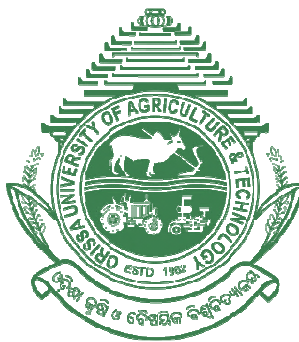


Genetic study of yield variation in lowland rice genotypes

*A Thesis submitted to the
Orissa University of Agriculture and Technology
in Partial fulfilment of the Requirement for the degree of
Master of Sciences in Agriculture
(Plant Breeding and genetics)*

By

VUPPULURI MYTHILI
Adm. No. 02PBG/15



**DEPARTMENT OF PLANT BREEDING AND GENETICS
COLLEGE OF AGRICULTURE
ORISSA UNIVERSITY OF AGRICULTURE AND TECHNOLOGY
BHUBANESWAR
2018**



**ORISSA UNIVERSITY OF AGRICULTURE & TECHNOLOGY
DEPARTMENT OF PLANT BREEDING AND GENETICS
COLLEGE OF AGRICULTURE
BHUBANESWAR**

Dr. B. Pradhan
Professor

Bhubaneswar
Date: 13/6/18

CERTIFICATE - I

This is to certify that the thesis entitled “**Genetic study of yield variation in lowland rice genotypes**” submitted in partial fulfilment of the requirements for the award of the degree of **MASTER OF SCIENCE IN AGRICULTURE (PLANT BREEDING AND GENETICS)** to the Orissa University of Agriculture and Technology is a faithful record of *bona fide* and original research work carried out by **VUPPULURI MYTHILI** under my guidance and supervision. No part of this thesis has been submitted for any other degree or diploma.

It is further certified that the assistance and help received by her from various sources during the course of investigation has been duly acknowledged.

Banshidhar Pradhan
Chairman
Advisory committee 13/6/18



**ORISSA UNIVERSITY OF AGRICULTURE & TECHNOLOGY
DEPARTMENT OF PLANT BREEDING AND GENETICS
COLLEGE OF AGRICULTURE
BHUBANESWAR**

CERTIFICATE II

This is to certify that the thesis entitled "**Genetic study of yield variation in lowland rice genotypes**" submitted by **VUPPULURI MYTHILI** to the Orissa University of Agriculture and Technology, Bhubaneswar, in partial fulfilment of the requirements for the degree of **MASTER OF SCIENCE IN AGRICULTURE (PLANT BREEDING AND GENETICS)** has been approved by the student's advisory Committee and the external examiner.

Advisory Committee

Chairman: Dr. B. Pradhan
Professor & Head
Dept. of Plant Breeding & Genetics
CA, OUAT, Bhubaneswar

Bans. Pradhan
22/6/18

Members:

1. **Dr. D. Mishra**
Plant Breeder
AICRN on Potential Crops
CA, OUAT, Bhubaneswar

D. Mishra
22/6/18

2. **Dr. G.R. Rout**
Professor & Head
Dept. of Agril. Biotechnology
CA, OUAT, Bhubaneswar

G. Rout
22/6/18

M. Kar
22.6.18
External examiner

(Name and Designation)
(**Dr. Meera Kumari Kar**)
Principal Scientist
ICAR-NRRI, Cuttack

ACKNOWLEDGEMENT

Expression is not enough to express my deep and profound sense of gratitude and indebtedness, reverence and heartfelt thanks to my major advisor and chairman of advisory committee Dr. B. Pradhan, Professor and Head, Department of Plant Breeding and Genetics, College of Agriculture, OUAT, Bhubaneswar, for his painstaking guidance, great suggestions, constructive criticism and constant encouragement right from the conceptualization of the research work to preparation of the thesis.

It gives me immense pleasure to express my heartfelt thanks to Dr. G.R. Rout, Professor and Head, Department of Agricultural Biotechnology, college of Agriculture, OUAT, Bhubaneswar, member of the advisory committee for his generous advice and constant inspiration during the course of my study and investigation.

It gives me immense pleasure to express my heartfelt thanks to Dr. D.N. Mishra Breeder AICRN on potential crops, OUAT, Bhubaneswar as member of the Advisory Committee for his generous advice and constructive suggestions during the course of this scientific investigation.

I take this rare opportunity and proud privilege to extend my heartfelt and deep sense of gratitude to Honorary Professor Dr.S.R. Das, Professors Dr. D.N. Bastia, Dr. T.K. Mishra, , Assoc. Professor Dr. (Mrs.) Mansi Dash Dr.D. Lenka and (Mrs.) J. Kar, Asst. Professor of the Department of Plant Breeding and Genetics, for their valuable advice and encouragement during the course of investigation. I am highly obliged to Dr. M.C. Patnaik, Ex-Professor and Head, Department of Plant Breeding and Genetics, for CA, OUAT, BBSR, for his sustained help in developing the computer programmes for analysis of the experimental data and constructive suggestions for improvement of the manuscript.

I feel dearth of words to express my obligation and indebtedness to my parents, my sister and my dear friends, whose blessings, affection and constant inspiration lifelong dedication have helped my progress despite my odds in life.

I once again extend my gratitude to all those who have generously lend their helping hand for this endeavour.

Bhubaneswar
Date: 13/06/18.

V. Mythili
Vuppuluri Mythili
Admn. No. 02PBG/15

ABSTRACT

Rice plays a prominent role in Indian agriculture as it is the staple food for two third of the population of the country. Rice is grown under various climatic conditions of which lowland rice occupies an area about 14.4 million hectares, which accounts for 32.4 % of the total area under rice crop in the country. Productivity in rainfed lowland areas is typically very low, with yields of 1–2.5 t/ha. There is an urgent need to identify high yielding genotypes suitable for lowland condition. The goal intended to attain through this present experimentation “Genetic study of yield variation in lowland rice genotypes” was to study genetic basis of variability for yield and yield attributes, character association, construction of selection indices and genetic divergence among 34 lowland rice genotypes. The Present experiment was carried out during *kharif*, 2017, at Rice Research Station, Dept of Plant Breeding and Genetics, College of Agriculture, OUAT, Bhubaneswar. Observations were recorded for twelve characters containing eleven metric traits such as Days to 50% flowering, Plant height, Number of Productive tillers, Flag leaf Area, Panicle length, Panicle Exsertion, Spikelet Fertility %, Number of Fertile Grains per panicle, Panicle weight, 100grain weight, Single plant yield and a qualitative character cellulose.

The analysis of variance revealed that there exists a highly significant difference among the test genotypes for all the characters under study. This indicate the presence of wide genetic variability among the selected genotypes which was supported by mean performance, variance and range. The phenotypic coefficient of variation was found to be higher than that of genotypic coefficient of variation for all the characters studied among the set of materials. The estimates of PCV and GCV were lowest in case of days to 50% flowering (4.84&4.61) and cellulose (43.28&42.62) was found to be highest. characters like panicle length (69.76%) exhibited moderate heritability (40%-70%) and all other characters exhibit high heritability (>70%) suggesting effectiveness of selection on the basis of phenotypic expression of the traits. High heritability accompanied with high genetic advance was observed in Number of fertile grains per panicle, Panicle weight, cellulose, Single plant yield indicate that additive gene effect has played a major role in the expression of these characters and simple selection will improve these characters. The promising genotypes with respect to their yield performance were SBP-15, SBP-53, Hasanta, SBP-30, SBP-102 can be recommended for commercial cultivation or can be used in further breeding programmes. The high estimates of correlation at phenotypic and genotypic level was between yield and number of fertile grains per panicle ($r_p = 0.775$, $r_g = 0.964$). High direct effect on yield was manifested by number of fertile grains per panicle (0.359). Fertile grains per panicle exhibited highest indirect effect on yield via panicle exsertion (0.266). The predicted genetic advance from different indices at 10% selection intensity ranged from 4.53 q/ha in one-character index to 4.79 q/ha in eleven character index and it varied from 100.00 % in index 1 to 105.7 % in index 11 in terms of relative efficiency.

Thus, in terms of predicted genetic advance, the results of the present study brought out superiority of eleven character index over direct selection on yield per se. Genetic divergence studies by D^2 analysis among the 34 genotypes for 11 characters revealed that cluster III and V are more divergent from each other with an inter cluster distance of 512.30, it can be concluded that crosses involving genotypes from these clusters can produce desirable recombinants with greater heterotic effects. While the clusters VI and VII are less divergent from each other with an inter cluster distance of 118.70.

It can be thus concluded from the above investigation that wide variation was observed for 12 yield and yield contributing characters in 34 lowland rice genotypes. High yielding genotypes like SBP-15, SBP-53, Hasanta, SBP-30, SBP-102 can be used as variety owing to their stable performance with respect to all other characters.

CONTENTS

CHAPTER	TITLE	PAGENO
I	INTRODUCTION	1-3
II	REVIEW OF LITERATURE	4-29
III	MATERIALS AND METHODS	30-43
IV	RESULTS	44-69
V	DISCUSSION	70-79
VI	SUMMARY AND CONCLUSION	80-84
	REFERENCES	i-xi

LIST OF TABLES

TABLE	PARTICULARS	PAGE
3.1	List of 34 lowland rice genotypes used in the study	31
3.2	ANOVA with expectations of mean squares	35
3.3	ANCOVA with expectations of mean sum of products (MSP)	38
4.1	Analysis of variance for various characters of 34 lowland rice genotypes	45
4.2	Mean and range for various characters for 34 rice genotypes	46
4.3	Mean performance with respect to various characters for 34 lowland rice genotypes	49
4.4	Frequency of genotypes on performance ranking for 12 characters in 34 lowland rice genotypes	50
4.5	PCV, GCV, h^2 and GA estimates for various characters for 34 lowland rice genotypes	53
4.6	Estimation of phenotypic and genotypic correlation coefficient among 12 characters for 34 lowland rice genotypes	56
4.7	Direct and indirect effects of component traits on yield at phenotypic level for 34 rice genotypes	58
4.8	Index scores and mean yield of 34 lowland rice genotypes in the order of their superiority	60
4.9	Expected genetic advance and relative efficiency of selection index over direct selection on grain yield	61
4.10	Cluster composition of 34 genotypes on the basis of D^2 analysis	62
4.11	Average intra-cluster (diagonal) and inter-cluster distance (D^2 & D values) among 7 clusters of 34 genotypes.	63
4.12	Relative contribution of different characters to genetic divergence among 34 lowland rice genotypes	65
4.13	Cluster means in 34 genotypes for 11 different characters	65
4.14	The coefficient of first two canonical vectors (Z1 and Z2) for 11 characters of 34 lowland rice genotypes	66
4.15	Mean canonical values of 34 genotypes	67
4.16	Cluster composition of 34 genotypes on the basis of canonical analysis	69

LIST OF FIGURES

FIGURE	PARTICULARS	PAGE
3.1	Cellulose standard curve	34
4.1	PCV, GCV, h^2 and GA of 12 for 12 characters of 34 genotypes	52
4.2	Cluster Analysis	63
4.3	Group constellation of 34 lowland rice genotypes using two canonical variates	68

INTRODUCTION

Rice (*Oryza sativa* L., $2n = 24$) belongs to the family poaceae which occupies an important position in the agricultural development history and civilization of Asian nations. Rice is the second most widely cultivated cereal after wheat but it is the primary source of staple food for more than half of global population.

Rice occupies 11% of the world's total cultivated area which is estimated to have 161.54 million hectares during 2017-18 with a production and productivity of 487.46 million metric tonnes and 4.5 metric tonnes per hectare during 2017-18. (Rice Outlook April 2018). Rice occupies a pivotal role in Indian agriculture as it is the staple food for two thirds of the population of India. The area, production and productivity of rice in India is 433.88 Lakh ha, 104.32 million tonnes and 2404 kg/ha respectively (Annual report 2016-17). Jeypore tract of Odisha is regarded as the secondary centre of origin of rice having great genetic diversity of rice genotypes. Production of rice during the year 2016-17 was 97.94 lakh tonnes 66.71 per cent from the previous year. (Economic Survey Odisha 2016-17)

Rainfed Lowland Rice Eco System

About 60 million hectares of rainfed lowlands supply about 20% of the world's rice production. Rainfed rice environments experience many abiotic stresses, such as salinity, high uncertainty in timing, duration, and intensity of rainfall. Because of such environments the yields are so unreliable, farmers rarely apply fertilizer and take no interest to sow improved varieties. Productivity in rainfed lowland areas is typically very low, with yields of 1–2.5 t/ha. Rice farming is practiced in several agroecological zones in India. No other country in the world has such diverse rice ecosystems. In India, lowland rice area is about 14.4 million hectares, which accounts 32.4 % of the total area under rice crop in the country. Production is variable because of the lack of technology used in rice production.

There is an urgent need to identify high yielding genotypes suitable for lowland condition. Information on nature and magnitude of variability present in the existing material and association among the various characters is a prerequisite for any breeding programme for high yield and quality. Grain yield is a complex character which is not only influenced by its associated characters. These characters are governed by number of gene and also influenced by environment. Hence, to make selection effective, it is necessary to separate genetic variability from total variability which enable breeder to adopt strategies for involvement of suitable breeding programme.

The main aim of plant breeder is to improve the plant type in order to get increased yield. Yield is governed by a number of components and those components are influenced by several of the environmental factors, making it necessary to partition observed variability into heritable and non-heritable components. This would facilitate effective selection for simultaneous improvement of one or more yield influencing traits.

Since yield is associated with its component characters, it is essential to know the degree of mutual association (correlation) prevailing between yield and its component characters, which forms a basis for selecting the desirable genotypes. Therefore, the analysis of the inter-componential correlation is essential to expose the direct contribution of each of the components which is determined by path coefficient analysis (Wright, 1921).

Rational choice of parents evidently demands knowledge of genetic architecture and diversity of parental strain with regard to characters which are being sought to be improved. Towards this end, the multivariate analysis has been utilized in the quantification of degree of divergence between populations. Rather than inferring from the earlier used indices like morphological similarity, ecological diversity, phylogenetic relationship and similar other criteria. Mahalanobis., 1936 generalized distance estimated by D^2 statistics helps in gaining numerical estimates of genetic diversity and quantitative assessment of the relative contribution of different component characters to the total divergence.

When the population being handled is large, it is difficult to select genotype based on the yield figure alone. Further, because of the complexity of yield and its close association with component characters, direct selection for yield is often ineffective in bringing out expected results. In such situation the success of selection could be enhanced with the use of selection indices formulated based on discriminant function technique involving important character. For yield improvement in rice, in the past, efforts were concentrated mainly on improvement of morphological characters such as reduced plant height for avoidance of lodging, good tillering capacity for obtaining adequate number of panicle and spikelets, leaf angle for better light interception and resistance to pest and disease, etc.

Ethanol from biomass has become an increasingly popular alternative to gasoline. Rice straw has several characteristics that make it a potential feedstock for fuel ethanol production. It has high cellulose and hemicelluloses content that can be readily hydrolyzed into fermentable sugars. In terms of chemical composition, the straw

predominantly contains cellulose (32–47%), hemicellulose (19–27%) and lignin (5–24%) (Garrote *et al.*, 2002; Maiorella, 1983; Saha, 2003; Zamora and Crispin, 1995). Developing Sustainable liquid fuel production from cellulose feed stock is a major challenge and will require significant breeding efforts to maximize plant biomass production. So, the present investigation is carried out to estimate cellulose content from rice straw which is the major component that can be converted to bioethanol.

Keeping in view the problems and prospects of varietal improvement in lowland rice, the experiment was carried out to evaluate 34 lowland elite rice genotypes. Thus, the present investigation was undertaken in *kharif*, 2017 with the following objectives:

Objectives:

- To evaluate the performance of selected rice genotypes, in respect of yield and yield contributing characters and identify genotypes suitable to lowland conditions.
- To assess the extent of variability and partition it into heritable and non-heritable components.
- To study the extent of genotypic and phenotypic correlation between yield and its components.
- To estimate the direct and indirect effects of various grain yield contributing characters.
- To construct selection indices using multiple traits for greater efficiency of selection for yield.
- To study genetic divergence of the selected genotypes, using different multivariate approaches.
- To estimate the amount of cellulose from rice straw and association with other quantitative traits.

The information thus, gathered from the study would throw light on the prospects and potentialities for genetic improvement of productivity and aid selection through identification of character(s) for accelerating the pace of improvement in lowland rice.



REVIEW OF LITERATURE

Rainfed lowland rice is particularly grown in major river flood plains of south and South east Asia. It is defined as rice that is usually transplanted and grown in levelled bundled fields that are shallowly flooded with rain water. (IRRI, 1996). The present investigation relates to the study on variability, heritability, genetic advance, correlation, Path coefficient and genetic divergence analysis in a set of thirty four elite lowland rice genotypes for yield and quality characters during *Khariif*, 2017 season. Relevant literature on these aspects has been reviewed here under the following headings.

- 2.1 Genetic variability
- 2.2 Character association
 - 2.2.1 Correlation
 - 2.2.2 Path coefficient analysis
- 2.3 Selection indices
- 2.4 Multivariate analysis

2.1 Genetic variability

The basic aspect of any plant breeding programme is to assess the nature and magnitude of variability present in any crop species. According to Allard, 1960 yield is polygenically controlled quantitative character and is highly influenced by environment. The phenotypic character expression is a result of the interaction between genotype and environment. Hence the observed variation needs to be partitioned into variance due to genotype (heritable) and variance due to environment (non-heritable) for assessing the true breeding behaviour of the phenotype. The genetic variability proportion transmitted from parents to offspring is reflected as heritability. Heritability in broad sense refers to the genetic variation present in the population in relation to the total observed variance. Since broad sense heritability includes both additive and epistatic effects. It will be reliable only when accompanied by high genetic advance. Genetic advance refers to the improvement in the mean genotypic value of the selected plants over the base population. A brief review of studies on genotypic and phenotypic coefficients of variation, Heritability and Genetic advance in rice is presented here under.

Sedeek *et al.*, 2009 reported high GCV and PCV for no of filled grains per panicle, flag leaf area, grain yield per plant, no of tillers per plant, medium for panicle length, and plant height low for 1000 grain weight and no of panicles per plant. High heritability coupled with high genetic advance for vegetative phase, number of days to heading, flag leaf area, number of filled grains per panicle and grain yield per plant. This indicates that selection using these traits would certainly bring improvement in the genotypes.

Pandey *et al.*, 2009 identified acceptable amount of variability with in entire gene pool for all traits studied. Grain yield per hill, harvest index plant height, and biological yield per hill recorded high PCV and GCV. High heritability along with high genetic advance as percent of mean was registered for grain yield, plant height, biological yield, test weight, number of tillers per hill, harvest index and number of spikelets per panicle indicating the additive gene action in the expression of these characters.

Krishna *et al.*, 2010 studied 97 rice accessions with three check varieties and reported that highest magnitudes of PCV and GCV were observed for number of unfilled spikelets per plant, total number of spikelets per plant respectively. High estimates of heritability coupled with high genetic advance was found for total number of spikelets per plant and reported that highest magnitudes of phenotypic and genotypic coefficients of variation were recorded for number of unfilled spikelets per plant, total number of spikelets per plant respectively. High estimates of heritability coupled with high genetic advance was found for total number of spikelets per plant and number of filled spikelets per plant, indicating that they can be effectively improved through selection.

Akhtar *et al.*, 2011 indentified GCV and PCV in case of number of grains per panicle, number of tillers per plant, plot yield and plant height. Among these characters number of grains per panicle, number of tillers per plant and plot yield have more than 15% variation at phenotypic level. High heritability values related to days to maturity, number of grains per panicle, number of tiller per plant and plant height were obtained which indicated reasonable variation for these traits. This suggests that selection can be practiced using these traits to improve plot yield in rice.

Singh *et al.*, 2011 evaluated eighty one rice genotypes for thirteen quantitative traits to examine the nature and magnitude of variability, heritability (broad sense) and genetic advance. Analysis of variance revealed that the differences among eighty one genotypes were significant for all the characters except flag leaf width. Among all the traits number of spikelets per panicle exhibited high estimates of GCV and PCV followed by harvest index, grain yield per hill and number of panicles per hill. Broad sense heritability was highest for biological yield per hill, which suggested that this trait would respond to selection owing to their high genetic variability and transmissibility. High heritability coupled with high genetic advance was recorded for number of spikelets per panicle, biological yield per hill, plant height and harvest index. Thus, it is interpreted that the characters viz., number of spikelets per panicle, biological yield per hill, plant height and harvest index were controlled by additive gene action, which could be improved through simple selection methods.

Sohrabi *et al.*, 2012 observed higher magnitudes of GCV and PCV for flag leaf length to width ratio, spikelet fertility, and days to flowering. High heritability along with high genetic advance was registered for yield per plant, days to flowering, and flag leaf length-to-width ratio suggesting preponderance of additive gene action in the gene expression of these characters.

Singh *et al.*, 2013 observed high GCV and PCV only for one trait (Number of spikelets per panicle) while plant height, flag leaf length, flag leaf width, panicle length, harvest index and grain yield per plant showed moderate GCV and PCV. Number of spikelets per panicle recorded high GCV and PCV value suggested the selection of these traits may be efficient for improvement of upland rice. Number of tillers per plant recorded high PCV and low GCV indicating that environmental effect is more than genotypic effect. Rest of the yield component traits viz., days to 50 per cent flowering and test weight exhibited low GCV and PCV estimates indicated that it may be governed by non-additive genes and recombination breeding may be helpful for improvement of grain yield through selection of these traits. High heritability was recorded for days to 50 % flowering, plant height, flag leaf length, flag leaf width, number of spikelets per panicle and grain yield per plant while panicle length, harvest index and test weight showed moderate heritability estimates. Number of productive tillers per plant showed low heritability & low genetic advance estimates. High

estimates of heritability coupled with high genetic advance as per cent of mean was observed for plant height, flag leaf length, flag leaf width, number of spikelets per panicle and grain yield per plant, while days to 50 % flowering and test weight showed moderate heritability coupled with moderate genetic advance as per cent of mean.

Basavaraja *et al.*, 2013 conducted field experiment to study the extent of genetic variability in yield and yield attributing traits under irrigated conditions. Genetic parameters of variability and heritability of 13 characters were studied in 100 genotypes of local rice. The maximum GCV and PCV were observed for test weight, number of productive tillers per plant, number of spikelet per panicle, amylose per cent and grain yield per plant(g). High heritability coupled with high genetic advance as per cent of mean were observed for days to 50 % flowering, test weight, number of spikelets per panicle, spikelet fertility %, protein % and grain yield per plant(g) will be useful for further breeding programme.

Ogunbayo *et al.*, 2014 conducted experiment in 12 different environments for 48 rice genotypes. PCV was higher than GCV in all the environments. High heritability coupled with high genetic advance was observed for grain yield indicating that selection can be done phenotypically for this character & preponderance of additive gene action.

Shrivastava *et al.*, 2015 under taken investigation to study the extent of variability and genetic parameters with 85 restorer (R) lines, 30 maintainer (B) lines and 15 male sterile (A) lines for thirty yield and its components characters. The magnitude of PCV was higher than the GCV for all the traits, indicating less environmental influence. High GCV and PCV were recorded with low magnitude of differences for unfilled spikelets per panicle, seed yield per plant, filled spikelets per panicle, panicle weight per plant, total spikelets per panicle, biological yield per plant, effective tillers per plant, tillers per plant, spikelet density, spikelet fertility, harvest index, culm length, flag leaf width and panicle index. High heritability coupled with high genetic advance as per cent of mean were recorded for unfilled spikelets per panicle, filled spikelets per panicle, total spikelets per panicle, seed yield per plant, panicle weight per plant, biological yield per plant, spikelet fertility, spikelet density, harvest index, panicle index, length breadth ratio, 1000 seed weight, length breadth ratio of decorticated seed, tillers plant-1, head rice recovery, effective tillers per plant, flag leaf width, culm length, plant height, flag leaf length, hulling percent, milling

percent, decorticated seed length, decorticated seed width, seed length, seed width, panicle length and days to heading indicating the additive gene effects in the genetic control of these traits and can be improved by simple selection in the present breeding material.

Khare *et al.*, 2015 reported high heritability coupled with high to moderate PCV and GCV and genetic advance as per cent of mean was recorded for grain yield per plant, plant height, test weight, fertile spikelet per panicle, total grains per panicle and number of effective tillers per plant. High heritability coupled with low genetic advance as per cent mean were observed in days to maturity and days to 50 % flowering.

Khatun *et al.*, 2015 evaluated forty-three genotypes in randomised complete block design with three replications. All genotypes exhibited a wide and significant variation for 22 traits. The highest PCV and GCV were recorded for the number of filled grains per panicle and yield per plant (g). The highest heritability was found for photosynthetic rate, transpiration rate, stomatal conductance, intercellular CO₂, and number of filled grains per panicle and yield per plant (g). The selected best trait of the number of filled grains per panicle and yield per plant (g), which showed high heritability and high genetic advance, could be used as a selection criterion for hybridisation programmes in the future. He suggested that the PCV was higher than the GCV for all traits, which reported large environmental effect, whereas small differences reveal a high genetic influence. The small differences between the PCV and GCV for most of the traits, such as Days to flowering, Days to maturity, and Grain length, represented some degree of environmental influence on the phenotypic expression of these characters. It also suggests that selection based on these characters would be effective for future crossing programmes. The other traits, which showed a higher difference between PCV and GCV, indicated that the environmental effect on the expression of those traits is higher and that selection based on these characters is not effective for further yield improvement.

Islam *et al.*, 2016) revealed that most of the growth traits showed higher PCV compared to yield and yield component traits. The high PCV was observed for unfilled grains per panicle, secondary branches per panicle, 1000 grain weight, and filled grains per panicle. Whereas days to maturity, panicle length, days to flowering, and plant height were found with lower values. The higher GCV was associated with 1000-grain

weight, whereas the value was fairly low in case of panicle length. Narrow differences between PCV and GCV observed for most of the traits. In this study, flag leaf area, secondary branches per panicle, filled grains per panicle, grain length, grain breadth, grain length breadth ratio, and 1000-grain weight showed high heritability and high genetic advance indicated the presence of additive genes controlling these characters.

Abebe *et al.*, 2017 evaluated 36 rice genotypes at two locations to study genetic variability, heritability and genetic advance for grain yield and 13 yield associated traits. Higher PCV and GCV values were exhibited by plant height, culm length, number of unfilled grain per panicle, biomass yield and grain yield, which suggests the possibility of improving this trait through selection. The highest heritability was recorded for culm length followed by plant height, biomass yield and panicle length. High to medium heritability coupled with high GCV and high genetic advance as percentage of means were exhibited for plant height, biomass yield, grain yield and number of unfilled grain per panicle.

Karande *et al.*, 2017 observed High genotypic coefficient of variation, high heritability with high genetic advance as per cent of mean for grain yield per plant, total tillers per plant, productive tillers per plant and grains per panicle, whereas days to initiation of flowering, days to 50 % flowering and days to maturity had high heritability with low genetic advance as per cent of mean, indicating that the inheritance of these characters are controlled by dominance and epistatic gene actions rather than additive gene action.

Limbani *et al.*, 2017 found higher estimates of GCV and PCV for number of non-effective tillers per plot, number of unfilled grains per panicle, harvest index, grain yield per plot and number of effective tillers per plot which also had high heritability coupled with high genetic advance indicating better scope for improvement of these traits by an effective selection. This indicated that these characters were governed by additive genes and selection would be rewarding for their improvement. The high heritability and moderate genetic advance (% mean) was observed for head rice recovery, milling percentage, plant height, days to 50% flowering and panicle length indicating that these characters were governed by both additive and non-additive gene effect thereby suggesting that reciprocal recurrent selection would be beneficial to improve these traits.

Harsha *et al.*, 2017 undertaken study on twenty-nine rice genotypes to determine, genetic variability, the nature of association among different yield attributes and their direct and indirect contribution towards yield. A high degree of variation was observed for all characters studied. Estimates of PCV and GCV were higher for the number of effective tillers per plant, flag leaf area, yields per plant and for test weight. Small differences between GCV and PCV were recorded for all the characters studied which indicated less influence of environment on these characters. The broad sense heritability estimates for the traits observed are leaf length, test weight, days to 50% flowering, leaf width, days to maturity and least for panicle length. The presence of high heritability with high genetic advance showed additive effects of the gene on the character and they response to selection effectively as they are least affected by the environmental condition.

Iqbal *et al.*, 2018, evaluated Fourteen elite rice genotypes following randomized complete block design with three replications. The magnitudes of PCV and GCV were higher (>20%) in all the studied traits, except physiological maturity, reflecting wide spectrum of variability and offering greater opportunities for selection. Similarly, the magnitude of broad-sense heritability and genetic advance as percent of mean was moderate to high for majority of traits, indicating additive gene action in their inheritance hence, amenable for simple selection.

Kishore *et al.*, 2018 worked on thirteen quantitative traits in twenty rice genotypes. Significant difference for all the quantitative traits was observed among the genotypes indicating presence of variability and scope of selection. Higher estimates of PCV than GCV for all the traits reflected influence of environmental factor on these traits with variable influence. The characters fertile spikelet per panicles, test weight, yield per plant, harvest index, biological yield per plant and flag leaf width showed greater influence of environment reflecting scope of improvement of these traits by providing favourable environment whereas least influenced traits cannot be improved even in favourable condition but may be good for selection. The traits plant height, effective tillers per plant, flag leaf length, test weight and biological yield per plant showed high estimates of heritability and genetic advance implies additive genetic component and can be used for selection in early segregating generations.

2.2 Character Association

Selection of traits contributing simultaneously to a character will improve it in subsequent segregation population given by Aishah *et al.*, 2014. Most of the characters of interest to breeders are complex and are the result of the interaction of a number of component traits. Understanding the relationship between yield and its components is of paramount importance for making the best use of these relationships in selection. Study of character association helps the breeder in fixing selection criteria for grain yield in parental lines, such that selections will be effective in isolating the plants with desired combination of characters. Phenotypic correlation is the correlation of phenotypic values and is subjected to changes in the environment. It measures the environment deviation together with non-additive gene action. Genotypic correlation is the correlation of breeding value (Additive + Additive x Additive epistatic) gene action. Hence, knowledge of association between different characters is highly essential for planning a sound breeding programme.

2.2.1 Correlation

Several workers have studied the correlation coefficients in rice and contradictory association have been reported for almost all the character pairs which may be due to the different experimental material handled by them. A brief review of studies on correlation coefficients in rice are presented below.

Sankar, 2006 reported that single plant yield had significant positive correlation with days to 50 per cent flowering, productive tillers per plant, panicle length and grains per panicle. This indicates the relative utility of all these traits for selection. Positive significant inter correlations were found between days to 50 per cent flowering and panicle length. Plant height was significantly inter correlated with panicle length and 100 seed weight. Significant inter correlations were recorded between panicle length and grains per panicle and between 100 seed weight and spikelet fertility.

Karad and Pol, 2008 observed in their study with rice genotypes that the grain yield had positive correlation with almost all the characters except 1000 grain weight at both phenotypic and genotypic levels. They found that genotypic correlation estimates were higher than phenotypic correlation with grain yield per plot.

Kole and Hasib, 2008 conducted an investigation to determine interrelationships among yield and yield contributing characters in scented rice. Grain yield per plant had positive and significant correlation with plant height, flag leaf length and panicle weight at both genotypic and phenotypic levels, while days to flower and panicle number per plant showed significant and negative correlation with grain yield at both genotypic and phenotypic levels.

Chandra Reddy *et al.*, 2009 correlation studies in rice revealed positive genotypic correlation coefficients for most of the characters under study. Character association analysis revealed significantly positive association of grain yield per plant with number of productive tillers per plant, 1000 grain weight, panicle length and number of grains per panicle.

Jayasudha and Sharma, 2010 observed the inter relationship, among yield components, plant height is positively and significantly associated with panicle length, flag leaf area and pollen fertility (%). Panicle length itself is positively correlated with flag leaf area and pollen fertility (%). In turn, pollen fertility was significantly and positively correlated with spikelet fertility (%) and harvest index. Selection for pollen fertility (%) indirectly increases the spikelet fertility (%), which in turn increases the grain yield per plant. Tillers per plant was significantly and positively correlated with productive tillers per plant. Flag leaf angle was significantly positively correlated with second leaf angle and third leaf angle. Second leaf angle in turn was significantly correlated with third leaf angle. The correlation analysis, however, did not reveal any significant association of grain yield per plant with flag leaf area (length x breadth), flag leaf angle, second leaf angle and third leaf angle. This may be due to a high negative indirect effect via flag leaf area. The correlation studies facilitate the assessment of the chance for mutual improvement of two traits by common selection.

Nandan *et al.*, 2010 studies correlation on thirty three rice genotypes and found strong positive association of yield with days to 50% flowering, plant height, number of grains per panicle, number of spikelets per panicle and spikelet fertility.

Pankaj *et al.*, 2010 studied correlation using 48 genotypes of rice for grain yield, its components and quality characters and found that grain yield exhibited significant positive correlation with grains per panicle, spikelets per panicle and effective tillers

per plant at maturity at both phenotypic and genotypic levels. Total tillers per plant had correlation with grain yield per plant at phenotypic level only. Significant negative genotypic correlation with days to 50% flowering and days to maturity revealed that early maturing genotypes yielded high under Palampur condition

Akhtar *et al.*, 2011 reported that the genetic and phenotypic correlation coefficients among paddy yield and yield contributing traits showed that most of the traits have higher genetic correlation coefficients than corresponding phenotypic correlation coefficients because the relationship was affected by environment at phenotypic level, indicated the low phenotypic correlation coefficients. Plot yield revealed significant positive genetic association with number of grains per panicle, days to maturity and 1000 grain weight and while negative relationship with plant height both at phenotypic and genetic levels. The findings suggest that paddy yield can be improved in these rice genotypes by using these traits as selection criteria in succeeding generations. Plant height was found negatively correlated with number of grains per panicle, no of tillers per plant and plot yield. Negative correlation coefficient of plant height with plot yield indicates that tallness in rice reduces the plot yield due to high accumulation of photosynthates in vegetative parts as compared to reproductive parts (i.e. seed formation and grain filling) and lodging susceptibility.

Selvaraj, 2011 observed characters like plant height, number of tillers per plant, number of productive tillers per plant, panicle length, filled grains per panicle and test weight had significant positive association with grain yield. Results of path-coefficient analysis revealed that, test weight exhibited maximum positive direct effect on grain yield per plant followed by filled grains per panicle, plant height, panicle length, number of tillers per plant and days to 50% flowering and they contributed primarily to yield and could be relied upon for selection of genotypes to improve genetic yield potential of rice.

Idris *et al.*, 2012 observed positive phenotypic and genotypic correlation coefficient between grain yield and number of filled grains per panicle, harvest index, panicle length and number of grains per panicle.

Ukaoma *et al.*, 2013 stated that of all the characters evaluated, only number of grains per plant had the highest and significant correlation with grain yield ($r=0.7643$). Days to booting and days to 50% heading had negative but high correlation.

Singh *et al.*, 2013 identified that genotypic correlation coefficient were higher than the corresponding phenotypic correlation coefficient, indicated the characters are governed by additive gene action and are useful in yield improvement. Grain yield is ultimate objective of any breeding programme. In this study, it showed positive and significant correlation with the yield component traits viz., plant height and panicle length at both level, whereas in addition to these traits number of productive tillers per plant showed positive and significant correlation with seed yield per hill at genotypic level only. In general, plant height showed negative association with grain yield in rice but here in this study it showed positive association. It also significantly correlated with number of productive tillers per plant, flag leaf length and number of spikelets per panicle. Days to 50 per cent flowering showed negative and significant correlation with grain yield per plant.

Ogunbayo *et al.*, 2014 reported that grain yield had high significant positive correlation with panicle length, leaf width, grain length, no of panicles per metre scale and 1000 grain weight, indicating that these are the important yield related traits and could be used for selection in rice breeding programme.

Khare *et al.*, 2015 reported that the genotypic correlation coefficient was found to be higher than phenotypic correlation coefficient except for days to maturity indicating a strong inherent association for grain yield per plant and other traits also. Days to 50 per cent flowering, days to maturity, plant height, panicle length, fertile spikelet per panicle, total grains per panicle and spikelet fertility showed strong positive and significant association with grain yield per plant both at genotypic and phenotypic levels. The association studied indicating grain yield of rice can be improved by selecting germplasm having higher performances for these traits.

Das, 2015 investigated that the estimates of genotypic correlation were higher than that of phenotypic correlation indicating that the environmental causes of correlation had affected the genetic cause, thereby reducing the reliability of phenotypic correlation for use in crop improvement programme. Highest estimates of correlation both at genotypic and phenotypic level was between yield and number of effective tillers per plant. It was followed by number of fertile grains per panicle, fertility %, harvest index. The rest of the characters had non-significant correlation with yield. The result revealed that days to 50% flowering had significant positive correlation with

plant height, panicle length and number of fertile grains per panicle. The plant height had positive significant correlation with panicle length, number of fertile grains per panicle. The panicle length showed positive correlation with number of fertile grains per panicle. The number of effective tillers per plant exhibited positive significant correlation with fertility % and harvest index.

Gour, 2017 reported that genotypic and phenotypic correlation coefficients among yield and yield contributing traits have higher genotypic correlation coefficients than corresponding phenotypic correlation coefficients indicating a low influence of environmental factors and relative stability of the genotypes. Panicle weight per plant followed by biological yield per plant, Number of tillers per plant, filled spikletes per plant, Harvest index and 1000 seed weight six exhibited significant positive association with seed yield per plant indicating the importance of these traits as selection criteria in succeeding generations for yield improvement. 1000 grain yield per plant had positive significant association with grain yield per plant, harvest index, panicle length per plant, panicle weight per plant, biological yield per plant and plant height. Yield per plant had showed significant phenotypic and genotypic correlation with grain yield per plant and harvest index. Harvest index showed positive significant association with plant height, panicle weight per plant, panicle length per plant, days to 50% flowering, Days to maturity, 1000 seed weight and Filled spikletes per plant.

Sangaré, 2017 based on the correlation values obtained in his study, indicated that selection of plants with more tillers could indirectly be used for developing plants with a high number of panicles. Plant height showed moderate to high significant positive phenotypic correlation with flowering time, number of grains per panicle and grain yield, which suggests that high yielding and late flowering rice varieties could be developed by indirectly selecting for taller plants. However, selection for taller plants may increase lodging, which would negatively affect grain yield. On the other hand, late flowering and late maturity require availability of sufficient moisture for a long period of time, which may not be possible in areas where there is limited rain within a short period of time. Plant height exhibited a negative correlation with number of tillers and number of panicle in both phenotypic and genetic level suggesting that selection for short genotypes would result in developing varieties with a higher number of tillers and panicles.

Karande *et al.*, 2017 reported that the genotypic and phenotypic correlation coefficient among all these traits showed that the genotypic correlation of yield was positive and significant with total and productive tillers per plant, spikelet fertility, 1000 grain weight and straw yield per plant. On the other hand, phenotypic correlation of yield was positive and significant with productive tillers per plant, spikelet fertility and straw yield per plant and days to maturity.

Harsha *et al.*, 2017 The correlation analysis was done to reveal the association between yield and its component traits. Genotypic correlations found higher than phenotypic correlations for all the character studied. The direction of phenotypic and genotypic correlations was almost the same for most of the character combinations. Grain yield per plant showed the significant positive correlation number of effective tillers per plant, panicle length and test weight. Plant height significant positive correlation with a number of effective tillers per plant, panicle length and leaf width. A number of effective tillers per plant showed significant positive correlation with leaf length, leaf width and yield per plant. Thus, improvement in yield can be enhanced by indirect selection for effective tillers per plant and leaf width.

Edukondalu *et al.*, 2017 studied 15 characters in 40 genotypes and found that magnitudes of genotypic correlation were found to be higher than phenotypic correlations. The results indicated that grain yield per plant showed significant positive association with number of tillers per plant, panicle length and milling percentage.

Kishore *et al.*, 2018 considered both correlation between the traits Panicle length, biological yield per plant, harvest index and test weight showed true association with grain yield per plant having significant and positive correlation with high positive direct effect. Hence for implication of direct selection these traits should be considered.

Goswami and Seth, 2018 evaluated Twenty hybrids along with three cytoplasmic sterile lines (IR 58025A, IR 98897, IR 56256A, DRR 9A and DRR10A) and eighteen pollen parents were studied for character association for yield and its components. It was observed that the magnitude of association varied in hybrids and parents. In hybrids the yield was primarily influenced by 100 grain weight, effective tillers per plant and number of fertile grains per panicle. In case of parents, grain yield per plant found to be significantly and positively correlated with days to 50% flowering,

panicle length, effective tillers per plant and number of fertile grains per panicle. Characters like effective tiller number per plant and fertile grains per panicle were significantly and positively correlated with each other as well as with grain yield per plant.

2.2.2 Path Coefficient Analysis

Shivaprasad *et al.*, 2013 studied the path coefficient analysis & revealed that panicle exertion showed the highest negative direct effect on grain yield followed by radical length (cm), seedling maturity, number of tillers per plant and days to maturity.

Gopikannan and Ganesh, 2013 carried out an experiment to study the correlation and path analysis in 10 parents and their F1 hybrids of rice (*Oryza sativa* L.) under sodic environment. Character association of the yield and its attributing traits revealed that significant positive association of grain yield per plant with number of productive tillers per plant, panicle length, spikelet fertility percentage, number of filled grains per panicle, proline content, total chlorophyll content and chlorophyll stability index.

Yadav and Suresh, 2013 path coefficient analysis revealed that harvest index had the highest positive direct effect (1.02) on grain yield. Grain yield linearly correlated with number of spikelets/panicle, tillers/plant, panicles/plant, biological yield and harvest index. Therefore, these traits may be used in the selection for improvement of yield components in rice.

Awasthi and Lal, 2014 conducted experiment comprising of 25 entries planted in a compact family block design with three replications. HUR 3022, HUR 105 and Sarjoo 52 were planted as lines and Nagina 22, Anjali and Birsa Gora were treated as testers. The experiment was conducted in two water regimes, irrigated and rainfed conditions, respectively. All experimental materials were tested under both the conditions. Observations were recorded on 20 randomly selected plants per replication for eleven characters viz., seedling height (SH), plant height (PH), stomatal behavior (SB), leaf rolling (LR), stay green (SG), panicle weight (PW), percent filled grains (PFG), spikelet per panicle (SPP), thousand grain weight (TGW), yield per plant (YPP) and proline content (PC). The mean values recorded for eleven characters in F2 generation were used for statistical analysis. The results of this research showed that indirect selections for increasing the number of SPP and decreasing SH and PH under

both the conditions can be suitable to improve paddy yield of rice in breeding programs. The component traits such as, PC, SB, LR, SG, PFG, TGW and YPP singly or in combinations appear to be most important towards enhancing seed yield and also drought tolerance in transgressive segregants.

Premkumar *et al.*, 2014 conducted Path coefficient analysis using single plant yield as a dependent variable and other yield contributing and grain quality traits were considered as independent variable. Three yield contributing characters viz., days to 50% flowering, number of productive tillers per plant and panicle length exhibited high and positive direct effects on single plant yield. Hence, selection based on these traits could help to bring simultaneous improvement of yield, yield attributes.

Saikumar *et al.*, 2014 carried out path analysis and found that Harvest index exhibited maximum positive direct effect on grain yield under both the conditions; in addition, filled grains per panicle, spikelet fertility and biomass had positive direct effect on grain yield under both irrigated and lowland drought stresses state. Hence, for improving the rice yield under lowland drought ecology, a genotype should possess a large number of panicles per plant, filled grains per panicle, high spikelet fertility and maintains higher biomass and harvest index.

Aye *et al.*, 2015 stated that the results of path coefficient analysis showed that different direct and indirect effect on yield. Number of panicles per hill possessed high positive direct effect and high correlation value to yield per plant at continuous flooding and saturated irrigation indicating number of panicle per hill should be used as target selection trait to improve yield per plant. In intermittent irrigation, number of spikelets per panicle and filled grain percent should be used as target traits to improve yield per plant because these traits showed high positive direct effect and high correlation. Thus, one can conclude from the findings of present study that selection of traits with high positive significant association and high positive direct effect on grain yield can help improving yield.

Shinde *et al.*, 2015 conducted path analysis and revealed that days to maturity, straw yield, plant height & harvest index exerted positive direct effect on grain yield. days to 50% flowering, productive tillers per plant, panicle length, spikelets per panicle, spikelet fertility and 1000 grain weight exhibited negative direct effect on grain yield.

However these traits influenced the yield through positive indirect effects via days to maturity, Straw yield , plant height & harvest index. The residual effect in the present study was high, it indicates besides the characters studied, there were some more attributes which contributes to grain yield. From this study it indicated that Days to maturity, Straw yield, plant height & harvest index can be used as direct selection for yield improvement and remaining traits can be chosen for indirect selection.

Devi *et al.*, 2016 conducted path analysis & reveals that test weight (3.48), effective tillers (1.57), and filled grains per panicle (1.41) had positive direct effect on grain yield per plant. Among the quality traits kernel length followed by milling percent and kernel elongation ratio had direct effect on head rice recovery.

Patel *et al.*, 2016 conducted path analysis & revealed that straw yield per plant, grain length, Harvest index, days to maturity, protein content, no of tillers per plant and no of grains per panicle were having high positive direct effect with grain yield, while grain L:B ratio, panicle length, grain breadth, 1000 grain weight, days to 50% flowering were having negative direct effect. Based on the above results it is suggested that more emphasis should be given on panicle length, no of grains per panicle, straw yield and harvest index for improvement of grain yield.

Priyanka *et al.*, 2016 conducted path analysis and reported that among the yield components studied number of grains per panicle, harvest index and biomass are important as the correlation coefficient as well as the direct effects were high. Another important character to be considered for high yield is the panicle length, however length of the panicle always never yields higher because of loosely packed spikelets and selection should be for compact and dense spikelets.

Behera *et al.*, 2017 observed from the path coefficient analysis that high direct positive effect on grain yield was manifested by harvest index followed by days to 50% flowering and moderate direct effect by plant height, kernel length, fertile grains per panicle and 100 seed weight thus, indicating the importance of such traits as criteria for selection in that order for realization of higher productivity.

Hijam *et al.*, 2017 observed from path coefficient analysis that Days to 50 per cent flowering, number of effective tillers per plant, filled grains per panicle, grain breadth, grain L:B ratio and harvest index had positive direct effect on yield. Based on

overall magnitudes of heritability, genetic advance, correlation and path analysis, number of effective tillers per plant, filled grains per panicle, grain breadth and 1000 grain weight should be given emphasised for selecting high yielding genotypes.

Yugandhar *et al.*, 2017 conducted Path coefficient analysis & revealed that, highest positive direct effect on grain yield per plant was exerted by total number of productive tillers per plant followed by grains per panicle, test-weight, number of productive tillers per m² and panicle length indicating that selection for these characters was likely to bring about an overall improvement in single plant yield directly.

Sowjanya *et al.*, 2017 path analysis studies revealed that harvest index, plant height at 30 days after transplanting, total number of tillers per plant, days to 50 % flowering exerted maximum positive direct effect on grain yield per plant. Therefore, during selection main attention need to be given for traits like plant height at 30 DAT, productive tillers per plant, panicle weight, panicle length and harvest index.

Das *et al.*, 2017 studied phenotypic path analysis through direct and indirect effect on contribution of various growth parameter indicated the highest positive direct effect on yield of grain was due to straw yield followed by filled grains. Number of chaffs per panicle showed highest negative direct effect. Further, yield of straw and number of filled grains per panicle exhibited the highest positive indirect effect across the characters. It was followed by number of ear bearing tiller per m², length of panicle and leaf area index.

Sahu *et al.*, 2017 studied path analysis and reported that Biological yield and harvest index had positive direct effect on grain yield, hence selection of these two traits for grain yield will be effective.

Yadav and Suresh, 2018 reported that the yield components such as plant height, flag leaf width, flag leaf length, tillers per plant, panicles per plant, panicle length, number of spikelets per panicles, days to maturity, biological yield, harvest index, test weight and seed yield had a direct effect on yield if other components kept constant. But the magnitude of direct effect of harvest index was maximum. An overall analysis of path coefficient suggested that panicles per plant, tillers per plant, number of spikelets per plant, biological yield and plant height should be given the maximum consideration for yield improvement and appropriate selection indices should be formulated using these traits.

2.3 Selection Indices

Rabiei *et al.*, 2004 calculated 20 selection indices were based on two methods (optimum and base) and 10 differing trait combinations with different economic weights genetic advances for other traits such as panicles per plant and grain yield per plant, which are yield-related components, based on indices 4 and 8 were more than that for index.

Sabouri *et al.*, 2008 suggested that among 14 selection indices which were calculated based on two methods (optimum and base) and combinations of 12 traits with various economic weights. the indices 5, 6 and 9 calculated by optimum and base indices were the best indices. Finally, selecting for 1000-grain weight, number of panicles per plant and panicle length by using their phenotypic and/or genotypic direct effects (path coefficient) as economic weights should serve as an effective selection criterion for using either the optimum or base index. The optimum indices, however, had the higher relative efficiency than the base indices in this research and are recommended for improving the grain yield in rice.

Fazlalipour *et al.*, 2008 indicated that selection for biomass, harvest index (%) and grain yield per plant using genotypic path coefficients and their heritability as economic values would be a suitable selection criterion for improving population.

Bastia *et al.*, 2008 assessed thirty two upland rice genotypes for study of genetic variability and construction of selection indices for enhancing selection efficiency. And stated that the relative efficiency of selection on the basis of selection indices is expected to increase upto 114.371%. On the basis of selection criteria, the promising genotypes selected were OR 1752-3, OR 1603-7, OR 2088-4, OR 2087-2, OR 1659-3, OR 2049-1, OR 2048-1, OR 2069-1, OR 2077-5 and OR 1920-7.

Kanbar *et al.*, 2008 Understanding the relationship between root system and yield related traits is an important objective in crop breeding programs. Canonical correlation analysis has been adopted to study the strength of association between the root morphological traits and grain yield components under low-moisture stress and well-watered conditions and to find the root morphological characters that have the largest influence on grain yield and its components under the two conditions. This study revealed that root to shoot length and weight ratios and root dry weight were had the largest effect on plant height, shoot dry weight and grain yield under well-watered condition.

Habib *et al.*, 2013 evaluated selection indices for yield were constructed using different combinations of characters. Different selection indices, their expected genetic advances with relative efficiencies are analysed. It was observed that selection for individual characters like filled grains per panicle, plant height and days to maturity have higher relative efficiencies over straight selection for grain yield.

Singh *et al.*, 2013 conducted an experiment with 11 genotypes of upland rice during *Kharif* 2009 and 2010. Which revealed that the expected genetic advance and relative efficiency of selection indices was ranged from 0.13 (Index III) – 33.23 per cent (Index XXI) and 4.20 ((Index III) 1093.09 per cent (Index XXI), respectively. Two genotypes from index XXI and three genotypes from index XVI were isolated as diverse parent with Vandana and can be used in crossing programme to obtain the better heterotic cross combinations with high relative efficiency and good characters combination and may helpful to improve the grain yield in upland rice.

Aslam *et al.*, 2014 conducted a Study of selection indices in 76 rice genotypes of Bangladesh through discriminate functions and observed that Bhute shalot possessed the highest selection score index (301.41) and rank as the best followed by Hati bajore, Jamai naru, Bazra muri and Enghi which suggests that the highest scoring genotypes might be recommended for farmer's cultivation for better yield.

Choudary *et al.*, 2017 observed that selection of many characters create difficulty at many stages and it was not maintained properly. So, looking to the simplicity of assigning weight and to get higher genetic gain and percent relative efficiency Index (I256) is suggested to select the genotypes for rice grain yield improvement which was combinations of plant height, 1000 grain weight and harvest index.

Chandrashekhar and Shailaja, 2017 constructed 63 selection indices based on 6 characters in all possible combinations. And observed that the highest genetic advance of 60.17 was obtained when selection was simultaneously based on discriminant function of two-character combination viz., Spikelet fertility (X3) + Biomass (X4). When three characters considered, selection index with spikelet fertility (X3) + biomass (X4) + harvest index (X5) were taken together, the genetic advance increased to 65.63. Selection index with combination of four characters viz., spikelet fertility (X3) + biomass (X4) + harvest index (X5) + grain yield per plant (X6) resulted in increased

genetic gain of 71.63. Among five-character combinations, productive tillers per plant (X1) + spikelet fertility (X3) + biomass (X4) + harvest index (X5) + grain yield per plant (X6) showed increase in genetic gain of 73.99. The discriminant function that includes all the six characters (X1+X2+X3+X4+X5+X6) including grain yield per plant gave the highest genetic gain of 79.56, over other selection indices with two, three, four and five-character combinations. Thus, study revealed that the selection index which includes more than one character gave high genetic gain indicating the usage of construction of selection indices for operating simultaneous improvement of grain yield and several other characters.

Biswaranjan *et al.*, 2017 stated that direct selection for grain yield *per se* is often not reliable as grain yield is a complex trait, controlled by non-additive gene action and is believed to have low heritability. No single trait could be taken as an adequate criterion of selection for yield, therefore, selection indices provide a useful method by making use of several correlated traits for greater efficiency of selection in yield. During investigation selection indices were constructed with grain yield as the economic criterion and thirteen different characters namely grain yield per plant (GYP), days to 50% flowering(DF), plant height (PH), panicle length(PL), number of effective tillers per plant(ETN), flag leaf area (FLA), fertile grain number(FGN), fertility percentage(F%), kernel length(KL), kernel breadth(KB), L/B ratio(LB), 100-seed weight(SW), harvest index(HI), were chosen for the construction of thirteen character indices. The thirteen-character index including all the thirteen traits was used for the selection of genotypes. The promising genotypes occupying better ranking in the thirteen-character index were selected for their future use.

2.4 Genetic Divergence

Monika *et al.*, 2008 conducted an experiment for the assessment of genetic diversity among the rice varieties cultivated in Punjab was done using Mahalanobis D^2 statistics based on eleven agro-morphological traits. Nineteen cultivars were grouped into four different clusters revealing sufficient amount of variability among the genotypes. The clustering pattern revealed non-correspondence of geographic diversity with genetic divergence. Days to 50% flowering and plant height contributed considerably, accounting for 61% of total divergence. The highest inter-cluster divergence (76.33) between clusters I and II maybe utilized in heterosis as well as in

recombination breeding. Further, selection within cluster IV, having maximum intra-cluster distance (11.64), maybe exercised based on the highest mean for the desirable traits, which could be used for improvement through inter-varietal hybridization.

Bisht et al., 2008 Thirteen landraces of paddy, collected from the Nanakosi microwatershed in Almora district of Uttarakhand, were evaluated for the pattern of genetic diversity using multivariate analysis of Mahalanobis D² statistics. These landraces formed seven distinct clusters, three with one landrace each, two with two, and the rest had three landraces each.

Kayode *et al.*, 2008 Showed that Canonical discriminant analysis have given traits such as panicle length, grain size (weight and length), tillering ability, number of days to heading and maturity were the main discriminatory characteristics.

Subudhi *et al.*, 2009 evaluated forty one promising rice varieties of eastern India for physico- chemical and cooking characters to study the diversity pattern among the genotypes. The genotypes were grouped into ten clusters. Maximum 11 genotypes were grouped in cluster IV followed by ten in cluster I. The clusters VI, VIII, IX and X are represented by single genotype namely Gayatri, Hanseswari, Satyakrishna and Saket-4 respectively indicating high degree of heterogeneity among the genotypes. The intra cluster distance is highest in cluster IV(D=13.41) followed by cluster V(D=10.16), cluster II(10.05) and lowest in cluster VII(D=7.31).

Pandey *et al.*, 2009 conducted D² statistics the 40 genotypes of rice were grouped into 7 clusters Among the different clusters cluster VI consisted maximum number of genotypes (11genotypes) followed by cluster III (9 genotypes), cluster V (8 genotypes) and cluster I (4 genotypes), while cluster II and IV (each 3 genotypes) and cluster VII included 2 genotypes. The pattern of group constellation proved the existence of significant amount of variability.

Akter *et al.*, 2009 estimated genetic divergence using Mahalanobis's statistic (D²) and principal component analysis. Cluster analysis revealed 44 restorers were grouped into 5 clusters. The lines chosen from the same ecogeographic region were found scattered in different clusters which indicated that genetic diversity and geographic distribution were not necessarily related. The intercluster distances were higher than the intra-cluster distance reflecting wider genetic diversity among the

genotypes of different groups. The highest inter-cluster distance was observed between cluster II & V followed by I and IV where the highest intra-cluster distance was found in the cluster I indicated that the highly divergent types existed in these clusters.

Ubarhonde *et al.*, 2009 the basis of D2 analysis 44 rice genotypes were grouped into nine clusters and three ungrouped clusters. Cluster I was the largest and contained 22 genotypes. Rest of the clusters contained 2-3 genotypes. The genotype belonging to ungrouped cluster X, namely, NDR 1130- I showed promise for early maturity, long grain size and grain yield/plant. The highest intra cluster distance was observed in cluster IX, containing two genotypes differing mainly for maturity and grain yield/plant. The most distant clusters were Cluster IV and ungrouped cluster XII. The genotypes of cluster IV showed promise for rain-fed condition with regard to days to maturity, effective tillers/plant, grain yield/plant and chlorophyll content. Contribution (%) towards the total divergence was maximum through grain breadth followed by chlorophyll content, grain length and total tillers/plant.

Shahidullah *et al.*, 2009 stated the contribution of each of five canonical discriminant functions for explaining the variance along with its corresponding eigenvalue and canonical correlation coefficient was calculated. It was found that the function 1 (the first principal component) accounted for 61.7% of the total variance and the function 2 explained 22.9% of the total variance. In the cumulative effect, functions 1 and 2 absorbed 84.6% of the total dispersion. Since canonical correlation values for functions 1 and 2 were very close to unity, this result indicated strong association between discriminant scores and the groups. The coefficient of thousand kernel weight, kernel length and L/B ratio were highest in function 1. Coefficients with large absolute values corresponding to variables should have greater discriminating ability. Therefore, these three characters were the major contributors to function 1 for explaining 61.7% of the total dispersion. Largest absolute values for elongation ratio and amylose content under function 2 indicated that these two traits were mainly responsible for explaining 22.9% of the total variance.

Banumathy *et al.*, 2010 evaluated for eight yield and yield attributing characters using D² analysis, to study the diversity pattern among the genotypes. Based on the analysis, the genotypes were grouped into 11 clusters. Maximum number of 16 and 15 genotypes were grouped under cluster XI and I respectively, while clusters II, IV, V,

VI, VIII, IX and X had only two genotypes each and clusters III and VII consisting of 3 and 5 genotypes respectively.

Kanbar *et al.*, 2010 described that Three canonical variables were generated to find the optimal combinations of variables needed to discriminate between two groups. Canonical variable one had the highest correlation with shoot dry weight followed by plant height.

Shaarma *et al.*, 2011 Genetic divergence using D^2 statistic in sixty three rice genotypes was studied on the basis of 18 yield and quality characters. The genotypes were grouped into 8 different clusters, in which, cluster VII was the largest having 16 genotypes. Highly significant variations were found amongst the rice genotypes with regard to all the characters studied except for kernel elongation ratio. Based on mean performance, genetic distances and clustering pattern, the genotypes; Pusa Basmati-1 and Taraori Basmati of cluster II, Sarju-52, Narendra Usar-3 and Narendra-80 of cluster IV, Badshah Bhog, MTU-7029 and BPT-5204 of cluster VI and Malviya-36, Kanakjeer and Super Basmati of cluster VIII proved to be promising for use in hybridization programme.

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

Garg *et al.*, 2011 an investigation was carried out with the forty eight genotypes of rice to study the nature and magnitude of genetic divergence using D^2 statistics. Seventeen yield and quality traits were recorded on the genotypes raised in the Randomized block Design with three replications. The forty eight genotypes were

grouped into five clusters based on Euclidean cluster analysis with cluster I containing the maximum of 18 genotypes. Maximum intra-cluster distance was observed in cluster I indicating greater genetic divergence between the genotypes belonging to this cluster. Days to maturity, gel consistency and days to 50 per cent flowering contributed 74.55 per cent of total divergence. Maximum inter-cluster distance was recorded between clusters II and III followed by clusters III and IV indicating wide genetic diversity and it may be used in rice hybridization programme for improving yield.

Latif *et al.*, 2011 conducted an experiment and The genotypes were grouped into 7 clusters according to Mohalanobis's D^2 statistics and canonical vector analysis. On the basis of cluster distances, high yielding along with highly susceptible genotype, Bangladesh Rice Research Institute (BRRI) dhan29 could be crossed with resistant genotypes, BR 6017-3-3-4-1 and Zong-yu 7. Similarly, BRRI dhan28 could be crossed with Qing Liali No.1 for the development of blast resistant rice varieties with higher yield

Ali *et al.*, 2011 revealed that canonical discriminant analysis identified eight agro-morphological traits (panicle number per plant, panicle length, plant height, flag leaf width, grain length, width, length:width ratio, and volume) as the main discriminatory characters among the rice accessions and between the subpopulations.

Chanbeni *et al.*, 2012 The nature and magnitude of genetic divergence were estimated in 70 rice genotypes using Mahalanobis D^2 – statistics by considering 13 quantitative characters. The genotypes were grouped into nine clusters. Cluster I and cluster III constituted maximum number of genotypes (12 each). The genotypes falling in cluster VII (2907) had the maximum divergence, which was closely followed by cluster V (2027) and cluster I (1762). The inter cluster distance was maximum between cluster VI and VII (18054) followed by cluster III and IX (12520), suggesting that the genotypes constituted in these clusters may be used as parents for future hybridization programme.

Sanni *et al.*, 2012 envisaged that the canonical discrimination revealed the composition of the accessions differs chiefly in number of days to 50% heading, maturity, grain characters, tiller number, and plant height. The result of the canonical discriminant analysis confirmed the results of both the PCA and cluster analysis.

Anandan *et al.*, 2013 evaluated forty four salt tolerant rice genotypes from different geographic regions Mahalanobis D^2 analysis. The D^2 statistics grouped the genotypes into 12 distinct clusters. Consisting of 19 genotypes, Cluster I was the largest cluster, followed by Cluster II with nine genotypes. Meanwhile, Clusters III, IV, VI, VII, IX, and XII were mono-genotypic clusters. The maximum intercluster distance was exhibited between Cluster IX and X (144.91), followed by Clusters II and X (131.87), as well as clusters VII and X (126.27). The number of grains per panicle (42.71%), followed by the grain yield per plot (29.81%), was the major contributor to the total divergence.

Kumar, 2015 an investigation was carried out to assess the nature and magnitude of genetic diversity was in 57 genotypes of rice using Mahalanobis D^2 statistics. They were evaluated for thirteen yield and yield attributing characters and based on D^2 analysis, 57 genotypes were grouped into 13 clusters. Clusters II and IV was the largest cluster containing 14 genotypes each followed by cluster III with 11 genotypes. The pattern of distribution of genotypes within different clusters was random and independent of geographical origin or region of adaptation. The characters like days to maturity (34.21%), days to flowering (27.44), grain length (19.55%) and grain width (12.16%) contributing maximum towards diversity. Hence these characters can be given consideration for selection of genotypes for future breeding programmes.

Chopkar and Sarawgi, 2017 studied 81 aromatic rice germplasm, collected from different locations of Chhattisgarh were evaluated for divergence analysis. Observations were recorded on five randomly selected plants for 16 agromorphological and quality characters. Based on relative magnitude of D^2 estimates 81 genotypes which were grouped into nine clusters. A wide range of variation was observed in cluster means for all the characters studied. The genotypes from cluster II having desired mean value for quality characters like hulling, milling and head rice recovery percentage and panicle length; cluster VII having high value for kernel length and length breadth ratio and cluster V for earliness and high yield could be incorporated in hybridization for developing high yielding, early maturing with good quality aromatic rice variety.

Singh *et al.*, 2017 evaluated Twenty rice landraces and grouped them into five different clusters based on the inter-cluster genetic distances. This indicated presence

of considerably diverse rice genotype in the set of material understudy. Clustering pattern indicated that 13 out of 20 genotypes belong to the same cluster i.e. cluster I. On the other hand, four genotypes belong to cluster II and III, IV, V consists of one genotype each. Among all the characters, biomass (kg per ha) contributed the maximum to the diversity by taking first rank, followed by grain yield per plant(g), harvest index, grain yield per plot(kg) and kernel breadth (mm).

Irappa *et al.*, 2018 To assess the divergence among 150 germplasm lines of rice, Mahalanobis's D^2 statistics were applied. The analysis of variance revealed highly significant mean sum of squares due to germplasm for all traits except for panicle length, the number of tillers per plant and number of productive tillers per plant indicating adequate genetic diversity exists among the lines. The 150 germplasm lines grouped into 8 clusters, where clusters I and II were the largest containing 56 and 54 genotypes, respectively followed by cluster IV with 17 genotypes. The maximum inter-cluster distances observed between cluster III and IV followed by cluster III and VII. The most important character was contributing to the total divergence number of spikelets per panicle (49.80 %) followed by the number of grains per panicle (26.02 %) and plant height (20.37 %). Among the 150 lines studied for genetic divergence ten germplasm lines viz., IET-16675, IET-16690, IET-13713, IET-16964, IET-14819, IET-13257, IET-16907, IET-8319, IET-16688, IET-13875 were found to be best which could be intercrossed to recover proper recombinants and desirable segregants.



MATERIAL AND METHODS

The Present investigation on “Genetic study of yield variation in lowland rice genotypes” was carried out during *kharif* 2017, at Rice Research Station, Dept. of Plant Breeding and Genetics, College of Agriculture, OUAT, Bhubaneswar. Crop management was done as per recommended lowland rice cultivation practices. The material utilized and the methodologies adopted in the present study are described below.

3.1 Experimental material

The material for the present study consisted of 34 lowland rice genotypes including 5 checks namely Swarna, Pooja, Upahar, Hasanta, Ashutosh. These genotypes are collected and maintained at Rice Research Station, Orissa University of Agriculture and Technology, Bhubaneswar. The details of the parentage of the test entries are presented in Table 3.1.

3.2 Methods

3.2.1 Experimental lay out

The experiment was laid out in Randomized Block Design with two replications which consisted of 34 genotypes. The spacing maintained was 20 cm between rows and 15 cm between plants with in a row. Recommended agronomic practices were followed during crop growth period to raise a good crop.

3.2.2 Cultural operations

The genotypes were sown on 4th August, 2017 in nursery. Recommended cultural practices of irrigation, fertilizer application and plant protection measures for raising nursery of paddy were followed.

The seedlings of genotypes were transplanted in the main plot on 05th September, 2017 in Randomized Block Design with two replications. Each of the entries was transplanted in 4 rows with 24 plants in each row. A spacing of 20 cm between rows and 15 cm between plants within a row was maintained.

Table 3.1 List of 34 lowland rice Genotypes used in the study

Sl. No	Genotype	Parentage
1	SBP-3	CN 1918/ Jagannath
2	SBP-15	CN 1920/ Gayatri
3	SBP-27	Rajendra mahsuri/ CN 1039
4	SBP-30	Rajendra mahsuri/ CN 1039
5	SBP-32	Mahalaxmi/ CN 1231-11-7
6	SBP-33	Mahalaxmi/ CN 1231-11-7
7	SBP-34	Mahalaxmi/ CN 1231-11-7
8	SBP-35	Mahalaxmi/ CN 1231-11-7
9	SBP-53	Prachi/ CN 1039-9
10	SBP-84	CN 1918/Kanchan// Bahudev
11	SBP-89	CN 1918/Kanchan// Bahudev
12	SBP-102	Manika/Purnendu// IR 49830-7
13	SBP-122	Santepheap 3/ IR 49830-7// Rajendra mahsuri
14	SBP-149	CR1009 / IR 49830-7
15	SBP-150	CR1009 / IR 49830-7
16	SBP-151	Hatidostisali/ Ranjit
17	SBP-168	CN 1499/ CN 1131-4-1-5
18	SBP-196	CN 1234-12-1/ OR 1898-8
19	SBP-198	CN 1234-12-1/ OR 1898-8
20	SBP-234	Savitri/ CRLC 899
21	SBP-235	Gayatri/ Raghukunwar
22	SBP-236	Gayatri/ Raghukunwar
23	SBP-237	Sudhir/ Swarna
24	SBP-238	Sudhir/ Swarna
25	SBP-241	Abhaya/ RD 15/Mahsuri
26	SBP-242	SBIR 67495-M-2-1-1-1/ IR 80409-B-37-4/Kanchan
27	SBP-250	SBIR 67495-M-2-1-1-1/ IR 80409-B-37-4
28	SBP-251	SBIR 67495-M-2-1-1-1/ IR 80409-B-37-4
29	SBP-328	Gayatri/ FL496// IR49830-7
30	Swarna	Vasista/Mahsuri
31	Pooja	Vijaya/ T-141
32	Upahar	Mahsuri/IR 62
33	Hasanta	OR 1206-26-2/OR-1534-129
34	Ashutosh	OR1301-32/IR52561

3.2.3 Method of sampling and recoding observation

Five plants were selected at random for each entry in the replication for recording the observation on 11 metric characters and cellulose. The average of observations recorded of these five plants were considered for statistical analysis. The characters on which observation were recorded are described below.

3.2.3.1 Days to 50 per cent flowering

The total number of days taken from the date of sowing to complete exertion of the panicle tip above the sheath of the flag leaf in 50 per cent of the total plants in the net plot.

3.2.3.2 Plant height (cm)

Height of the plant was measured at maturity from the base of plant to the tip of main panicle was measured in centimetres.

3.2.3.3 Productive tillers per plant

The number of ear bearing tillers, which produced healthy panicles were counted on each plant at the time of maturity.

3.2.3.4 Flag leaf area (cm²)

It was measured to the nearest square centimetre by multiplying the conversion factor (0.8) to the product of length (measured in centimetre from the junction to the tip of the leaf lamina) and breadth measured in centimetre where it is maximum of the flag leaf.

3.2.3.5 Panicle length (cm)

The panicle length measured as the total length from the base of panicle to the tip of the panicle measured to the nearest centimetre.

3.2.3.6 Panicle exertion (cm)

The total length of the peduncle from its base to the point where it coincides with the flag leaf collar is recorded. Depending on whether, the panicle base was above, below or in line with the flag leaf collar, the exertion measurements were given positive, negative and zero values respectively.

3.2.3.7 Spikelet fertility (%)

It was computed as the ratio of number of fertile grains per panicle to total number of grains expressed in percentage. This was averaged over five samples.

3.2.3.8 Number of fertile grains per panicle

It was recorded as the average no of fertile grains from the panicles of 5 sample tillers.

3.2.3.9 Panicle weight (g)

The panicle weight is measured as the total weight of five panicles and average weight was recorded in grams.

3.2.3.10 Test weight (100 grain weight) (g)

Weight of one hundred randomly selected filled grains was recorded in grams.

3.2.3.11 Single plant yield (g)

Panicles from a single plant were harvested at maturity, threshed, cleaned and sun dried to 12 per cent moisture content and the weight was recorded in grams.

3.2.3.12 Cellulose (micro gram)

The Cellulose from rice straw was estimated and expressed in terms of microgram of cellulose per gram of straw sample taken.

Cellulose estimation method

Plant materials

Thirty four plant samples of two replications including 5 checks are sundried for 2 weeks prior to analysis. After removing the panicles, the above ground parts are sun dried and then oven dried at $45 \pm 3^{\circ}\text{C}$ for 3 hours. The sample was weighed and kept for drying at 45°C for 1 hour. The process was repeated until the change in mass of the sample is $<1\%$ in 1 hour.

Isolation of cellulose

Principle

Cellulose undergoes acetolysis with acetic / nitric reagent forming acetylated cellodextrins which get dissolved & hydrolysed to form glucose molecules on treatment with 67% sulphuric acid. The glucose molecule is dehydrated to form hydroxy methyl furfural which forms green coloured product with anthrone & the colour intensity is measured at 630 nm.

Procedure

1. The dried sample was macerated in a grinder and 1 g of sample from each genotype was taken.

2. To the sample 3 ml of 10:1 mixture of Acetic/ Nitric reagent is added in a test tube & mixing done in vortex mixer.
3. Then the tubes are placed in a water bath at 100° c for 30 min
4. The contents were cooled and centrifuged for 15 – 20 min & supernatant was discarded
5. To the residue 10 ml of 67% of conc sulphuric acid was added and allowed it to stand for 1 hr.
6. To 1 ml of the above solution 100 ml of water was added to dilute
7. To 1 ml of the diluted solution 10 ml of Anthrone reagent was added. Then the tubes were heated in boiling water bath for 10 mins.
8. The samples develop green colour and the colour was measured at 630nm in Spectrophotometer
9. The blank with anthrone and distilled water is kept along with the sample and the OD value was measured at 630 nm
10. OD value was compared to the standards prepared and the cellulose content in 1g of the straw sample is measured.

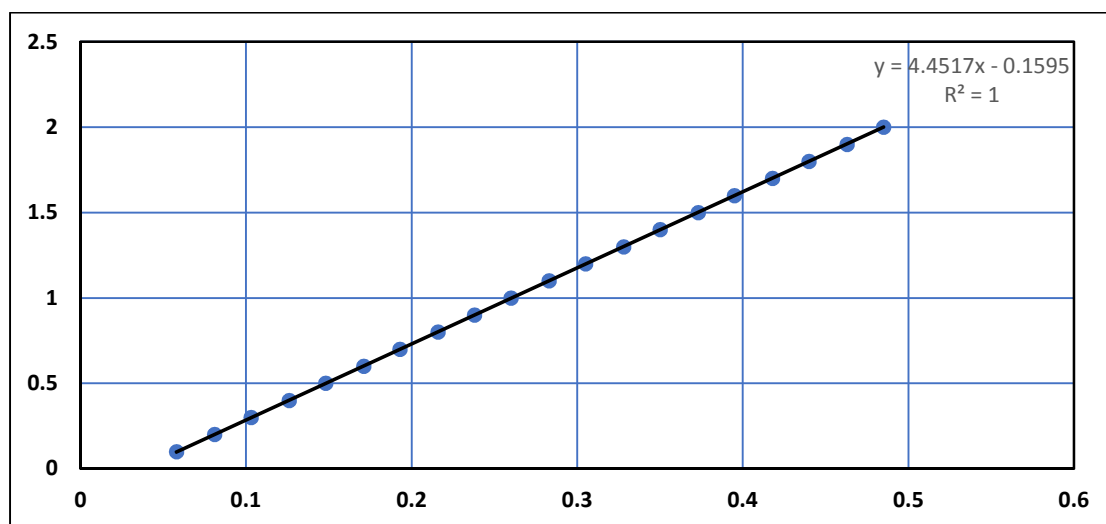


Figure 3.1: Cellulose standard curve

3.3 Statistical analysis

The data was subjected to statistical analysis based on the sample means observed for each character.

3.3.1 Analysis of variance (ANOVA)

The data of mean value for all the characters were analysed for their variance following Randomized Block Design outlined by Panse and Shukhatme, 1985. The analysis of variance was done on the basis of the following model:

$$Y_{ij} = M + g_i + r_j + e_{ij}$$

Where,

Y_{ij} = Phenotypic observation of the i^{th} genotype in j^{th} replication

M = general mean

g_i = Effect of i^{th} genotype

e_{ij} = random error associated with i^{th} genotype in j^{th} replication

The structure of analysis of variance is as follows:

Table 3.2 ANOVA with expectations of mean squares

Source	d.f	M.S.	E (MS)	F
Replication	(r-1)	M_r	$\sigma_e^2 + g\sigma_r^2$	M_r / M_e
Genotypes	(g-1)	M_g	$\sigma_e^2 + r\sigma_g^2$	M_g / M_e
Error	(r-1) (g-1)	M_e	σ_e^2	

Where,

r = no of replications

g = no of genotypes

M_r , M_g and M_e stand for sum of squares due to replication, genotype and error respectively.

3.3.2 Estimation of mean, range, standard error and critical differences

Mean

The mean value of each character was determined by summing up all the observations and dividing them by corresponding number of observations.

$$\bar{X} = \frac{1}{N} \sum x_i$$

Where,

N = Number of observations

x_i = Variable

Range

The lowest and highest mean values for each character were taken as the range.

Standard error of mean

$$SEM = \sqrt{\frac{EMS}{r}}$$

Standard error of difference between two means [SE.d. (m)]

SE.d. (m) was calculated with the help of error mean square from ANOVA table

$$S.E.d.(M) = \sqrt{\frac{2EMS}{(r \times t)}}$$

Where, r = Number of replications,

EMS = Error Mean sum of square

t = t value at error degree of freedom at 5% and 1% level of significance

Critical difference (CD)

The significant difference between means of any two genotypes was tested by 't' – test through computation of critical difference (CD)

$$CD = \sqrt{\frac{2EMS}{r}} \times t$$

Where,

EMS = error mean sum of squares

r = number of replications

t = value of 't' at 5 % or 1 % level of significance at error degrees of freedom

Variance

Genotypic and Phenotypic variances were calculated as per the formulae Burton and Devane, 1952.

From the structure of Analysis of Variance

Error variance = $\sigma_e^2 = M_e$

Genotypic variance = $\sigma_g^2 = (M_g - M_e)/r$

$$\text{Phenotypic variance} = \sigma_p^2 = \sigma_g^2 + \sigma_e^2$$

$$\text{GCV} = \text{Genotypic standard deviation} / \text{grand mean} \times 100$$

$$\text{PCV} = \text{Phenotypic standard deviation} / \text{grand mean} \times 100$$

$$\text{CV} = \frac{\sqrt{\text{EMS}}}{\bar{x}} \times 100$$

PCV and GCV were classified as per Sivasubramanian and Menon, 1973 and as shown below: 0-10 per cent - Low; 10 -20 per cent - Moderate; >20 per cent – High.

3.3.3 Heritability in broad sense (h^2)

Heritability (broad sense) was estimated for all the characters as the ratio of genotypic variance to the total variance as suggested by Lush, 1949.

$$h_{bs}^2 = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100$$

3.3.4 Expected Genetic Advance (GA)

Genetic advance for each character was estimated by using the following formula of Johnson *et al.*, 1955.

$$\text{GA} = h^2 \times K \times \sigma_p$$

Where,

h^2 = Heritability estimate

K = Selection differential which is equal to 2.06 at 5 per cent intensity of selection.

σ_p = Phenotypic standard deviation

Further the genetic advance as per cent of mean was computed by using the following Formula

$$\text{GA as per cent of mean} = \frac{\text{GA}}{\text{Grand mean}} \times 100$$

Genetic advance as per cent of mean was categorized according to Johnson *et al.*, 1955, as given below.

0 -15 per cent = Low;

15 - 30 per cent = Moderate

>30 per cent = High

3.3.5 Analysis of Covariance

The analysis of Covariance between all possible pairs of characters was done on the mean values following the procedure of randomized block design analysis by Panse and Sukhatme, 1954. The Structure of analysis of covariance is as follows.

Table 3.3 ANCOVA with expectations of mean sum of products (MSP)

Source	Degrees of freedom	M.P	Expected M.P
Replication	(r-1)	Mr_{xy}	$\sigma_{exy} + g \sigma_{rxy}$
Genotypes	(g-1)	Mg_{xy}	$\sigma_{exy} + r \sigma_{rxy}$
Error	(r-1)(g-1)	Me_{xy}	σ_{exy}

Where,

r = number of replications

g = number of genotypes

Mr_{xy} , Mg_{xy} , and Me_{xy} stand for mean sum of products between pairs of characters due to replication, genotype and error, respectively. From the structure of the analysis of covariance the following estimates were computed

$$\text{Error covariance} = \sigma_{exy} = Me_{xy}$$

$$\text{Genotypic covariance} = \sigma_{exy} = \frac{(Mg_{xy} - Me_{xy})}{r}$$

$$\text{Phenotypic covariance} = \sigma_{pxy} = \sigma_{grxy} + \sigma_{exy}$$

3.3.6 Estimation of correlation coefficients

The genotypic and phenotypic correlation coefficients were computed between the pairs of characters adopting the following formula.

$$\text{Genotypic correlation coefficient, } (r_g) = \frac{\sigma_{gxy}}{(\sigma_{gx} \times \sigma_{gy})}$$

$$\text{Phenotypic correlation coefficient, } (r_p) = \frac{\sigma_{pxy}}{(\sigma_{px} \times \sigma_{py})}$$

Where, σ_{gxy} = Genotypic covariance between two traits X and Y

σ_{pxy} = Phenotypic covariance between two traits X and Y

σ_{gx} and σ_{gy} stand for genotypic standard deviation of X and Y, respectively.

σ_{px} and σ_{py} stand for Phenotypic standard deviation of X and Y, respectively.

To test the significance of the phenotypic correlation coefficients, the estimated values were compared with the table values by Fisher and Yates, 1963 at (n-2) degrees of freedom at the 5% and 1% levels of significance.

3.3.7 Path coefficient analysis

The method of analysis by path coefficients requires a cause-and-effect relationship among correlated variables. Path coefficients are standardized partial regression coefficients which individually provide a measure of the direct effect of a causal factor on the effect variable. They permit partitioning of the correlations between a causal factor and the effect variable into components of direct and indirect effects and thus, give a better picture of associations of the causal factors with the effect of variable.

In the present study, yield was taken as the effect with eleven other characters related to yield and the causal factors. The path coefficients were obtained by following simultaneous equations which give the basic relationship between correlations and path coefficients in a system of correlated causes Dewey and Lu, 1959

$$\begin{aligned}
 r_{1-11} &= p_{1-11} + r_{1.2} p_{2.11} + r_{1.3} p_{3.11} + \dots + r_{1.10} p_{10.11} \\
 r_{2.10} &= r_{2.1} p_{1.11} + p_{2.11} + r_{2.3} p_{3.11} + \dots + r_{2.10} p_{10.11} \\
 &\dots\dots\dots \\
 &\dots\dots\dots \\
 r_{10.11} &= r_{10.1} p_{1.11} + r_{10.2} p_{2.11} + r_{10.3} p_{3.11} + \dots + p_{10.11}
 \end{aligned}$$

3.4 Construction of selection indices

Application of discriminate function as a basis for making selection on several characters simultaneously was aimed at discriminating the desirable genotypes from undesirable ones on the basis of their phenotypic performance. The selection index for different character combinations were constructed considering grain yield per plant as ultimate economic criterion. The indices were of the following form.

$$I_x = b_1x_1 + b_2x_2 + b_3x_3 + \dots\dots\dots b_n x_n$$

Where,

x's = character means of a particular genotype included in the index

b's = relative weights to be signed to the characters in computing the single index value I_x for each genotype on which the selection is based

The b values which would maximize the expected genetic advance in yield from index selection were obtained by solving the following simultaneous equations as suggested by Hazel (1943).

$$\begin{aligned}
 b_1p_{1.1} + b_2p_{1.2} + b_3p_{1.3} + \dots + b_n p_{1. n} &= G_{1. y} \\
 b_1p_{2.1} + b_2p_{2.2} + b_3p_{2.3} + \dots + b_n p_{2. n} &= G_{2. y} \\
 b_1p_{3.1} + b_2p_{3.2} + b_3p_{3.3} + \dots + b_n p_{3. n} &= G_{3. y} \\
 &\dots \\
 &\dots \\
 b_1p_{n.1} + b_2p_{n.2} + b_3p_{n.3} + \dots + b_n p_{n. n} &= G_{n. y}
 \end{aligned}$$

Where,

P = phenotypic variance/ covariance

G = genotypic covariance between a particular character and grain yield

3.4.1 Character combination and group indices

Since grain yield was a complex trait, controlled by non-additive gene action and is believed to have low heritability, hence direct selection for grain yield per se is often not reliable and effective further inter-genotypic competition and large experimental error associated with yield measurements often bias the out come of selection for high yield. Therefore, several workers in different crop plants have emphasized the importance of indirect selection for yield through the use of component traits governed by genes with additive effect and with strong correlation on grain yield. As no single trait can be taken as adequate criterion of selection for yield therefore selection indices provide a useful method by making use of several correlated characters for greater efficiency of selection in yield.

During the present investigation selection indices were constructed with grain yield as economic criterion and eleven different characters namely days to 50 % flowering plant height, panicle length, number of productive tillers, panicle weight, flag leaf area, panicle exsertion, number of fertile grains per panicle, spikelet fertility %, 100 seed weight, single plant yield were chosen for the construction of eleven selection indices. The eleven character index including all the eleven traits was used for the selection of genotypes. These genotypes which occupied better rankings in the above selection indices were selected for future use.

The following eleven characters namely (x_1) DF- Days to 50% flowering (x_2) PH-Plant height (cm), (x_3) EF- number of Effective tillers, (x_4) FA- Flag leaf Area (cm^2), (x_5) PL- Panicle length (cm), (x_6) PE- Panicle Exsertion (cm), (x_7) SF- Spikelet fertility %, (x_8) FG- number of Fertile Grains / panicle, (x_9) PW- Panicle weight(g), (x_{10}) TW- 100grain weight (g), (x_{11}) SPY- Single plant yield (g) were chosen on the basis of heritability and phenotypic correlation for the construction of nine selection indices. The number of characters in the combination was increased each time by the inclusion of characters one after the other such that the indices varies from single character to a complete eleven character index.

3.4.2 Genetic advance and relative efficiency of indices

The expected genetic advance from selection indices was constructed on the basis of model suggested by smith, 1936 in following manner.

Where,

K = standardized selection differential which takes the values of 2.06 at 5% selection intensity

G_{iy} = genotypic covariance between i^{th} character and yield

B_i = index value of the i^{th} character

The relative efficiency of an index was estimated as the ratio of the expected genetic advance from index selection to that from direct selection on the basis of yield and was expressed in percentage.

3.4.3 Criteria of selection

On the basis of genetic advance values two selection indices including SPY- Single plant yield as single character and combination of all the eleven characters was used for the selection of genotypes from the present set of material. Those cultures which occupy better rankings in all the above selection indices were selected during the course of the present investigation for their future use.

3.5 Multivariate approach in grouping the genotypes

In view of the inadequacy of the single variable statistical approach, the observations on different quantitative traits were utilized to calculate the genetic divergence and classify the genotypes into different groups following multivariate approach of Mahalanobis D^2 -statistic and Canonical analysis following Rao, 1952.

3.5.1 D²-analysis

3.5.2 Multivariate test of significance

After testing for difference between genotypes for each of the 11 characters, a simultaneous test of significance difference in mean values of the 11 correlated variables of 34 genotypes was carried out using Wilk's Lambda (λ) criterion and V-statistics Rao, 1952.

$$\lambda = \frac{|W|}{|W + Q|} = \frac{|\text{Diterminant of error matrix}|}{|\text{Determinant of error + Genotype matrix}|}$$

Where,

W = error sum of squares and sum of product matrix

Q = genotype sum of squares and sum of product matrix

$$V - \text{statistics} = - \left(n - \frac{p+q+1}{2} \right) \log_e \lambda$$

Where,

n = sum of degrees of freedom for error and genotypes

p = number of characters

q = degrees of freedom for genotypes

The V-statistics is distributed approximately as χ^2 with pq degrees of freedom.

Thus, the required test of significance could be performed using χ^2 distribution.

3.5.4 Average Inter and Intra-Cluster Distance

Average intra- cluster distance was calculated as follows:

$$\text{Average intra-cluster distance (D}^2\text{)} = \frac{\sum \sigma_i^2}{n}$$

Where, σ_i^2 = sum of distance between all possible combinations

n = number of genotypes included in a character

Its square root represents the distance within cluster (intra – cluster distance).

For calculating the inter-cluster distance, the average D² values of all possible combinations of genotypes in one cluster with those in the other was computed and its square root was used to represent the statistical distance between two clusters (inter-cluster distance). Their relationship was represented diagrammatically.

3.5.5 Contribution of different characters towards divergence

The relative contribution of different characters to the total D² distance between each pair of genotypes was given by a score of 1–11 (as there are 11 characters) based on the magnitude of the D² values due to each character. Rank-1 represents the highest

while Rank 11 indicates the lowest contribution. Per cent contribution of a character to divergence was calculated as follows.

$$\text{Contribution of character (X)} = \frac{N(X) \times 100}{n}$$

Where,

$N(X)$ = Number of genotypic contribution which were ranked first for character X out of the total genotypic contribution of n combinations.

The genotypes were grouped into clusters on the basis of D^2 values following Tocher's method as described by Rao 1952. The criterion of grouping was that any two genotypes belonging to the same cluster should have a smaller D^2 than those between genotypes belonging to different clusters.

3.5.6 Canonical analysis

Canonical analysis was also done following Anderson 1958 and the Z1 and Z2 values corresponding to the first two canonical vectors plotted as a supplement to grouping by Tocher's method. Grouping of the population was inferred from their relative dispersion in the Z1-Z2 graph.



RESULTS

The results of the present study on “Genetic study of yield variation in lowland rice genotypes” are based on the data recorded in the field experiment conducted at Rice Research Station, Dept. of Plant Breeding and Genetics, College of Agriculture, OUAT, Bhubaneswar. The data was collected on 12 different yield, contributing characters such as days to 50% flowering, plant height (cm), number of productive tillers, flag leaf Area (cm²), panicle length (cm), panicle exertion (cm), spikelet Fertility %, number of fertile grains per panicle, panicle weight(g), 100- grain weight (g), cellulose (µg), single plant yield (g) for the assessment of genetic variability, character association, construction of selection indices and genetic divergence studies. The observation on days to 50% flowering were recorded on plot basis and the rest of the characters were estimated on the average of five randomly selected plants in each replication.

The genetic variability existing among the genotypes was analysed using Analysis of variance (ANOVA) and the different parameters of variability such as range, mean, PCV, GCV, heritability, GA were estimated. The nature and extent of variation among the yield attributing characters was measured. Genotypic and Phenotypic correlation analysis among the yield attributing characters were observed. The direct and indirect effects on yield via the component traits was studied using path coefficient analysis. Superior genotypes were selected by constructing selection indices. Genetic divergence among the genotypes was estimated using multivariate analysis such as Mahalanobis D²-analysis and Canonical analysis. The results obtained in the present investigation were presented under the following headings.

4.1.1 Analysis of variance for various characters of 34 lowland rice genotypes

The analysis of variance was carried out among 12 different characters and presented in the Table 4.1. The analysis of variance and F-test revealed that there exists a highly significant difference among the test genotypes for all the characters under study. These indicate the presence of wide genetic variability among the selected genotypes (Table 4.1). The variance due to replications were found significant for number of productive tillers, spikelet fertility (%) and cellulose. The mean and range of different characters has been presented in Table 4.2.

Table 4.1 Analysis of variance for various characters of 34 lowland rice genotypes

Sl. No.	Characters	Mean sum of squares (df)		
		Replication (1)	Genotype (33)	Error (33)
1.	DF	9.956	53.886**	4.941
2.	PH (cm)	7.496	253.131**	45.794
3.	EF	38.250**	8.553**	1.826
4.	FA (cm ²)	22.997	61.745**	10.544
5.	PL (cm)	0.563	9.169**	2.773
6.	PE (cm)	0.104	1.084**	0.091
7.	SF (%)	221.739**	262.778**	27.965
8.	FG	37.835	1135.551**	24.802
9.	PW (g)	0.207	0.904**	0.066
10.	TW (g)	0.004	0.202**	0.006
11.	Cellulose (µg)	2.904*	17.590**	0.533
12.	SPY(g)	5.445	17.030**	2.000

*Significant at 5 % level of probability ** Significant at 1 % level probability

Figures in parenthesis indicate degrees of freedom for corresponding sources of variation

DF- Days to 50% flowering

PH- Plant height (cm)

EF- Number of effective tillers

FA- Flag leaf area (cm²)

PL- Panicle length (cm)

PE- Panicle exertion (cm)

SF- Spikelet fertility %

FG- Number of fertile grains / panicle

PW- Panicle weight(g)

TW- 100- grain weight (g)

SPY- Single plant yield (g)

4.1.2 Mean performance for various characters of 34 lowland rice genotypes

The overall mean and range of each character are presented in Table 4.2. The mean performance of 34 lowland rice genotypes for 12 characters is presented in Table 4.3. The genotypes were classified as high (H), medium (M), low(L) basing on overall

mean and S.E for each character as per the following criteria. Values more than mean+S.E ($\bar{X}+S.E$) as high(H); values in between mean $\pm$ SE ($\bar{X}\pm SE$) as medium(M); values less than mean-S. E ($\bar{X}-S.E$) as low (L). All the 34 genotypes for the 12 characters studied were grouped as H, M or L according to the values of each genotype (Table 4.3) on the basis of above criteria.

Table 4.2 Mean and range for various characters for 34 lowland rice genotypes

Sl. No	Characters	Mean	Range
1.	DF	107.26	96-118
2.	PH (cm)	109.59	89.60-141.50
3.	EF	9.75	6.5-15.0
4.	FA (cm ²)	27.85	16.90-39.11
5.	PL (cm)	23.87	16.85-28.20
6.	PE (cm)	2.10	0.85-3.42
7.	SF (%)	64.73	41.5-87.74
8.	FG	99.17	52.5-160
9.	PW (g)	2.07	0.80-3.96
10.	TW (g)	1.97	1.41-2.64
11.	Cellulose (μ g)	6.85	3.16-12.85
12.	SPY(g)	7.42	1.94-12.93

Days to 50% flowering

The varietal mean for days to 50% flowering ranged from 96 days in SBP-53 to 118 days in Ashutosh with overall mean of 107.26 days. Twenty three genotypes were found earliest with respect to days to 50% flowering, below 110.40days. eleven genotypes were found late with respect to the character under study above 110.40 days.

Plant height (cm)

The overall mean of Plant height was 109.59cm, with a range of 89.60 cm in Swarna to 141.50 cm in SBP-150. Twelve genotypes recorded medium plant height between 106.45-119.15 cm and 15 genotypes less than 106.45 cm. For 7 genotypes it was higher than 119.15cm. This clearly indicates the height shows considerable variability among genotypes.

Number of effective tillers per plant

The overall mean of all genotypes for number of productive tillers per plant was 9.75 and range varies from 6.5 to 15.0 in SBP-234 and SBP-15 respectively. 7 genotypes showed more number of panicles i.e. above 12.

Flag leaf area (cm²)

Among the genotypes, SBP-15 had the lowest flag leaf area and the highest flag leaf area was present in SBP-151 and the variability range of flag leaf area of the genotypes was 16.90 cm² to 39.11 cm² with an overall mean of 27.85cm². Seven genotypes recorded highest flag leaf area of above 32.43 cm² and Six genotypes showed lowest flag leaf area of 23.27 cm².

Panicle length (cm)

The range of panicle length for all the genotypes ranged from 16.85 cm to 28.20 cm. The panicle length was lowest for Swarna and SBP-53 exhibited highest panicle length with an overall mean of 23.87cm. Twenty seven genotypes recorded medium panicle length between 21.52 cm to 26.22 cm and four genotypes recorded high panicle length of more than 26.22cm. Three genotypes recorded shorter panicle length i.e. below 21.52cm.

Panicle exertion (cm)

SBP-250 exhibited lowest panicle exertion of 0.85 cm and SBP-15 exhibited highest panicle exertion of 3.42 cm respectively with an overall mean of 2.10 cm. Eleven genotypes exhibited fully exerted panicles and fourteen genotypes exhibited partially exerted panicles.

Spikelet fertility %

The overall mean of spikelet fertility % was 64.73% and range was 41.5 % - 87.74%. The highest range was found in SBP-235 and the lowest range was observed in SBP-15. Seven genotypes exhibited high spikelet fertility of above 72.20% and nine genotypes exhibited low spikelet fertility of below 57.26%. Eighteen genotypes recorded medium spikelet fertility between 57.26% to 72.20%.

Number of fertile grains / panicle

The lowest fertile grains observed in case of Pooja and highest in case of Hasanta with a range from 52.5 to 160, the overall mean observed is 99.17 grains. Twenty one genotypes recorded more number of fertile grains per panicle above i.e. 121.28 and six genotypes recorded less number of fertile grains i.e. below 77.06.

Panicle weight (g)

The overall mean of panicle weight was 2.07 g and range from 0.80g to 3.96g. The lowest was observed in SBP-150 and highest was observed in Hasanta. Twenty genotypes recorded medium panicle weight of 1.71 gm to 2.43 gm, 10 genotypes below 1.71gm and four genotypes recorded more panicle weight above i.e. 2.43gm.

100 - grain weight (g)

The range was 1.41 g in SBP-151 to 2.64 g in SBP-53 and the overall mean of 100 grain weight of all the genotypes was 1.97 gm. Eleven genotypes recorded medium 100 grain weight of 1.86 gm to 2.08 gm, 12 genotypes below 1.86gm and eleven genotypes recorded more test weight of above 2.08gm.

Cellulose (µg)

The range of cellulose content among the test genotypes is 1.86 g to 12.85 g. The highest cellulose content observed in case of SBP-84 and lowest in case of Ashutosh. The overall mean of all the genotypes is 6.85 grams. Twelve genotypes recorded high cellulose content of above 7.8grams.

Single plant yield

The single plant yield of all test genotypes showed a variation from 1.94 gram in SBP-150 and 12.93 gram in SBP-15 with overall mean of 7.42 grams. Nine genotypes recorded highest yield per plant of above 9.42grams.

Table 4.3 Mean performance with respect to various characters for 34 lowland rice genotypes

Sl. No	Genotype	DF	PH	EF	FA	PL	PE	SF	FG	PW	TW	Cellulose	SPY
1	SBP-3	105.50(M)	106.45(L)	9.00(M)	28.97(M)	22.65(M)	2.10(M)	66.28(M)	74.50(L)	1.83(M)	2.04(M)	12.48(H)	8.35(M)
2	SBP-15	111.00(H)	102.35(L)	15.00(H)	16.90(L)	22.75(M)	3.42(H)	87.74(H)	136.5(H)	2.38(M)	2.14(H)	4.95(L)	12.93(H)
3	SBP-27	114.50(H)	94.00(L)	9.00(M)	23.90(M)	24.55(M)	2.05(M)	53.28(L)	77.50(M)	2.26(M)	2.32(H)	7.05(M)	6.40(M)
4	SBP-30	102.50(L)	107.95(M)	12.50(H)	25.18(M)	24.14(M)	3.32(H)	75.65(H)	132.0(H)	3.28(H)	1.87(M)	5.75(L)	12.14(H)
5	SBP-32	104.00(L)	97.35(L)	9.00(M)	27.04(M)	23.93(M)	1.60(L)	68.64(M)	99.00(M)	2.11(M)	2.17(H)	6.91(M)	8.87(M)
6	SBP-33	105.00(M)	98.10(L)	10.00(M)	24.69(M)	19.10(L)	1.99(M)	66.50(M)	105.50(M)	2.28(M)	1.88(M)	6.26(M)	9.72(H)
7	SBP-34	104.00(L)	114.38(M)	11.50(M)	26.47(M)	24.30(M)	2.84(H)	69.50(M)	125.00(H)	1.20(L)	1.89(M)	12.44(H)	10.12(H)
8	SBP-35	102.50(L)	111.90(M)	9.00(M)	30.56(M)	23.95(M)	3.04(H)	71.50(M)	110.00(M)	2.33(M)	2.05(M)	5.53(L)	7.78(M)
9	SBP-53	96 (L)	124.40(H)	14.00(H)	32.17(M)	28.20(H)	2.88(H)	79.00(H)	125.00(H)	2.93(H)	2.64(H)	3.41(L)	12.70(H)
10	SBP-84	103.50(L)	123.90(H)	8.00(M)	34.39(H)	24.43(M)	1.50(L)	69.99(M)	99.00(M)	2.40(M)	2.10(H)	12.85(H)	5.56(M)
11	SBP-89	103.50(L)	118.70(M)	7.50(L)	36.6(H)	22.15(M)	1.75(M)	69.50(M)	91.50(M)	1.97(M)	2.21(H)	7.47(M)	5.92(M)
12	SBP-102	108.50(M)	121.50(H)	12.50(H)	21.21(L)	27.82(H)	2.48(M)	76.00(H)	122.50(H)	2.38(M)	2.09(H)	6.49(M)	10.94(H)
13	SBP-122	112.50(H)	110.90(M)	8.00(M)	19.74(L)	24.40(M)	2.75(H)	69.50(M)	111.0(M)	3.16(H)	2.29(H)	3.16(L)	8.23(M)
14	SBP-149	108.50(M)	124.80(H)	7.50(L)	25.53(M)	24.37(M)	1.41(L)	61.47(M)	97.03(M)	2.13(M)	2.03(M)	3.55(L)	5.74(M)
15	SBP-150	104.00(L)	141.50(H)	7.50(L)	27.33(M)	26.51(H)	1.90(M)	48.94(L)	59.50(L)	0.80(L)	1.74(L)	8.19(H)	1.94(L)
16	SBP-151	103.50(L)	113.75(M)	9.00(M)	37.99(H)	21.35(L)	3.22(H)	68.79(M)	128.50(H)	2.13(M)	1.41(L)	5.72(L)	5.66(M)
17	SBP-168	113.50(H)	107.30(M)	7.50(L)	25.87(M)	23.87(M)	1.91(M)	60.83(M)	70.50(L)	1.57(L)	2.03(M)	8.70(H)	5.40(L)
18	SBP-196	103.50(L)	120.80(H)	8.50(M)	25.79(M)	24.00(M)	1.20(L)	82.15(H)	94.50(M)	2.89(M)	2.63(H)	11.89(H)	9.45(H)
19	SBP-198	108.50(M)	129.50(H)	10.50(M)	30.83(M)	23.80(M)	1.59(L)	60.40(M)	84.50(M)	1.85(M)	2.63(H)	7.96(H)	6.04(M)
20	SBP-234	102.00(L)	103.60(L)	6.50(L)	28.24(M)	23.38(M)	1.59(L)	44.57(L)	78.50(M)	1.56(L)	1.60(L)	9.64(H)	3.97(L)
21	SBP-235	113.50(H)	104.68(L)	10.00(M)	32.48(H)	22.40(M)	1.53(L)	41.50(L)	67.50(L)	1.27(L)	1.47(L)	8.99(H)	3.80(L)
22	SBP-236	114.00(H)	99.35(L)	9.50(M)	31.37(M)	23.97(M)	2.74(H)	45.50(L)	111.0(M)	1.91(M)	1.61(L)	10.21(H)	7.06(M)
23	SBP-237	114.00(H)	102.00(L)	8.50(M)	26.12(M)	24.35(M)	1.88(M)	68.54(M)	105.0(M)	2.16(M)	1.78(L)	5.11(L)	4.44(L)
24	SBP-238	103.50(L)	106.05(L)	7.50(L)	30.68(M)	24.45(M)	3.16(H)	63.67(M)	107.5(M)	1.67(L)	2.02(M)	9.19(H)	5.85(M)
25	SBP-241	105.00(M)	113.45(M)	9.50(M)	30.21(M)	27.16(H)	1.30(L)	69.31(M)	76.50(L)	1.36(L)	1.74(L)	8.63(H)	5.64(M)
26	SBP-242	107.00(M)	103.85(L)	9.00(M)	35.15(H)	24.39(M)	1.63(L)	66.04(M)	100.75(M)	1.95(M)	1.71(L)	5.61(L)	9.30(M)
27	SBP-250	109.50(M)	102.00(L)	10.00(M)	24.91(M)	24.71(M)	0.85(L)	48.88(L)	85.50(M)	1.75(M)	1.48(L)	5.24(L)	4.05(L)
28	SBP-251	113.50(H)	107.63(M)	13.50(H)	24.37(M)	21.85(M)	1.17(L)	47.25(L)	83.20(M)	1.55(L)	1.65(L)	5.63(L)	5.74(M)
29	SBP-328	112.50(H)	115.30(M)	9.00(M)	39.11(H)	25.90(M)	1.39(L)	66.04(M)	96.50(M)	2.32(M)	2.24(H)	7.48(M)	10.13(H)
30	Swarna	103.50(L)	89.60(L)	9.00(M)	18.66(L)	16.85(L)	1.31(L)	65.68(M)	77.80(M)	0.99(L)	1.67(L)	3.40(L)	4.81(L)
31	Pooja	101.50(L)	93.55(L)	10.00(M)	22.41(L)	24.60(M)	1.48(L)	56.89(L)	52.50(L)	1.25(L)	1.95(M)	1.98(L)	3.44(L)
32	Upahar	113.50(H)	107.55(M)	12.50(H)	20.39(L)	23.10(M)	2.49(M)	54.50(L)	106.00(M)	2.41(M)	2.01(M)	3.57(L)	9.00(M)
33	Hasanta	101.50(L)	101.45(L)	12.00(H)	35.40(H)	23.85(M)	2.93(H)	78.81(H)	160.0(H)	3.96(H)	1.95(M)	5.74(L)	12.75(H)
34	Ashutosh	118.00(H)	106.50(M)	9.50(M)	26.18(M)	24.30(M)	2.88(H)	77.82(H)	120.00(M)	2.35(M)	1.83(L)	1.80(L)	8.26(M)
	GM	107.26	109.59	9.75	27.85	23.87	2.1	64.73	99.17	2.07	1.97	6.85	7.42
	CD	4.52	13.76	2.75	6.6	3.39	0.61	10.76	31.82	0.52	0.16	1.49	2.88
	CV(%)	2.07	6.17	13.86	11.66	6.98	14.35	8.17	15.78	12.46	4.04	10.66	19.07

(H), (M), (L) indicate high, Medium, low mean performance.

Bold figures indicate minimum and maximum values.

Table 4.4 Frequency of genotypes on performance ranking for 12 characters in 34 lowland rice genotypes

Sl. No	Characters	High	Medium	Low
1.	DF	11	8	15
2.	PH (cm)	7	12	15
3.	EF	7	21	6
4.	FA (cm ²)	7	21	6
5.	PL (cm)	4	27	3
6.	PE (cm)	11	9	14
7.	SF (%)	7	18	9
8.	FG	7	21	6
9.	PW (g)	4	20	10
10.	TW (g)	11	11	12
11.	Cellulose (µg)	12	6	16
12.	SPY(g)	9	17	8

4.1.3 Genotypic and phenotypic coefficient of variation

From the investigation it was found that phenotypic coefficient of variation was found to be higher than that of genotypic coefficient of variation for all the characters studied among the set of materials.

The estimates of phenotypic coefficients of variations (PCV) ranged from 4.84 for days to 50% flowering to 42.62 for cellulose.

Phenotypic coefficient of variability was low (below 10 %) for characters like days to 50 per cent flowering (4.84%) and panicle length (8.97). The estimates of PCV were moderate (10-20%) for plant height (10.27), flag leaf area (19.95), spikelet fertility (17.71), 100 grain weight (16.16). These estimates were high (> 20%) for number of effective tillers (21.21), panicle exsertion (35.12), filled grains per panicle (24.03), panicle weight (32.51), cellulose (43.28), single plant yield (39.25).

The estimates of genotypic coefficient of variation ranged between 4.61 for days to 50% flowering to 42.62 for cellulose. The GCV estimates showed that the genotypic variability was low (below 10%) for days to 50% flowering (4.61), plant height (9.29) and panicle length (7.49). The estimates of GCV were moderate (10-20%) for number of effective tillers (18.81), flag leaf area (18.17), spikelet fertility (16.74), 100- seed weight (15.90). These estimates were high (> 20%) for panicle exsertion (33.62), filled grains (21.28), panicle weight (31.30), cellulose (42.62), single plant yield (36.97) indicates better scope for genetic improvement in the characters through simple selection. (Table 4.5)

Relatively higher difference in magnitudes of GCV and PCV exists for number of productive tillers (18.81% and 21.21%), fertile grains per panicle (21.28% and 24.03%), single plant yield (36.97% and 39.35%) indicates the influence of environmental fluctuations on these traits. Relatively low difference in GCV and PCV for rest of the characters i.e days to 50% flowering, Plant height, Panicle length, Flag leaf area, Spikelet fertility, 100 seed weight, panicle exsertion, panicle weight and cellulose indicates that these are mostly governed by genetic factors and minor environmental effect.

4.1.4 Heritability and genetic advance

The heritability in broad sense and genetic advance for all the characters are presented in the table 4.5. It is the measurement of relative importance of hereditary and environmental factors in the expression of the characters. It is an index to quantify the extent of transmission of particular character from parents to the offsprings.

The estimates of heritability ranged from 69.76% for panicle length to 96.97% for cellulose. Characters like panicle length (69.76%) exhibited moderate heritability (40%-70%) and all other characters exhibit high heritability (>70%) suggesting effectiveness of selection on the basis of phenotypic expression of the traits.

The expected genetic advance over mean for different characters ranged from 7.74 for days to 50% flowering to 73.86 for cellulose. Low (0-15%) expected genetic advance was reported in case of days to 50 per cent flowering (7.74), panicle length (11.01) plant height (14.80) moderate (15-30%) genetic advance was reported for number of productive tillers (29.36), flag leaf area (29.12), spikelet fertility % (27.85), 100-seed weight (27.55). For characters like panicle exsertion (56.65), number of fertile grains per panicle (33.17), panicle weight (53.02), cellulose (73.86), single plant yield (61.12), reported high (> 30%) genetic advance.

Characters like days to 50 per cent flowering and plant height observed high heritability accompanied with low genetic advance. High heritability with moderate genetic advance was observed in number of productive tillers, flag leaf area, spikelet fertility %, 100-seed weight. High heritability accompanied with high genetic advance was observed in number of fertile grains per panicle, panicle weight, cellulose, single plant yield. panicle length exhibited moderate heritability with low genetic advance.

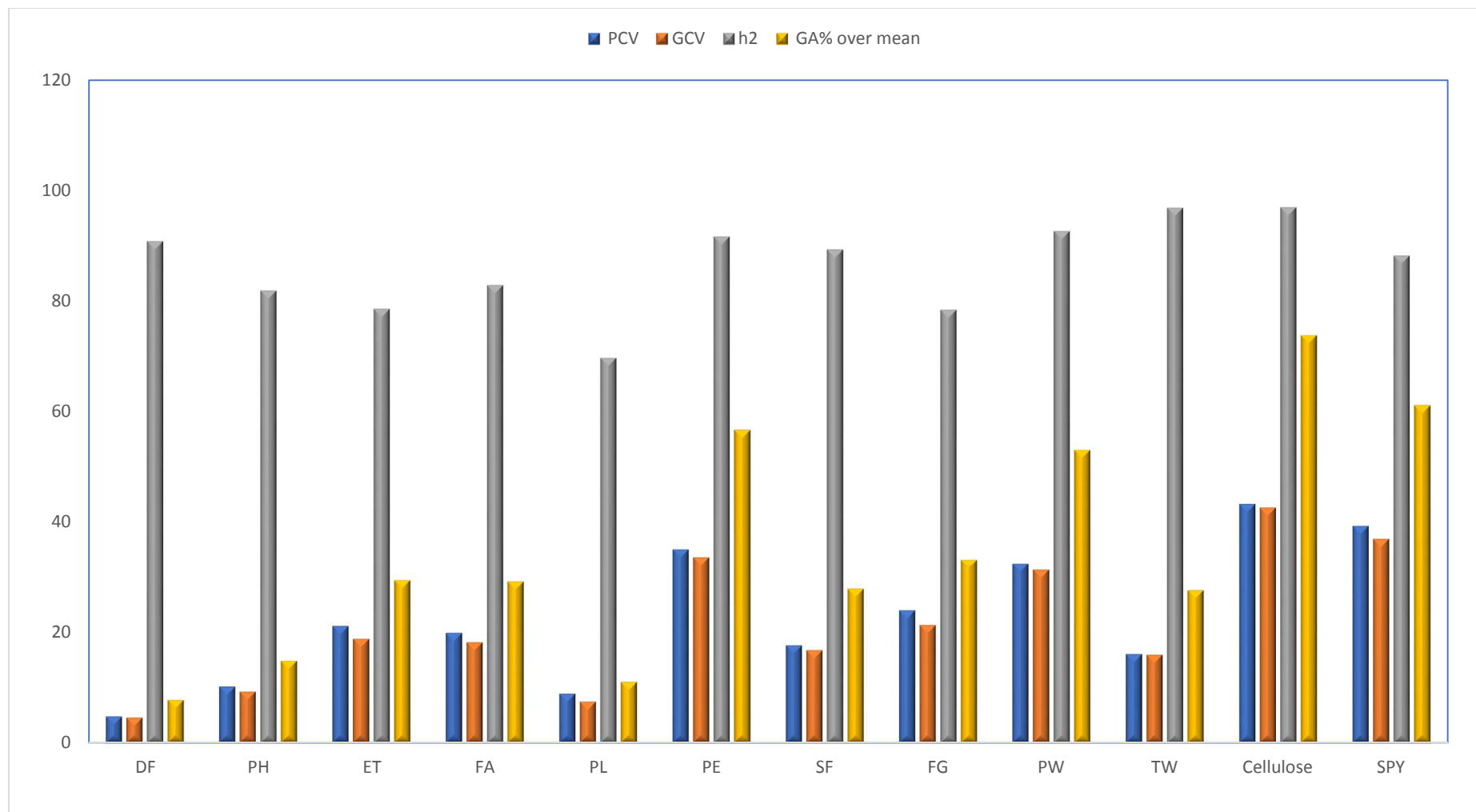


Figure 4.1 PCV, GCV, h^2 and GA of 12 for 12 characters of 34 genotypes

Table 4.5 PCV, GCV, h^2 and GA estimates for various characters for 34 lowland rice genotypes

Sl. No	Haracters	PCV	GCV	h^2	GA (10%)	GA% over mean
1.	DF	4.84	4.61	90.83	8.30	7.74
2.	PH (cm)	10.27	9.29	81.91	16.22	14.80
3.	EF	21.21	18.81	78.65	2.86	29.36
4.	FA (cm ²)	19.95	18.17	82.92	8.11	29.12
5.	PL (cm)	8.97	7.49	69.76	2.63	11.01
6.	PE (cm)	35.12	33.62	91.65	1.19	56.65
7.	SF (%)	17.71	16.74	89.36	18.03	27.85
8.	FG	24.03	21.28	78.44	32.90	33.17
9.	PW (g)	32.51	31.30	92.66	1.10	53.02
10.	TW (g)	16.16	15.90	96.88	0.54	27.55
11.	Cellulose (μ g)	43.28	42.62	96.97	5.06	73.86
12.	SPY(g)	39.35	36.97	88.26	4.53	61.12

4.2 Character association

Correlation coefficients between yield and yield components viz., days to 50 per cent flowering, plant height, number of productive tillers per plant, Flag leaf area, panicle length, panicle exsertion, spikelet fertility, number of fertile grains per panicle, panicle weight and 100 grain weight and cellulose were estimated for all the rice genotypes. The genotypic and phenotypic correlations between yield and its component characters were computed separately. The results are presented in Table 4.6. The results revealed that in general, the direction of genotypic and phenotypic correlations were identical for various characters, though the magnitude of genotypic correlations were slightly higher than phenotypic correlation coefficients for most of the characters under study indicating influence of environment in their relationship. The results obtained from correlations analysis (phenotypic / genotypic) are presented character wise here under.

4.2.1 Phenotypic and genotypic correlation

From table 4.6 it can be deduced that the significant Phenotypic correlation(r_p) ranges from 0.355 (between plant height and 100 grain weight, flag leaf area and

cellulose) to 0.775 (between number of filled grains per panicle and single plant yield). Out of 78 estimates of r_p with seed yield, only 19 found highly significant. None of the negative correlation values are found significant.

The genotypic correlation (r_g) ranges from 0.354 (between number of productive tillers and spikelet fertility %) to 0.964 (between number of fertile grains per panicle and single plant yield). Out of the 78 estimates 23 were negative only one was found significant. Among the 55 positive estimates 22 were found highly significant. All of the remaining Positive values were recorded as non-significant.

4.2.2 Correlation of yield with component traits

The high estimates of correlation at phenotypic level was between yield and number of fertile grains per panicle (0.775). It was followed by panicle weight (0.721), spikelet fertility% (0.709), number of productive tillers (0.634), panicle exertion (0.547), 100- grain weight (0.439). The character panicle length is positive and non-significant. The characters like days to 50% flowering, plant height, flag leaf area and cellulose found negatively correlated and non-significant at phenotypic level. (Table 4.6)

At genotypic level, number of fertile grains (0.964) was found to have high positive and significant correlation with single plant yield. It was followed by spikelet fertility % (0.806), panicle weight (0.790), number of productive tillers (0.723), panicle exertion (0.607), and 100grain weight (0.474). Panicle length is positive and non-significant. The characters like Days to 50% flowering, plant height, flag leaf area and cellulose found negatively correlated and non-significant at phenotypic level. (Table 4.7)

4.2.3 Correlation among other component traits

Out of the 66 estimates of phenotypic correlations for 12 characters, 13 were found positive and highly significant. None of the negative correlation values were found significant. 16 estimates of genotypic correlations were found to be positive and significant where as one of the estimate is negative and significant at genotypic level.

Plant height had positive significant correlation with Panicle length ($r_p = 0.496$, $r_g = 0.657$), 100 grain weight ($r_p = 0.355$, $r_g = 0.377$) at both phenotypic and genotypic level. It had positive significant genotypic correlation with flag leaf area ($r_g = 0.372$).

Number of productive tillers had positive significant correlation with Panicle exertion ($r_p = 0.365$, $r_g = 0.404$), number of fertile grains ($r_p = 0.486$, $r_g = 0.611$). It had negative significant correlation with flag leaf area ($r_g = -0.354$) at genotypic level. It had positive significant genotypic correlation with spikelet fertility ($r_p = 0.354$).

Flag leaf area had positive significant correlation with cellulose ($r_p = 0.355$, $r_g = 0.391$) at both phenotypic and genotypic level. It is nonsignificant with other characters.

Panicle length had significant positive genotypic correlation with 100 grain weight ($r_g = 0.394$).

Panicle exertion had positive significant correlation with number of fertile grains ($r_p = 0.740$, $r_g = 0.859$), spikelet fertility % ($r_p = 0.448$, $r_g = 0.502$), panicle weight ($r_p = 0.446$, $r_g = 0.480$).

Spikelet fertility % had positive significant correlation with fertile grains per panicle ($r_p = 0.651$, $r_g = 0.769$), Panicle weight ($r_p = 0.594$, $r_g = 0.642$), 100 grain weight ($r_p = 0.488$, $r_g = 0.528$).

Panicle weight had positive significant correlation with 100 grain weight ($r_p = 0.447$, $r_g = 0.473$).

4.2.4 Analysis of path coefficient

Grain yield is based on the net effect produced by various yield components interacting with one another. The association of different component characters among themselves and with yield is quite important for devising an efficient selection criterion for yield. The total correlation between yield and its component characters may be some times misleading, as it might be an over-estimate or under-estimate because of its association with other characters. Hence, indirect selection by correlated response may not be sometimes fruitful.

When many characters are affecting a given character, splitting total correlation into direct and indirect effects of cause as devised by Wright, 1921 would provide more meaningful interpretation to the cause of association between the dependent variable like yield and independent variables like yield component characters. If the correlation coefficient between caused factor and the effect is almost equal to its direct effect, then correlation explains the true relationship and direct selection of this trait will be effective.

Table 4.6 Estimation of phenotypic and genotypic correlation coefficient among 12 characters for 34 lowland rice genotypes

Characters	Corrl. coeff.	DF	PH (cm)	EF	FA	PL (cm)	PE (cm)	SF %	FG	PW (g)	TW (g)	Cellulose (µg)
PH (cm)	r _p	-0.118										
	r _g	-0.127										
EF	r _p	0.071	-0.071									
	r _g	0.053	-0.089									
FA	r _p	-0.201	0.291	-0.283								
	r _g	-0.190	0.372*	-0.354*								
PL (cm)	r _p	0.011	0.496**	0.089	0.175							
	r _g	0.069	0.657**	0.049	0.091							
PE (cm)	r _p	-0.018	-0.018	0.365*	-0.029	0.090						
	r _g	-0.011	-0.069	0.404*	-0.007	0.077						
SF %	r _p	-0.238	0.132	0.298	-0.022	0.122	0.448**					
	r _g	-0.273	0.156	0.354*	-0.004	0.204	0.502**					
FG	r _p	-0.011	0.003	0.486**	0.096	0.079	0.740**	0.651**				
	r _g	-0.026	-0.031	0.611**	0.072	0.108	0.859**	0.769**				
PW (g)	r _p	0.012	0.023	0.309	0.084	0.180	0.446**	0.594**	0.732**			
	r _g	0.017	0.027	0.320	0.090	0.248	0.480**	0.642**	0.907**			
TW (g)	r _p	-0.088	0.355*	0.114	-0.047	0.316	0.073	0.488**	0.120	0.447**		
	r _g	-0.088	0.377*	0.131	-0.065	0.394*	0.056	0.528**	0.122	0.473**		
Cellulose (µg)	r _p	-0.133	0.247	-0.289	0.355*	0.069	-0.151	-0.131	-0.178	-0.216	0.053	
	r _g	-0.130	0.261	-0.333	0.391*	0.087	-0.162	-0.158	-0.202	-0.222	0.058	
SPY (g)	r _p	-0.037	-0.026	0.634**	-0.032	0.156	0.547**	0.709**	0.775**	0.721**	0.439**	-0.095
	r _g	-0.034	-0.063	0.723**	-0.059	0.115	0.607**	0.806**	0.964**	0.790**	0.474**	-0.120

r>/ 0.339 significant at 5% level*

r>/ 0.436 significant at 1% level**

The correlation coefficient is positive and the direct effects are negative or negligible, the indirect effects seem to be the cause of correlation. In such situations the other factors influencing the trait have to be considered simultaneously. Correlation coefficients may be negative but the direct effect may be positive and high. Under these conditions a restricted simultaneous selection model is to be followed i.e., restrictions are to be imposed to nullify the undesirable indirect effects in order to make use of the direct effects. With this background, in present investigation the direct and indirect effects of different yield contributing traits and grain quality parameters on yield were estimated using genotypic and phenotypic correlation coefficients and are presented in Table 4.7. As discussed in character association here also the results of both phenotypic and genotypic path coefficient analysis of yield, its contributing characters and grain quality parameters are discussed here under (Table 4.7).

It was revealed from the table that high direct effect to yield was manifested by number of fertile grains per panicle (0.359) followed by number of productive tillers (0.346), 100 grain weight (0.261), spikelet fertility % (0.208), panicle weight (0.104), flag leaf area (0.083), panicle length (0.04), days to 50% flowering (0.01). The other traits like plant height (-0.168), panicle exertion (-0.008) exhibited negative direct effect on yield at phenotypic level.

Fertile grains per panicle exhibited highest indirect effect on yield via panicle exertion (0.266) followed by number of fertile grains per panicle via panicle weight (0.263), fertile grains per panicle via spikelet fertility % (0.234). Plant height showed negative direct effect on yield (-0.168). other characters showed small and nominal effects.

At genotypic level number of productive tillers (0.536) exhibited maximum direct effect on yield followed by spikelet fertility%(0.440), panicle weight (0.348), flag leaf area (0.204), 100 grain weight (0.119) and panicle exertion (0.108). The characters like plant height (-0.178), panicle length (-0.034), number of fertile grains (-0.140) exhibited negative direct effect on single plant yield. Spikelet fertility% had positive indirect effect via 100 -grain weight (0.63). similarly, number of fertile grains per panicle via spikelet fertility%(0.339), number of productive tillers (0.327).

Thus, from the foregoing observations on direct and indirect effects, the traits like number of fertile grains per panicle, panicle weight, 100-grain weight, panicle exertion along with single plant yield may be considered as important selection criteria for realization of high and stable yields. Plant height must be selected against in order to get high and stable yield as it exhibited negative direct effect on yield.

Table 4.7 Direct and indirect effects of component traits on yield at phenotypic and genotypic level for 34 rice genotypes

Characters	Path coeff.	DF	PH (cm)	ET	FA	PL (cm)	PE (cm)	SF %	FG	PW (g)	TW (g)	Correl. with SPY
DF	P _p	0.010	0.020	0.025	-0.017	0.000	0.000	-0.049	-0.004	0.001	-0.023	-0.037
	P _g	0.078	0.023	0.028	-0.039	-0.002	-0.001	-0.120	0.004	0.006	-0.010	-0.034
PH (cm)	P _p	-0.001	-0.168	-0.025	0.024	0.020	0.000	0.027	0.001	0.002	0.093	-0.026
	P _g	-0.010	-0.178	-0.048	0.076	-0.022	-0.007	0.069	0.004	0.009	0.045	-0.063
EF	P _p	0.001	0.012	0.346	-0.024	0.004	--0.003	0.062	0.175	0.032	0.030	0.634
	P _g	0.004	0.016	0.536	-0.072	-0.002	0.044	0.156	-0.085	0.111	0.016	0.723
FA	P _p	-0.002	-0.049	-0.098	0.083	0.007	0.000	-0.005	0.035	0.009	-0.012	-0.032
	P _g	-0.015	-0.066	-0.190	0.204	-0.003	-0.001	-0.002	-0.10	0.031	-0.008	-0.059
PL (cm)	P _p	0.000	-0.083	0.031	0.015	0.040	-0.001	0.025	0.028	0.019	0.082	0.156
	P _g	0.005	-0.117	0.026	0.019	-0.034	0.008	0.090	-0.015	0.086	0.047	0.115
PE (cm)	P _p	0.000	0.003	0.126	-0.002	0.004	-0.008	0.093	0.266	0.046	0.019	0.547
	P _g	-0.001	0.012	0.216	-0.001	-0.003	0.108	0.221	-0.120	0.167	0.007	0.607
SF %	P _p	-0.002	-0.022	0.103	-0.002	0.005	-0.003	0.208	0.234	0.062	0.127	0.709
	P _g	-0.021	-0.028	0.190	-0.001	-0.007	0.054	0.440	-0.107	0.223	0.63	0.806
FG	P _p	0.000	-0.001	0.168	0.008	0.003	-0.006	0.135	0.359	0.076	0.031	0.775
	P _g	-0.002	0.006	0.327	0.015	-0.004	0.093	0.339	-0.140	0.316	0.014	0.964
PW (g)	P _p	0.000	-0.004	0.107	0.007	0.007	-0.003	0.123	0.263	0.104	0.117	0.721
	P _g	0.001	-0.005	0.171	0.018	-0.008	0.052	0.283	-0.127	0.348	0.056	0.790
TW (g)	P _p	-0.001	-0.060	0.039	-0.004	0.012	-0.001	0.101	0.043	0.047	0.261	0.439
	P _g	-0.007	-0.067	.070	-0.013	-0.013	0.006	0.232	-0.017	0.165	0.119	0.474

Phenotypic path: P (R)= 0.403, R² (%)= 83.79

Genotypic path : P(R)= 0.054, R² (%)= 99.71

4.3 Selection indices

During the present investigation selection indices were constructed with grain yield as the economic criteria and eleven different characters namely single plant yield (SPY), days to 50% flowering (DF), plant height (PH), number of productive tillers (ET), flag leaf area (FA), panicle length (PL), panicle exertion (PE), panicle weight (PW), spikelet Fertility % (SF), number of Fertile grains/ panicle (FG), 100 seed weight (TW), were chosen for the construction of eleven character indices. The eleven character index including all the eleven traits was used for the selection of genotypes. Those genotypes which occupied better rankings in the above selection indices were selected for their future use.

The expected genetic advance in yield from selection and different selection indices over direct selection on yield is presented in (Table 4.8). The predicted genetic advance from different indices at 10% selection intensity ranged from 4.53 q/ha in one-character index to 4.79 q/ha in eleven character index and it varied from 100.00 % in index 1 to 105.7 % in index 11 in terms of relative efficiency. Thus, in terms of predicted genetic advance, the results of the present study brought out superiority of eleven character index over direct selection on yield per se (Table 4.9).

The index scores and eleven selection index for yield along with index and yield ranking of 34 genotypes have been presented in the Table 4.8. As per the mean index score (12.18), 16 genotypes out of 34 test genotypes were above the mean index.

The promising genotypes occupying better ranking in eleven character index were selected for future use. The ten top ranking genotypes are SBP-15, Hasanta, SBP-53, SBP-30, SBP-102, SBP-34, SBP-196, SBP-32, SBP-33 and Upahar presented in table 4.8.

It is imperative to note that SBP-15, Hasanta, SBP-53, SBP-30, SBP-102 were found to be most promising among the test genotypes based on selection index score and they also exhibited highest mean yield.

Table 4.8 Index scores and mean yield of 34 lowland rice genotypes in the order of their superiority

Rank	Genotype	Index score	Genotype	Mean yield(g)
1	SBP-15(2)	17.97	SBP-15(2)	12.93
2	Hasanta(33)	17.92	Hasanta(33)	12.75
3	SBP-53(9)	17.27	SBP-53(9)	12.70
4	SBP-30(4)	15.29	SBP-30(4)	12.14
5	SBP-102(12)	15.03	SBP-102(12)	10.94
6	SBP-34(7)	14.76	SBP-34(7)	10.13
7	SBP-196(18)	13.94	SBP-196(18)	10.12
8	SBP-32(5)	13.73	SBP-32(5)	9.72
9	SBP-33(6)	13.55	SBP-196(18)	9.45
10	Upahar(32)	13.38	SBP-242(26)	9.30
11	SBP-328(29)	13.37	Upahar(32)	9.00
12	Ashutosh(34)	13.37	SBP-32(5)	8.87
13	SBP-122(13)	13.04	SBP-3(1)	8.35
14	SBP-35(8)	12.66	Ashutosh(34)	8.26
15	SBP-242(26)	12.39	SBP-122(13)	8.23
16	SBP-198(19)	12.38	SBP-35(8)	7.78
17	SBP-238(24)	11.86	SBP-236(22)	7.06
18	SBP-236(22)	11.70	SBP-27(3)	6.40
19	SBP-27(3)	11.60	SBP-198(19)	6.04
20	SBP-151(16)	11.57	SBP-89(11)	5.92
21	SBP-89(11)	11.48	SBP-238(24)	5.85
22	SBP-237(23)	11.48	SBP-149(14)	5.74
23	SBP-84(10)	11.38	SBP-251(28)	5.74
24	SBP-3(1)	10.97	SBP-151(16)	5.66
25	SBP-251(28)	10.94	SBP-241(25)	5.64
26	SBP-149(14)	10.82	SBP-84(10)	5.56
27	Swarna(30)	10.62	SBP-168(17)	5.40
28	SBP-241(25)	9.88	Swarna(30)	4.81
29	SBP-250(27)	9.61	SBP-237(23)	4.44
30	SBP-168(17)	9.58	SBP-250(27)	4.05
31	Pooja(31)	8.87	SBP-234(20)	3.97
32	SBP-234(20)	8.26	SBP-235(21)	3.80
33	SBP-235(21)	8.00	Pooja(31)	3.44
34	SBP-150(15)	5.65	SBP-150(15)	1.94

Table 4.9 Expected genetic advance and relative efficiency of selection index over direct selection on grain yield

Index No./ Number of characters	Characters	Expected genetic advance	Relative efficiency in per cent
1	Y	4.53	100.00
2	Y+DF	4.53	100.00
3	Y+DF+PH	4.53	100.00
4	Y+DF+PH+PT	4.54	100.22
5	Y+DF+PH+PT+FA	4.54	100.22
6	Y+DF+PH+PT+FA+PL	4.55	100.44
7	Y+DF+PH+PT+FA+PL+PE	4.56	100.66
8	Y+DF+PH+PT+FA+PL+PE+SF%	4.63	102.21
9	Y+DF+PH+PT+FA+PL+PE+SF%+FG	4.69	103.53
10	Y+DF+PH+PT+FA+PL+PE+SF%+FG+PW	4.70	103.75
11	Y+DF+PH+PT+FA+PL+PE+SF%+FG+PW+TW	4.79	105.7

4.4 Multivariate analysis of genetic divergence

Simultaneous variation of all the 11 i.e. excluding cellulose characters for 34 genotypes were tested for assessing the nature of genetic divergence among them, following Mahalanobis D^2 -statistic and Canonical analysis.

4.4.1 Group constellation using D^2 analysis

The D^2 values was estimated by using Mahalanobis' D^2 statistics described by Rao (1952), for all the combinations among 34 genotypes on the basis of 11 characters studied were represented. The group constellations were obtained following Tochers method. The magnitude of D^2 values indicated considerable genetic diversity among the genotypes.

The observed variability of D^2 values ranged from 13.48 between SBP-35 and SBP-238 to 919.15 between SBP-151 and SBP-196. From the above experiment it is concluded that some genotypes were highly similar and the rest are distinct or genetically diverse. Highest distance between SBP-151 and SBP-196 may be due to wide difference in Test weight.

By applying Tochers method (Table 4.10), all the 34 lowland genotypes were classified in to 7 clusters. The Cluster I included 15 genotypes indicating the lack of significant genetic differences among them. cluster II was the second largest with 7 genotypes grouped together. cluster III contained 6 genotypes, Cluster IV and V contained 2 genotypes each. Cluster VI and VII contained 1 genotype each indicating that these two genotypes SBP-15 and Hasanta were much more divergent than rest of the genotypes, justifying their individual identity.

4.4.2 Intra – and inter – cluster divergence.

From the observations of (Table 4.11) it is reflected that III and V are more divergent from each other with an inter cluster distance of 512.30, it can be deduced that crosses involving genotypes from these clusters can produce desirable recombinants with greater heterotic effects. While the clusters VI and VII are less divergent from each other with an inter cluster distance of 118.70. Results presented in table indicated that genotypes of cluster V are more diverse as compared to the genotypes included in other clusters.

Table 4.10 Cluster composition of 34 genotypes on the basis of D² analysis

Cluster	No. of genotypes	Genotypes included in the cluster
I	15	SBP-35(8), SBP-238(24), SBP-3(1), SBP-33(6), SBP-242(26), SBP-34(7), SBP-89(11), SBP-30(4), SBP-237(23), Ashutosh(34), Upahar(32), SBP-32(5), SBP-84(10), SBP-168(17), SBP-102(12)
II	7	SBP-250(27), SBP-251(28), SBP-234(20), SBP-241(25), SBP-149(14), SBP-235(21), SBP-150(15)
III	6	SBP-27(3), SBP-122(13), SBP-328(29), SBP-198(19), SBP-53(9), SBP-196(18)
IV	2	Pooja(31), Swarna(30)
V	2	SBP-236(22), SBP-151(16)
VI	1	SBP-15(2)
VII	1	Hasanta(33)

Table 4.11 Average intra-cluster (diagonal) and inter-cluster distance (D^2 & D values) among 7 clusters of 34 genotypes

Clusters	I(15)	II(7)	III(6)	IV(2)	V(2)	VI(1)	VII(1)
I	77.58 (8.80)	135.39 (11.63)	173.57 (13.17)	146.90 (12.12)	203.18 (14.25)	120.03 (10.95)	169.80 (13.03)
II		86.09 (9.27)	286.91 (16.93)	123.17 (11.09)	205.12 (14.32)	293.18 (17.12)	355.10 (18.84)
III			106.39 (10.31)	298.19 (17.26)	512.30 (22.63)	201.17 (14.18)	292.19 (17.09)
IV				83.34 (9.12)	272.88 (16.51)	243.06 (15.59)	359.06 (18.94)
V					109.87 (10.48)	305.77 (17.48)	262.55 (16.20)
VI						0.00	118.70 (10.89)
VII							0.00

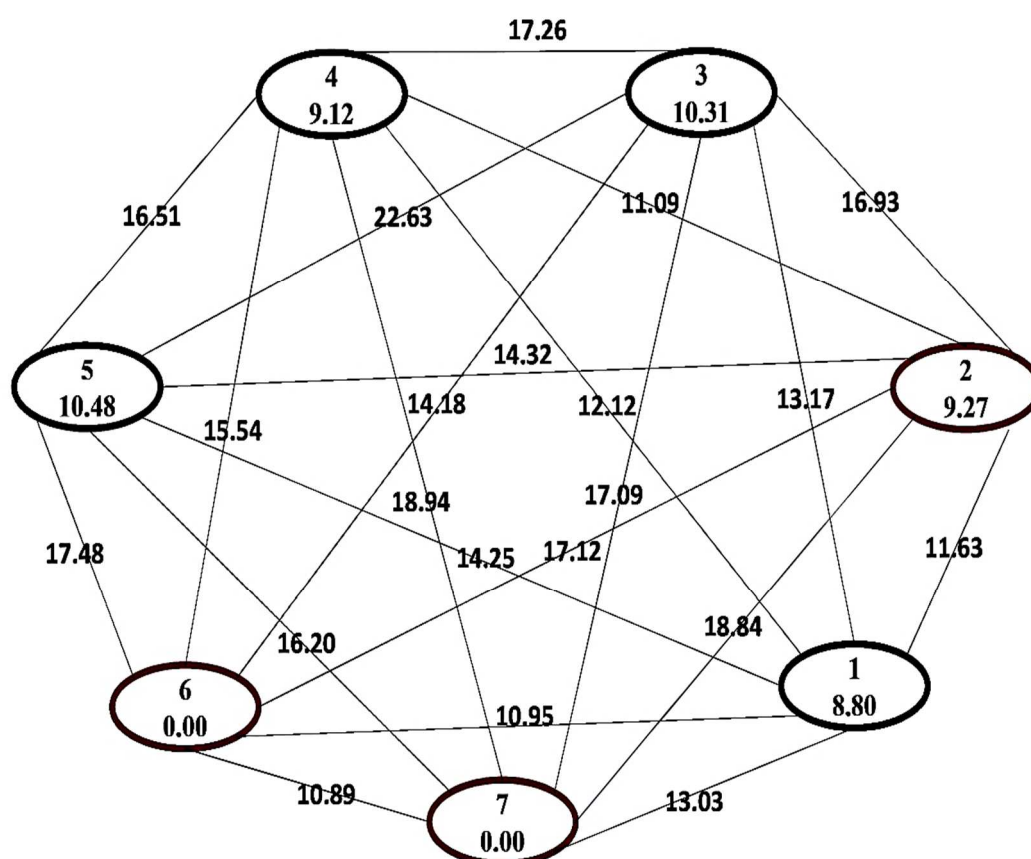


Figure 4.2 Cluster Analysis

4.4.3 Relative contribution of characters to genetic divergence

The contribution of different characters towards genetic divergence was worked out (Table 4.12) by employing the standard methods. The relative contribution (in per cent) of each character to total divergence was assessed in two ways : (i) average D^2 for individual character over 561 combinations as suggested by Singh, 1981 and (ii) rank total for individual character, over all the paired combination (Murty and Quadri, 1966).

The lowest rank total indicates highest contribution to genetic divergence. The estimation using both the methods gave the same order of relative contribution with regards to highest and lowest values in all the cases except for Days to 50% flowering and Spikelet fertility%.

Based on the average D^2 values over 561 paired combinations, it was found that the highest contribution was by 100 grain weight (38.62%). Next highest contributions in decreasing order was by panicle weight (13.40) followed by panicle exertion (9.72), single plant yield (9.00), days to 50% flowering (6.52), spikelet fertility (6.36), flag leaf area (4.33), panicle length (3.39), plant height (3.28), number of productive tillers (3.02), number of fertile grains per panicle (2.36).

In the method of percentage rank total, exactly similar results were obtained. 100 grain weight was found to contribute maximum (i.e., lowest value of 1867) and Fertile grains per panicle was found to contribute minimum (Table 4.12)

4.4.4 Characterization of the D^2 based clusters among 34 rice genotypes

An analysis of relative contribution of characters to divergence has been presented in Table 4.13. Cluster I is characterised by moderate grain yield, panicle weight, 100 seed weight, plant height, flag leaf area. Cluster II is characterised by low panicle exertion, spikelet fertility, grain yield. Cluster III exhibited superior mean performance for plant height, panicle length, low grain yield per plant. Cluster IV is characterised by lowest Days to 50% flowering, plant height, panicle length, fertile grains per panicle, panicle weight, single plant yield, panicle exertion. Cluster V contained low 100 seed weight. Cluster VI recorded highest days to 50 per cent flowering and number of productive tillers, panicle exertion, spikelet fertility%, single plant yield and lowest flag leaf area. Cluster VII is characterised by high flag leaf area, number of fertile grains per panicle, panicle weight, single plant yield.

Table 4.12: Relative contribution of different characters to genetic divergence among 34 lowland rice genotypes

Sl. No.	Characters	Average D ²	Percentage of total D ²	Rank Total	Relative % of Rank Total
1.	DF	10.91	6.52(5)	3391	9.1(6)
2.	PH	5.48	3.28(9)	3966	10.71(9)
3.	PT	5.06	3.02(10)	4082	11.02(10)
4.	FA	7.24	4.33(7)	3715	10.03(7)
5.	PL	5.67	3.39(8)	3929	10.61(8)
6.	PE	16.26	9.72(3)	2873	7.75(3)
7.	SF%	10.63	6.36(6)	3331	8.99(5)
8.	FG	3.95	2.36(11)	4322	11.67(11)
9.	PW	22.42	13.40(2)	2608	7.04(2)
10.	TW	64.61	38.62(1)	1867	5.04(1)
11.	SPY	15.06	9.00(4)	2942	7.94(4)
	Total			37026	

Table 4.13 Cluster means in 34 genotypes for 11 different characters

Sl. No.	Characters	I(15)	II(7)	III(6)	IV(2)	V(2)	VI(1)	VII(1)	Group Means
1.	DF	107.23	108.00	108.83	99.75	108.75	111.00	101.50	107.26
2.	PH	108.90	113.95	115.82	91.57	106.55	102.35	101.45	109.59
3.	PT	9.57	9.21	9.83	9.50	9.25	15.00	12.00	9.75
4.	FA	27.97	27.58	28.59	20.53	34.68	16.90	35.40	27.85
5.	PL	23.80	24.34	25.14	20.73	22.66	22.75	23.85	23.87
6.	PE	2.30	1.39	1.98	1.39	2.98	3.42	2.93	2.10
7.	SF%	68.33	51.70	68.39	61.28	57.15	87.74	78.81	64.73
8.	FG	104.58	78.25	98.17	65.15	119.75	136.50	160.00	99.17
9.	PW	2.13	1.49	2.57	1.12	2.02	2.39	3.96	2.07
10.	TW	1.98	1.67	2.46	1.81	1.51	2.14	1.95	1.97
11.	SPY	8.11	4.41	8.82	4.13	6.36	12.93	12.75	7.42

4.7.5 Canonical analysis

Another method of grouping the genotypes as suggested by Rao (1952) is canonical analysis. The two canonical roots accounted for 70.5% of the total variability, thus qualifying for graphic presentation (Table 4.14). The mean values of the first two canonical vectors Z_1 and Z_2 (Table 4.15) were used as coordinates in plotting a two-dimensional dispersion complex (Fig 4.3). The Scatter points were found more or less in agreement with the results of D^2 analysis. Thus, it had agreement with Tocher's method though with some deviations.

The 34 genotypes were grouped in to 8 different clusters (Table 4.16 and Fig 4.3). The cluster I being the largest cluster included 24 genotypes whereas cluster II had 3 genotypes, cluster III had 2 genotypes. Rest of the clusters i.e IV,V,VI,VII,VIII were found to have single constituent genotype in each.

The Cluster I have 24 genotypes indicated to possess close resemblance among them. Similarly cluster II and III containing 3 and 2 respectively also indicated much similarity with respect to different traits on which observations are recorded. All the monogenotypic clusters i.e cluster IV,V,VI,VII,VIII representing SBP-196,SBP-198,SBP-150,SBP-235,SBP-151 respectively seems to be more divergent from rest of the genotypes.

Table 4.14 The coefficient of first two canonical vectors (Z_1 and Z_2) for 11 characters of 34 lowland rice genotypes

Sl. No	Characters	Z_1	Z_2
1	Days to 50% flowering	0.001	-0.018
2	Plant height (cm)	0.077	-0.105
3	Productive tillers	0.039	0.151
4	Flag leaf Area (cm ²)	-0.051	-0.018
5	Panicle length (cm)	0.112	-0.081
6	Panicle exertion (cm)	-0.089	0.522
7	Spikelet fertility %	0.195	0.291
8	Filled grains	0.054	0.240
9	Panicle weight	0.327	0.447
10	Test Weight	0.906	-0.203
11	Single plant yield	0.043	0.551
Variances accounted for (%)		45.1%	25.4%

4.5.1 Contribution of characters to genetic divergence

The coefficients of first two canonical vectors (Z_1 and Z_2) presented in (Table 4.14 and 4.15) reflects relative importance of the characters contributing towards

divergence. It was observed that the important characters responsible for genetic divergence were panicle weight and test weight in the first axis. Panicle exertion, spikelet fertility%, filled grains, panicle weight. single plant yield in the second axis in that order, thus suggesting much difference among the test entries with respect to these traits. Due to low values of canonical roots the population did not qualify for better graphic representation hence not suitable for comparing with grouping obtained earlier using D^2 statistics.

Table 4.15 Mean canonical values of 34 genotypes

Variety	Z1	Z2
1	37.85	-4.87
2	41.91	3.20
3	45.32	-6.48
4	38.44	4.85
5	43.32	-4.51
6	36.69	-0.87
7	34.47	-2.03
8	37.81	-.85
9	49.65	-1.76
10	41.32	-6.90
11	39.60	-6.72
12	44.20	-2.60
13	47.34	-1.30
14	42.01	-8.07
15	32.55	-13.17
16	24.64	2.05
17	39.08	-7.84
18	53.22	-6.88
19	47.25	-11.39
20	32.09	-7.08
21	27.68	-8.35
22	30.61	-1.37
23	37.88	-4.50
24	35.74	-2.43
25	36.13	-8.92
26	34.38	-3.07
27	34.10	-8.53
28	33.55	-8.61
29	43.25	-5.99
30	32.13	-6.38
31	38.12	-10.15
32	40.19	-2.80
33	40.15	7.21
34	37.28	0.26

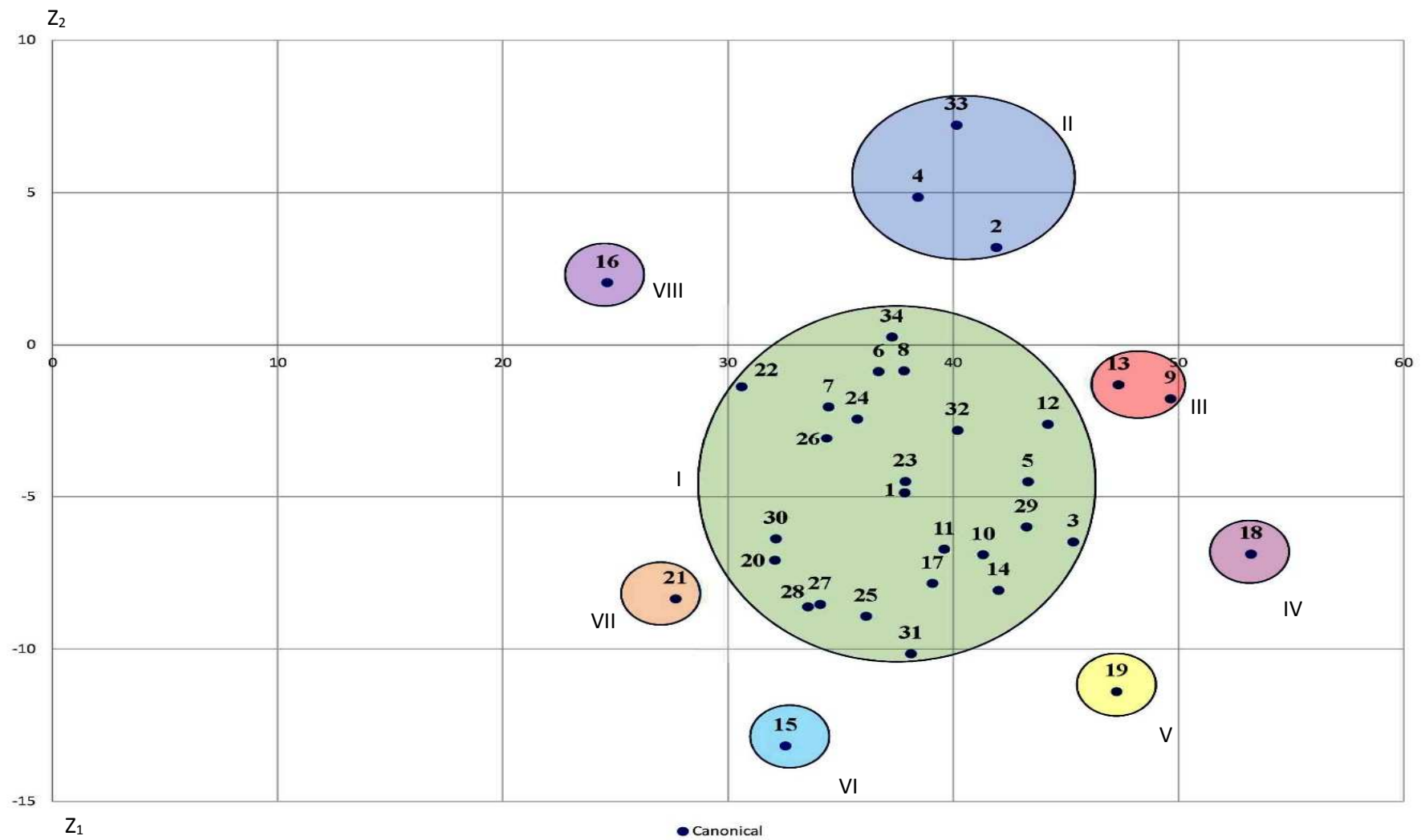


Figure 4.3 Group constellation of 34 lowland rice genotypes using two canonical variates

Table 4.16 Cluster composition of 34 genotypes on the basis of canonical analysis

Cluster	No. of genotypes	Genotypes included in the cluster
I	24	SBP-3(1), SBP-27(3), SBP-32(5), SBP-33(6), SBP-34(7), SBP-35(8), SBP-84(10), SBP-89(11), SBP-102(12), SBP149(14), SBP-168(17), SBP-234(20), SBP-236(22), SBP-237(23), SBP-238(24), SBP-241(25), SBP-242(26), SBP-250(27), SBP-251(28), SBP-328(29), Swarna(30), Pooja(31), Upahar (32), Ashutosh (34)
II	3	SBP-15(2), SBP-30(4), Hasanta (33)
III	2	SBP-53(9),SBP-122(13)
IV	1	SBP-196(18)
V	1	SBP-198(19)
VI	1	SBP-150(15)
VII	1	SBP-235(21)
VIII	1	SBP-151(16)



DISCUSSION

In rice the grain yield is complex trait governed by additive gene action of different yield and yield contributing traits. Lack of suitable rice varieties with high yield and resistance to various biotic and abiotic stresses is the major constraint for high productivity lowlands rice farms of Odisha. Therefore, there is a need for enhancement of genetic yield potential of rainfed low land rice genotypes.

Present study on “Genetic study of yield variation in lowland rice genotypes” emphasises towards the selection of best performing genotypes under lowland rice situation using different genetic studies. The genetic analysis tools used in the present study are the study on variability, heritability, genetic advance, correlation, Path-coefficient and genetic divergence analysis and also selection indices of 12 different traits in 34 lowland rice genotypes were studied.

Knowledge of the extent and pattern of genetic variability in a population is essential for the assessment of the nature of genetic mechanism and it facilitates the selection of high yielding genotypes either for direct use as a variety or to be used in different breeding programmes. Information on the extent and nature of interrelationship among characters helps in formulating efficient scheme of selection for different traits. The characters which have high positive correlation with yield can be used in the indirect selection for yield improvement. Path coefficient analysis helps the breeders to explain direct and indirect effects and hence has extensively been used in plant breeding activities. Selection is an integral part of a plant breeding programme by which genotypes with high productivity coupled with better quality in a given environment could be developed. However, selection for high yield is difficult because of its complex nature. Selection indices are constructed to find the best genotypes. Different multivariate techniques namely D²-analysis by Mahalanobis and Canonical analysis methods are employed for the analysis of divergence and the genotypes are grouped together based on their relative genetic similarity or divergence.

5.1 Genetic Variability

5.1.1 Analysis of variance for various characters in 34 lowland rice genotypes

A genetic variability study was conducted using 34 lowland rice genotypes for 12 different characters of yield and its components. The analysis of variance showed

significant difference among the genotypes for all the characters studied even at 1% level of significance (Table 4.1). A wide range of variation was observed among the 34 lowland rice genotypes for all the 12 traits. This suggested that there is inherent genetic difference among the genotypes for all the characters studied. However, the replication differences were significant for the characters i.e. number of productive tillers and spikelet fertility which might be due to the fact that the experimental plot had inherent soil heterogeneity.

5.1.2 Mean performance for 12 characters of 34 lowland rice genotypes

The performance of the genotypes was determined by mean values for eleven quantitative characters and cellulose which were carefully recorded and presented in Table 4.2

Days to 50% flowering is a stable agronomic trait as it was less influenced by the environment. The overall mean value of the character is 107.26 days. It ranged from 96-118 days among the genotypes. Out of the total 34 genotypes evaluated, 15 genotypes were observed to have recorded lower than mean-S.E value i.e less than 104.12 days. Eight genotypes recorded medium duration between 104.12-110.40 days. Eleven genotypes recorded high duration of above 110.40 days for days to 50% flowering. The range of variation of the genotypes indicated that upper limit of the variation was 22.91% higher than the lower limit, where it was 20.51% higher than mean for the character under study.

In the present investigation, there was wide variability in plant height ranging from 89.60 cm to 141.50cm with a general mean of 109.59 cm. Twelve genotypes recorded medium plant height between 106.45-119.15cm and 15 genotypes less than 106.45cm indicating short stature which is a desirable character in crop improvement. The range of variation of the genotypes indicated that the upper limit of the variation was 57.9% higher than the lower limit, where it was 47.35% higher than the mean.

Number of productive tillers is one of the major yield attributing trait in rice. In this investigation, number of productive tillers was calculated and the mean values were tabulated (4.2). It ranged from 6.5-15.0 among the genotypes with overall mean of 9.75. Seven genotypes were found statistically superior than the rest. The range of variation of the genotypes was 87.17% higher than the mean value , indicating a great variability among the genotypes for this character.

The spectrum of variation for flag leaf area was observed to be in a range of 16.90 cm² to 37.99 cm² with an overall mean of 27.85 cm² among the genotypes. The range of variation of the genotypes was 75.72% higher than the mean value, indicating a great variability among the genotypes for this character.

Panicle length for all the genotypes ranged from 16.85 cm to 28.20 cm with an overall mean of 23.87cm. Twenty seven genotypes recorded medium panicle length between 21.52 cm to 26.22 cm and four genotypes recorded high panicle length of more than 26.22cm. Three genotypes recorded shorter panicle length of below 21.52cm. The range of variation of the genotypes indicated that the upper limit of variation was 67.35% higher than the lower limit where as it was 47.54% higher than mean value, indicating a great variability among the genotypes.

Panicle exertion ranged from 0.85 cm to 3.42 cm respectively with an overall mean of 2.10 cm. Eleven genotypes exhibited fully exerted panicles and fourteen genotypes exhibited partially exerted panicles.

The overall mean of spikelet fertility % was 64.73% and range was 41.5 % - 87.74% which is one of the key yield contributing character. Seven genotypes exhibited high spikelet fertility of above 72.20% and nine genotypes exhibited low spikelet fertility of below 57.26%. Eighteen genotypes recorded medium spikelet fertility between 57.26% to 72.20%. The range of variation of the genotypes was 71.43% higher than the mean value

Number of fertile grains per panicle ranged from 52.5 to 160, the overall mean observed is 99.17 grains. Twenty one genotypes recorded more number of fertile grains per panicle above 121.28 and six genotypes recorded less no of fertile grains below 77.0.

The overall mean of panicle weight was 2.07g and it ranged from 0.80g to 3.96g. Twenty genotypes recorded medium panicle weight of 1.71g to 2.43g,10 genotypes below 1.71g and four genotypes recorded more panicle weight above 2.43g.

One hundred seed weight of different genotypes used in the study varied from 1.41 g to 2.64 g and the overall mean was 1.97 gm. Eleven genotypes recorded medium 100 grain weight of 1.86 gm to 2.08 gm,12 genotypes below 1.86gm and eleven genotypes recorded more test weight of above 2.08gm. SBP-53(2.64) was considered

as best for this trait among the 34 genotypes. The range of variation of the genotypes indicated that the upper limit of variation was 87.23% higher than the lower limit where as it was 62.43% higher than mean for this character.

The range of cellulose content is 3.16 g to 12.85 g. The overall mean of all the genotypes is 6.85 grams. Twelve genotypes recorded high cellulose content of above 7.8grams.

Improvement in the single plant yield is the results from favourable and unfavourable combinations of component traits and the ultimate aim of plant breeding activities showing a wide range of variation among the genotypes. The test genotypes showed a variation from 1.94 g to 12.93 g with overall mean of 7.42 g. SBP-15(12.93), SBP-30(12.14), SBP-53(12.70),Hasanta(12.75) these four genotypes recorded highest yield per plant of above 12.00g. Nine genotypes recorded highest yield per plant of above 9.42g.

It is evident from the aforesaid discussion that the genotypes included in the study exhibited a wide range of variability in respect of all the eleven characters. The mean performance of SBP-15(15) followed by SBP-53(14), SBP-251(13), SBP-30(12.5), Upahar(12.5) was highest for number of productive tillers per plant Where as Hasanta(160), SBP-15(136.5),SBP-30(132),SBP-151(128.5),SBP-53(125) for number of fertile grains per panicle and SBP-53(2.64) for 100 seed weight.

Among the 34 genotypes, SBP-15(12.93g) recorded the highest single plant yield, followed by SBP-84(12.70), SBP-30(12.14g), SBP-196(11.89).SBP-30 was found to be the early flowering genotype(102.5 days) among the top yielders in the investigation.

It is further suggested that due to enormous variations present, the test genotypes have the merit to be used as the base population in varietal improvement programme. The variation among the genotypes is therefore ascribed to the genetic diversity owing to the improvement of diverse parents in the development of breeding lines. Similar findings pertaining to the presence of high amount of genetic variability for the different traits including seed yield have been reported by Shrivastava 2015, Praveen Pandey *et al.*, 2009, Khatun *et al.*, 2015, Harsha *et al.*, 2017, Chandan Kishore *et al.*, 2018.

5.1.3 Genotypic and phenotypic coefficient of variation

The coefficient of variability encompasses the genetic variation that responds to selection. The genotypic components and their magnitude for yield and its component characters influence the selection strategies to be adopted by the breeders, being the heritable part of the total variability. Besides, an idea about the nature of gene action can be derived from a relative comparison of heritability and genetic advance. The magnitude of variability with regard to phenotypic and genotypic coefficient of variation for all 12 characters are presented in Table 4.5

The magnitude of phenotypic coefficient of variation (PCV) estimates in the present study was found to be slightly higher than their respective genotypic coefficient of variations (GCV) for all the studied characters which might be the result of influence of environment on the development of characters. Similar report noticed earlier by many researchers like Ogunbayo 2014, Idris 2014 and Tefera Abebe 2017 in rice. The difference between PCV and GCV estimates were relatively low for all the traits except for no. of productive tillers, fertile grains per panicle and single plant yield, indicating less environmental influence on these traits. Thus, selection based on phenotypic performance of these characters would be effective to bring about considerable genetic improvement.

Phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were categorized as low (0-10%), moderate (10-20%) and high (>20%) as indicated by Sivasubramanian and Madhavamenon. Therefore, according to the classification high PCV and GCV values were recorded for panicle exertion, filled grains per panicle, panicle weight, cellulose, single plant yield, which suggests the possibility of improving these traits through selection. No of effective tillers has high PCV and moderate GCV. Similar results were also reported by khatun *et al.*, 2015, Mazid *et al.*, 2013, Pandey and Anurag 2010, Sabu *et al.*, 2009 and Kiani, 2013 for filled grains per panicle and single plant yield. Augustina, Sabu *et al.*, 2009 and Kiani, 2013 for panicle weight. On the other hand, the estimates of GCV and PCV were low in the present study for days to 50 per cent flowering and panicle length and Plant height. Padmaja *et al.*, 2008, Laxuman *et al.*, 2010, Shrivastava 2015, Sangaré, 2017 for days to fifty per cent flowering & plant height. Sabu *et al.*, 2009 and Kiani, 2013, for panicle length.

5.1.4 Heritability and Genetic Advance

High heritability does not always indicate high genetic gain; heritability coupled with high genetic advance should be used in predicting the ultimate effect for selecting superior varieties. Keeping in view that, consideration of heritability and genetic advance together prove more useful in predicting the resultant effect of selection on phenotypic expression (Johnson *et al.*, 1955).

The estimates of heritability ranged from 69.76% for panicle length to 96.97% for cellulose. Characters like panicle length (69.76%) exhibited moderate heritability (40%-70%) and all other characters exhibit high heritability (>70%) suggesting effectiveness of selection on the basis of phenotypic expression of the traits.

The expected genetic advance over mean for different characters ranged from 7.74 for Days to 50% flowering to 73.86 for cellulose. Low (0-15%) expected genetic advance was reported in case of days to 50 per cent flowering (7.74), panicle length (11.01) plant height (14.80). Moderate (15-30%) genetic advance was reported for no of productive tillers (29.36), flag leaf area (29.12), spikelet fertility % (27.85), 100-seed weight (27.55). For characters like panicle exsertion (56.65), No of fertile grains per panicle (33.17), Panicle weight (53.02), Cellulose (73.86), Single plant yield (61.12), reported high (> 30%) genetic advance.

High heritability accompanied with moderate to high genetic gain for no. of fertile grains per panicle, panicle weight, no. of productive tillers, flag leaf area, spikelet fertility (%), 100-seed weight, cellulose, single plant yield indicating presence of additive gene action and hence selection based on phenotypic performance would be effective. Similar results were obtained by Shrivastava 2015, Gour 2017, Basavaraja 2013, Singh 2013, Khare 2014, Karande *et al.*, 2017, Chandan Kishore *et al.*, 2018, Bhinda *et al.*, 2017, Lingaiah *et al.*, 2014, Limbani (2017), Babu 2012 and Tripathi 2018. Characters like days to 50 per cent flowering, plant height observed high heritability accompanied with low genetic advance indicates the predominance of epistasis and dominant gene action (non - additive gene action) and selection for such traits may not be rewarding, in that case heterosis breeding may be useful. Similar reports were obtained by Karande *et al.*, 2017, Ashish Kumar Panigrahi 2017, Sabesan *et al.*, 2009, Sangaré 2017 for Days to 50% flowering, Sangaré 2017, Konate *et al.*, 2016 for plant height.

5.2 Character association

The nature and extent of association among the component characters with grain yield per plant would be helpful to decide the major contribution towards grain yield. Yield is a complex polygenic trait for which direct selection may not be effective always. So that component traits would be helpful in the improvement of yield. The results on correlations revealed that genotypic correlation coefficient was higher than the corresponding phenotypic correlation coefficient, indicating strong inherent association between the traits under study. The association between yield and yield component traits are presented in Table 4.6. Grain yield is ultimate objective of any breeding programme. In this study, positive and significant correlation with the yield component traits viz., no. of fertile grains per panicle, panicle weight, spikelet fertility%, no. of productive tillers, panicle exertion, 100 grain weight were observed. The rest of the characters had non- significant correlation with yield.

The character panicle length (0.156) is positive and non-significant. The characters like Days to 50% flowering (-0.037), plant height (-0.026), flag leaf area (-0.032) and cellulose (-0.095) found negatively correlated and non-significant.

From the results it is inferred that high no. of productive tillers, fully exerted panicles which increases pollination and therefore increasing no of fertile grains per panicle and thus increasing spikelet fertility%, high test weight, panicle weight contributes to single plant yield. The findings indicated that plants with heavy panicles tend to have high number of fertile grains thereby increasing rice yield. The positive correlation that was obtained between number of grains and weight of panicles implies that increasing the weight of panicle would also effectively increase the number of grains per plant and thus increase grain yield. This indicated that all these characters were important for yield improvement. Similar results were observed by Baloch *et al.*, 2016, Sravan *et al.*, 2016, Harsha *et al.*, 2017, Padmaja *et al.*, 2011, Babu *et al.*, 2012, Patel *et al.*, 2014 and Rao *et al.*, 2014, Rathod 2017, Das 2015 for test weight, no. of productive tillers. Ekka *et al.*, 2011, Mohanty *et al.*, 2012, Sravan *et al.*, 2012, Reddy *et al.*, 2013, Patel *et al.*, 2014 and Rahman *et al.*, 2014, Rathod 2017, Das 2015, Karande 2017, Kumar and Saravanan (2012) and Minnie *et al.*, 2013, for number of filled grains per panicle and spikelet fertility. Augustina 2013 Sarath *et al.*, 1969, Shashidhar *et al.*, 2005, Girish *et al.*, 2006, Ketan & Sarkar 2014, Gour 2017 and Shrivastava *et al.*, 2014 for Panicle weight.

5.2.1 Path analysis of yield components

The correlation coefficient of component traits with grain yield were partitioned in to direct and indirect effects following path coefficient analysis, to ascertain further conclusive evidence on choice of characters required for selection of high yielding genotypes. The path coefficient analysis not only specify the effective measure of direct and indirect causes of association, but also depicts the relative importance of each factor involved in contributing to the final product of yield.

A trait with high positive and direct effect on grain yield reveals its effectiveness towards the direct selection. Characters with High direct effect along with positive and high indirect effect through other traits provides a better chance to be selected through breeding programmes.

At phenotypic level, high direct effect on yield was manifested by number of fertile grains per panicle (0.359) followed by number of productive tillers (0.346), 100 grain weight (0.261), spikelet fertility % (0.208), Panicle weight (0.104), flag leaf area (0.083), panicle length (0.04), Days to 50% flowering (0.01). The other traits like plant height (-0.168), Panicle exertion (-0.008) exhibited negative direct effect on yield at phenotypic level. The indirect effects were recorded small and nominal for many character pairs with few exceptions.

Fertile grains per panicle exhibited highest indirect effect on yield via panicle exertion (0.266) followed by no. of fertile grains per panicle via panicle weight (0.263), fertile grains per panicle via spikelet fertility % (0.234). Plant height showed negative direct effect on yield (-0.168). other characters showed small and nominal effects.

At genotypic level Number of productive tillers (0.536) exhibited maximum direct effect on yield followed by spikelet fertility% (0.440), panicle weight (0.348), flag leaf area (0.204), 100 grain weight (0.119), panicle exertion (0.108). The characters like plant height (-0.178), panicle length (-0.034), number of fertile grains (-0.140) exhibited negative direct effect on single plant yield. Spikelet fertility% had positive indirect effect via 100 grain weight (0.63). similarly, number of fertile grains per panicle via spikelet fertility% (0.339), number of productive tillers (0.327).

Thus, from the above observations on direct and indirect effects on yield, it is concluded that traits like no. of fertile grains per panicle, no of productive tillers, 100 grain weight, spikelet fertility %, panicle weight and panicle exertion should be

considered as important selection criteria for increasing yield. Similar findings were reported by Rathod *et al.*, 2017, Padmaja *et al.*, 2011, Lingaiah *et al.*, 2014 and Rahman *et al.*, 2014, Solanki and Tiwari 2013 and Islam *et al.*, 2015, Shankar *et al.*, 2016, Harsha 2017, for number of productive tillers per plant and 1000-grain weight, and Padmaja *et al.*, 2011, Mohanty *et al.*, 2012, and Sarker *et al.*, 2014, Das 2015, Gour 2017 for number of filled grains per panicle, Pradhan *et al.*, 2015 for spikelet fertility%

5.3 Selection indices

Plant breeding programmes are mostly aimed at selection of high yielding genotypes with better quality. But selection on the basis of yield *per se* in the initial stage of evaluation is often, not effective owing to low heritability. Smith (1936) suggested the use of selection index which provides means for making use of correlated characters for higher efficiency for selection of yield. Inter- genotypic competition and large experimental errors associated with yield measurement often bias outcome of selection for higher yield. Therefore, several workers in different crop plants have emphasized the importance of indirect selection for yield of component traits governed by genes with additive effect and strong correlation with yield.

In the present study selection indices were constructed with grain yield as the economic criteria and eleven different characters namely Grain yield per plant (GYP), Days to 50% flowering (DF), Plant height (PH), No of productive tillers (PT), Flag leaf area (FA), Panicle length (PL), Panicle exertion (PE), Spikelet Fertility percentage (SF%), Fertile grain number (FG), Test weight (TW), were chosen for the construction of eleven character indices. The results of the study indicated that the eleven character index is superior to any other index with an efficiency % of 105.7. The genotypes which are better performing with eleven character index are selected for further breeding programmes. It indicates that the eleven character index is far superior to the yield *per se* alone. The results obtained were similar to (Biswaranjan *et al.*, 2017, Chandrashekhar and Shailaja, Choudary *et al.*, 2017, Aslam *et al.*, 2014, Singh *et al.*, 2013, Habib *et al.*, 2013, Kanbar *et al.*, 2008, Bastia *et al.*, 2008, Fazlalipour *et al.*, 2008, Sabouri *et al.*, 2008, Rabiei *et al.*, 2004.

5.4 Genetic divergence

The genetic diversity in crop improvement is very important which helps in choosing recombinant parents for breeding programs. Mohalanobis D²-statistic is extensively used by many of the scientists to quantify genetic divergence among the

genotypes in a number of crop plants (Murthy and Arunachalam, 1966). This technique provides both discrimination among populations on the basis of genetic diversity and assessment of the relative contribution of individual characters to the total divergence. Genetic diversity between the genotypes determines the heterosis of their crosses. As most diverse parents produce most successful hybrid.

In the present study the D^2 -analysis as well as Canonical analysis was conducted for assessing the nature and degree of divergence among 34 genotypes of lowland rice for 12 different characters. The objective of this study is to group these genotypes based on their genetic diversity and select the divergent genotypes for the crop improvement programme. Out of 7 different clusters, cluster III and V are more divergent from each other with an inter cluster distance of 512.30. While the clusters VI and VII are less divergent from each other with an inter cluster distance of 118.70. Least intra-cluster distance was observed in cluster I with highest no of genotypes of 15 presented in (Table 4.11). The genotypes of cluster V are more diverse of all the clusters with an intra cluster distance of 10.48 containing two genotypes. The character which contributes to most of the divergence is test weight with a D^2 value of 64.61 (Table 4.12). The close planting and hybridization of the genotypes belonging to the most divergent clusters promotes crop improvement. These results are in agreement with Joshi Monika *et al.*, 2008

5.4.1 Canonical analysis

Canonical discriminant analysis examines the differences in the morphological variables and indicates the relative contribution of each variable to the genotype discrimination simultaneously.

The coefficients of first two canonical functions (Z1 and Z2) presented in (Table 4.15) which accounts for 70.5% of the divergence. The first canonical discriminant function Z1 is dominated by the contribution of the characters test weight, panicle length and plant height and the second canonical discriminant function Z2 is dominated by single plant yield and panicle exertion. The canonical analysis suggests that the panicle weight, test weight, Panicle exertion, spikelet fertility%, filled grains, panicle weight and single plant yield were the principle discriminatory characters.



SUMMARY AND CONCLUSION

Improvement of crop mainly depends upon a wide genetic variability in germplasm collection followed by adopting suitable breeding methods. The breeding methods to be adopted in the improvement of crop are in turn decided primarily by the amount of genetic variability. Estimation of GCV, PCV, heritability and genetic advance enables the breeder to decrease the size of germplasm collection by selecting the best performing genotypes and for the selection of characters responsible. The correlation studies are used to define the relation between the quantitative characters responsible for the yield. The Multivariate studies like Mahalanobis D^2 and canonical analysis were used in the present study to assess the genetic divergence in 34 lowland rice genotypes which helps in gaining numerical estimates of genetic diversity and quantitative assessment of the relative contribution of different component characters to the total divergence.

The present investigation “Genetic study of yield variation in lowland rice genotypes” was carried with the following objectives:

- To evaluate the performance of selected rice genotypes, in respect of yield and yield contributing characters and identify genotypes suitable to lowland conditions.
- To assess the extent of variability and partition it in to heritable and non-heritable components.
- To study the extent of genotypic and phenotypic correlation between yield and its components.
- To estimate the direct and indirect effects of various grain yield contributing characters.
- To construct selection indices using multiple traits for greater efficiency of selection for yield.
- To study genetic divergence of the selected genotypes, using different multivariate approaches.
- To estimate the amount of Cellulose from rice straw and association with other quantitative traits.

The field experiment of the present study using 34 lowland rice genotypes including 5 checks namely Swarna, Pooja, Upahar, Hasanta, Ashutosh was conducted at Rice Research Station OUAT Bhubaneswar during the *kharif* 2017.

- a) Observations were recorded on 11 quantitative traits viz., Days to 50% flowering, Plant height, Number of Effective tillers, Flag leaf Area, Panicle length, Panicle Exsertion, Spikelet Fertility, Number of Fertile Grains / panicle, Panicle weight, 100 grain weight, Single plant yield, and cellulose.
- b) Days to 50% flowering was measured with 50 per cent of the total plants in the net plot. For the remaining characters the average of observations recorded of five plants per plot were considered for statistical analysis.
- c) Statistical analysis was conducted to estimate the genetic variability of different parameters by ANOVA. The genotypes were classified as high (H), medium(M),low(L) basing on overall mean + S.E for each character as per the following criteria. Values more than mean+S.E ($\bar{x}+S.E$) as high(H); values in between mean+SE($\bar{x}+SE$) as medium(M); values less than mean-S.E($\bar{x}-S.E$) as low (L).
- d) Correlation was carried out to determine the inter relationships among the traits studied. Path coefficient analysis was studied to assess the direct and indirect effects of the traits on yield. Mahalanobi's D^2 statistics and canonical analysis were conducted to study the nature and extent of genetic diversity.
- e) The results from the study of variability by the assessment of GCV, PCV, heritability and genetic advance (Table 4.1) indicated wide range of variation among the 34 genotypes valuated for the 11 traits considered.
- f) Correlation studies were carried out to determine the nature and extent of relationship among different traits and their contribution to the yield in numerical value at both phenotypic and genotypic level. It was studied on then basis of cause and effect relationship.
- g) Path coefficient analysis was also performed to determine the net effect produced by various yield components interacting with one another.
- h) Selection indices were constructed with Single plant yield (SPY), as the economic criteria and eleven different characters were chosen for the construction of eleven

character indices. The eleven character index including all the eleven traits was used for the selection of rice genotypes.

- i) The assessment of genetic divergence using Mahalanobis's D^2 statistics resulted in 7 clusters with two monogenotypic clusters and the large cluster The Cluster I included 15 genotypes indicating the lack of significant genetic differences among them. Then the intra and inter cluster distances were calculated to find out the genetic divergence and closeness among the obtained clusters. The relative contribution (in per cent) of each character to total divergence was assessed in two ways :(i) average D^2 for individual character over 561 combinations and (ii) rank total for individual character, over all the paired combination.
- j) Canonical analysis was also carried out to study the genetic divergence among the genotypes.

A brief description of the salient findings from the present investigation and the inferences are presented below.

1. The analysis of variance indicated that significant variation was observed among the 32 lowland rice genotypes for all the 12 characters evaluated.
2. Eleven genotypes were found late with respect to the Days to 50% flowering above 110.40 days, 7 genotypes it was higher than 119.15cm, 7genotypes showed more no of panicles of above 12, seven genotypes recorded highest flag leaf area of above 32.43 cm², four genotypes recorded high panicle length of more than 26.22 cm, Eleven genotypes exhibited fully exerted panicles and fourteen genotypes exhibited partially exerted panicles, Seven genotypes exhibited high spikelet fertility of above 72.20%, Twenty one genotypes recorded more number of fertile grains per panicle above 121.28, four genotypes recorded high panicle weight above , eleven genotypes recorded high 100 seed weight above , 12 genotypes recorded high cellulose content above ,
3. The heritability ranges from 69.76% (Panicle length) to 96.97% (cellulose). Characters like panicle length (69.76%) exhibited moderate heritability (40%-70%) and all other characters exhibit high heritability (>70%).
4. The expected genetic advance over mean for different characters ranged from 7.74 (Days to 50% flowering) to 73.86 (Cellulose). Three characters reported

low GA over mean those are Days to 50 % flowering, Panicle length and Plant height. Moderate genetic advance was reported for number of productive tillers, Flag leaf area, Spikelet fertility % and 100seed weight. For characters like Panicle exsertion Number of fertile grains per panicle, Panicle weight, Cellulose, Single plant yield, reported high genetic advance.

5. High heritability accompanied with low genetic advance was reported by Characters like days to 50 per cent flowering and plant height. High heritability with moderate genetic advance was observed in Number of effective tillers, Flag leaf area, Spikelet fertility % and 100 seed weight. High heritability accompanied with high genetic advance was observed in Number of fertile grains/ panicle, Panicle weight, cellulose and Single plant yield. Panicle length exhibited moderate heritability with low genetic advance.
6. No negative phenotypic correlation was found significant whereas the lowest significant positive phenotypic correlation (0.355) was observed between plant height and 100 grain weight and highest correlation (0.775) was between number of filled grains/ panicle and single plant yield.
7. Out of 78 estimates only 23 are negative of which only 1 is significant. And among 55 positive estimates 22 were highly significant. with the highest genotypic correlation (0.964) between number of fertile grains per panicle and single plant yield and the lowest (0.354) between number of productive tillers and spikelet fertility %.
8. At phenotypic level of the eleven characters estimated 9 characters showed positive direct effect on yield with highest (0.359) in case of number of fertile grains per panicle. The two traits that showed negative direct effect on yield were plant height and Panicle exsertion.
9. Phenotypically fertile grains per panicle exhibited highest indirect effect on yield via panicle exsertion (0.266).
10. At genotypic level Number of productive tillers (0.536) exhibited maximum direct effect on yield. The characters like plant height, panicle length and number of fertile grains/ panicle exhibited negative direct effect on yield.

11. Genotypically spikelet fertility% has highest positive indirect effect via 100 grain weight (0.63) on yield.
12. The predicted genetic advance from different indices at 10% selection intensity ranged from 4.53 q/ha in one-character index to 4.79 q/ha in eleven character index and it varied from 100.00 % in index 1 to 105.7 % in index 11 in terms of relative efficiency. Thus, in terms of predicted genetic advance, the results of the present study brought out superiority of eleven character index over direct selection on yield per se.
13. SBP-15, Hasanta, SBP-53, SBP-30, SBP-102 were found to be most promising among the test genotypes based on selection index score and they also exhibited highest mean yield
14. By using Tochers method all the 34 lowland genotypes were classified in to 7 clusters of which The Cluster I is the largest with 15 genotypes followed by cluster II with 7 genotypes and cluster III contained 6 genotypes, Cluster IV and V contained 2 genotypes each. Cluster VI and VII were monogenotypic clusters much more divergent than rest of the genotypes. The genotypes of III and V are more divergent with highest inter cluster distance of 512.30 while the genotypes of VI and VII are less divergent with an inter cluster distance of 118.70.
15. 100 seed weight contributed for the maximum divergence among the 34 genotypes with 38.62 of total percentage of D^2 .
16. As a supplement to D^2 , Canonical analysis was carried out by calculation of Z_1 and Z_2 and presentation of genotypes in a scatter diagram.

It can thus be concluded from the above investigation that wide variation was observed for twelve yield and yield attributing characters in 34 rice genotypes. SBP-15, Hasanta, SBP-53, SBP-30, SBP-102 can be used as varieties owing to their stable performance with respect to all other characters. By virtue of their divergence from all the genotypes.



REFERENCES

- Abebe T, Alamerew S and Tulu L. 2017. genetic variability, heritability and genetic advance for yield and its related traits in rainfed lowland rice (*Oryza sativa* L.) Genotypes at Fogera and Pawe, Ethiopia, *Advanced Crop Science and Technology*, **5**(2): 1-8.
- Akhtar N, Nazir MF, Rabnawaz A, Mahmood T Safdar M.E, Asif M and Rehman A. 2011. Estimation of heritability, correlation and path coefficient analysis in fine grain rice (*Oryza sativa* L.), *The Journal of Animal & Plant Sciences*, **21**(4): 660-664.
- Akter A, Hasan MJ, Paul AK, Mutlib MM and Hossain MK. 2009. Selection of parent for improvement of restorer line in rice (*Oryza Sativa* L.), *SAARC Journal of Agriculture*, **7**(2): 43-50.
- Ali ML, McClung, Jia MH, Kimball JA. 2015 A Rice Diversity Panel Evaluated for Genetic and Agro-Morphological Diversity between Subpopulations and its Geographic Distribution, *AGRIS*, **51**(5) 2021- 2035.
- Allard RW. 1960. *Principles of Plant Breeding*. John Wiley and sons. Inc., New
- Anandan A, Eswaran R and Prakash M. 2011. Diversity in rice genotypes under salt affected soil based on multivariate analysis. *Pertanika Journal of Tropical Agriculture and Science*, **34**(1): 33-40.
- Annual report 2017-18, *Department of Agriculture, Cooperation & Farmers Welfare*, Ministry of Agriculture & Farmers Welfare, Government of India, Krishi Bhawan, New Delhi-110 001, www.agricoop.nic.in.
- Ashish G and Vishal S. 2018. Correlation study between yield components in WA based rice hybrids, *International Journal of Plant Sciences (Muzaffarnagar)*, **13**(1): 127-130.
- Aslam M.S, Islam MM, Hassan L, Begum SN and Gupta R. 2014. Study of Correlation, Magnitude of Genetic Diversity and Selection Indices in Popular Rice (*Oryza sativa* L.) Landraces of Bangladesh, *International Journal of Innovation and Applied Studies*, **8**(3): 1329.

- Augustina UA, Iwunor OP and Ijeoma OR. 2013. Heritability and character correlation among some rice genotypes for yield and yield components. *Journal of Plant Breeding and Genetics*, **1**(2): 73-84.
- Awasthi S and Lal JP. 2014. Genotypic correlation and path analysis study in rice (*Oryza sativa* L.) Under irrigated and rainfed conditions, *Annals of Plant Sciences*, **3**(12): 916-920.
- Banumathy S, Manimaran R, Sheeba A, Manivannan N, Ramya B, Kumar D and Ramasubramanian GV. 2010. Genetic diversity analysis of rice germplasm lines for yield attributing traits. *Electronic Journal of Plant Breeding*, **1**(4): 500-504.
- Baradhan G and Thangavel P. 2011. D² analysis in rice (*Oryza sativa* L.). *Plant Archives*, **11**(1): 373-375.
- Basavaraja T, Asif M, Mallikarjun SK and Gangaprasad S. 2013. Variability, heritability and genetic advance for yield and yield attributing characters in different local rice (*Oryza sativa* L.) cultivars. *Asian Journal of Bio Science*, **8**(1): 60-62.
- Bastia D, Mishra TK and Das SR. 2008. Genetic variability and selection indices for grain yield in upland rice, *ORYZA-An International Journal on Rice*, **45**(1): 72-75.
- Bisht V, Rao KS, Maikhuri RK and Nautiyal AR. 2008. Genetic divergence of paddy landraces in Nanakosi micro-watershed of Uttarakhand Himalaya, *Journal of Tropical Agriculture*, **45**(1): 48-50.
- Biswaranjan B, Simanchal S, Rajesh KK and Ritu KP. 2017. Selection indices for yield and yield contributing characters in slender grain rice genotypes, *International Journal of Current Research*, **9**(09): 56977-56979.
- Chandra BS, Reddy TD, Ansari NA and Kumar SS. 2009. Correlation and path analysis for yield and yield components in rice (*Oryza sativa* L.), *Agricultural Science Digest*, **29**(1): 45-47.

- Chaudhary AP, Parmar DJ, Muniya SD and Darji VB. 2017. Construction of selection index using simple correlation coefficients and path coefficients (direct effects) as a weight in rice (*Oryza sativa* L.), *International Journal of Current Research* **9**(7): 53864-53869.
- Das S. 2015. Genetic studies of yield variation in mid duration irrigated rice. *IOSR Journal of Agriculture and Veterinary Science*, **8**(4): 41-43.
- Deepa SP, Sheeba A and Anbumalarmathi J. 2006. Variability and character association studies in rice. *Agric. Sci. Digest*, **26**(3): 182-184.
- Devi KR, Chandra BS, Lingaiah N, Hari Y and Venkanna V. 2017. Analysis of variability, correlation and path coefficient studies for yield and quality traits in rice (*Oryza sativa* L.). *Agricultural Science Digest-A Research Journal*, **37**(1): 1-9.
- Dewey DR and Lu KH. 1959. A correlation and path coefficient analysis of components of crested wheat grass seed production, *Agronomy journal*. **51**:515-518
- Edukondalu B, Reddy VR, Rani TS, Kumari CA and Soundharya B. 2017. Studies on Variability, Heritability, Correlation and Path Analysis for Yield, Yield Attributes in Rice (*Oryza sativa* L.), *International Journal of Current Microbiology Applied Science* **6**(10): 2369-2376.
- Fazlalipour M, Rabiei B, Samizadeh LH and Rahim SH. 2008. Multi-trait Selection for Screening Elite Genotypes of an F₂ Rice Population. *JWSS-Isfahan University of Technology*, **11**(42): 41-52.
- Fisher RA and Yates F. 1963. Statistical tables for biological, agricultural, and medical research. **6.**, rev. and enl. New York: Hafner Pub. Co.
- Garg P, Pandey DP and Kaushik RP. 2011. Genetic divergence for yield and quality traits in rice (*Oryza sativa* L.). *Journal of Rice Research*, **4**(1): 1-5.
- Garrote G, Dominguez H and Parajo JC. 2002. Autohydrolysis of corncob: study of non-isothermal operation for xylooligosaccharide production. *Journal of food and Engineering*, **52**:211–218

- Gopikannan M and Ganesh SK. 2013. Inter-relationship and path analysis in rice (*Oryza sativa* L.) under sodicity. *Indian Journal of Science and Technology*, **6**(9): 5223-5227.
- Gour L, Koutu GK, Singh SK, Patel DD, Shrivastava A and Singh Y. 2017. Genetic variability, correlation and path analyses for selection in elite breeding materials of rice (*Oryza sativa* L.) genotypes in Madhya Pradesh.
- Habib SH, Iftakharuddaula KM, Bashir MK, Akter K and Hossain MK. 2013. Genetic variation, correlation and selection indices in advanced breeding lines of rice (*Oryza sativa* L.). *Bangladesh Journal of Plant Breeding and Genetics*, **20**(1): 25-32.
- Haradani CS and Shailaja H. 2017. Trait association and construction of selection indices in rice (*Oryza sativa* L.) under aerobic condition, *International Journal of Agriculture Sciences*, **9**(30): 4416-4421.
- Harsha ID, Kumar S and Mohammed T. 2017. Assessment of genetic variability and inter-character association studies in rice genotypes (*Oryza sativa* L.), *International Journal of Current Microbiology and Applied Science*, **6**(9): 2041-2046.
- Hazel LN. 1943. The genetic basis for constructing selection indices, *Genetics*, **28**:476-490
- Hemant S, Ritu RS and Verulkar. 2017. Genetic variability and character association study for different morphological traits and path analysis for grain yield of rice under irrigated and rainfed condition, *Electron journal of Plant Breeding*, **8**(1): 38-45.
- Idris AE, Justin FJ, Dagash YMI and Abuali AI. 2012. Genetic variability and inter relationship between yield and yield components in some rice genotypes, *American Journal of Experimental Agriculture*, **2**(2): 233.
- Immanuel SC, Pothiraj N, Thiagarajan K, Bharathi M and Rabindran R. 2011. Genetic parameters of variability, correlation and pathcoefficient studies for grain yield and other yield attributes among rice blast disease resistant genotypes of rice (*Oryza sativa* L.). *African Journal of Biotechnology*, **10**(17): 3322-3334.

- Iqbal T, Hussain I, Ahmad N, Nauman M, Ali M, Saeed S, Zia M and Ali F. 2018. Genetic variability, correlation and cluster analysis in elite lines of rice, *Journal of Scientific Agriculture*, **2**: 85-91.
- Irappa BM, Lakshmana D and Chandana BC. 2018. Genetic divergence study for yield and its components traits in rice, *Green Farming* **9**(1): 18-20.
- Islam MZ, Khalequzzaman M, Bashir MK, Ivy NA, Haque MM and Mian, MAK. 2016. Variability assessment of aromatic and fine rice germplasm in Bangladesh based on quantitative traits. *The scientific world journal*, Article ID 2796720
- Jayasudha S and Deepak S. 2010. Genetic parameters of variability, correlation and path-coefficient for grain yield and physiological traits in rice (*Oryza sativa* L.) under shallow lowland situation, *Electronic Journal of Plant Breeding*, **1**(5): 1332-1338.
- Joshi MA, Singh P, Sarao NK, Sharma RC and Bharaj TS. 2008. Genetic diversity among rice varieties cultivated in Punjab, *ORYZA-An International Journal on Rice*, **45**(4): 277-279.
- Kanbar A, Toorchi M and Shashidhar H. 2009. Relationship between root and yield morphological characters in rainfed low land rice (*Oryza sativa* L.), *Cereal Research Communications*, **37**(2): 261-268.
- Kanbar A, Toorchi M, Motohashi T, Kondo K and Shashidhar H.E. 2010. Evaluation of discriminant analysis in identification of deep and shallow rooted plants in early segregating generation of rice (*Oryza sativa* L.) using single tiller approach, *Australian Journal of Basic and Applied Sciences*, **4**(8): 3909-3916.
- Karad SR and Pol KM. 2008. Character association, genetic variability and path coefficient analysis in rice (*Oryza sativa* L.), *International Journal of Agricultural Sciences* **4**(2): 663-666.
- Karande SS, Thaware BL, Bhawe SG and Devmore JP. 2017. Genetic Variability and Character Association Studies on Some Exotic Germplasm Lines in Kharif Rice (*Oryza sativa* L.), *Advanced agriculture and technology journal*, **1**(1): 110-114.

- Khare R, Singh AK, Eram S and Singh PK. 2015. Genetic variability, association and diversity analysis in upland Rice (*Oryza sativa* L), *SAARC Journal of Agriculture*, **12**(2): 40-51.
- Kishore C, Kumar A, Pal AK, Kumar V, Prasad BD and Kumar A. 2018. Character Association and Path Analysis for Yield Components in Traditional Rice (*Oryza sativa* L.) Genotypes, *International Journal of Current Microbiology and Applied Science* **7**(3): 283-291.
- Kole PC and Hasib KM. 2008. Correlation and regression analysis in scented rice, *Madras Agriculture Journal*, **95**(6): 178- 182
- Krishna T, Kavita A and Pushpalata T. 2010. Genetic variability, heritability and genetic advance for quantitative traits in rice (*Oryza sativa* L.) accession, *Agricultural & Biological Research*, **26**(1): 13-19.
- Kumar V. 2015. Genetic diversity and character association studies for some economic traits in rice (*Oryza sativa* L.), *The Bioscan*, **10**(2): 899-904.
- Latif MA, Rahman MM, Kabir MS, Ali MA, Islam MT and Rafii, MY. 2011. Genetic diversity analyzed by quantitative traits among rice (*Oryza sativa* L.) genotypes resistant to blast disease, *African Journal of Microbiology Research*, **5**(25): 4383-4391.
- Liakat AM, McClung AM, Jia MH, Kimball JA, McCouch SR and Georgia CE. 2011. A rice diversity panel evaluated for genetic and agro-morphological diversity between subpopulations and its geographic distribution. *Crop Science*, **51**(5): 2021-2035.
- Limbani PL, Gangani MK and Pandya MM. 2017. Genetic Variability, Heritability and Genetic Advance in Rice (*Oryza sativa* L.), *International Journal of Pure and Applied Bioscience*, **5**(6): 1364-1371.
- Maiorella BI. 1983. *Ethanol industrial chemicals*. *Biochem Fuels*, Pergamon Press, Oxford: 861–914.

- Nachimuthu VV, Robin S, Sudhakar D, Raveendran M, Rajeswari S and Manonmani S. 2014. Evaluation of rice genetic diversity and variability in a population panel by principal component analysis, *Indian journal of Science and Technology*, 7(10): 1555-1562.
- Nandan R and Singh S.K. 2010. Character association and path analysis in rice (*Oryza sativa* L.) genotypes. *World Journal of Agricultural Sciences*, 6(2): 201-206.
- Nor AH, Harun AR, Rafii YM, Norain MN and Izzah JN. 2014. Correlation Analysis on Agronomic Characters in F1 population derived from a cross of Pongsu Seribu 2 and MR 264. In *Research and Development Seminar*.
- Odisha Economic Survey 2016-17, Planning and Convergence Department, Directorate of Economics and Statistics, Government of Odisha.
- Ogunbayo SA, Ojo DK, Sanni KA, Akinwale MG, Toulou B, Shittu A, Idehen EO, Popoola AR, Daniel IO and Gregorio GB. 2014. Genetic variation and heritability of yield and related traits in promising rice genotypes (*Oryza sativa* L.), *Journal of Plant Breeding and Crop Science*, 6(11): 153-159.
- Ovung CY, Lal GM and Rai PK. 2012. Studies on genetic diversity in Rice (*Oryza sativa* L.), *Journal of Agricultural Technology*, 8(3): 1059-1065.
- Ovung S, Lal CY and Rai PK. 2012. Studies on genetic diversity in Rice (*Oryza sativa* L.), *Journal of Agricultural Technology*, 8(3): 1059-1065.
- Pandey P, Anurag PJ, Tiwari DK, Yadav SK and Kumar B. 2009. Genetic variability, diversity and association of quantitative traits with grain yield in rice (*Oryza sativa* L.), *Journal of Bio-Science*, 17: 77-82.
- Pankaj G, Pandey DP and Dhirendra S. 2010. Correlation and Path Analysis for Yield and its Components in Rice (*Oryza sativa* L.), *Crop Improvement*, 37 (1): 46-51
- Pate JR, Saiyad MR, Prajapati KN, Patel RA and Bhavani RT. 2014. Genetic variability and character association studies in rainfed upland rice (*Oryza sativa* L.), *Electronic Journal of Plant Breeding*, 5(3): 531-537.

- Premkumar R, Gnanamalar RP and Anandakumar CR. 2015. Correlation and path coefficient analysis among grain yield and kernel characters in rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*, **6**(1): 288-291.
- Priyanka D, Gulati JML and Sarthak P. 2017. Correlation and phenotypic path coefficient studies in rice under system of aerobic rice production, *Oryza*, **54**(2): 246-248.
- Priyanka G, Senguttuve P, Sujatha M, Sravanraju N, Beulah P, Naganna P, Revathi P, Kemparaju KB, Prasad ASH, Suneetha K and Sreedevi, B. 2016. Correlation between traits and path analysis co-efficient for grain yield and other components in direct seeded aerobic rice (*Oryza sativa* L.), *Advance Research Journal of Crop Improvement*, **7**(1): 40-45.
- Rabiei B, Valizadeh M, Ghareyazie B and Moghaddam M. 2004. Evaluation of selection indices for improving rice grain shape, *Field Crops Research*, **89**(2-3): 359-367.
- Rahimi M, Ramezani M and Kordrostami M. 2017. Selecting Best Rice Varieties under Drought Stress and Non-Stress Conditions Using Selection Indices, *Journal of Agricultural sciences*, **27**(4): 473-480.
- Rao, CR. 1952. Advanced statistical method in biometrics research. Newyork: John weley & sons
- Rice Outlook, RCS-18D, April 12, 2018 USDA, *Economic Research Service*.
- Rita C and Sarawgi AK. 2017. Study of genetic diversity for agro-morphological and quality characters in diverse aromatic rice germplasm, *Oryza*, **54**(3), pp.342-345.
- Sabouri H, Rabiei, B. and fazlalipour M. 2008. Use of selection indices based on multivariate analysis for improving grain yield in rice. *Rice Science*, **15**(4): 303-310.
- Saha BC. 2003. Hemi-cellulose bioconversion. *Indian Microbiology and Biotechnology*, **30**:279–291

- Saikumar S, Saiharini A, Ayyappa D, Padmavathi G and Shenoy VV. 2014. Heritability, correlation and path analysis among yield and yield attributing traits for drought tolerance in an interspecific cross derived from. *Notulae Scientia Biologicae*, **6**(3): 338.
- Sangaré JR, Konaté AK, Cissé F and Sanni A. 2017. Assessment of genetic parameters for yield and yield related-traits in an intraspecific rice (*Oryza sativa* L.) population. *Journal of Plant Breeding and Genetics*, **5**(2): 45-56.
- Sanni KA, Fawole I, Guei RG, Ojo DK, Somado, EA, Tia DD, Ogunbayo SA and Sanchez I. 2008. Geographical patterns of phenotypic diversity in *Oryza sativa* landraces of Côte d'Ivoire, *Euphytica*, **160**(3), pp.389-400.
- Sanni KA, Fawole I, Ogunbayo A, Tia D, Somado EA, Futakuchi, K, Sié M, Nwilene FE and Guei RG. 2012. Multivariate analysis of diversity of landrace rice germplasm. *Crop Science*, **52**(2): 494-504.
- Sedeek SEM, Hammoud SAA, Ammar MH and Metwally TF. 2009. Genetic variability, heritability, genetic advance and cluster analysis for some physiological traits and grain yield and its components in rice (*Oryza sativa* L.), *Journal of Agriculture Research*, **35**(3): 858-878.
- Shahidullah SM, Hanafi MM, Ashrafuzzaman M, Ismail MR and Khair A. 2009. Genetic diversity in grain quality and nutrition of aromatic rice, *African Journal of Biotechnology*, **8**(7).
- Sharma SK, Nandan R, Singh SK, Sharma AK, Kumar S, Sharma PK, Singh, MK and Kumar V. 2011. Genetic divergence in rice (*Oryza sativa* L.) genotypes under irrigated condition. *Progressive Agriculture*, **11**(2): 321-325.
- Shinde SR, Kamlesh K and Pawar RM. 2015. Genetic studies in upland rice (*Oryza sativa* L.). *International Journal of Plant Sciences (Muzaffarnagar)*, **10**(1): 33-37.
- Shiva Prasad G, Sujatha M, Rao SV, Chaitanya and Parashuram P. 2013. Character Association and Path Analysis in Rice (*Oryza sativa* L.) Genotypes for cold tolerance. *Helix* **3**: 349-352

- Shrivastava A, Mishra DK, Koutu GK and Singh SK. 2014. Genetic parameters for grain yield and its attributes in parental lines of hybrid rice, *Jawaharlal Nehru Krishi Vishwa Vidyalaya Jabalpur 482004 (Madhya Pradesh) India*: 275.
- Shrivastava A, Mishra DK, Koutu GK, Singh SK, Prakash V and Sohgaure N. 2015. Assessment of genetic diversity of restorer and maintainer lines of rice using SSR markers, *The Ecoscan*, **9**(1&2): 265-269.
- Singh CM, Babu GS, Kumar B and Mehandi S. 2013. Analysis of quantitative variation and selection criteria for yield improvement in exotic germplasm of upland rice (*Oryza sativa* L.). *The Bioscan*, **8**(2): 485-492.
- Singh SK, Singh CM and Lal GM. 2011. Assessment of genetic variability for yield and its component characters in rice (*Oryza sativa* L.). *Research in Plant Biology*, **1**(4).
- Sohrabi M, Rafii MY, Hanafi MM, Akmar SNA and Latif MA. 2012. Genetic diversity of upland rice germplasm in Malaysia based on quantitative traits. *The Scientific World Journal*, Article ID 416291: 1-9
- Sowjanya PR, Raghavendra P and Shailaja H. 2017. Trait association studies to determine selection indices in two F3 segregating populations of rice (*Oryza sativa* L.), under aerobic condition, *Oryza*, **54**(3): 276-281.
- Subudhi HN, Meher J, Bose LK and Das S. 2009. Genetic diversity studies of promising rice varieties of eastern India based on quality characters, *ORYZA-An International Journal on Rice*, **46**(4): 271-274.
- Tuhina KM, Hanafi MM, Rafii YM, Wong MY, Salleh FM and Ferdous J. 2015. Genetic variation, heritability, and diversity analysis of upland rice (*Oryza sativa* L.) genotypes based on quantitative traits, *BioMed research international*, Article ID 290861: 1-7
- Ubarhande VA, Prasad R, Singh RP, Singh SP and Agrawal RK. 2009. Variability and diversity studies in rain-fed rice (*Oryza sativa* L.). *Indian Journal of Plant Genetic Resources*, **22**(2): 134.

- Umarani E, Radhika K, Padma V and Subbarao LV. 2017. Variability, heritability and genetic advance for agro-morphological and grain quality parameters in landraces of rice (*Oryza sativa* L.), *Environment and Ecology*, **35**(3), pp.1682-1687.
- Wright, S. 1921. Correlation and causation, *Journal of Agriculture Research*. **20**:557-585
- Yadav S and Suresh BG. 2018. Path coefficient analysis for yield and yield yomponents in diverse rice genotypes. *International Journal of Current Microbiology and Applied Science* Special Issue **6**: 998-1004.
- Zamora R and Crispin JAS (1995) Production of an acid extract of rice straw, *Acta Cient Venez* **46**:135–139.
- Zheng XZ, Lan YB, Zhu JM, Westbrook J, Hoffmann WC and Lacey RE. 2009. Rapid identification of rice samples using an electronic nose, *Journal of Bionic Engineering*, **6**(3): 290-297.

