plant vigour, basal leaf sheath, panicle exsertion, stigma colour, panicle type, seed coat colour, and hull colour whereas leaf pubescence, apiculus colour, and awning shows no variability.
5. Based on the relative magnitude of D^2 statistics, the genotypes were grouped into 5 clusters. The highest intra-cluster distances were recorded for Cluster 3 and Cluster 5 while the highest inter-cluster distance was recorded between 3 and 5 followed by Cluster 2 and 4. However, Cluster 1, 2 and 3 exhibited higher mean values for most of the important traits, hence genotypes from these 3 clusters could be used as parents in hybridization programme to develop high yielding N use efficient genotypes.
6. Genotypes in cluster 3 and 4 viz., Taposen Youli, Yarba (SARS−3), Shyekenyii, Tsushvuri and Amusu had the highest levels of variability.
7. Genotypes from clusters 1 and 3 have desirable characteristics (grain N%, PNUE, NUtE, BY, and NHI) such as Thupfu Lha, RCM-9, and Taposen Youli may be selected for intercrossing.
8. Check variety RCM-9 falls under Cluster 1 which has high values for days to 50% flowering and days to maturity.
9. The correlation analysis revealed that grain yield per plant had moderate to strong positive correlation with panicle weight, spikelet fertility, harvest index, NUtE and 100 grain weight both at genotypic and phenotypic levels, respectively. Therefore, these traits can be used as primary selection criteria for improving NUE in rice.
10. High positive direct effects of grain N%, harvest index and NUtE on grain yield were found by path coefficient analysis at genotypic and phenotypic levels.

11. Grain N%, harvest index and NUtE are the main direct contributor to the total variation in grain yield, thus these three traits should be given prior attention for genetic improvement of grain yield in rice.
12. The pooled analysis of variance showed that genotypes varied significantly across environments for all the characters.
13. The characters panicle length, spikelet fertility, PNUE, NUtE, NHI, GN%, 100 grain weight, and grain yield per plant were also found to have strong linear GxE interactions.
14. In the present investigation, Kezie (SARS-94) and RCM-9 were found to have above average stability for grain yield per plant. Thus, these could be considered as potential genotypes for general adaptability to all the environments. Among all the genotypes, Kezie (SARS-94) exhibited above average stability for harvest index, grain N%, NUtE, NHI and grain yield per plant.
15. Since the genotype Kezie (SARS-94) possessed stability for grain yield per plant along with NUtE this genotype would be suitable for N non-limiting environment.
16. Among 29 traits studied, for grain yield per plant Tsushvuri performed the best across all the three environments.
17. Among the three environments, environment 2 and 3 (E_2 and E_3) were considered favourable in terms of environmental index.
18. Correlation based on stability parameters suggested that the mean performances, responses and stability of the genotypes for various characters were relatively independent to each other.

CONCLUSION

In Nagaland, upland rice is grown predominantly during *Kharif* season and NUE of rice is low due to higher leaching, runoff and denitrification during the season. As the state N fertilizer consumption for rice cultivation is very low, there is a need for identification and development of high

yielding N use efficient genotypes. In the present investigation, Kezie (SARS-94) exhibited better mean performance and stability for yield and its component characters can be used for general cultivation or breeding for both N limiting and non-limiting conditions. The genotypes Thupfu Lha, Amusu and Tsushvuri may also be utilized in breeding programme for developing N responsive HYVs. Thus, this study justifies initiation of a new programme for development of N use efficient cultivars especially for rainfed upland rice ecosystem of Nagaland making use of potential genetic material identified through the present investigation.

FUTURE PROSPECTS

1. As the present study was conducted with only 28 upland rice genotypes of Nagaland, screening large number of genotypes only for NUE would be helpful in identifying N use efficient genotypes.
2. This study further supports the utilization of potential genetic material present in the genotypes for the development of nitrogen use efficient varieties in rainfed upland rice.
3. Further investigation utilizing biochemical and molecular analysis of the aforementioned varieties is warranted.
4. The best genotypes that lack one or two important characters can be improved by incorporating them into crossing programs.

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APPENDICES

Appendix I

Meteorological Data recorded at ICAR Medziphema during the period of study (April 2021 to December 2021)

Month	Temperature (ºC)		Relative Humidity (%)		Total Rainfall (mm)	Avg. Sunshine hour (h)
	Max	Min	Max	Min		
April	33.1	17.9	87	34	59.6	7.0
May	32.8	21.9	90	58	85.4	4.7
June	33.1	24.3	93	69	117.4	3.4
July	33.3	24.8	92	72	272.2	3.9
August	32.6	24.6	93	72	138.8	3.2
September	33.1	23.8	94	68	116.2	5.9
October	32.1	22.1	95	68	130.0	6.4
November	28.5	14.8	96	51	0.0	7.9
December	25.1	11.3	95	51	16.4	6.3

Appendix II

Meteorological Data recorded at ICAR Medziphema during the period of study (April 2022 to December 2022)

Month	Temperature (ºC)		Relative Humidity (%)		Total Rainfall (mm)	Avg. Sunshine hour (h)
	Max	Min	Max	Min		
April	30.9	19.9	90	68	175.7	4.2
May	30.5	21.9	92	71	224.4	4.0
June	32.0	23.9	95	72	160.8	2.6
July	33.6	24.3	92	69	375.8	5.0
August	33.3	24.1	94	70	261.8	4.8
September	33.0	23.8	91	69	161.2	5.2
October	30.5	21.3	94	69	94.8	5.3
November	28.4	14.8	96	58	0.0	8.0
December	25.7	11.7	96	53	15.4	6.3

Appendix III

Stability parameters of grain yield, yield components, NUE and its yield related traits in 28 upland rice genotypes

S.No	Name of genotype	Germination percentage			Days to 50% flowering			Days to maturity			Plant height		
		Mean	b1	s2di	Mean	b1	s2di	mean	b1	s2di	Mean	b1	s2di
1	Sungmangtsuk (SARS-1)	70.00	6.02	-60.61	70.00	6.02	-60.61	135.61	-12.61	-0.11	108.92	0.69	-1.09*
2	Apuapa (SARS-61)	26.67	2.29	-60.61	66.67	5.73	-60.61	137.33	9.45	0.40**	112.79	1.39	31.78
3	Kezie (SASRS-94)	71.67	6.16	-60.61	90.00	7.74	-60.61	134.5	1.1	0.2	112.49	0.92	-3.11
4	Korea Tsuk	96.67	8.30	-60.61	31.11	20.00	-60.61	134.72	14.04	-0.14*	113.71	0.49	39.04
5	Longkhum Tsuk (SASRS-2)	92.22	10.00	-60.41	76.11	2.00	-60.41	135.78	-6.27	0.02	122.78	3.06	6.11***
6	Yarba (SARS-3)	36.67	3.15	-60.61	66.67	5.73	-60.61	138.56	-0.4	-0.14	110.03	2.9	10.99***
7	Tsushvuri	93.33	8.03	-60.61	26.67	2.29	-60.61	135.22	-4.28	-0.08*	115.18	0.45	10.53
8	Chali	90.00	7.74	-60.61	100.00	8.59	-60.61	135.56	-3.95	1.32	121.12	1.29	-4.29
9	Chishoghi	73.33	6.30	-60.61	67.78	-4.00	-60.61	133.89	-0.48	-0.14	126.76	2.86	-4.47***
10	Thangmo Red	66.67	5.73	-60.61	93.33	8.03	-60.61	137.5	2.78	0.05	134.03	1.47	6.08
11	Thangma White	90.00	7.74	-60.61	73.33	6.30	-60.61	133.94	0.48	-0.14	125.67	1.09	26.09
12	Chahashye	31.11	20.00	-59.82	26.67	2.29	-59.82	134.22	-0.4	-0.14	139.84	-0.09	6.01
13	Taposen Youli	76.11	2.00	-58.83	90.00	7.74	-58.83	135.22	-9.68	-0.13**	122.04	0.83	20.95
14	Kedayishye	66.67	5.73	-60.61	76.67	6.59	-60.61	135.78	-0.87	-0.16	125.76	0.11	116.89
15	Shyekenyii	26.67	2.29	-60.61	86.67	7.45	-60.61	136.28	-2.14	-0.14	138.52	0.82	6.37
16	Amusu	100.00	8.59	-60.61	90.00	7.74	-60.61	136.28	4.36	-0.15*	148.84	-0.05	1.33
17	Ongpangsuk	67.78	-4.00	-53.47	93.33	8.03	-53.47	135.17	2.37	0.37	134	-0.27	-0.74
18	Moyatsuk	93.33	8.03	-60.61	28.89	-20.00	-60.61	134	1.57	-0.16	141.07	0.86	-3.33
19	Sulijak	73.33	6.30	-60.61	27.78	20.00	-60.61	134.78	-0.95	-0.1	143.87	1.89	-3.7
20	Moya Chali	90.00	7.74	-60.61	66.67	5.73	-60.61	135.11	0.8	0.96	139.33	0.79	12.92
21	Tsungmiki	76.67	6.59	-60.61	90.00	7.74	-60.61	134.89	-3.95	1.32	146.95	0.79	42.1
22	Manen Red (SARS-5)	86.67	7.45	-60.61	71.67	6.16	-60.61	134.44	12.13	-0.04	123.49	1.29	-4.78
23	Pfukhi Lha	90.00	7.74	-60.61	96.67	8.30	-60.61	135.33	10.06	1.44*	118.98	1.13	-2.08
24	Rosho Lha	93.33	8.03	-60.61	92.22	10.00	-60.61	135.22	4.59	0.24	106.9	0.72	47.57
25	Tungo	28.89	-20.00	-59.82	36.67	3.15	-59.82	134.94	0.31	-0.03	139.37	2.12	46.86
26	Ngoni	27.78	20.00	-59.82	93.33	8.03	-59.82	142.83	5.23	-0.15	101.65	-0.4	24.26
27	Thupfu Lha	66.67	5.73	-60.61	90.00	7.74	-60.61	161.11	5.71	-0.15*	100.14	0.3	-4.95
28	RCM-9	90.00	7.74	-60.61	73.33	6.30	-60.61	170.06	0.55	0.74	82.03	0.54	10.53

Signifcance at 1% level of probability-**, Signifcance at 5% level of probability-*

Stability parameters of grain yield, yield components, NUE and its yield related traits in 28 upland rice genotypes (*contd…*)

S.No	Name of genotype	Flag leaf length			Flag leaf breadth			Flag leaf area			No. of ear bearing tillers		
		mean	b1	s2di	mean	b1	s2di	mean	b1	s2di	mean	b1	s2di
1	Sungmangtsuk (SARS-1)	34.82	-0.17	-1.16	2.08	9.78	0.02**	53.81	-2.9	12.02	12.78	0.12	0.02
2	Apuapa (SARS-61)	43.61	1.56	-1.16	2.13	-7.34	0.01	69.97	5.73	16.94*	13.78	-1.08	-0.05
3	Kezie (SASRS-94)	45.02	1.38	-0.08	2.25	-12.36	0.01	76.04	12.49	-3.52	14.06	1.08	-0.05
4	Korea Tsuk	42.97	0.66	-1.14	2.29	-6.8	0	73.97	6.49	-1.9	14.39	2.59	1.77**
5	Longkhum Tsuk	38.5	-0.72	-1.13	2.06	-1.23	0	59.35	-0.06	-2.98	15.72	2.27	0.03
6	Yarba (SARS-3)	23.41	-1.53	-0.29	2	-4.62	0	35.1	-1.18	-2.65	15.11	-0.56	0.24
7	Tsushvuri	30.77	2.02	2.02	2.08	-17.14	0.02**	48.08	10.56	37.24**	15.06	-0.27	0.29
8	Chali	33.01	1.28	0.75	2.17	3.39	0	53.64	0.32	8.53	14.11	-0.23	-0.04
9	Chishoghi	34.78	0.77	-0.74	2.18	9.44	0	56.71	-4.33	-2.95	13.78	0.12	0.02
10	Thangmo Red	39.09	0.19	-0.22	2.21	-7.82	0	64.67	4.61	8.88	13.67	1.04	0.23
11	Thangma White	25.51	2.18	0.21	2.02	-2.37	0	38.59	5.13	-3.53	14.78	0.12	0.02
12	Chahashye	36	0.03	-0.24	2.08	11.11	0.01**	56.16	-5.03	20.35**	15.11	0.32	1.62
13	Taposen Youli	28.61	0.55	-0.27	1.72	-2.25	0	36.57	0.89	-3.34	15.06	0.23	-0.04
14	Kedayishye	44.18	6.42	32.52*	2.02	8.59	0	66.61	6.46	74.53**	13.67	1.19	0.05
15	Shyekenyii	16.93	0.37	-0.05	2.06	-1.81	0.01	26.04	1.26	5.8	14.44	1.49	0.07
16	Amusu	41.32	0.07	2.34	2.03	1.23	0	62.72	-1.59	-1.33	14.06	3.12	0.55***
17	Ongpangsuk	31.57	0.66	-1.15	1.69	-1.69	0	40.52	0.19	-3.37	15.17	3.6	0.04***
18	Moyatsuk	39.2	1.6	0.36	2.09	1.98	0	61.59	1.88	0.33	14.56	3.33	0.72***
19	Sulijak	35.58	0.31	-0.99	1.63	11.92	0.08**	45.86	-14.7	-2.9	15.72	0.9	0.08
20	Moya Chali	36.61	-0.99	-1.15	2.18	3.31	0.01	59.83	-4.64	-0.05**	13.39	2.47	0.51*
21	Tsungmiki	26.77	-0.19	4.62	2.08	3.41	0.01	41.62	-3.39	0.05	14.06	0.41	0.05
22	Manen Red (SARS-5)	34.33	1.39	-0.57	1.92	5.01	0	49.7	-0.76	-0.88	13.94	1.31	-0.05
23	Pfukhi Lha	28.27	2.02	-0.47	2.08	1.87	0.01	44.04	4.19	-0.61	14.06	0.74	-0.03
24	Rosho Lha	27.98	0.35	-0.85	1.69	4.43	0	35.32	-2.25	-3.52	14.06	1.58	0.35
25	Tungo	28.83	2.77	4.24	2.17	6.12	0	46.31	3.03	15.54	15	1.7	0.08
26	Ngoni	43.68	2.21	0.76	2.26	-5.45	0.01	74.83	7.6	1.5	13.67	1.19	0.05
27	Thupfu Lha	34.2	1.95	1.17	1.96	10.82	0.02**	59.25	-3.32	11.42**	15.61	-1.28	1.08***
28	RCM-9	27.91	0.87	-0.81	1.38	6.47	0.05	32.38	1.34	-3.17	15.5	0.5	0.4

Signifcance at 1% level of probability-**, Signifcance at 5% level of probability-*

Stability parameters of grain yield, yield components, NUE and its yield related traits in 28 upland rice genotypes (*contd…*)

S.No	Name of genotype	Panicles per plant			Panicle length			Panicle weight			Spikelet fertility		
		mean	b1	s2di	mean	b1	s2di	mean	b1	s2di	mean	b1	s2di
1	Sungmangtsuk (SARS-1)	5.06	0.97	-0.01	26.86	-6.38	-0.65***	2.67	0.15	-0.01	77.96	-2.19	-19.2
2	Apuapa (SARS-61)	5.44	0.11	-0.04	23.66	6.42	-0.70***	4.99	0.03	0.13	76.96	-2.65	-20.06
3	Kezie (SASRS-94)	5.72	0.75	0.14	31.09	0.96	-0.62	4.74	-1.56	-0.03**	84	-2.31	-17.77
4	Korea Tsuk	5.61	0.54	0.05	28.27	1.95	2.62	3.16	-0.7	0.01	61.25	-0.65	3.09
5	Longkhum Tsuk	5.67	1.72	0.06	27.92	-1.4	-0.5	3.49	-0.16	0.01	75.68	4.99	-12.02
6	Yarba (SARS-3)	5.33	1.08	0.06	27.66	1.49	1.77	4.66	1.47	0.12	84.05	2.25	-16.32
7	Tsushvuri	5.83	3.12	0.10**	26.33	3.12	0.1	4.57	4.06	0.27**	85.5	5.57	-13.56
8	Chali	5.5	1.08	0.06	24.96	4.31	-0.51**	4.3	0.58	0.33	72.48	1.55	-5.41
9	Chishoghi	5.44	1.94	0.12	25.13	0.42	4.84	3.33	0.89	0.28	78.44	11.27	-16.27***
10	Thangmo Red	5.06	0.86	0.12	23.26	-0.04	2.37	2.66	1.93	0.1	66.17	-2.45	-16.28
11	Thangma White	5.56	-1.4	0.01***	24.73	0.24	-0.35	2.45	1.02	0.06	87.87	0.8	-14.62
12	Chahashye	6	1.29	-0.04	26.77	1.94	0.45	3.59	1.65	0.38	78.81	7.46	-19.54**
13	Taposen Youli	5.78	0.86	-0.05	30.39	0.54	-0.69	3.05	1.44	0.02	77.51	-4.27	-11.83
14	Kedayishye	5.5	-0.22	0	30.2	0.94	-0.22	4.73	0.68	0.06	81.24	5.09	-18.04
15	Shyekenyii	5.11	2.37	-0.05	27.74	2.82	-0.29	3.39	2.14	0.37*	76.26	6.67	-10.81
16	Amusu	5.33	0.32	0.1	26.76	2.63	1.77	4.87	-0.81	0.74**	83.46	4.24	-14.56
17	Ongpangsuk	4.94	-0.86	0.12**	25.49	0.04	-0.66	4.54	-2.39	0.17***	80.32	-7.32	-20.11*
18	Moyatsuk	5.28	0.86	-0.05	30.27	0.19	1.13	4.61	2.76	0.06*	80.37	1.3	-19.43
19	Sulijak	5.78	0.32	-0.04	26.9	0.26	0.31	3.71	-2.22	-0.03**	84.43	4.33	-20.17
20	Moya Chali	5.28	2.37	-0.05	26.96	1.5	2.25	5.02	0.52	0.05	81.25	1.86	-19.76
21	Tsungmiki	5.28	1.08	-0.03	30.61	0.45	-0.69	4.13	4.17	0.07**	64.47	7.28	2.45
22	Manen Red (SARS-5)	5	1.18	0.21	27.55	2.3	-0.69	3.4	3.66	0	82.59	-3.44	-8.88
23	Pfukhi Lha	5.44	-1.29	0.31***	27.83	0.33	-0.66	4.63	0.26	0.06	84.72	-1.93	-16.72
24	Rosho Lha	5.11	3.45	0.04***	30.19	-1	-0.41	3.63	1.08	0.05	67.56	-3.18	-10.16
25	Tungo	5.22	2.69	-0.04	27.4	-0.08	-0.35	4	1.68	0.19	70.5	0.23	-14.24
26	Ngoni	5.5	1.94	0.27	28.69	-0.16	0.45	3.73	1.47	-0.01	55.07	-11.14	15.32
27	Thupfu Lha	5.94	0.32	-0.04	23.02	2.93	1.23	4.66	2.98	-0.03*	81.04	3.2	-20.16
28	RCM-9	5.28	0.54	0.05	22.25	1.29	0.59	3.59	1.22	-0.02	72.99	1.44	-10.43

Signifcance at 1% level of probability-**, Signifcance at 5% level of probability-*

Stability parameters of grain yield, yield components, NUE and its yield related traits in 28 upland rice genotypes (*contd*…)

S.No	Name of genotype	Root length			Root dry weight			Stem dry weight			Harvest index		
		mean	b1	s2di	mean	b1	s2di	mean	b1	s2di	mean	b1	s2di
1	Sungmangtsuk (SARS-1)	26.58	-0.09	5.73	6.29	-0.38	0.00***	12.33	-0.38	-0.02**	20.66	0.88	-4.94*
2	Apuapa (SARS-61)	26.76	1.28	-0.02	6.96	0.31	0.07**	12.47	-0.99	0.12***	27.77	0.45	-5.05
3	Kezie (SASRS-94)	27.04	-7.51	2.82***	7.12	2.42	0.73***	15.18	-0.92	0.32***	31.34	1.27	-4.69
4	Korea Tsuk	25.92	1.27	0.66	6.43	-0.78	0.04***	13.97	0.8	0.45**	25.5	2.08	-5
5	Longkhum Tsuk	27.64	-2.05	6.34***	6.94	0.59	0.01	13.34	2.68	-0.05***	26.9	0.72	-2.58
6	Yarba (SARS-3)	26.78	-4.83	0.01***	7.25	1.19	0.04	14.93	1.79	0.06	23.83	-0.04	-4.09
7	Tsushvuri	27.69	1.49	1.9	7.38	-0.62	-0.02***	14.01	3.69	0.30***	26.64	0.22	-2.19
8	Chali	26.82	1.87	1.65	6.85	-0.02	0.11***	13.84	1.28	-0.05	27.88	1.36	-4.59
9	Chishoghi	26.81	3.06	4.02**	6.9	1.16	-0.02	14.01	0.23	-0.05*	25.45	1.44	-5
10	Thangmo Red	28.37	-2.59	4.33***	7.25	-1.89	1.35*	17.14	0.49	-0.02**	20.78	1.28	-5.05
11	Thangma White	28.59	-0.84	-0.04**	6.98	1.73	0.99**	16.09	2.42	1.76**	28.38	4.8	-5.04***
12	Chahashye	27.14	-4.3	5.52***	7.51	-0.66	2.18***	13.66	-0.06	0.22**	26.79	0.9	-4.28
13	Taposen Youli	28.86	6	-0.04***	7.96	0.47	0	14.63	4.68	0.58***	24.17	3.46	-3.67
14	Kedayishye	27.84	3.54	1.78	6.43	-0.83	0.03***	14.02	-0.38	0.07**	31.69	2.87	-4.24
15	Shyekenyii	26.79	3.21	15.39	6.27	1.86	-0.01**	14.91	-0.24	-0.01**	30.33	2.08	-4.26
16	Amusu	29.97	0.58	0.11	6.4	-0.24	0.14***	16.54	1.42	-0.02	40.76	1.32	-4.16
17	Ongpangsuk	27.19	-0.12	1.1	6.72	1.3	1.72	14.67	4.29	0.13**	19.2	-0.87	-0.79
18	Moyatsuk	27.02	4.87	1.80***	6.88	1.91	0.50**	13.93	-5.03	0.00***	30.86	-3.17	232.03***
19	Sulijak	28.27	3.35	7.85***	6.66	3.23	0.61***	14.24	-1.01	-0.05***	20.92	-0.49	-5.02
20	Moya Chali	27.41	1.94	1.96	6.81	0.34	0.00**	14.64	-1.11	0.22***	38.42	1.32	-3.69
21	Tsungmiki	26.83	-0.13	6.67	7.04	1.73	0.29**	15.76	0.04	0.07*	32.14	-2.09	-3.65
22	Manen Red (SARS-5)	26.2	4.02	3.30***	6.64	1.88	0.09**	14.6	-0.54	-0.05*	43.63	1.05	-4.61***
23	Pfukhi Lha	27.16	1.28	8.2	6.08	3.22	0.41***	12.73	1.55	-0.02	39.93	3.81	-5.02***
24	Rosho Lha	27.61	2.67	4.61**	6.94	1.86	0.04**	13.65	-1.1	0.34***	32.73	-0.34	-1.6
25	Tungo	27.33	5.26	2.94***	6.91	3.33	-0.02	11.87	4.21	0.26***	34.42	-0.05	4.59
26	Ngoni	28.85	-0.66	2.47***	6.97	2.63	0.01	14.54	5.09	0.35***	40.95	0.08	7.09
27	Thupfu Lha	26.59	0.58	5.81	6.45	1.97	0.22***	16.19	4.13	0.05***	41.81	2.84	-1.04
28	RCM-9	27.97	4.85	0.17***	5.77	0.3	0.17*	14.85	0.98	0.02	36.11	0.84	-3.97

Signifcance at 1% level of probability-**, Signifcance at 5% level of probability-*

Stability parameters of grain yield, yield components, NUE and its yield related traits in 28 upland rice genotypes (*contd…*)

S.No	Name of genotype	Total nitrogen			Crude protein			Chlorophyll a			Chlorophyll b		
		mean	b1	s2di	mean	b1	s2di	mean	b1	s2di	mean	b1	s2di
1	Sungmangtsuk (SARS-1)	1.65	2.49	0.18**	6.08	0.91	-0.01*	16.82	-0.52	-3.84***	23.70	1.50	-3.13
2	Apuapa (SARS-61)	1.51	-1.83	0	6.08	0.91	0.25	12.59	1.31	-3.86	21.04	1.65	-3.38
3	Kezie (SASRS-94)	1.87	9.52	0.00*	6.38	-0.51	0.05	10.44	0.42	-3.80***	19.38	2.05	-3.44
4	Korea Tsuk	2.35	0.82	0	6.43	0.54	-0.01**	11.04	0.47	-3.87***	19.96	1.74	-3.46
5	Longkhum Tsuk	2.03	-4.95	0.04*	6.14	1.23	0.27	11.93	0.13	-3.86	19.49	1.77	-3.48
6	Yarba (SARS-3)	2.11	-0.95	0.35	5.56	1.72	0.09**	11.23	1.03	-3.87***	19.57	1.67	-3.40
7	Tsushvuri	1.72	-2.6	0.07*	6.22	1.04	0.33	12.34	0.39	-3.86***	21.64	1.62	-3.33
8	Chali	1.86	6.02	0	6.34	0.96	0.03	11.08	1.78	-3.86***	20.56	1.62	-3.34
9	Chishoghi	2.43	-5.44	0.03*	6.21	0.96	0.1	13.21	-0.3	-3.85***	23.26	0.65	-3.51
10	Thangmo Red	2.19	-5.84	0.02	6.49	1.15	0.59	11.86	1.26	-3.87***	20.57	0.69	-3.51
11	Thangma White	1.59	2.56	0.01*	6.29	1.7	0.39**	11.53	0.48	-3.78***	20.10	-1.27	-3.49
12	Chahashye	1.93	7.71	0	6.13	0.82	0.16**	12.84	0.55	-3.87***	22.61	0.00	-3.51
13	Taposen Youli	2.12	3.04	0.02*	5.99	0.58	0.12**	12.93	0.17	-3.86***	22.38	-0.29	-3.51
14	Kedayishye	2.54	-9.23	0.06	6.47	1.45	0.01**	13.22	1.25	-3.87**	23.18	0.61	-3.51
15	Shyekenyii	2.16	-0.2	0.01	5.93	1.17	-0.01*	11.02	0.35	-3.86***	20.35	0.43	-3.51
16	Amusu	1.94	-2.22	0	6.25	1.3	0.11*	12.11	3.18	-3.87***	21.37	1.15	-3.51
17	Ongpangsuk	2.55	-12.05	0.59	6.35	1.39	-0.01	12.64	-1.1	-3.84***	23.05	0.48	-3.40
18	Moyatsuk	2.48	9.49	0	6.8	0.41	0.04**	11.43	2.31	-3.87***	20.60	0.73	-3.46
19	Sulijak	2.4	-3.32	0.02	6.46	0.89	0.06	12.82	-0.1	-3.79***	22.43	-1.03	-3.03
20	Moya Chali	2.52	7.39	0.07*	6.44	1.55	0.02**	11.67	0.76	-3.86***	20.69	0.09	-3.48
21	Tsungmiki	2.06	4.4	0.07*	6.1	1.22	0.32	22.55	-0.65	-3.87***	30.72	-0.12	-3.44
22	Manen Red (SARS-5)	2.31	6.52	0.00*	6.36	1.32	0.00**	24.58	3.67	-3.87***	34.06	1.21	-3.38
23	Pfukhi Lha	2.11	3.51	0.00*	6.43	0.58	0.09**	25.06	3.15	-3.87***	36.08	0.85	-3.51
24	Rosho Lha	2.47	7.27	0.8	5.93	0.94	0.52**	22.68	5.71	-3.85***	35.65	2.65	-3.09
25	Tungo	2.26	5.04	0.00*	6.09	1.29	-0.01	23.11	-3.18	-3.65***	32.86	1.32	-2.71
26	Ngoni	2.25	-10.24	0.00*	6.77	0.57	-0.01**	23.58	4.89	-3.86***	34.13	1.87	-3.51
27	Thupfu Lha	1.99	6.34	0.01*	6.37	1.2	-0.01	23.97	0.42	-3.70***	32.13	2.41	-2.80
28	RCM-9	1.83	4.73	0.24*	6.1	0.71	0.07	24.09	0.16	-3.87***	31.08	1.93	-3.51

Signifcance at 1% level of probability-**, Signifcance at 5% level of probability-*

Stability parameters of grain yield, yield components, NUE and its yield related traits in 28 upland rice genotypes (*contd*…)

S.No	Name of genotype	Total chlorophyll			Amylose content			Grain N%			PNUE		
		mean	b1	s2di	mean	b1	s2di	mean	b1	s2di	mean	b1	s2di
1	Sungmangtsuk (SARS-1)	21.36	0.05	-2.61	7.24	-1.02	-1.52	1.64	-2.67	-0.004	11.46	0.52	0.39
2	Apuapa (SARS-61)	18.65	0.75	-2.62	6.97	1.51	-1.52	1.82	0.83	-0.004	11.94	0.62	0.22
3	Kezie (SASRS-94)	17.17	-0.12	-2.55	6.19	1.70	-1.51	1.76	1.83	-0.004	12.76	0.09	0.25
4	Korea Tsuk	17.78	0.23	-2.63	10.74	0.76	-1.52	1.72	0.83	-0.004	11.75	0.62	0.70
5	Longkhum Tsuk	17.44	-0.03	-2.63	9.19	0.72	-1.52	1.93	2.50	-0.004	12.51	0.85	-0.01
6	Yarba (SARS-3)	17.38	0.58	-2.62	10.10	2.58	-1.53	1.31	0.17	-0.004	13.38	1.67	0.02
7	Tsushvuri	19.34	0.31	-2.62	8.95	0.06	-1.52	1.56	-3.17	-0.004	12.61	1.25	0.04
8	Chali	18.09	1.18	-2.60	6.85	1.87	-1.52	1.79	-1.17	-0.004	12.21	0.73	0.14
9	Chishoghi	20.63	0.23	-2.61	6.19	-0.97	-1.52	1.80	4.50	-0.004	12.43	0.94	-0.03
10	Thangmo Red	18.21	1.64	-2.63	8.78	1.86	-1.52	1.64	-3.67	-0.004	13.79	1.69	0.75
11	Thangma White	17.85	-0.44	-2.56	10.34	2.76	-1.48	2.07	6.33	-0.004	13.57	0.31	-0.03
12	Chahashye	20.05	0.51	-2.63	10.53	0.67	-1.52	2.01	10.17	-0.004	12.84	1.86	0.09
13	Taposen Youli	19.87	-0.09	-2.63	14.70	1.10	-1.52	1.62	-0.17	-0.004	14.04	0.99	-0.02
14	Kedayishye	20.52	1.48	-2.63	7.83	1.50	-1.53	1.98	-4.00	-0.004	12.10	0.79	1.42
15	Shyekenyii	18.03	0.67	-2.63	9.06	0.01	-1.52	1.43	-2.50	-0.004	12.23	1.14	-0.03
16	Amusu	18.88	2.69	-2.62	6.80	1.89	-1.52	1.78	5.00	-0.004	12.64	1.71	0.46
17	Ongpangsuk	20.46	-1.57	-2.57	8.61	-1.09	-1.52	1.59	-2.33	-0.004	12.29	2.31	0.06
18	Moyatsuk	18.28	2.00	-2.63	8.84	1.84	-1.52	2.04	3.33	-0.004	11.84	0.94	0.07
19	Sulijak	19.90	3.26	-2.38	6.81	1.93	-1.51	2.18	4.17	-0.004	12.20	0.36	0.50
20	Moya Chali	18.36	1.21	-2.62	8.06	0.82	-1.52	2.06	4.67	-0.004	12.40	1.32	0.52
21	Tsungmiki	27.31	1.56	-2.61	10.08	1.00	-1.52	1.83	4.67	-0.004	13.02	0.75	0.38
22	Manen Red (SARS-5)	30.27	3.16	-2.63	6.64	0.98	-1.53	1.63	-1.33	-0.004	12.30	0.58	-0.01
23	Pfukhi Lha	32.07	0.32	-2.60	9.05	0.04	-1.52	1.77	1.50	-0.004	10.98	1.24	0.85
24	Rosho Lha	31.66	6.09	-2.61	7.07	1.98	-1.52	1.52	0.83	-0.004	12.29	0.68	0.41
25	Tungo	29.17	-2.82	-2.60	8.00	-1.05	-1.52	1.88	4.00	-0.004	11.69	0.96	2.55
26	Ngoni	31.23	-1.33	-2.62	7.55	1.70	-1.52	2.05	-4.00	-0.004	12.72	1.20	1.11
27	Thupfu Lha	29.22	5.48	-2.54	7.15	1.96	-1.51	1.88	-1.00	-0.004	12.72	1.29	0.01
28	RCM-9	30.75	1.03	-2.63	7.37	0.89	-1.52	1.73	-1.33	-0.004	11.74	0.61	-0.02

Signifcance at 1% level of probability-**, Signifcance at 5% level of probability-*

Stability parameters of grain yield, yield components, NUE and its yield related traits in 28 upland rice genotypes (*contd…*)

S.No	Name of genotype	NUtE			BY			NHI			100 grain weight			Grain yield per plant		
		mean	b1	s2di	mean	b1	s2di	mean	b1	s2di	mean	b1	s2di	mean	b1	s2di
1	Sungmangtsuk (SARS-1)	7.03	0.35	0.06	30.22	-7.95	-120.90	50.91	-2.29	-0.08	2.55	0.01	-1.22	3.56	0.48	0.02
2	Apuapa (SARS-61)	7.76	1.42	0.00	20.52	-6.41	-120.79	53.57	0.82	-2.39	4.67	0.00	-1.22	5.42	0.5	0
3	Kezie (SASRS-94)	7.53	1.13	-0.01	20.96	8.66	-120.90	50.58	1.81	-2.39	4.34	-0.04	-1.22	4.66	1.34	0
4	Korea Tsuk	7.52	0.94	-0.01	22.42	1.17	-120.90	50.58	0.82	-2.39	3.87	-0.01	-1.22	4.18	12.39	0.06**
5	Longkhum Tsuk	7.19	-0.25	0.08	26.99	2.38	-120.90	55.22	2.47	-2.38	3.77	0.13	-1.22	3.83	0.08	0
6	Yarba (SARS-3)	8.82	2.87	0.09	21.71	-4.11	-120.84	38.97	0.16	-2.39	4.17	0.18	-1.22	5.49	0.81	0
7	Tsushvuri	8.62	2.55	1.24	19.66	-3.83	-120.89	49.59	-3.13	-2.37	7.55	25.67	-1.22	6.64	0.48	0
8	Chali	7.56	0.70	0.04	19.42	-7.47	-120.83	54.56	-1.15	-2.39	4.33	1.29	-1.22	4.85	0.43	0
9	Chishoghi	7.53	1.18	0.55	19.56	-4.75	-120.89	49.25	4.45	-2.34	3.58	0.43	-1.22	4.21	9.82	0.28**
10	Thangmo Red	7.61	-1.28	-0.01	20.30	7.57	-120.88	52.57	-3.62	-2.36	2.77	-0.04	-1.22	3.83	0.51	0
11	Thangma White	7.56	-0.14	1.05	22.57	6.31	-120.89	55.56	6.26	-2.30	2.83	0.05	-1.22	3.72	-1.89	0.05**
12	Chahashye	7.86	0.91	1.53	22.45	1.87	-120.90	49.92	10.04	-2.14	4.32	-0.01	-1.22	4.48	0.06	0
13	Taposen Youli	7.33	-1.28	0.07	83.25	-8.39	-120.62	48.59	-0.16	-2.39	3.16	0.21	-1.22	3.26	0.34	0
14	Kedayishye	7.30	-0.65	0.02	20.61	-0.59	-120.90	63.18	-3.95	-2.36	4.18	0.10	-1.22	4.34	-0.16	0
15	Shyekenyii	7.74	1.61	0.51	22.59	-8.98	-120.77	45.27	-2.47	-2.38	4.15	-0.07	-1.22	4.58	0.54	0
16	Amusu	8.60	2.67	0.38	28.65	1.02	-120.88	48.26	4.94	-2.33	4.62	-0.01	-1.22	6.3	0.19	0
17	Ongpangsuk	7.74	1.51	0.33	25.39	7.39	-120.71	49.92	-2.30	-2.38	4.61	0.00	-1.22	4.95	0.54	0
18	Moyatsuk	7.29	0.63	0.10	24.73	10.36	-120.76	57.55	3.29	-2.37	5.34	-0.01	-1.22	5.1	-12.2	0.43**
19	Sulijak	6.95	0.43	0.45	28.97	1.35	-120.89	60.86	4.12	-2.35	4.16	0.01	-1.22	3.73	10.4	0.39**
20	Moya Chali	7.88	0.85	0.28	23.48	0.82	-120.90	56.88	4.61	-2.34	4.65	-0.09	-1.22	5.57	-0.69	0
21	Tsungmiki	7.89	1.86	0.27	29.23	6.29	-120.82	49.92	4.61	-2.34	4.64	0.00	-1.22	5.07	0.09	0
22	Manen Red (SARS-5)	7.46	1.05	0.11	26.67	3.39	-120.89	49.92	-1.32	-2.39	3.60	0.46	-1.22	4.28	0.71	0
23	Pfukhi Lha	7.23	2.52	0.10	23.25	5.86	-120.88	51.24	1.48	-2.39	4.54	-0.08	-1.22	4.79	0.76	0
24	Rosho Lha	7.59	1.76	0.30	20.78	8.18	-120.86	44.61	0.82	-2.39	4.16	0.02	-1.22	4.47	0.17	0.15
25	Tungo	7.24	2.43	0.00	24.30	-1.63	-120.89	52.24	3.95	-2.36	4.55	-0.05	-1.22	4.63	0.37	0
26	Ngoni	7.02	-0.08	0.06	21.13	1.25	-120.90	65.17	-3.95	-2.36	3.87	0.01	-1.22	4.24	0.46	0
27	Thupfu Lha	8.01	1.48	0.15	21.71	0.49	-120.90	57.21	-0.99	-2.39	4.64	-0.23	-1.22	6.28	0.32	0
28	RCM-9	7.23	0.83	0.08	26.14	7.75	-120.88	52.90	-1.32	-2.39	3.74	0.06	-1.22	4.19	1.15	0

Signifcance at 1% level of probability-**, Signifcance at 5% level of probability-*

Plate 1a. General view of the experimental plot

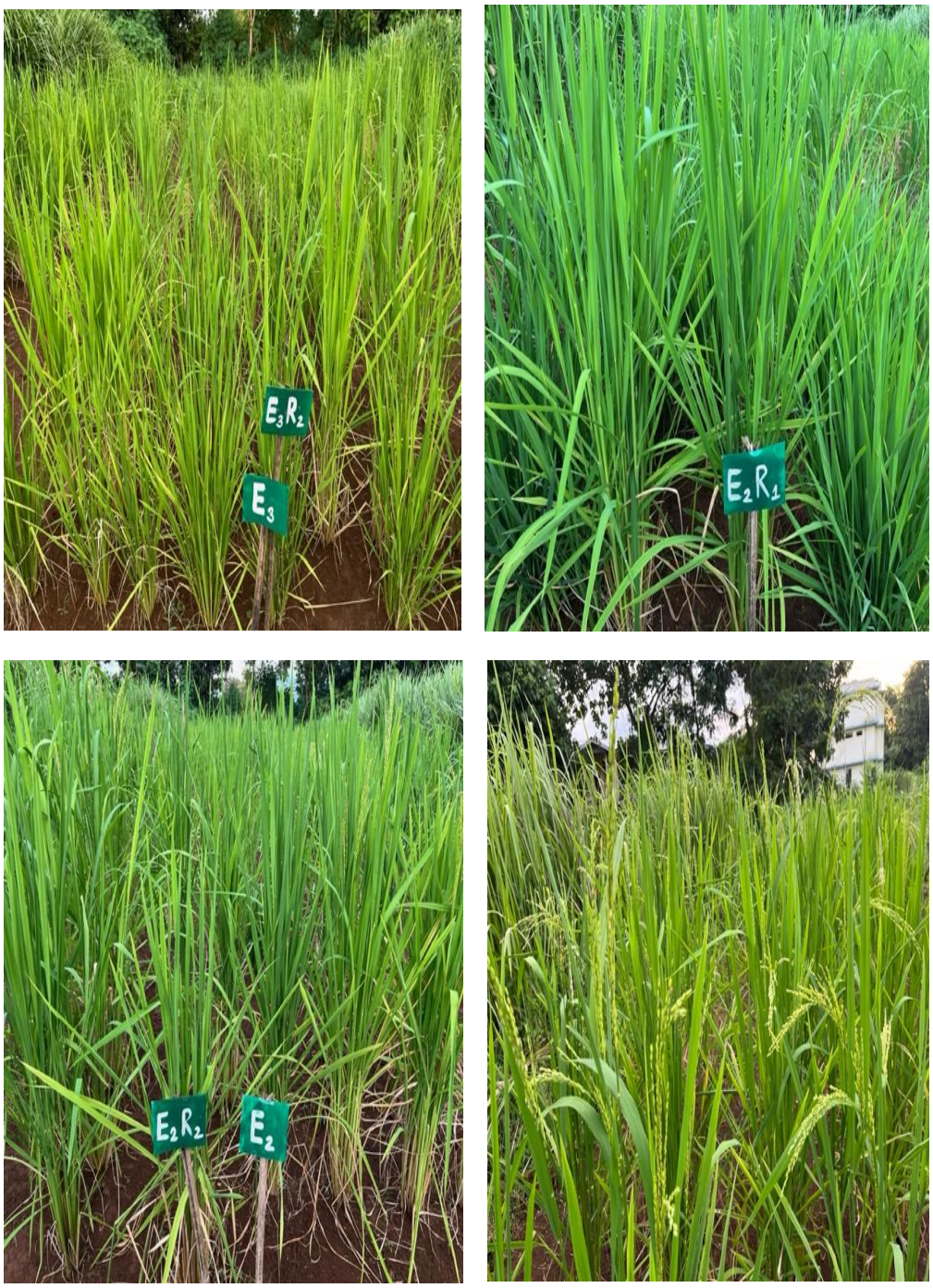
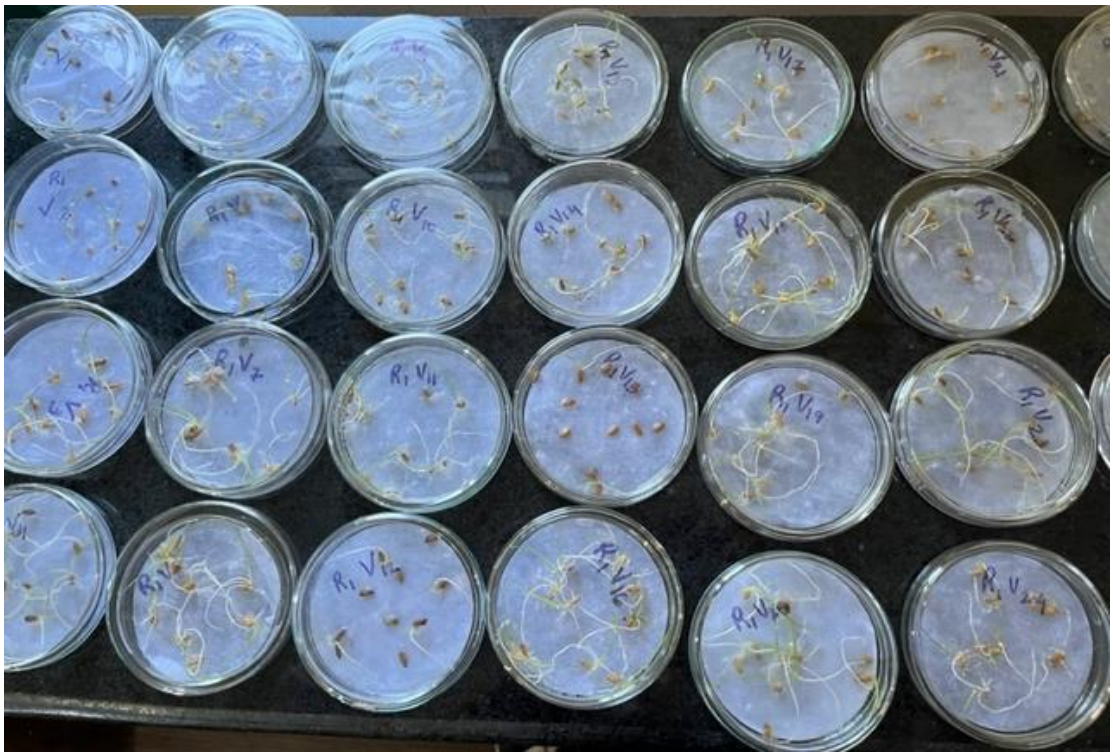


Plate 1b. General view of the experimental plot

Plate 2. Rice plant infected by brown spot in the field

Plate 3. Rice plant infested by gundhi bug and termites

Plate 4. Estimating nitrogen using Micro-Kjeldahl method



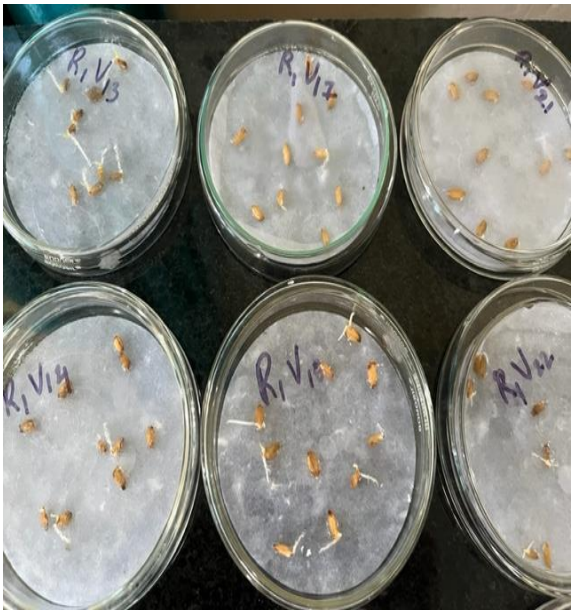


Plate 5. Germination percentage among 28 upland rice genotypes

Plate 6. Amylose content estimation using spectrophotometer

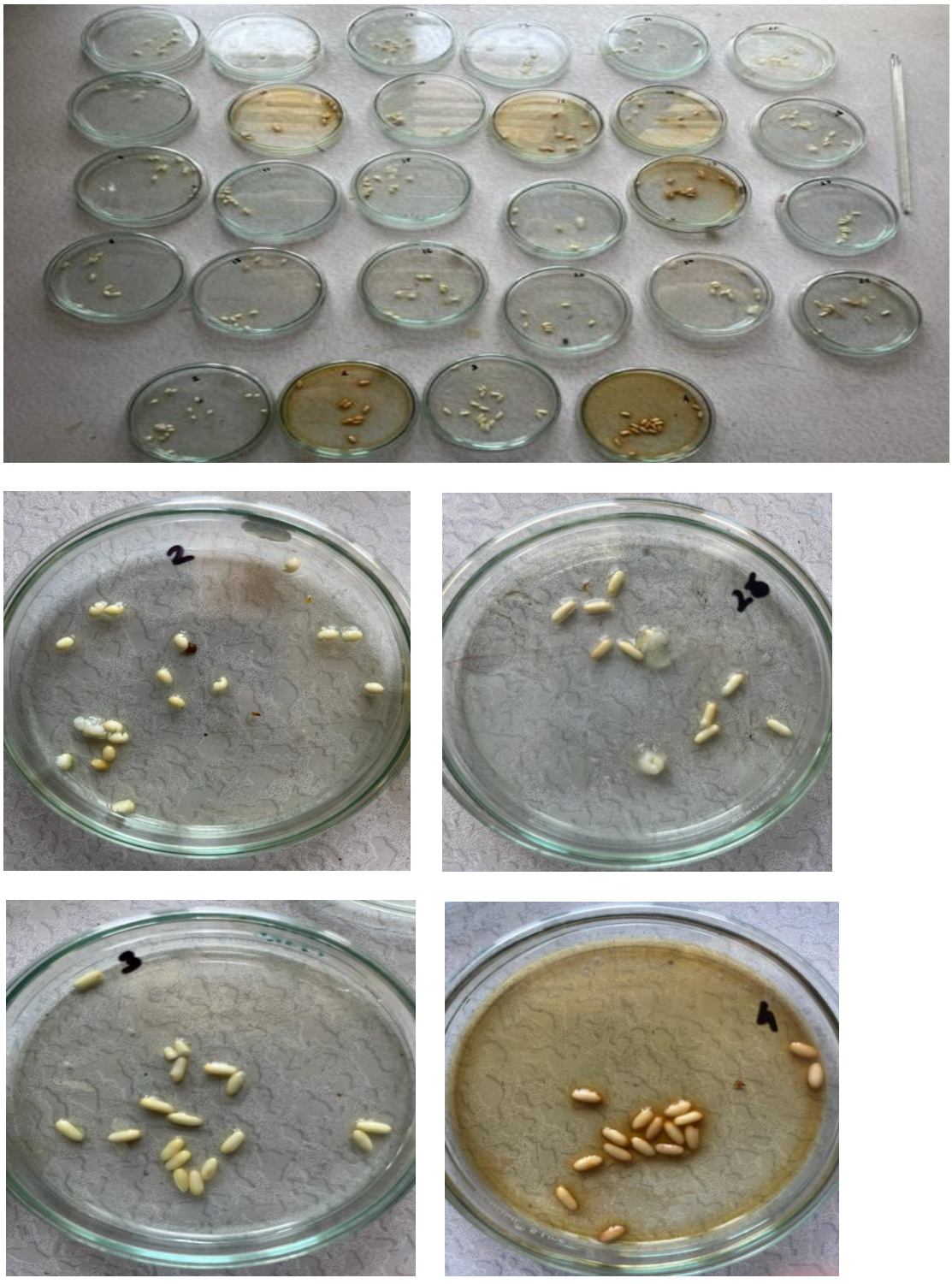


Plate 7. Estimation of Gelatinization temperature (°C) in rice genotypes