

**VARIABILITY FOR NUTRITIONAL AND  
BIOCHEMICAL QUALITY PARAMETERS  
IN COLORED RICE GENOTYPES  
(*Oryza sativa* L.)**

**By**  
**PEKETI SRI DEVI**  
**B.Sc. (Ag.)**

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**CHAIRPERSON: Dr. B. KRISHNA VENI**



**ANGRAU**

**DEPARTMENT OF GENETICS AND PLANT BREEDING  
AGRICULTURAL COLLEGE, BAPATLA – 522 101  
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**2018**

## DECLARATION

I, **Ms. PEKETI SRI DEVI**, hereby declare that the thesis entitled **“VARIABILITY FOR NUTRITIONAL AND BIOCHEMICAL QUALITY PARAMETERS IN COLORED RICE GENOTYPES (*Oryza sativa* L.)”**, submitted to **Acharya N. G. Ranga Agricultural University** for the degree of **Master of Science in Agriculture** in the major field of **Genetics and Plant Breeding** is the result of original research work done by me. I also declare that no material contained in the thesis has been published earlier in any manner.

Place:

**(PEKETI SRI DEVI)**  
**I.D. No. BAM- 16-24**

Date:

# CERTIFICATE

Ms. **PEKETI SRI DEVI** has satisfactorily prosecuted the course of research and that the thesis entitled “**VARIABILITY FOR NUTRITIONAL AND BIOCHEMICAL QUALITY PARAMETERS IN COLORED RICE GENOTYPES (*Oryza sativa* L.)**” submitted is the result of original research work and is of sufficiently high standard to warrant its presentation to the examination. I also certify that neither the thesis nor its part there of has been previously submitted by her for a degree of any university.

**Date:**

**(B. KRISHNA VENI)**

**Chairperson**

# CERTIFICATE

This is to certify that the thesis entitled “**VARIABILITY FOR NUTRITIONAL AND BIOCHEMICAL QUALITY PARAMETERS IN COLORED RICE GENOTYPES (*Oryza sativa* L.)**” submitted in partial fulfillment of the requirements for the degree of ‘Master of Science in Agriculture’ in the major field of **Genetics and Plant Breeding** of the Acharya N.G. Ranga Agricultural University, Lam, Guntur, is a record of the bonafied original research work carried out by **Ms. PEKETI SRI DEVI** under our guidance and supervision. The subject of the thesis has been approved by the student’s advisory committee.

No part of the thesis has been submitted by the student for any other degree or diploma. The published part and all assistance received during the course of the investigations have been duly acknowledged by the author of the thesis.

## **Thesis approved by the Student Advisory Committee**

Chairperson : **Dr. B. KRISHNA VENI**  
Scientist (Plant Breeding)  
ARS, Bapatla - 522 101

---

Member : **Dr. J. DAYAL PRASAD BABU**  
Assistant Professor  
(Genetics and Plant Breeding)  
Student Affairs Section  
ANGRAU, Lam, Guntur - 522 034

---

Member : **Sri. D. SANDEEP RAJA**  
Scientist (Biochemistry)  
AICRP on PHET  
Bapatla - 522 101

---

**Date of Final Viva-voce**

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*Place:*

*Date:*

*(Peketi Sri Devi)*

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## LIST OF SYMBOLS AND ABBREVIATIONS

ASV	:	Alkali spreading value
AAE	:	Ascorbic Acid Equivalent
&	:	And
$\sigma_p^2$ (or) $V_p$	:	Phenotypic variance
$\sigma_g^2$ (or) $V_g$	:	Genotypic variance
$\sigma_e^2$ (or) $V_e$	:	Environmental variance
ANOVA	:	Analysis of variance
AUC	:	Area Under Hydrolysis Curve
°C	:	Degree centigrade
CD	:	Critical difference
Cm	:	Centimeter
CV	:	Coefficient of variation
COV	:	Covariance
d.f	:	Degrees of freedom
DFF	:	Days to 50% Flowering
<i>et al.</i> ,	:	and coworkers
Fig.	:	Figure
Fe	:	Iron
F <sub>1</sub>	:	First F <sub>1</sub> ial generation
G	:	Gram
GA	:	Genetic advance
GAM	:	Genetic advance as per cent of mean
GCV	:	Genotypic coefficient of variation
GI	:	Glycemic Index
GL	:	Glycemic Load
ha	:	Hectare

$h^2$ (b)	:	Heritability in broad sense
IIRR	:	Indian Institute of Rice Research
K	:	Selection differential
kg ha <sup>-1</sup>	:	Kilograms per hectare
L	:	Litre
L/B	:	Kernal length to breadth ratio
Max.	:	Maximum
mg	:	Milli grams
Min.	:	Minimum
ml	:	Milli litre
mm	:	Millimeter
Mss	:	Mean Sum of Square
nm	:	Nano meters
No.	:	Number
NS	:	Non-significant
PCV	:	Phenotypic coefficient of variation
<i>per se</i>	:	As such with mean
ppm	:	Parts Per Million
<i>QE</i>	:	Quercetin Equivalent
R	:	Correlation coefficient
RBD	:	Randomized Block Design
RDS	:	Rapidly Digestible Starch
RPM	:	Revolutions per minute
RS	:	Resistant Starch
S	:	Significant
SS	:	Sum of Square
SDS	:	Slowly Digestible Starch
TFC	:	Total Flavonoid Content
TPC	:	Total Phenol Content

%	:	Per cent
VER	:	Volume expansion ratio
<i>Via</i>	:	Through
<i>viz.,</i>	:	Namely
XRF	:	X ray fluorescence spectrometry
$\bar{X}$	:	Grand mean
/	:	Per
<	:	Less than
>	:	Greater than
Zn	:	Zinc

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# ABSTRACT

Name of the Author : **P. SRI DEVI**  
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The present investigation was carried out during *kharif*, 2017 at Agricultural College Farm, Bapatla with 26 rice (*Oryza sativa* L.) genotypes to obtain information on the nature and extent of variability, heritability, genetic advance as per cent of mean, correlation and the magnitude of direct and indirect effects of yield and physicochemical, nutritional and biochemical quality characters on grain yield of different colored rice (*Oryza sativa* L.) genotypes.

The analysis of variance revealed significant differences among the genotypes for all characters *viz.*, days to 50% flowering, panicle length (cm), plant height (cm), ear bearing tillers per plant, grain yield per plant (g), test weight (g), number of filled grains per panicle, total number of grains per panicle, fertility %, water uptake, alkali spreading value, amylose content (%), protein content (%), total starch content (%), total phenol content (mg/100g), total antioxidant activity (mg AAE/100g), flavonoid content (mg QE/100g), Zn content (ppm), Fe content (ppm), glycemic index, slowly digestible starch (%), rapidly digestible starch (%) and resistant starch (%) except for solid loss, volume expansion ratio and L/B ratio.

Among the brown pericarp colored genotypes, BPT 5204, a popular variety with excellent cooking quality traits manifested all the quality parameters in the desirable range and had a low GI value. Another variety BPT 2270 along with BPT 2660, a minikit culture also recorded low GI coupled with other desirable quality traits. All these genotypes possess medium slender grain type. BPT 2595 had high RS content and flavanoid content among brown rice genotypes. But the phenol content, flavonoid content and antioxidant activity was low in brown colored genotypes when compared with red and black genotypes. Among red pericarp colored genotypes, BPT 3139 manifested low GI along with high antioxidant activity, high protein and Zn content. Whereas Jyothi, Matta Triveni and BPT 3111 recorded high antioxidant activity coupled with high Zn and Iron content and high grain yield. Among black pericarp colored genotypes, BPT 2848 manifested highly desirable quality parameters along with high yield potential. It also recorded high protein content, high flavonoid content, high SDS & RS content coupled with low GI value. Hence these can be recommended for inclusion in diabetic diet.

High GCV and PCV coupled with high heritability and high genetic advance as percent of mean were recorded for test weight, number of filled grains per panicle and total number of grains per panicle among yield components, while among quality traits solid loss, water uptake, alkali spreading value, total phenol content, total antioxidant activity, flavonoid content, zinc and iron content are controlled by additive type of gene action. Thus apparently substantial contribution of additive genetic variance is involved in the expression of these traits. Hence, good response to selection can be attained for improvement of these traits. All other remaining traits studied manifested low to moderate estimates for genotypic and phenotypic coefficient of variation, moderate to high heritability estimates and low to high genetic advance as percent of mean indicating the role of both additive and non-additive gene effects in the expression of these traits.

The results of correlation studies revealed that panicle length, plant height, ear bearing tillers per plant, test weight and fertility %, along with amylose content, protein content, total starch content, total phenol content, total antioxidant activity, flavonoid content, Zn content, Fe content, glycemic index and rapidly digestible starch exhibited positive correlation with grain yield suggesting simultaneous improvement of these traits with grain yield.

Studies of path coefficient analysis revealed positive direct effects coupled with positive correlation coefficients of grain yield with panicle length, plant height, test weight, fertility %, amylose content, protein content, total starch content, total phenol content, Zn content and Fe content suggesting that simple selection of all the above traits would bring improvement to grain yield in rice.

## Chapter – I

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# Introduction

## Chapter I

# INTRODUCTION

Rice (*Oryza sativa* L.) is one of the most important cereal crops in the tropics as well as parts of temperate regions in the world. It is the most widely eaten staple in the world with global consumption levels more than tripling from 156 million tons to 456 million tons between 1960 and 2010 (IRRI, 2010). Rice is not only the major source of energy, but also the major source of protein and a significant source of fiber and essential micronutrients (Uphoff, 2008). Rice is the only cereal, cooked and consumed as a whole grain and quality considerations are much more important than for any other food crops (Hossain *et al.*, 2009). Rice has approximately 87% carbohydrates, 7-8% proteins and very low in fat content (Selvakumar *et al.*, 2014a) and rice consumption varies from 60 kg to 220 kg in Asian countries and about 12 kg per capita in North America. Dependency on rice is very high among poor people in parts of Asia. Recent studies suggest that the high consumption of rice accelerates the development of diabetes (Hu *et al.*, 2012). A high dietary glycemic load (predominantly from rice) has been associated with increased risk of type 2 diabetes in Chinese (Villegas *et al.*, 2007), Japanese (Nanri and Mizoue, 2008) and Indian (Mohan *et al.*, 2009) populations. The prevalence of lifestyle-related chronic diseases and conditions, such as obesity, cardiovascular disease, certain cancers and type II diabetes is continuing to grow at an alarming pace throughout the world. The total number of people with Type II diabetes mellitus (DM) is projected to rise from 171 million in 2000 to 366 million in 2030 ( Wild and Roglic, 2004).

Brown rice is the regular rice which has its bran and germ intact. Brown rice is a whole grain rich in protein, fiber, fat, B complex vitamins and minerals like calcium, phosphorus and iron. White rice is produced from the polishing of brown rice that removes the pericarp, seed-coat, testa, aleurone layer and embryo which results in the loss of fat, protein, crude and neutral detergent fiber, ash, vitamins, and polyphenols whilst increasing starch content (Shobana *et al.*, 2011). Starch constitutes about 80-90% of dry mass of milled rice. Due to the removal of the bran layer, white rice has a lower total dietary fiber content (0.7–2%) than brown rice (3–4%) (Juliano and Bechtel, 1985). The energy content of brown rice is slightly higher than white rice due to lipids in the bran (Juliano, 2003). White rice elicits a relatively large glycemic response and is

thus associated with exacerbating impaired glucose tolerance (Sun *et al.*, 2010). It contributes a large glycemic load (GL) to the diets of those in countries where it is the main staple food due to both the large quantity eaten and its greater GI. These countries incidentally are also those where diabetes rates are markedly increasing (Chan *et al.*, 2009 and Shaw *et al.*, 2010).

In addition to common white-rice varieties, there are some speciality rices such as the colored ones (black also known as purple, brown and red). (Chaudhary, 2003) quoted China as the richest country in black rice resources (62%) followed by Sri Lanka (8.6%), Indonesia (7.2%), India (5.1%), Philippines (4.3%), Bangladesh (4.1%) and few in Malaysia, Thailand and Myanmar. Colors in the rice are due to the deposition of large amounts of anthocyanin or proanthocyanidin pigment in the rice coat (Chaudhary, 2003). Pigmented rice has been consumed since time immemorial, in most of the countries of Southeast Asia (Tananuwong and Tewaruth, 2010). Nowadays, whole grain pigmented rice has been categorized as one of the potent functional foods since it contains high amounts of phenolic compounds (Yawadio *et al.*, 2007). The concentration of total phenolics in the grain has been positively associated with the antioxidant activity (Itani *et al.*, 2002; Goffman and Bergman, 2004 and Zhang *et al.*, 2006), with potential beneficial effects on health, such as reduction of oxidative stress (Ling *et al.*, 2001 and Hu *et al.*, 2003), aid in the prevention of cancer (Hudson *et al.*, 2000; Hu *et al.*, 2003; Hyun and Chung, 2004 and Chen *et al.*, 2006), in the control of blood lipids and related diseases, which may help in the prevention of cardiovascular problems (Ling *et al.*, 2001), and in the prevention of the complications of diabetes (Morimitsu *et al.*, 2002 and Yawadio *et al.*, 2007). Black rice is an excellent alternative to white and brown rice, due to its nutrient density, high fiber content and rich antioxidant content. In addition, colored rice contains higher levels of proteins, vitamins and minerals than common white rice while red rice is good source of fibre, antioxidants, magnesium and iron and has more health benefits than white rice.

Increased income levels and self-sufficiency induced rice availability for consumption has brought a shift in the consumer as well as market preferences for better grain quality. Consumer's choice of rice varieties are largely based on grain and cooking qualities. With sharp increase in lifestyle related health problems, scientists are looking at quality traits other than carbohydrates, proteins and fat in food stuffs (primary metabolites) (Zhang *et al.*, 2005). As the consumers become more health

conscious and more aware of the benefits of functional foods, diets containing bio-active compounds (secondary metabolites) such as antioxidants have received greater attention. The total antioxidant activity which is positively correlated with the total soluble phenolic compounds (TSPCs) are found in higher concentration in genotypes with red and black pericarp colour when compared to those with a light brown pericarp colour (Tian *et al.*, 2004). Owing to several health promoting impacts associated with anthocyanins, such as anti-oxidative, anti-inflammatory and anti-carcinogenic effects, coloured rice is considered as a functional food and food ingredient in many Asian countries.

Rice is a traditional staple food and primary dietary source of carbohydrates for most Asians and is increasingly playing the same role in African diets. Improving the carbohydrate quality of this popular commodity offers potential as a dietary strategy for preventing and managing type II diabetes and its co-morbidities, thereby promoting population health and alleviating the public health burden of chronic diseases. Low GI diets are effective in the prevention and treatment of type II diabetes (Barclay *et al.* 2008; Gnagnarella *et al.* 2008 and Jenkins *et al.* 2002). However, rice improvement programmes have not been able to focus on the development of varieties with potential for reducing the incidence and severity of type II diabetes because variability for GI in rice is unknown, the genetics of GI are unknown and phenotyping tools for nutritional traits such as GI (standardized *in vitro* methods) are not available until recently.

Even though, many studies elucidating the variability and associations among physical and chemical quality parameters and yield components were reported earlier, the studies on biochemical parameters of rice grain and their relationship with other quality traits and yield components are very meagre. Further, studies on different components of rice starch and glycemic index of rice varieties are essential for improving the carbohydrate quality and lowering the GI of staple foods which offers potential as a dietary strategy for preventing and managing type II diabetes. Selecting the low GI rice genotypes of high nutritional value from existing germplasm collection may be an efficient and reliable way to deliver benefits to farmers and society (Fitzgerald *et al.*, 2011 and Jain *et al.*, 2012). Hence, the present investigation was taken up with the following objectives.

**Objectives:**

1. To study the variability for yield components, physical, nutritional and biochemical quality parameters.
2. To study the association among yield components and quality parameters.
3. To study the direct and indirect effects of yield components and quality parameters on yield of rice crop.

**Chapter – II**

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# **Review of Literature**

## Chapter – II

# REVIEW OF LITERATURE

Rice is a major staple food for half of the world's population, providing 50 to 80% of daily calorie intake (Khush, 2005). Carbohydrates, proteins, fatty acids and micronutrients (vitamins and trace minerals) are the major nutrient components in rice. Popularly eaten white rice contains low level of essential micronutrients, leading to development of micronutrient deficiency upon continuous consumption which warrants the situation of developing micronutrient and vitamin rich rice through genetic engineering (Ye *et al.*, 2000). Consumption of increased quantity of polished rice grains (high GI food) has also been shown to contribute for higher insulin resistance and dyslipidemia (low-high density lipoprotein) among the Asian population. With the majority of world's population consuming rice as staple food, developing therapeutic rice varieties with enhanced nutritive value will have greater impact on preventing the above life style disorders.

Literature pertaining to variability & correlation of grain yield and different physicochemical characters with nutritional and biochemical quality traits is very meager. Very few studies were conducted regarding glycemic index of rice, different portions of starch (RDS, SDS and RS) and its relation to GI and other quality traits.

Review of literature pertaining to the present investigation in rice is presented under the following headings

2.1 Variability, Heritability and Genetic advance

2.2 Character association

2.3 Path analysis

## **2.1. VARIABILITY, HERITABILITY AND GENETIC ADVANCE AS PER CENT OF MEAN**

### **2.1.1 Variability for yield and yield components**

Knowledge on the nature and magnitude of variability present in any crop species plays a vital role in formulating a successful breeding programme for developing superior cultivars. Estimation of genetic variability in conjunction with heritability and genetic advance gives a clear indication of possible improvement that can be achieved through selection.

Heritability is the measure of transmission of characters from generation to generation. Broad sense heritability gives an idea about portion of observed variability attributable to genetic differences (Gangashetty *et al.*, 2013). The actual portion of heritable variation present in a population in relation to the total variation determines the consistency of performance of selection in succeeding generations.

Devi *et al.* (2010) conducted genetic variability, heritability and genetic advance studies on 110 rice genotypes for sixteen grain quality characters and grain yield. Studies revealed that single plant yield, volume expansion ratio, gel consistency, alkali spreading value and amylose content exhibited high GCV, heritability and genetic advance.

Nandan *et al.* (2010) conducted variability studies to evaluate thirty three rice genotypes for identifying their efficiency with respect to 20 yield and quality traits. Number of grains per panicle, number of spikelets per panicle exhibited the highest GCV and PCV. High heritability coupled with high genetic advance was registered for number of grains per panicle, number of spikelets per panicle and plant height.

Pandey and Anurag (2010) evaluated 22 genotypes of indigenous rice for yield and quality contributing traits to assess the genetic variability and heritability. Maximum value of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was recorded for head rice recovery. High broad sense heritability was exhibited by test weight followed by grain yield per hill while lowest heritability was observed for volume expansion ratio. Highest genetic advance was recorded for milling percentage and lowest genetic advance was recorded for volume expansion ratio.

Sunayana *et al.* (2010) studied the variability among 100 rice genotypes for quality traits and observed that high GCV and PCV were found for alkali spreading value. Total soluble sugar content showed high heritability coupled with high genetic advance whereas alkali spreading value and grain widening ratio manifested high heritability along with moderate genetic advance.

Yadav *et al.* (2010) conducted genetic variability studies on 40 rice genotypes for yield and its component traits and observed that higher magnitude of genotypic (GCV) and phenotypic coefficients of variation (PCV) was recorded for traits like seed

yield per hill, number of spikelets per panicle, number of tillers per hill and plant height. High heritability was observed for traits like plant height, seed yield per hill, test weight and number of spikelets per panicle.

Aktar *et al.* (2011) conducted variability and heritability studies on ten rice genotypes for yield and yield contributing traits and observed that highest genotypic as well as phenotypic coefficients of variation were obtained in case of number of grains/panicle followed by number of tillers/plant, paddy yield and plant height. High heritability values were observed for number of grains/panicle, number of tillers/plant and plant height.

Prasad *et al.* (2011) assessed 52 genotypes of rice to study the genetic variability for yield and its component characters and observed that characters like spikelet sterility and productive tillers showed high PCV and GCV. All the characters *viz.*, panicle length, spikelet sterility, test weight, seed yield/plant, plant height, tillers/plant, days to 50% flowering and productive tillers showed high genetic advance as percent of mean.

Bekele *et al.* (2013) evaluated sixty four rice genotypes to study the variability for grain zinc concentrations and yield related traits and reported that phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were highest for grain zinc concentration, number of tillers per plant, number of productive tillers per plant and grain yield per plant. Low values of PCV and GCV recorded for days to maturity. High heritability coupled with high genetic advance as percent mean were recorded for all the traits in this study except days to maturity.

Dhanwani *et al.* (2013) evaluated 21 F<sub>1</sub> crosses to assess the genetic variability, heritability and genetic advance for 13 quantitative and 19 quality traits in rice. Among the characters the high percent of GCV and PCV was recorded for biological yield, alkali spreading value and lowest for days to 50% flowering and hulling percentage. The highest heritability was exhibited by plant height and kernel length. The genetic advance as percentage of mean was highest for biological yield, alkali spreading value and lowest for days to 50% flowering and milling percentage.

Raja *et al.* (2013) conducted experiment to study the extent of genetic variability in yield and yield attributing traits and concluded that maximum genotypic co-efficient of variability and phenotypic co-efficient of variability were observed for

test weight, number of productive tillers per plant, number of spikelet per panicle, amylose per cent and grain yield/plant (g). High heritability coupled with high genetic advance as per cent of mean were observed for days to 50 per cent flowering, test weight, number of spikelet per panicle, per cent of spikelet fertility, protein per cent and grain yield/plant (g).

Sanghera *et al.* (2013) evaluated 14 red rice ecotypes from temperate region to assess the genetic variability for grain yield and component traits and observed that genotypic and phenotypic coefficients of variation were high for grain yield, secondary branches per panicle and panicle weight. High heritability coupled with genetic advance was recorded for traits *viz.*, days to 50% flowering, days to maturity, plant height, panicle weight, grain length, grain width and L/B ratio.

Veni *et al.* (2013) conducted genetic variability studies on seventy rice (*Oryza sativa* L.) genotypes for yield, yield components and quality parameters and observed that high GCV was exhibited by water uptake followed by grain yield per plant and test weight. Highest broad sense heritability was exhibited by days to 50% flowering, volume expansion ratio while genetic advance as per cent of mean was high for grain yield followed by water uptake and test weight.

Dhurai *et al.* (2014) conducted experiment using thirty two rice genotypes to estimate the genetic variability, heritability and genetic advance for grain yield and yield contributing traits in rice and reported that number of grains per panicle and grain yield per plant showed relatively high GCV and PCV estimates whereas high estimates of heritability coupled with high genetic advance as percent of mean were obtained for number of effective tillers per plant, plant height, panicle length, number of grains per panicle, L/B ratio, 1000-grain weight and grain yield per plant.

Gokulakrishnan *et al.* (2014) assessed the heritability, genetic advance, phenotypic and genotypic coefficient of variation among yield, quality and its component characters in twenty three genotypes of rice and concluded that high magnitude of phenotypic and genotypic coefficients of variation were observed for panicle weight. Panicle length and days to 50 per cent flowering exhibited the lowest GCV and PCV. High values for heritability was observed for grain yield per plant while high genetic advance was obtained for number of grains per panicle. High genetic advance coupled with high heritability was exhibited by grain breadth, grain L/B ratio, plant height, number of grains per panicle and grain yield per plant.

Naseem *et al.* (2014) conducted genetic variability studies on twenty genotypes of rice (*Oryza sativa* L.) for yield and yield related traits and reported that grain yield per plant showed the highest GCV and PCV followed by number of spikelets per panicle and plant height.

Rahman *et al.* (2014) evaluated seven advanced fine grain rice lines *viz.*, S-1, S-2, S-5, AL-33(II), AL-36, AL42(II) and AL-44(I) to study the variability parameters. The results revealed that plant height, number of effective tillers/hill, number of total tillers/hill, panicle length, number of filled spikelets/panicle, number of unfilled spikelets/panicle, grain yield/plant, and grain yield/plot exhibited the highest PCV values than GCV. Number of in-effective tillers/hill, weight of 1000 seeds showed the same GCV and PCV values. High heritability along with high genetic advance in percentage of mean was exhibited by number of ineffective tillers/plant.

Bhati *et al.* (2015) conducted genetic variability studies on 30 elite rice (*Oryza sativa* L.) genotypes for grain yield and quantitative traits. Highest genotypic coefficient of variance (GCV) phenotypic coefficient of variance (PCV) was observed for grain yield per hill. High estimates of heritability coupled with high genetic advance were observed for plant height and spikelets per panicle.

Bhuvanewari *et al.* (2015) evaluated F<sub>2</sub> segregating populations of two black rice crosses *viz.*, cross I ( Chakhao amubi ×RCM 23 ) and cross II (RCM 14×RCM 23) to study the genetic variability of yield and yield components. Productive tillers and filled spikelets per panicle showed high PCV & GCV in both crosses. whereas, panicle length showed low GCV and PCV in both the crosses. Plant height, fertility(%) and 1000 grains weight showed high heritability. Except panicle length, all the remaining traits *viz.*, plant height, productive tillers, filled spikelets, fertility (%), 1000 grains weight and grain yield per plant depicted high genetic advance as per cent mean.

Devi *et al.* (2015) evaluated ninety two rice (*Oryza sativa* L.) genotypes to estimate the genetic variability and heritability for 14 physicochemical and cooking quality traits and observed that water uptake, gel consistency and alkali spreading value exhibited high estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). Highest broad sense heritability and genetic advance was obtained for water uptake , amylose content and gel consistency.

Ekka *et al.* (2015) evaluated 96 rice germplasm accessions to study the variability among yield attributing and quality traits. Studies revealed that highest genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was observed for number of effective tillers per plant and grain yield per plant. High heritability coupled with high genetic advance was noticed for number of effective tillers per plant, number of filled grains per panicle and grain yield per plant.

Gampala *et al.* (2015) evaluated 80 rice genotypes to study the genetic variability, heritability and genetic advance for grain yield and quality traits. The result revealed that highest PCV was observed for grain yield per hill and number of spikelets per panicle while highest GCV was observed for number of spikelets per panicle. High estimates of heritability was observed for number of spikelets per panicle, test weight, plant height, days to 50% flowering, whereas grain yield per hill had lowest heritability. High genetic advance was observed for number of spikelets per panicle and plant height. High heritability coupled with high genetic advance was observed for plant height, panicle length and grain yield per plant.

Patil *et al.* (2015) screened sixty one rice genotypes to study the variability and heritability. They observed that grain yield per plant exhibited highest PCV and GCV followed by grain Fe content. Low PCV and GCV was exhibited by panicle length, days to first flowering and days to maturity. High heritability and high genetic advance as per cent of mean was manifested by grain yield per plant. Moderate heritability along with high genetic advance was recorded for grain Zn and Fe content.

Sala *et al.* (2015) conducted a study to assess the variability for iron and zinc content along with quality traits in dehusked rice grains and reported that ADT 37 x IR68144-3B-2-2-3 showed high mean value for the characters *viz.*, kernel length, kernel breadth after cooking, iron content. TRY (R) 2 x Mapillaisamba had high mean value for the characters *viz.*, zinc content, breadth wise expansion ratio. High heritability coupled with high genetic advance was observed in ADT37 x IR68144-3B-2-2-3 only for iron and zinc content.

Samak *et al.* (2015) conducted experiment to study the genetic variability among protein content, Zn content and Fe content in segregating generations of rice from a cross BPT × HPR 14 and reported that total grain protein showed moderate heritability along with moderate genetic advance as percent of mean whereas zinc and iron content showed high heritability coupled with high genetic advance as percent of mean.

Savitha and Kumari (2015) evaluated four traditional land races and six improved high yielding varieties to study the genetic variability among yield and yield component traits. They reported moderate values of PCV & GCV for days to 50% flowering, plant height, number of productive tillers per plant and single plant yield. High heritability coupled with high genetic advance was observed for days to 50 % flowering, plant height and number of productive tillers per plant

Umesh *et al.* (2015) assessed 24 rice genotypes to study different genetic parameters for yield attributing and quality characters and reported that spikelets/panicle and alkali spreading value showed the highest GCV and PCV. High heritability (in broad sense) was noted for plant height and 100-seed weight while genetic advance was highest for number of spikelets/panicle and lowest for spikelet fertility among yield component traits and for quality traits it was highest for alkali spreading value.

Bitew *et al.* (2016) carried out an experiment to assess the extent of genetic variability for yield and yield related traits among 22 rice genotypes. And concluded that high level of genotypic and phenotypic coefficients of variation was recorded for traits like grain yield, number of effective tillers per plant and unfilled grains per panicle. High heritability coupled with moderate genetic advance as percent of mean was observed for thousand grain weight.

Chowdhury *et al.* (2016a) evaluated 65 rice genotypes to study the variability among cooking quality parameters and yield. They observed that gel consistency showed the highest GCV and PCV values. High heritability along with high genetic advance was recorded for amylose content and yield per plant.

Chowdhury *et al.* (2016b) evaluated 65 diverse rice germplasm to study the variability among yield contributing characters and yield. Highest GCV and PCV was observed for 1000 grain weight and lowest for grain yield/plant. Higher estimates of heritability along with genetic advance was observed in all the traits except for zinc, protein content and number of panicles/plant.

Devi *et al.* (2016a) evaluated 27 rice genotypes to assess the genetic variability, heritability and genetic advance for grain yield and quality traits and observed that among the characters studied, yield per plant and filled grains per panicle exhibited the

higher estimates of PCV and GCV. The estimates of PCV and GCV were low for the characters *viz.*, kernel elongation ratio, days to 50% flowering, kernel length, kernel width, panicle length and L/B ratio. High heritability in broad sense and high genetic advance as percent of mean were exhibited by six traits *viz.*, effective tillers, plant height, filled seeds per panicle, test weight, yield per plant and length/breadth ratio.

Ernawati *et al.* (2016) assessed the brown rice of local varieties to study the genetic parameters and reported that high heritability estimates were found for grain yield, plant height, number of productive tillers and number of filled grains per panicle. While 1000 grain weight exhibited low heritability.

Kumar *et al.* (2016) evaluated eighty one rice genotypes for thirteen quantitative traits to examine the nature and magnitude of variability, heritability and genetic advance as percent of mean. And concluded that number of tillers per hill exhibited highest genotypic coefficient of variation and phenotypic coefficient of variation followed by number of panicles per hill and number of spikelets per panicle whereas high heritability coupled with high genetic advance was recorded for number of spikelets per panicle followed by grain yield and plant height.

Mohan *et al.* (2016) evaluated 44 rice genotypes to study the variability among yield parameters. Days to 50 % flowering, plant height and panicle length exhibited low levels of PCV and GCV indicating less variability among the genotypes for these traits. whereas, number of grains per panicle and 1000 grain weight recorded high estimates of PCV and GCV indicating the presence of high degree of variation for these traits among the genotypes. High heritability along with high genetic advance was observed for number of grains per panicle and 1000 grain weight indicating the predominance of additive gene affects in controlling these traits.

Pavan *et al.* (2016) evaluated 22 rice genotypes to study variability among yield and quality traits and reported that high GCV and PCV coupled with high heritability and genetic advance as percent of mean were exhibited by filled grains per panicle, alkali spreading value.

Rukminidevi *et al.* (2016) evaluated 50 traditional rice varieties and 7 popular rice varieties to study the variability among the biometrical traits along with Fe and Zn content. Studies revealed that highest GCV and PCV was observed for single plant

yield while low heritability was manifested by number of productive tillers/plant. Single plant yield recorded the highest genetic advance followed by Zn content and Fe content.

Sameera *et al.* (2016) evaluated 25 rice genotypes for their variability with regard to yield and yield components and the results revealed that high variability, heritability and genetic advance as per cent mean were exhibited by productive tillers per plant, number of grains per panicle and number of filled grains per panicle while days to maturity recorded high heritability coupled with low genetic advance as per cent of mean.

Bhinda *et al.* (2017) carried out experiment to obtain information on genetic variability, heritability and genetic advance for yield contributing and quality traits in advance breeding lines of rice (*Oryza sativa* L.). Studies revealed that alkali spreading value exhibited highest GCV and PCV followed by filled grains per panicle whereas high heritability coupled with high genetic advance was reported for plant height, filled grains per panicle, number of grains per panicle and days to 50% flowering.

Devi *et al.* (2017) studied the variability for yield and quality traits in 27 rice genotypes. Higher PCV and GCV were observed for yield per plant and filled grains per panicle. High heritability in broad sense coupled with high genetic advance as percent of mean were exhibited by effective tillers, plant height, filled grains per panicle, test weight, yield per plant and length/breadth ratio.

Jan *et al.* (2017) studied fourteen agro-morphological traits among 35 rice (*Oryza sativa* L.) genotypes for the assessment of genetic variability and observed that harvest index manifested the highest values of GCV and PCV while lowest GCV and PCV were exhibited by 1000 grain weight. High broad sense heritability coupled with high genetic advance was observed for number of spikelets per panicle and number of filled grains per panicle.

Lakshmi *et al.* (2017) evaluated fifty five aromatic rice genotypes for yield and component characters to study the genetic variability, heritability and genetic advance. The results revealed that number of filled grains per panicle, grain yield per plant, kernel length and L/B ratio recorded high GCV and PCV. Days to 50% flowering and kernel breadth recorded low GCV and PCV. High heritability coupled with high

genetic advance as percent of mean was registered for plant height, number of productive tillers per plant, panicle length, number of filled grains per panicle, grain yield per plant, kernel length and L/B ratio.

Nandini *et al.* (2017) evaluated 324 traditional rice varieties in Karnataka for grain yield and yield attributing characters. High heritability coupled with high genetic advance was observed for days to 50% flowering, grain length, grain breadth and L/B ratio. Days to 50% flowering, productive tillers/ plant L/B ratio and 1000 grain weight exhibited high genotypic variance, high heritability coupled with high expected genetic gain.

Sahu *et al.* (2017) evaluated 215 indigenous rice landraces of Chhattisgarh, India. to estimate the components of genetic variability for grain quality traits. High heritability coupled with high genetic advance as percent mean was observed for all the grain quality traits except for hulling percent and milling percent. High phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was observed for alkali spreading value and gel consistency.

Shaik *et al.* (2017) conducted experiment to study the genetic parameters for yield and yield attributing characters in forty rice genotypes and reported that high phenotypic and genotypic coefficient of variation was recorded for yield per plant followed by total number of grains per plant. Low phenotypic and genotypic coefficient of variation was observed for number of filled grains per panicle, panicle length and days to 50% flowering. High heritability coupled with high genetic advance as percent of mean was registered for yield per plant, effective tillers per square meter, total number of grains per plant, effective tillers per plant and 1000 grain weight.

Supriya *et al.* (2017) evaluated 25 rice germplasm accessions to study the genetic variability among quality, yield and yield related traits and reported that highest values for genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) was observed for seeds per panicle followed by days to 50 per cent flowering, plant height, yield per plant and number of effective tillers among yield related traits. For quality traits, highest values for genotypic and phenotypic coefficients of variation were observed for alkali spread value and L/B ratio. High heritability coupled with genetic advance as percent of mean was observed for days to 50% flowering, effective tillers per plant, test weight, number of grains per panicle, grain yield per plant, L/B ratio and alkali spreading value.

Behera *et al.* (2018) conducted experiment to study genetic variability in forty-nine elite slender grain rice genotypes for yield and yield component characters and concluded that both PCV and GCV were high for grain yield and fertile grains per panicle. High heritability estimates were associated with moderate to high genetic gain over mean for days to 50% flowering, plant height, panicle length, fertile grains/panicle and fertility percentage.

Hari *et al.* (2018) evaluated 36 rice genotypes to study the genetic variability among yield component traits and physical quality traits. Studies revealed that high PCV coupled with GCV was recorded for alkali spreading value whereas high heritability coupled with high genetic advance as per cent of mean was observed for total number of tillers per plant, number of grains per panicle, water uptake, alkali spreading value, amylose content and grain yield per plant.

Mamata *et al.* (2018) evaluated two F<sub>2</sub> populations of rice *viz.*, 'Rajamudi × BR-2655' and 'Rathnachoodi × BR-2655' to estimate the variability, heritability, genetic advance and genetic advance as percent of mean. High PCV and GCV values were observed for grain yield per plant and low PCV and GCV was observed for thousand grain weight and panicle length. Plant height, spikelet fertility and grain yield per plant had high heritability along with high genetic advance as per cent of mean. Both the crosses registered high broad sense heritability coupled with high genetic advance.

## **2.2. CORRELATION OF GRAIN YIELD WITH YIELD COMPONENTS AND QUALITY TRAITS**

Correlation coefficient is a measure of the degree of closeness and linear relationship between two variables. The study of correlations between different characters may help the plant breeder to know how improvement in one character will bring simultaneous changes in other characters. The yield of a plant is polygenic and highly influenced by the environment. Hence, direct selection for yield may not be effective. But most of the component characters are simply inherited and less subjected to environmental variations. Therefore, for indirect selection through selecting these component characters, it is essential to have the knowledge of genetic correlations among the factors contributing to the yield that leads to most effective method of selection by use of favorable contributions of characters and to minimize the retarding effect of antagonistic correlations (Singh and Bains, 1967).

Devi *et al.* (2010) conducted correlation studies on 110 rice genotypes for sixteen grain quality characters and grain yield. Studies revealed that single plant yield had highly significant and positive genotypic association with hulling percent, milling per cent, head rice recovery, L/B ratio, elongation ratio after cooking and volume expansion ratio.

Kumar *et al.* (2010) evaluated thirty crosses in rice to study the association among the grain quality components. Grain yield had a significant positive association with kernel breadth after cooking at phenotypic, genotypic and environmental level. Head rice recovery had a significant positive association with kernel breadth after cooking at phenotypic, genotypic and environment level and significant positive correlation with water uptake at genotypic level. Kernel length after cooking had a significant negative association with kernel breadth after cooking at genotypic level.

Nandan *et al.* (2010) conducted character association studies to evaluate thirty three genotypes for identifying their efficiency with respect to 20 yield and quality traits. Grain yield per plant was found to be positive and significantly correlated with days to 50% flowering, grains per panicle, spikelets per panicle, spikelet fertility percentage, kernel elongation ratio and plant height. Significantly negative association was observed for panicle length, 1000 grain weight, L/B ratio with the yield.

Aktar *et al.* (2011) conducted association studies among yield and yield contributing traits in ten rice genotypes. They reported that number of grains /panicle and 1000-grain weight showed significant positive association with yield while plant height showed the negative association with yield both at phenotypic and genetic levels.

Prasad *et al.* (2011) assessed 52 genotypes of rice to study the character association for yield and its component characters. They reported that plant height (cm) exhibited a positive and non significant association with number of tillers per plant and days to 50% flowering. Days to maturity exhibited positive and significant correlation with plant height and days to 50% flowering.

Nagesh *et al.* (2012) evaluated 48 rice hybrids to study the phenotypic and genotypic association among grain iron, zinc, yield attributes and grain yield. They observed that grain yield was positively correlated with number of productive tiller per

plant, test weight and number of grains per panicle. Positive correlation between iron and zinc content was observed while there is no correlation between grain iron and zinc content with grain yield.

Bekele *et al.* (2013) evaluated sixty four rice genotypes to study the association for grain zinc concentrations and yield related traits. The study concluded that grain zinc concentration showed significant positive correlation with 100 grain weight. Number of tillers per plant had significant positive correlation with number of productive tillers per plant. Plant height exhibited a significant positive correlation with grain yield per plant.

Nivedhitha *et al.* (2013) evaluated M<sub>3</sub> generation of rice to study the association among yield components and quality traits with grain yield. Studies revealed that selection for higher number number of productive tillers, number of fertile grains per panicle, spikelet fertility, test weight and kernel length would improve the yield.

Sanghera *et al.* (2013) evaluated 14 red rice ecotypes from temperate region to assess the character association among grain yield and component traits. Studies revealed that grain yield was positively and significantly associated with panicle length, number of grains per panicle, number of tillers per plant both at genotypic and phenotypic levels.

Shabir *et al.* (2013) evaluated 79 rice genotypes to assess character association among yield and yield component traits and reported that highly positive significant association for grain yield with all other parameters such as plant height, number of tillers per plant, panicle length, 1000 grain weight, number of grains per panicle and fertility %.

Veni *et al.* (2013) conducted genetic correlation studies on seventy rice (*Oryza sativa* L.) genotypes for yield, yield components and quality parameters. They reported that days to 50 per cent flowering, productive tillers per plant, panicle length, head rice recovery and volume expansion ratio manifested significant positive association with grain yield.

Lakshmi *et al.* (2014) evaluated seventy genotypes of rice (*Oryza sativa* L.) to study the nature and extent of correlation among yield and yield attributing characters. The results revealed that grain yield per plant is positively and significantly associated with number of productive tillers per plant, plant height and kernel length.

Naseem *et al.* (2014) conducted correlation studies on twenty genotypes of rice (*Oryza sativa* L.) for yield and yield related traits and concluded that number of productive tillers per plant, number of spikelets per panicle, number of grains per panicle and 1000 grain weight had a highly positive and significant genotypic and phenotypic correlation with grain yield per plant.

Rahman *et al.* (2014) evaluated seven advanced fine grain rice lines *viz.*, S-1, S-2, S-5, AL-33(II), AL-36, AL42(II) and AL-44(I) to study the association among yield and yield contributing characters. Studies revealed that number of effective tillers/hill number of filled spikelets/panicle and weight of 1000-grains showed the positive association with grain yield/plant. Panicle length, number of unfilled spikelets/panicle showed significant and negative association with grain yield/plant.

Bhati *et al.* (2015) conducted correlation studies on 30 elite rice (*Oryza sativa* L.) genotypes for grain yield and quantitative traits and reported that grain yield per hill was positively and significantly correlated with harvest index, biological yield per hill, test weight and plant height at both genotypic and phenotypic level.

Bhuvanewari *et al.* (2015) evaluated F<sub>2</sub> segregating populations of two black rice crosses *viz.*, cross I ( Chakhao amubi × RCM 23 ) and cross II (RCM 14×RCM 23) to study the association among yield and yield components. They observed that in both crosses, number of productive tillers per plant, filled spikelets, fertility% and 1000 grains weight showed significant positive correlation with grain yield. Grain yield showed significant positive correlation with panicle length in cross I, positive non significant correlation in Cross II.

Devi *et al.* (2015) conducted correlation studies on ninety two rice (*Oryza sativa* L.) genotypes for 14 physicochemical and cooking quality traits. Hulling percent showed significant and positive correlation with milling percent, head rice recovery and kernel length after cooking with kernel elongation ratio and L/B ratio. Alkali spreading value showed positive and significant correlation with water uptake and kernel length.

Ekka *et al.* (2015) evaluated 96 rice germplasm accessions to study the association among yield attributing and quality traits and observed that positive and significant association of head rice recovery percentage was observed with days to 50% flowering, number of filled grains per panicle, spikelet sterility percentage and milling percentage at both genotypic and phenotypic levels. Head rice recovery percentage was also negatively associated at both phenotypic and genotypic level with number of effective tillers per plant, 100 seed weight, paddy breadth and kernel breadth.

Patil *et al.* (2015) screened sixty one rice genotypes to study the association among grain yield and its component traits. Studies revealed that highest positive correlation was observed for grain yield per plant with 100 grain weight, number of productive tillers per plant and number of grains per panicle. There was a significant positive correlation between grain Fe and Zn content. Fe content had significant positive correlation with grain yield while Zn content had negative and non-significant correlation with grain yield.

Precilla *et al.* (2015) assessed the association between grain quality parameters in 24 rice genotypes and observed that highly positive and significant correlation was found between kernel length after cooking and linear elongation ratio. Kernel breadth after cooking showed high and significant correlation with breadth elongation ratio.

Xu *et al.* (2015) conducted study to analyze the relationship between grain yield, yield components, and grain quality of 300 rice germplasms. Studies revealed that grain yield had a significant positive correlation with the brown rice and head rice whereas number of panicles, number of grains per panicle and 1000 grain weight had a significant negative correlation with the brown rice and head rice ratios.

Abdala *et al.* (2016) conducted correlation studies on eleven F<sub>1</sub> generation lines derived from crosses between aromatic and non-aromatic parental landraces. They observed that, there was a strong and highly significant positive correlation between brown rice width and paddy grain width. There was a highly significant positive correlation between the brown rice length and brown rice shape. The aroma sense correlated negatively with grain width.

Chowdhury *et al.* (2016a) evaluated 65 rice genotypes to study the association among cooking quality parameters and yield. Studies revealed that significant positive correlation was observed between amylose content with respect to elongation ratio and

alkali spreading value and also between elongation ratio and gel consistency. Amylose content showed significant negative correlation with gel consistency. Yield/plant had non-significant association with all the quality parameters (amylose content, elongation ratio, alkali spreading value and gel consistency).

Chowdhury *et al.* (2016b) evaluated 65 diverse rice germplasm to study the association among yield contributing characters, iron, zinc, protein and yield. Studies revealed that significantly positive correlation between grain zinc content and iron content was observed. But, zinc and iron content did not affect protein content. Grain yield manifested a positive and significant correlation with different yield attributing traits *i.e.* with 1000 grain weight, filled grains per panicle, panicle length and number of panicle per plant. Negative non-significant correlation was observed between grain yield and grain iron and zinc content.

Ernawati *et al.* (2016) assessed brown rice local varieties to study the association among the characters and observed that there was a significant correlation among the grain yield and total number of productive tillers per hill, panicle length, total number of grains per panicle, weight of 100 grains and grain weight per panicle in brown rice.

Pavan *et al.* (2016) evaluated 22 rice genotypes to study association among yield components and quality traits with yield. Studies revealed that plant height, panicle length, filled grains per panicle, test weight and kernel length showed significant positive correlation with grain yield. Amylose content showed negative and non significant association with grain yield.

Ratna *et al.* (2016) studied the correlation for twelve grain characters (before cooking) and eight characters (after cooking) on distinct six lines *viz.*, S1, S2, S5, 42(i), 42(ii) and 44(i) of Basmati rice. The results of correlation study revealed that hulling percent had highly significant positive relationship with milling per cent, HRR per cent and kernel breadth of milled rice. Kernel breadth of cooked rice showed a significant positive relationship with alkali spreading value at genotypic level. Water uptake exhibited a significant negative relationship with alkali spreading value but an insignificant negative relationship with volume expansion per cent and elongation ratio.

Sameera *et al.* (2016) conducted character association studies on 25 rice genotypes with regard to yield and yield components and observed that yield was positively associated with number of tillers per plant, productive tillers per plant, number of grains per panicle and number of filled grains per panicle.

Jan *et al.* (2017) studied association among agro-morphological traits and grain yield among 35 rice (*Oryza sativa* L.) genotypes and observed that at both genotypic and phenotypic levels, the harvest index showed significantly positive correlation with grain yield per hill followed by plant height. Days to 50% flowering showed significant negative correlation with grain yield per hill.

Lakshmi *et al.* (2017) evaluated fifty five F<sub>7</sub> generation aromatic rice genotypes to study the character association among yield and yield contributing traits. Correlation studies revealed that grain yield per plant had significant positive association with panicle length, number of filled grains per panicle, 1000-grain weight, kernel length and L/B ratio both at phenotypic and genotypic level. Days to 50% flowering was recorded significant negative correlation with grain yield per plant at both genotypic and phenotypic levels.

Priya *et al.* (2017) conducted character association studies among yield and quality traits to evaluate 40 genotypes of rice and observed that traits like productive tillers per plant, grains per panicle, test weight, panicle length, days to maturity, kernel breadth, plant height, days to 50% flowering and kernel length were found to possess significant positive association with grain yield per plant at phenotypic level.

Sowmiya and Venkatesan (2017) carried out experiment with 48 rice genotypes to explore correlation for yield and yield contributing characters. The genotypic correlation coefficients showed higher magnitude than phenotypic correlation coefficients. The genetic correlation revealed that grain yield per plant had strong negative and significant association with days to first flowering at both genotypic and phenotypic levels. Number of tillers per plant exhibited significant positive correlation with number of panicles per plant at both genotypic and phenotypic levels.

### **2.3. PATH ANALYSIS STUDIES**

Path analysis is an important tool to partition the correlation coefficients into direct and indirect effects of independent variable and dependent variable. Though, correlation gives information about the components of complex character like yield, it

will not provide an exact picture of relative importance of direct and indirect contributions of the component characters on yield. Thus, correlation studies coupled with path analysis would give a better insight into cause and effect relationship between different pairs of characters.

The available literature on path analysis studies in rice were presented in below.

Kumar *et al.* (2010) evaluated thirty crosses of rice to study path analysis among the grain quality components. Brown rice length manifested a highest positive direct effect on head rice recovery followed by milling percentage. Kernel length showed highest negative direct effect on head rice recovery, while hulling percentage showed a positive indirect effect on head rice recovery through milling percentage.

Nandan *et al.* (2010) conducted Path coefficient analysis studies to evaluate thirty three genotypes for identifying their efficiency with respect to 20 yield and quality traits. Days to 50% flowering, grains per panicle and plant height had positive direct effects on grain yield while effective tillers, 1000 grain weight had negative direct effect on grain yield.

Pankaj *et al.* (2010) evaluated forty eight rice genotypes and path coefficient analysis of these lines revealed highest positive direct effect of grain length on grain yield, followed by effective tillers/plant at maturity, plant height at maturity, and days to maturity at genotypic level was observed whereas length/breadth ratio had a negative direct effect.

Yadav *et al.* (2010) conducted path coefficient analysis studies on 40 rice genotypes for yield and it's component traits. Path coefficient at genotypic level revealed that number of tillers per hill, panicle length, number of spikelet per panicle, plant height and test weight had direct positive effect on seed yield per hill and days to 50% flowering, number of panicles per plant manifested direct negative effect.

Aktar *et al.* (2011) evaluated 10 rice genotypes for direct and indirect effects of yield component traits on grain yield. Path coefficient analysis studies revealed that 1000 grain weight has highest positive direct effect followed by days to maturity. Number of grains panicle<sup>-1</sup> showed negative direct effect but positive indirect effects through number of tillers plant<sup>-1</sup>, plant height and 1000 grain weight. Number of tillers plant<sup>-1</sup> had high indirect effect through plant height and negative indirect effect *via* with 1000grain weight.

Hasan *et al.* (2011) carried out path analysis studies in twenty four rice genotypes and reported that fertility % possessed the highest positive effect on grain yield followed by thousand grain weight and number of effective tillers per hills. Days to 50% flowering and days to maturity had negative significant effect with yield.

Prasad *et al.* (2011) assessed 52 genotypes of rice to study the direct and indirect effects of yield component traits on yield. Studies revealed that seedling growth (cm) exerted the highest direct positive effect on grain yield followed by panicle length, days to 50% flowering. Panicle exertion showed the highest negative direct effect on grain yield followed by number of tillers per plant and days to maturity.

Nagesh *et al.* (2012) evaluated 48 rice hybrids to study the direct and indirect effects of component traits on grain yield. Studies revealed that grain length had highest positive direct effect on grain yield followed by number of productive tillers per plant, number of grains per panicle and test-weight. No direct effect of grain iron and zinc content were observed on grain yield.

Rangare *et al.* (2012) carried out an investigation to study direct and indirect effects of various traits on grain yield and results revealed that number of fertile tiller per plant, days to 50% flowering, test weight and panicle length all had important role in the improvement of grain yield in rice at genotypic and phenotypic levels.

Seyoum *et al.* (2012) analyzed fourteen rice genotypes to understand direct and indirect contributions of characters under study towards grain yield. Results revealed that days to 50% flowering, plant height and panicle length exhibited high positive direct effect with grain yield while direct effects of panicles per plant and 1000 grain weight were negative indicating that direction selection can be practiced for these characters.

Sravan *et al.* (2012) conducted path analysis studies on thirty six diverse genotypes and reported that biological yield had the maximum direct effect on grain yield, followed by panicles per plant. The direct contribution of test weight and panicle length was positive but of low magnitude. The direct contribution of biological yield to grain yield was supported by indirect effects of panicles per plant, test weight, and panicle length.

Aditya and Bhartiya (2013) carried out path analysis studies in eighteen rice genotypes and found that L/B ratio had the highest positive direct effect on grain yield followed by kernel width, grains per panicle and tillers per plant. Highest positive but indirect effect was observed for kernel length *via* L/B ratio followed by thousand grain weight *via* L/B ratio. Plant height, days to 50 per cent flowering, days to maturity, tillers per plant, flag leaf length, panicles per plant, thousand grains weigh and kernel length grains per panicle were observed to contribute positively to an appreciable extent *via* L/B ratio.

Bekele *et al.* (2013) evaluated sixty four rice genotypes to study the direct and indirect effects of different traits on grain yield and reported that number of productive tillers per plant, plant height and grain breadth showed high positive direct effect on grain yield per plant. Days to 50 % flowering, grain zinc concentration had negative direct effect on grain yield per plant.

Nivedhitha *et al.* (2013) evaluated M<sub>3</sub> generation of rice to study the direct and indirect effects of yield components and quality traits with grain yield. Studies revealed that kernel breadth had highest positive direct effect followed by L/B ratio and plant height.

Sanghera *et al.* (2013) evaluated 14 red rice ecotypes from temperate region to assess the direct and indirect effect of component traits on yield. Path analysis revealed that days to 50% flowering and panicle density exhibited high positive direct effect and significant positive association with grain yield followed by days to maturity and plant height at genotypic level.

Veni *et al.* (2013) conducted path coefficient Analysis studies on seventy rice (*Oryza sativa* L.) genotypes for yield, yield components and quality parameters and observed that productive tillers exhibited the maximum direct effect on grain yield/plant followed by kernel breadth, L/B ratio, kernel length after cooking and panicle length. Test weight and kernel length exhibited negative direct effect on grain yield per plant.

Naseem *et al.* (2014) conducted path coefficient analysis studies on twenty genotypes of rice (*Oryza sativa* L.) for yield and yield related traits and concluded that number of productive tillers per plant, number of spikelets per panicle, number of grains per panicle and had positive direct effect on grain yield per plant.

Rahman *et al.* (2014) evaluated seven advanced fine grain rice lines *viz.*, S-1, S-2, S-5, AL-33(II), AL-36, AL42(II) and AL-44(I) to study the direct and indirect effects of yield contributing characters on yield. Studies revealed that plant height, number of effective tillers/hill, panicle length, 1000 grain weight exhibited positive direct effect on grain yield/plant. Number of ineffective tillers/hill and number of unfilled spikelets/panicle showed the negative direct effect on grain yield/plant.

Bhati *et al.* (2015) conducted path coefficient analysis studies on 30 elite rice (*Oryza sativa* L.) genotypes for grain yield and quantitative traits and reported that number of spikelets per panicle, number of tillers per hill and plant height had high positive direct effect on grain yield at both genotypic and phenotypic level.

Bhuvanewari *et al.* (2015) evaluated F<sub>2</sub> segregating populations of two black rice crosses *viz.*, cross I ( Chakhao amubi × RCM 23 ) and cross II (RCM 14 × RCM 23) to assess the direct and indirect effects of yield component traits on yield. In their study, they concluded that productive tillers per plant and filled grains had high positive direct effect on grain yield per plant. In cross I, 1000 grain weight showed high direct positive effect on grain yield. The indirect effect of spikelet fertility and 1000 grain weight *via* filled spikelets per panicle and productive tillers resulted in significant positive correlation with grain yield in both F<sub>2</sub> populations.

Ekka *et al.* (2015) evaluated 96 rice germplasm accessions to study the direct and indirect effects of yield attributing traits and quality traits on yield and reported that days to 50% flowering, panicle length, 100 seed weight, paddy length, milling percentage and brown rice breadth had positive direct effect on grain yield.

Patil *et al.* (2015) screened sixty one rice genotypes to study the direct and indirect effects of yield component traits on grain yield. They observed that number of productive tillers/plant, 100 grain weight, plant height, days to 50% flowering showed moderate to low direct effects on grain yield per plant. They did not observe any direct and indirect effect of grain Fe and Zn content on grain yield per plant.

Abdala *et al.* (2016) conducted path coefficient analysis studies on eleven F<sub>1</sub> generation derived crosses between aromatic and non-aromatic parental landraces. They observed positive direct effect of paddy grain length on brown rice grain length. The indirect effect of paddy grain length was detected for grain width, head rice recovery, milling recovery and gelatinization temperature. The direct effect of brown rice width on brown rice length was very high and positive.

Chowdhury *et al.* (2016b) evaluated 65 diverse rice germplasm to study the direct and indirect effects of yield contributing characters, iron, zinc, protein on yield. They reported that 1000 grain weight, number of filled grains per panicle, panicles per plant and panicle length had positive direct effect on grain yield. Grain iron content and grain zinc content showed negative to low indirect effects on grain yield *via* other characters.

Pavan *et al.* (2016) evaluated 22 rice genotypes to study the direct and indirect effects of yield components and quality traits on yield and reported that kernel breadth followed by plant height. L/B ratio, ear bearing tillers per plant and test weight exhibited maximum positive direct effect on grain yield. Filled grains per panicle, kernel length showed negative direct effect.

Sameera *et al.* (2016) evaluated 25 rice genotypes with regard for yield and yield components to assess the direct and indirect effects among themselves. Number of tillers per plant, productive tillers per plant and number of filled grains per panicle were noticed to exert high direct effects on grain yield per plant. Highest indirect effect on yield was exhibited by productive tillers per plant.

Jan *et al.* (2017) studied the direct and indirect effects of agro-morphological traits on yield among 35 rice (*Oryza sativa* L.) genotypes. Studies revealed that at genotypic level flag leaf length showed high direct positive effect with grain yield per hill followed by flag leaf width. days to maturity showed highest negative direct effect on grain yield per hill. At both genotypic and phenotypic levels, highest indirect effect on grain yield was observed by harvest index.

Lakshmi *et al.* (2017) evaluated fifty five F<sub>7</sub> generation aromatic rice genotypes to study the direct and indirect effects of yield contributing characters on yield and observed that kernel length manifested the highest direct effect on grain yield followed by number of filled grains per panicle, days to 50% flowering, kernel width and L/B ratio had negative direct effect on grain yield per plant.

Priya *et al.* (2017) conducted path coefficient studies among yield and quality traits to evaluate 40 genotypes of rice for yield and quality traits and concluded that kernel breadth, L/B ratio, productive tillers per plant, grains per panicle, test weight, days to 50% flowering, had significant positive direct effect on grain yield.

Shivani *et al.* (2018) conducted study to determine the degree of association between yield, yield attributing traits, grain Zinc and Iron concentration in 100 RIL population of Swarna x Type 3. Correlation studies revealed that grain yield per plant showed strong positive significant association with plant height and 1000seed weight. Positive non- significant association of grain yield per plant was observed with days to 50 per cent flowering, panicle length, number of filled grains per panicle and significant negative correlation was observed for grain iron and zinc concentration.

## **2.4. VARIABILITY AND CORRELATION STUDIES FOR QUALITY PARAMETERS**

### **2.4.1. Physicochemical quality traits, protein and micronutrients**

Diako *et al.* (2011) evaluated four commercial Ghanaian rice varieties for physicochemical characters and reported that imported rice types had highest length/width (L/W) ratios and Ex-Baika, Jasmine 85 and Marshall had good thousand grain weight than imported rice types. Marshall exhibited the highest protein (5.93%) and iron content (8.0 mg/kg). All varieties under study showed the highest gelatinization temperature and alkali spreading values.

Anuradha *et al.* (2012) analyzed brown rice of 126 accessions of rice genotypes for Fe and Zn concentration. They observed that both Fe and Zn were high in wild rice genotypes and least in japonica types. Among wild accessions SL-32 (*Oryza nivara*) was found to possess high iron and zinc content. Zn concentration was significantly correlated with the grain elongation.

Jain *et al.* (2012) conducted experiment in order to find out the most suitable method of cooking rice for diabetic patients. They reported that in steam cooked method, traditional method, microwave method and raw method amylose content was 17.35,19.67, 22.98 and 25.99 mg/ml) respectively. If amylose content is high, then glycemic index may be low and the rice grains will show high volume expansion and a high degree of flakiness. If amylose content was low, glycemic Index may be high and the rice grains will cook moist and sticky. (amylose content was inversely proportional to glycemic index) and they concluded that raw method of cooking rice is the most suitable for diabetic patients as the Glycemic Index will be lowest.

Mia *et al.* (2012) evaluated two land races (Ukunmadhu and Kataribough), one hybrid variety (BRRI dhan32 ) and one mutant variety (Binasail) of aromatic fine rice to assess the morpho-physiological and biochemical attributes in relation to yield. They reported that Ukonmodhu recorded the highest plant height and lowest L/B ratio while Kataribhog exhibited the maximum number of total tillers/hill and highest L/B ratio. BRRI dhan 32 showed the highest 1000 grain weight, grain yield and shortest panicle length and plant height. Highest protein content was recorded in Binasail (10.53%).

Oko *et al.* (2012) assessed the cooking quality and physico-chemical characteristics of 15 selected indigenous and five newly introduced hybrid rice varieties. Studies revealed that water uptake was significantly correlated with grain elongation during cooking, solids in cooking water, optimum cooking time, gelatinization temperature, amylose content and gel consistency. The negative correlation was observed between grain elongation during cooking and amylose content indicating that cultivars that elongate more during cooking would likely have a decreased content of amylose.

Subudhi *et al.* (2012) evaluated forty one rice varieties for grain yield, physicochemical and cooking characters. The results revealed that water uptake was highest in Tara and lowest in Tapaswini. Nuadhusara exhibited highest elongation ratio and lowest kernel length while volume expansion ratio is highest in Nua kalajeera and lowest in Udaya. Hybrids Ajay and Rajlaxmi possess high yield, kernel length and kernel length after cooking. Geetanjali possess high kernel length, kernel length after cooking and low kernel breadth. The varieties *viz.*, Ajay, Rajlaxmi, Varshadhan and Geetanjali are having good quality characters and yield better than check.

Tamanna *et al.* (2013) evaluated 8 BRRI (Bangladesh Rice Research Institute) varieties and two local varieties (Pajam and Chinigura) to study the effect of morphology of rice kernels on zinc and iron content. Studies revealed that the range of iron content in the parboiled group was 0.017 to 0.044 mg/g and in the unparboiled group it was 0.020 to 0.044 mg/g. Zinc content was found to be in the range of 0.022 to 0.070 mg/g for parboiled and 0.015 to 0.074 mg/g for unparboiled group. Shape of the kernels has a significant effect on the levels of zinc. Zn contents of short, medium and long-grain rice was 0.073, 0.037, and 0.027mg/g respectively.

Zhukova *et al.* (2013) evaluated six rice varieties for some biochemical parameters and reported that there was an inverse relationship between the amount of protein and amylose. Dalnevostochnii showed the highest protein content (10%) and lowest amylose content. Priozerni 61 had lowest protein content (7.5%) and highest amylose content. Khankayski 52 showed the highest starch content.

Laenoia *et al.* (2015) conducted study to compare the Zn and Fe contents in brown and white samples of six common Thai rice varieties and concluded that all Thai brown rice varieties had Fe (< 13 mg Fe/kg), and Zn (< 30 mg Zn/kg), while IR68144 was high in both Fe (16 mg Fe/kg) and Zn (40 mg Zn/kg). Concentration of Fe and Zn in white rice were lower than in brown rice.

Madhuri *et al.* (2015) studied the physico chemical characteristics of 15 milled and parboiled rice varieties. And reported that mean kernel length, breadth and L/B ratio of parboiled rice was greater as compared to milled rice. Highest thousand kernel weight was observed in Dodiga. Rice variety Dodiga (84.04%) had higher starch content, while Avinash variety recorded highest amylose content, lowest starch content and amylopectin lowest amylose and highest amylopectin was shown by Prasanna rice variety. L/B ratio of rice varieties did not show any significant correlation with starch and amylose content of rice varieties.

Mani *et al.* (2015) evaluated seeds of 100 traditional rice varieties for nutritional traits (protein, starch, amylose and amylopectin). GC/JH/2007/187 and GC/OR/2007/168 were identified with very high values for protein and amylose contents and high 100-seed weight while GC/JH/2007/228 showed the highest starch content. Amylose content was positively correlated with starch and negatively correlated with amylopectin.

Verma *et al.* (2015) conducted experiment to study the grain quality characteristics of Azad Basmati and to compared with other prominent basmati rice varieties. They reported that Azad Basmati exhibited high hulling, milling and the highest head rice recovery. Kernel dimensions of Azad Basmati were satisfactory in respect of breadth and length/breadth (L/B) ratio but kernel length was shorter than the desired minimum kernel length for Basmati rice. On cooking Azad Basmati exhibited highest kernel elongation ratio and volume expansion ratio. Amylose content of Azad Basmati variety was found higher than Basmati-370, Pusa Basmati-1 and Basumathi but shown low value when compare with Type-3 and Improved Pusa Basmati-1 varieties.

Panomjan *et al.* (2016) evaluated the concentration of Zn in rice caryopsis (intact with pericarp and embryo) and husk (palea and lemma) among 48 rice varieties. They reported that rice varieties Chaw Gam Preud, Leuang Hawm, Mai Yah, and Nahn Hak had the highest caryopsis Zn concentrations (> 29 mg Zn/kg). Zn concentration in the caryopsis and in the husk for the 48 rice varieties correlated significantly.

Pathak *et al.* (2016) assessed physicochemical properties of 22 pigmented glutinous rice varieties along with one non pigmented variety (Memon Bora) and reported that amylose content was lowest in Kmj Bora-61 (0.05 %) and highest in Kola Bora-5 (3.0 %), as compared to 0.4 % of non-pigmented-Memon Bora while alkali spreading value among the genotypes ranged from 4 to 7, against 7 of non-pigmented-Memon Bora. Highest protein content was recorded in Narul Bora (10.17 %) and lowest in Til Bora-2 (8.32 %) against 9.7% of non-pigmented Memon Bora. Highest Zn content (4.42 mg/100 g) was found in Kmj Bora-50 and lowest in Pakhori Bora (3.14 mg/100 g) where as non-pigmented-Memon Bora contained 3.902 mg/100 g. The highest Fe content was recorded in Kmj Bora-21 (4.21 mg/ 100 g) and lowest in Narul Bora (3.12 mg/100 g) as against 2.70 mg/100 g of non-pigmented Memon Bora.

Ritika *et al.* (2016) evaluated some Indian rice varieties of Basmati (Pusa Basmati-1, Pusa Basmati-1401, Pusa-2511, and Pusa Basmati-1509) and non-basmati (HKR-47, HKR-127) for physicochemical, cooking, pasting and textural properties. Studies revealed that L/B ratio of basmati grains was significantly higher than non-basmati grains. Among the studied varieties, HKR-47 and HKR-127 rice cultivars showed good physical characteristics (maximum hulling, head rice recovery, L/B ratio). The chemical properties (amylose content, alkali spreading value, gel consistency, gelatinization temperature) were excellent in basmati cultivars.

Lum *et al.* (2017) evaluated five rice varieties (white, red, black, brown and aroma rice) for physicochemical characteristics. Study revealed that L/B ratio was highest for red rice while black rice showed the lowest L/B ratio, 1000 grain weight, cooking time, highest water uptake ratio, elongation ratio and gruel solid loss. White rice showed the highest thousand grain weight and amylose content. Aromatic rice showed the highest starch content and lowest amylose content. Brown rice showed the lowest water uptake ratio and cooking time than other milled rice or polished rice. Cooking parameters of rice correlated well with each other and the elongation and water uptake ratios correlated positively with the L/B ratio. Cooking time of the rice varieties showed a strong negative correlation with water uptake ratio and elongation ratio.

Pathak *et al.* (2017) assessed fourteen pigmented hill rice cultivars along with a non-pigmented one to determine the zinc, iron content and protein content. Highest protein content was recorded in 'Sakbothang' (11.42%) and lowest in 'Bijor' (9.27 %) against non colored rice variety 'Vandana' (10.84 %). Highest Zn content was found in 'Pakai'(4.28 mg/100g) and lowest in 'Bairing' (3.42 mg/100g) whereas 'Vandana' contained 2.58 mg/100g. Highest Fe content was recorded in 'IRAT 141' (4.18 mg/100g) and the lowest in 'Miren'(3.21 mg/100 g) as against 'Vandana' (2.67 mg/100g).

Siyee *et al.* (2018) assessed the grain quality characteristics of 60 upland rice seed samples (white, brown, red and purple) and the results revealed that highest protein content was found in the varieties of Chao Khoon (11.1%). Niaw Peak-peing exhibited highest Fe concentration (45.4 mg/kg), highest Zn concentration (24.1 mg/kg) was found in Leuang Yai and Kam Med-dam showed the highest antioxidant concentration (4.35 mg/g).

#### **2.4.2 Total phenolic compounds, flavonoid content and antioxidant activity**

Finocchiaro *et al.* (2010) evaluated the total antioxidant capacity (TAC) and poly phenols of Italian rice varieties which included three white, two black and five red varieties. The results revealed that colored rice genotypes had four times higher TAC than white ones. Black grained variety Artemide showed highest TAC (2 times higher than other pigmented one) and polyphenol content (2-3 times higher than other pigmented varieties).

Kim *et al.* (2010) evaluate different pigmented and non pigmented rice varieties (5 black rice, 2 red rice and one white rice) to assess the flavonoid content and reported that BR-2 (black rice) had more flavonoid content than red rice and white rice.

In a study conducted by Muntana and Prasong (2010) the total phenol content and antioxidant activity of thai white, red and black rice bran extracts were estimated and the results revealed that total phenol content of white, red and black rice brans were 0.8931-0.9884, 1.0103-1.0494, and 1.0810-1.2239 mg GAE mg<sup>-1</sup> respectively and antioxidant activity was highest for red rice followed by black rice bran and lowest for white rice bran. Positive correlation was observed between total phenol content and antioxidant activity in red rice bran extracts.

A study was conducted to determine the total phenolic and flavonoid contents as well as antioxidant activity in the water extracts of brown rice and rice bran from Sangyod, a red pigmented rice and Khao Dawk Mali 105, a commercial white-colored rice. The study concluded that phenolic compounds, flavonoids and antioxidant activity were highest in the water-soluble extract of Sangyod rice bran and the lowest in the water-soluble extract of Khao Dawk Mali 105 rice bran (Panunto *et al.*, 2010).

Sompong *et al.* (2011) analyzed nine red and three black rice varieties to determine the physicochemical and antioxidant properties and reported that the varieties Niaw Dam pleuak Dam (red) and Sung Yod Patthalung (black) showed highest protein content (10.9 and 10.4 respectively), red rice varieties (BG,LP,SR 11, SR12, SR13) had highest amylose content, black rice varieties (Niaw Dam pleuak Dam, Niaw Dam pleuak Khao) had lowest amylose content. Red rice varieties showed the total phenol content of 79.18 to 691.37 mg/100g. While black rice varieties had 336.69 to 665.16 mg/100g. Total equivalent antioxidant capacity of red rice was 2.08-12.29 m mol/100g and black rice was 4.98-12.03 m mol/100g.

Basu *et al.* (2012) conducted a study to evaluate and compare the carbohydrate content, antioxidant parameters in polished and unpolished seeds of three edible rice cultivars *viz.*, Swarna (SW), Gobindobhog (GB) and Pusa Basmati (PB) and they concluded that carbohydrate content was highest in PB seeds (both polished and unpolished), amylose content was highest in SW polished seeds and SW polished seeds were superior as compared to GB and PB cultivars in terms of antioxidant activity. Total phenol content was highest in unpolished seeds of Swarna and flavonoid content was highest in unpolished seeds of Pusa Basmati.

Chakuton *et al.* (2012) analysed the rice seed extracts of twelve colored and non-colored thai rice cultivars to determine the total phenolic content and antioxidant activity. Results showed that TPC of all cultivars with methanolic extract showed highest value (2.02-4.77 mg GAE/100g). Colored cultivar 53 showed the highest TPC (7.40 mg GAE/100g). DPPH scavenging activity of colored rice seed extracts was higher than non-colored rice extract.

Chen *et al.* (2012) assessed different colored rice varieties (black, red and green) and one white color rice variety to determine the total phenol content and antioxidant activity. They reported that red rice cultivars had highest antioxidant

capacity (69.91-130.32  $\mu\text{mol Trolox/g}$ ) than black rice (55.49-64.85  $\mu\text{mol Trolox/g}$ ), green rice (35.32  $\mu\text{mol Trolox/g}$ ) and white rice (21.81  $\mu\text{mol Trolox/g}$ ). Black rice showed highest phenol content (8.5g/100g) than red rice (0.1 g/100 g), green rice (159.95 mg/100 g) and white rice (124.81 mg/100 g).

Irkali *et al.* (2012) evaluated pigmented rice (red and black rice) and non pigmented rice to assess the total phenol content and flavonoid content. Studies revealed that total phenol content and flavonoid content were found to be more in black rice (87.87  $\mu\text{g/g}$  and 59.19  $\mu\text{g/g}$  respectively) than red rice (52.76  $\mu\text{g/g}$  and 24.71  $\mu\text{g/g}$ ) and white rice (30.15  $\mu\text{g/g}$  and 15.95  $\mu\text{g/g}$ ).

Lee *et al.* (2012) conducted a study to evaluate the antioxidant potential, flavonoids and polyphenol content in exotic rice germplasm. The results revealed that rice germplasm had tremendous variations with respect to total polyphenols (0.08–0.71 mg/g) and flavonoid contents (0.091–0.413 mg/g) and antioxidant activity (18–96%). Rice cultivars with red and black seed coat recorded higher total phenols and flavonoid content and antioxidant activity than cultivars with white seed coat color.

The antioxidant activity and total phenols of bran extracts of glutinous and non glutinous black rice cultivars were estimated in a study which revealed that black rice variety 1000-11-2-26 had the highest DPPH scavenging activity and total phenol content. Total phenolic content in bran extracts of the black rice samples ranged from 2.93 to 4.01 mg GAE per g (Pijitha *et al.*, 2013).

Saikia *et al.* (2012) analysed two pigmented (purple and red color) and two non-pigmented aromatic rice varieties for physicochemical properties, total phenols, flavonoids and antioxidant activity. And concluded that non-pigmented one had high amylose content than pigmented one. Red rice variety Chak-Hao-Amubi had highest total phenolic content (579.00 mg GAE  $100^{-1}\text{g}$ ) flavonoid content (220.5 mg QE  $100^{-1}\text{g}$ ) than purple colored and non-pigmented rice varieties. Both purple and red colored varieties had good DPPH radical scavenging activity of 94.19%, and 96.43% respectively.

Gunaratne *et al.* (2013) studied the antioxidant activity and nutritional quality of eight traditional red rice varieties and three light brown colored varieties and concluded that red rice varieties had highest total equivalent antioxidant capacity (8.01-17.88 m

mol/100 g) and highest total phenol content (590-1710 mg/100 g) than light brown varieties. Variety Kalu Heenati (red rice) had highest protein content (10.1%), while brown rice variety BG 300 had lowest protein content (6.15).

Walter *et al.* (2013) conducted a study to determine the concentration of total soluble phenolic compounds (TPSCs) and antioxidant activity (AOAs) of rice grains with light brown, red and black pericarp colors and reported that genotypes with red and black pericarp color had higher values of TPSCs and AOAs than those with a light brown pericarp color. Parboiling and cooking reduced the concentration of TPSCs especially in brown and polished grains.

Moko *et al.* (2014) analyzed two non colored and one colored rice varieties to determine the antioxidant activity and flavanoid content of rice bran. The results revealed that red variety had the highest DPPH scavenging radical activity (88.29 %) and highest total phenolic content. Cigeulis had 261.96 mg/g gallic acid, red variety 258.23 mg/g gallic acid and the lowest was recorded by Superwin variety 239.04 mg/g gallic acid. Antioxidant properties of colored rice bran were better than that of non colored rice bran.

Pengkumsri *et al.* (2015) studied physicochemical and antioxidative properties of three rice varieties (Chiang Mai-Black rice, Mali-Red rice and Suphanburi-1 Brown rice) and observed that rice bran extract of polar solvent of Chiang Mai Black rice contained higher concentration of phenols, flavanoids and antioxidant activity.

Rahman *et al.* (2015) conducted a study to assess the total phenol content, antioxidant activity and flavanoid content of joha rice (an aromatic indigenous rice of Assam) and reported that DPPH scavenging activity was  $81.45 \pm 2.29$   $\mu\text{g/ml}$ , total phenolic content was found  $74.86 \pm 2.474$  mg/gm equivalent of Gallic Acid and total flavanoid content was  $190.7 \pm 15.28$  mg/gm equivalent of Quercetin.

Pathak *et al.* (2016) assessed chemical and antioxidant properties of 22 pigmented glutinous rice varieties along with one non pigmented variety (Memon Bora) and reported that total phenolic content of 22 pigmented glutinous rice cultivars ranged from 53.45 to 80.16 mg GAE (100 g)<sup>-1</sup> against 29.12 mg GAE (100 g)<sup>-1</sup> in Memon Bora while the flavonoid content of 22 pigmented glutinous rice cultivars ranged from 45.57 to 60.76 mg QE (100 g)<sup>-1</sup>. Memon Bora had recorded flavonoid

content of 26.78 mg QE (100 g)<sup>-1</sup>. DPPH radical scavenging activity of 22 pigmented glutinous rice cultivars ranged from 14.54 to 21.73 %, where as no DPPH activity was detected in Memon Bora.

Veni *et al.* (2016) conducted experiment to determine the total phenol content and antioxidant activity in 18 rice genotypes (2 black, 3 red and 13 brown) and reported that black rice had highest amount of total phenols (576.1 mg/100 g) and antioxidant activity (11.14 mgAAE/100 g) than red rice and brown rice.

Pathak *et al.* (2017) assessed fourteen pigmented hill rice cultivars along with a non-pigmented one to determine the total phenol content, antioxidant activity and flavonoid content. Total phenolic content of 14 pigmented hill rice cultivars varied from 67.89–89.43 mg GAE/100 g against 'Vandana'(33.23 mg GAE/100 g) while pigmented rice cultivars exhibited flavanoid content of 57.75-78.74 mg QE/100 g whereas 'Vandana' had 24.58 mg QE/100 g. DPPH scavenging activity of 14 pigmented hill rice cultivars was 19.56-29.29%, whereas no DPPH activity has been detected in non-pigmented rice cultivar 'Vandana'. They reported a positive correlation between phenol content, antioxidant activity and flavanoid content.

Chay *et al.* (2017) conducted a study to determine the total phenolic content and antioxidant activity of waxy pigmented and non-pigmented rice varieties. And reported that the waxy pigmented rice exhibited a significantly higher total polyphenol content of 2074 µg GAE g<sup>-1</sup> compared to that of the waxy non-pigmented rice of 134 µg GAE g<sup>-1</sup> db. The percentage of DPPH inhibition (Antioxidant activity) increased along with the increasing concentration of total phenols. Waxy pigmented rice varieties had highest percentage of inhibition (75.37%) than non pigmented rice varieties (6.72%).

Raghuvanshi *et al.* (2017) conducted a study to evaluate and compare the physical characteristics, nutritional quality, antioxidant properties and glycemic index among red rice and white rice. Studies revealed that red rice had highest thousand kernel weight (18.3 g) than white rice. In all the parameters red rice proved to be superior to white rice, red rice had highest crude protein content (10.49%), total phenolic content (143.38 mg GAE/100g), flavonoid content (120 mg R.E. /100 g), DPPH scavenging activity (25%). Red rice was found to have a lower glycemic index (63.15) than white rice.

Shao *et al.* (2018) assessed 15 rice genotypes (5 non pigmented brown rice, 5 red rice and 5 black pigmented rice) to determine the total phenolic content (Folin ciocalteu method). And reported that colored rice genotypes (red rice: 6.55-51.86 mg/100g and black rice: 4.31-23.72 mg/100 g) had highest total phenolic content than non-colored rice (0.79-3.21 mg/100 g) genotypes.

### **2.4.3 Glycemic Index, Rapidly Digestible Starch, Slowly Digestible Starch & Resistant Starch**

Peisong *et al.* (2004) assessed three types of rice cultivars (*indica*, *japonica* and hybrid rice) to study the variability in starch digestibility. Results indicated that there were significant differences among glycemic responses of three types of rice. Amylose content had impact on estimated glycemic score (EGS) and resistant starch. *Japonica* rice had lower resistant starch content. Starch hydrolysis tends to be more quick and complete for the waxy and low amylose rice than for intermediate and high amylose rice.

Shu *et al.* (2009) evaluated seven rice mutants (RS4, RS9, RS12, RS13, RS14, RS25 and RS30) which differed in Resistant Starch (RS) content to elucidate the factors that play a role in slow digestibility. They reported that RS values ranged from 3.3 to 11.7%, when RS4 with the highest RS content, showed lowest HD (Degree of Hydrolysis) among all of these materials. In all mutants studied, lipids and proteins showed significant correlation to the RS content and also affected the HD greatly. With the decreased RS, the degree of starch hydrolysis increased. For rice varieties with different RS contents, the RS showed significant positive correlation with the degree of starch hydrolysis, whereas for those rice varieties with similar RS contents, the content of lipids and starch-lipid complex was shown to be a key factor for starch hydrolysis.

Deepa *et al.* (2010) studied the in vitro starch digestibility and glycemic indices of three rice varieties Njavara, Jyothi (pigmented rice varieties) and 'IR 64' (non-pigmented rice) with similar amylose content. Pigmented rice varieties showed more resistant starch content than the un-pigmented variety, IR 64. Highest digestible starch was showed by IR 64. Glycemic Index was highest for Njavara (74.8). They concluded that pigmented whole grain rice ('Njavara' and 'Jyothi') is a better source of dietary fibre and resistant starch.

Patindol *et al.* (2010) conducted study to assess the nutritionally important starch fractions (RDS, SDS, and RS) in cooked rice, making use of 16 rice cultivars. In their study they reported that some cultivars were identified as possessing high levels of RS (Bowman and Rondo) or SDS (Dixiebelle and Tesanai-2). Apparent amylose content correlated positively with RS, and negatively with RDS, and insignificantly with SDS. RS and SDS were not collinear it does not follow that a cultivar high in RS will also be high in SDS, and vice versa.

Odenigbo *et al.* (2013) evaluated five improved varieties (FARO 52, FARO 57, FARO 44, FARO 60 and FARO 61) and four local varieties (Kwandala, Yardass, Jeep and Jamila) to determine the levels of nutritionally important starch fractions. They reported that rapidly digestible starch (RDS) was lowest in Jamila (27.70%) and highest in FARO 61 (39.26%). While the local varieties had significant higher RS (2.71%) with a lower RDS (32.82%) compared with improved varieties (RS; 1.88% and RDS; 36.07%). RS was inversely related to RDS and starch digestion index (SDI). The SDI had a highly significant positive correlation with RDS. Slowly digestible starch fraction ranged between 35.04% (Jamila) and 44.03% (FARO 52) suggesting that Jamila and FARO 44 have less rapid digestion and glycemic responses.

Babu *et al.* (2014) conducted experiment for *invivo* GI estimation in ten rice varieties and reported that BPT 5204 was found to be low in GI (51.42), Dhan Rasi as medium GI and remaining varieties as high GI varieties. This study indicated that GI had negative correlation with amylose content and positive correlation with amylopectin.

Jeevitha *et al.* (2014) conducted a study to analyze the amylose content of two types of white rice namely White Rice 5% Broken (WR5%) and Fragrant White Rice (FWR) and determined its relationship with the glycemic index (GI) value. Amylose content of the WR5% (12.5%) was comparable to FWR (11.6). GI value of FWR (124) appeared to be comparable to the WR5% (87). This study observed that white rice categorized as low amylose may have high GI value.

Selvakumar *et al.* (2014a) characterized 50 rice accessions for high resistant starch content and reported that the variety kattanur exhibited high RS content (9.5%) followed by Kallurundaikar (9.3%) while lowest value for RS content was recorded in Jegatsal ( 2.1). and concluded that analysis of RS content in germplasm can help to use the natural variability for development of rice varieties with health benefits.

Selvakumar *et al.* (2014b) conducted biochemical analysis to find out the genetic variability and association of amylose content (AC), protein content (PC) and lipid content (LC) on resistant starch (RS) by using 50 rice accessions. And reported that amylose content and protein content have significant positive correlation on resistant starch content in rice. Hence analysis of biochemical association of quality characters on resistant starch content help in the selection process for development of rice varieties with health benefits.

Pongjanta *et al.* (2016) evaluated twelve pigmented rice varieties of rice grain with varying amylose content (low, medium and high) and different pigmented, three from each of four bran colors (white, brown, red and purple) to determine the correlation among total phenolic compounds and starch digestibility. They reported that red and purple pigmented flours had higher total phenolic compounds (TPC) and more resistant starch than that of white flours. The TPC and resistant starch content of the flours ranged between 7.83- 47.3 mg/L and 2.44–10.50% respectively, and produced 60-80 of estimated glycemic index. Total phenolic compound had significant negative correlation with estimated glycemic index and positive correlation with resistant starch content. Resistant starch content had negative correlations with estimated glycemic index.

Anitha *et al.* (2017) conducted a study to determine the glycemic index of rice varieties Pradhyumna (JGL-17004) and Anjana (JGL-11118). GI was estimated by *in vivo* method by selecting the clinically healthy adult subjects (n = 20) of age 19 - 25 years. cooked rice of these varieties containing 64 g digestible carbohydrate were administered to the participants, and the peak blood glucose response was obtained at different time intervals. Results had shown that GI values for Anjana (JGL-11118) was 52.7 and for Pradhyumna (JGL-17004) rice variety, GI value was 51.3 then these varieties were categorised as low glycemic index rice varieties.

Eight Bangladesh rice varieties were characterized for physico-chemical, biochemical quality parameters. The results revealed that BR 16 had low glycemic index (52.4) with high resistant starch content of 4.68%. it was found that GI has a negative correlation (-0.796<sup>\*</sup>) with apparent amylose content (AAC) and resistant starch had a positive correlation (0.787<sup>\*</sup>) with AAC. Regarding Zn and Fe availability, BRRI dhan 53 and BRRI dhan 62 are suitable for mineral intake Fe and Zn respectively among the tested high yielding varieties (Shozib *et al.*, 2018).

## Chapter – III

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# Materials and Methods

## Chapter III

# MATERIALS AND METHODS

The present investigation entitled “Variability for nutritional and biochemical quality parameters in colored rice genotypes (*Oryza sativa* L.)” was undertaken to study the variability and association among yield and quality parameters, along with direct and indirect effects of quality parameters on yield. And also to identify the rice genotypes with desirable nutritional and biochemical quality characteristics. The materials utilized and the methodologies adopted in the present study are described below.

### 3.1 MATERIAL

The experimental material consists of 26 released and advanced genotypes developed at Agricultural Research Station, Bapatla and varieties received from ARS Pattambi, Kerala (Matta Triveni, Annapurna, Aathira, Harsha, Jyothi and Samyuktha). Among the 26 genotypes seven had brown pericarp color and eight genotypes possess red pericarp color. The remaining eleven genotypes had black pericarp color. BPT 5204, a popular high yielding genotype with excellent cooking quality traits is used as check variety in the present study. The parentage of the genotypes used in the present investigation are given in Table 3.1. Photograph showing some of the genotypes used in the present study are shown in Fig 3.1.

**Table. 3.1 List of genotypes used in the present study**

S.No.	Genotype	Cross combination	Released and advanced cultures
<b>Light brown pericarp colored genotypes</b>			
1.	BPT 5204	GEB 24/TN1/ Mahsuri	} <b>Released varieties</b>
2.	BPT 2270	BPT 5204/CRMR 1523	
3.	BPT 2295	BPT 1768/ NLR 33641	
4.	BPT 2595	Mutant of BPT 2270	} <b>Advanced cultures</b>
5.	BPT 2782	NLR 145/ MTU 2077	
6.	BPT 2660	BPT 1768/ NLR 145	
7.	BPT 2776	BPT 2231/ NLR 145	
<b>Red pericarp colored genotypes</b>			
8.	Matta Triveni	Re-selection from Triveni	} <b>Released varieties</b>
9.	Annapurna	PTB 10/TN 1	
10.	Aathira	BR 51-46-1/C.2332-2-2	
11.	Harsha	M 210/ PTB 28	
12.	Jyothi	PTB 10/ IR 8	
13.	Samyuktha	Pureline selection from culture C3-2	
14.	BPT 3111	Swarna/ IRGC 18195// MTU 1081	} <b>Advanced cultures</b>
15.	BPT 3139	Cult. 01120305/ cult. 0910025-7	
<b>Black pericarp colored genotypes</b>			
16.	BPT 3137	RP Bio 226*1/1RGC 48493	} <b>Advanced cultures</b>
17.	BPT 3145	RP Bio 226/ IRGC26940// MTU 1081	
18.	BPT 3138	RP Bio 226*1/1RGC 18195	
19.	BPT 3136	RP Bio 226*1/1RGC 18195	
20.	BPT 3140	Swarna/1RGC 18195 /MTU 1081	
21.	BPT 3141	RP Bio 226*1/ 1RGC 30938	
22.	BPT 3142	RP Bio 226/ 1RGC 26940// MTU 1081	
23.	BPT 3143	RP Bio 226*1/ RGC 48493	
24.	BPT 2848	RP Bio 226*1/1RGC 48493	
25.	BPT 3144	RP Bio 226*1/1RGC 48493	
26.	BPT 2858	RP Bio 226*1/1RGC 48493	

### **BROWN RICE**



BPT 5204

BPT 2295

BPT 2270

### **RED RICE**



ANNAPURNA

BPT 3111

HARSHA

### **BLACK RICE**



BPT 3131

BPT 3142

BPT 3140

**Fig. 3.1 : Photograph showing some of the genotypes used in the present study**

## 3.2 METHODS

The present investigation on “Variability for nutritional and biochemical quality parameters in colored rice genotypes (*Oryza sativa* L.)” was carried out during *kharif*, 2017 at northern block of Agricultural College Farm, Bapatla, Guntur district of Andhra Pradesh. Bapatla was located at 15° 9' North and 80° 4' East longitude at an altitude of 5.49 m above mean sea level. Analysis pertaining to various nutritional and biochemical quality parameters was carried out at Biochemistry and Food Process Engineering Laboratory, Post Harvest Engineering and Technology (PHET), Agricultural College Campus, Bapatla.

### 3.2.1 Experimental Design

The experiment was conducted with 26 entries in Randomized Block Design (RBD) with three replications. All the genotypes were sown separately in each experimental unit by following direct sowing through manual dibbling method. Each experimental unit consisted of 3 m<sup>2</sup> and the spacing adopted was 20 cm between the rows and 15 cm between the plants. The detailed experimental technique for the present investigation has been furnished in the Table 3.2. Layout of the experimental design was shown in fig. 3.2

**Table 3.2. Experimental details of evaluation of rice (*Oryza sativa* L.) genotypes**

Location	Agricultural college farm, Bapatla
Season	<i>Kharif</i> , 2017
Entries	26
Design	Randomized Block Design (RBD)
Replications	Three
Spacing	20 cm × 15 cm
Plot size	3 m <sup>2</sup>
Row length	3 m
Number of rows	5
Fertilizers	120 kg N : 40 kg P <sub>2</sub> O <sub>5</sub> : 40 kg K <sub>2</sub> O ha <sup>-1</sup>

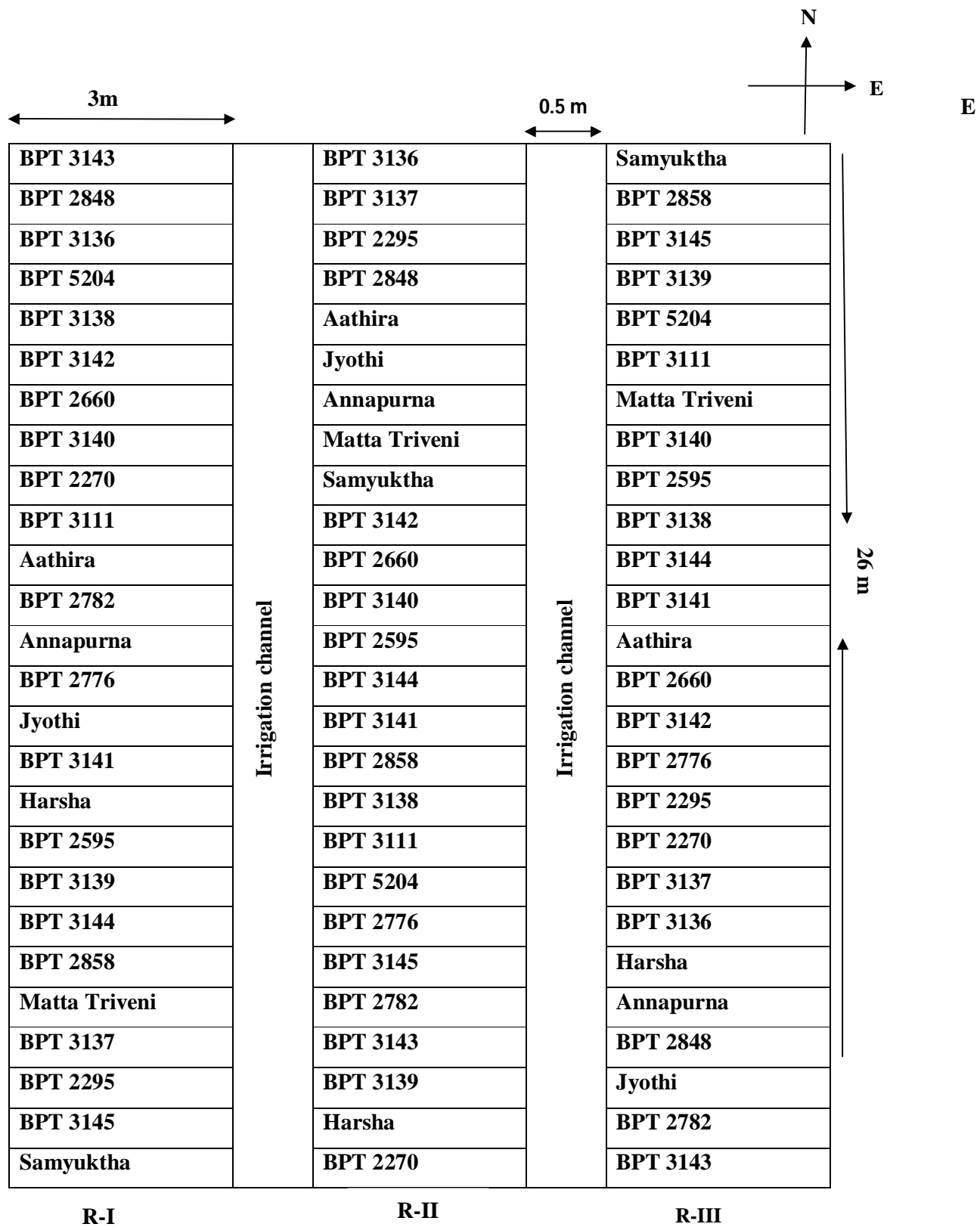


Fig. 3.2 Layout of Experimental design

### **3.2.2 Cultural operations in main field**

All the recommended package of practices were adopted throughout the crop growth period with need based plant protection measures. Fertilizers were applied at the rate of 120 kg N, 40 kg P<sub>2</sub>O<sub>5</sub> and 40 kg K<sub>2</sub>O ha<sup>-1</sup>. One third dose of nitrogen, entire dose of P<sub>2</sub>O<sub>5</sub> and ½ of the K<sub>2</sub>O were applied as basal dose. The remaining nitrogen was applied in two equal split doses one at 35 days after sowing and another at 70 days after sowing. Remaining ½ of the K<sub>2</sub>O was applied along with last dose of N.

### **3.2.3 Recording of observations**

Observations for grain yield and associated characters were recorded on ten randomly selected plants for each entry in each replication. The mean data was estimated for each character per each replication and utilized for final statistical analysis. The method of recording data for each trait is described below:

#### **3.2.3.1 Yield component traits**

##### **3.2.3.1.1 Days to 50% flowering (DFF)**

The total number of days taken from the date of sowing to complete exertion of the 50 percent of panicles in the net plot.

##### **3.2.3.1.2 Plant height (cm)**

The plant height was recorded measuring from the base of the plant to the tip of the main panicle at the time of harvest and is expressed in cm.

##### **3.2.3.1.3 Number of productive tillers per plant**

The number of ear bearing tillers were counted on each plant at the time of maturity and expressed on per plant basis

##### **3.2.3.1.4 Panicle length (cm)**

The length of panicles from each plant was measured in centimeters from neck node to the tip of top most grain in a panicle.

#### **3.2.3.1.5 1000 grain weight (g)**

One thousand well filled grains were counted from sample of each entry in each replication and weighed with the help of electronic top pan balance in grams.

#### **3.2.3.1.6 Grain yield per plant (g)**

Panicles from ten plants were harvested individually at maturity and then threshed, cleaned and sun dried to 12% moisture content and the average of ten plants weight was recorded in grams.

#### **3.2.3.1.7 Total number of grains per panicle**

Total number of grains were counted for each panicle of ten randomly selected panicles of each genotype in each replication and average value was calculated.

#### **3.2.3.1.8 Number of filled grains per panicle**

Number of filled grains per panicle of ten randomly selected panicles was counted and average value was calculated.

#### **3.2.3.1.9 Fertility percentage**

Spikelet fertility was estimated on five panicles per plant from ten randomly selected plants. Spikelet fertility was recorded as a proportion of the total number of filled grains to the total number of grains (filled + unfilled) per panicle and expressed in percentage

$$\text{Fertility \%} = \frac{\text{Total number of filled grains per panicle}}{\text{Total number of grains per panicle}} \times 100$$

#### **3.2.3.2 Grain quality characters:**

As the red and black pericarp colored genotypes are eaten as a whole grain without polishing, paddy from all these 26 genotypes was dehusked and used for estimation of physico-chemical, nutritional and biochemical quality parameters. Brown rice quality characteristics brown rice of Samba Mahsuri (BPT 5204) were used for comparison with red and black pericarp colored genotypes.

### 3.2.3.2.1 Kernel length (mm), kernel breadth (mm) and kernel L/B ratio

Ten rice kernels from each replication of the bulk sample of each entry were measured for length and breadth using a dial micrometer. Average of the length and breadth was taken in milli meters and L/B ratio was calculated. Based on kernel length and kernel L/B ratio, grain type was assigned following Ramaiah (1969) classification.

Grain type	Length	L/B ratio
Long Slender (LS)	6 mm and above	3 and above
Short Slender (SS)	Less than 6 mm	3 and above
Medium Slender (MS)	5.5 mm-6 mm	2.5-3.0
Long Bold (LB)	6 mm and above	Less than 3.0
Short Bold (SB)	Less than 6 mm	Less than 2.5

### 3.2.3.2.2 Volume Expansion Ratio

Five grams of rice sample was soaked in 15 ml of water for 5 minutes in 50 ml measuring cylinder. The volume of water was recorded after adding rice sample (Y-15). Rice cooked for 20 minutes in water bath and cooked rice sample was taken in 100 ml measuring cylinder (X) containing 50 ml water. The volume raised was recorded (X-50) and calculated by using the formula.

$$\text{Volume Expansion Ratio (VER)} = \frac{\text{Increase in volume after cooking (X-50)}}{\text{Increase in volume before cooking (Y-15)}}$$

### 3.2.3.2.3 Alkali spreading value

The time required for cooking is determined by gelatinization temperature. Gelatinization temperature is estimated by the extent of alkali spreading. Six whole milled grains without any cracks were taken and spread evenly in petri dishes containing 10 ml of 1.7 % KOH. These petri plates were kept at 30°C for 23 hours. The alkali spreading of the kernels were noted on a seven point scale and expressed as average of six values. Scoring was done by following the method described by Little *et al.* (1958).

<b>Kernel Spreading</b>	<b>ASV score</b>	<b>Clearing</b>
Kernel not effected	1	Kernel chalky
Kernel swollen	2	Kernel chalky, collar powdery
Kernel swollen, collar incomplete and narrow	3	Kernel chalky, collar cloudy
Kernel swollen, collar complete and wide	4	Center cottony, collar cloudy
Kernel split or segmented, collar complete wide	5	Center cottony, collar clearing
Kernel dispersed, merged with collar	6	Center cloudy, collar cleared
Kernel completely dispersed and intermingled	7	Center and collar cleared

<b>Classification</b>	<b>Alkali spreading value</b>	<b>Gelatinization temperature</b>
1-2	Low	High >74°C
3	Low-intermediate	High-Intermediate
4-5	Intermediate	Intermediate (70°C - 74°C)
6-7	High	Low (55°C - 69°C)

#### 3.2.3.2.4 Water Uptake

Two grams of head rice was taken in 10 ml of distilled water and boiled for 20 min in water bath at 85°C. 10 ml of distilled water was taken as control along with test sample. After boiling water was collected in measuring cylinder and the water level was measured. Water Uptake ratio was calculated by using the formula (DRR, 2006).

$$\text{Water Uptake} = (\text{water left in the control} - \text{water left in the test sample}) \times \frac{100}{2}$$

#### 3.2.3.2.5 Solid loss

Two grams of milled rice was cooked in 20 ml of distilled water for 20 min at 85°C. After cooking, grains were separated and cooking water was placed in pre-weighted petri plate ( $W_1$ ) and dried in oven at 50°C for 12 hours and the final weight ( $W_2$ ) was recorded. The solid loss was estimated by using the formula (Sidhu *et al.*, 1975).

$$\text{Solid loss} = (W_2 - W_1) \times \frac{100}{2}$$

#### 3.2.3.2.6 Amylose content (%)

Amylose is the linear fraction of starch, has a major influence on cooking quality and it plays an important role in determining the texture of cooked rice. Amylose content in rice was determined as per the method suggested by Juliano (1971).

A standard solution of amylose was prepared by taking 100 mg of amylose dissolved in 10 ml of 1 N NaOH and made to 100 ml with distilled water. An aliquot of 0.2 to 1.0 ml of this was taken and neutralized with 0.1 N HCL using Phenolphthalein as indicator and then 1 ml iodine reagent was added. For the test samples, 100 mg rice sample was taken and 1 ml distilled ethanol and 10 ml 1 N NaOH were added. Samples were incubated overnight at room temperature and then volume was made to 100 ml with distilled water. From this 2.5 ml of extract was taken, 20 ml distilled water was added, neutralized with 0.1 N HCL using Phenolphthalein as indicator and then 1 ml iodine reagent was added. Volume was made to 50 ml with distilled water and absorbance was recorded at 590 nm using spectrophotometer. The amylose content of the sample was calculated by using the slope value obtained from standard curve and expressed as percentage. After estimating the amylose content, the samples were classified as

### 3.2.3.2.7 Total starch content (%)

Total starch content was estimated by using Anthrone method (Hodge, J.E and Hofrieter, B.T. 1962). Rice sample of 0.5 g was taken and extracted with 10 ml of hot 80 % ethanol. Centrifuged at 2,500 RPM for 5 min and retained the residue, washed the residue with hot 80 % ethanol till the supernatants does not give color with anthrone reagent. The residue was dried on water bath and then 5 ml of distilled water and 6.5 ml 52 % perchloric acid was added to the residue. This was kept at 0°C for 20 min and the same was repeated twice and supernatant was pooled up and made to 100 ml with distilled water. Along with test samples glucose working standard was prepared with concentration of 10 mg/100 ml. An aliquot of 0.2 to 1.0 ml of glucose working standard was taken and made to 1 ml with distilled water. 4 ml anthrone reagent was added to the samples and then heated for 8 min at 80°C and read the absorbance at 630 nm using spectrophotometer. Total starch content in the test sample was calculated by comparing the O.D. values of the standards and the test samples and expressed as %.

### 3.2.3.2.8 Protein content (%)

Protein content was estimated by using Lowry's method (Lowry *et al.* 1951). Rice powder of 0.5 g was taken and extracted with 10 ml of 0.1 N NaOH. Then centrifuged at 2,500 RPM for 10 min. Supernatant of 0.1 ml was taken and made to 1 ml with distilled water. Bovine Serum Albumin (BSA) standard solution in an aliquot of 0.1 to 1.0 ml was taken and made to 1 ml with distilled water. 5 ml of alkaline reagent was added and samples were incubated for 10 min, then Folin-Ciocalteus (FC) reagent of 0.5 ml was added to the samples and incubated in dark chamber for 30 min. Then the absorbance at 660 nm was recorded using spectrophotometer. Protein content was calculated by comparing the O.D. values of the standard with test sample and expressed as %.

Classification	Amylose %
Waxy	1-2%
Very low	2-9%
Low	9-20%
Intermediate	20-25%
High	25-33%

### 3.2.3.2.9 Total Phenol Content (mg/100 g)

Total Phenol Content (TPC) was estimated by using Folin Ciocalteu method (Malik, C.P and Singh, M.B.1980). A powdered sample of 0.5 g was taken and extracted with 10 ml of hot 80% ethanol. Centrifuged at 10,000 RPM for 20 min and save the supernatant then 5 ml of 80% ethanol was added to the residue and again centrifuged to pool the supernatants, evaporated to dryness and dissolved the residue in 5 ml of distilled water. Filtration was done and 0.5 ml aliquot was taken. Along with this catechol standard was prepared and aliquot of 0.2 to 1.0 ml was taken and made up to 3 ml with distilled water. 0.5 ml Folin-Ciocalteus (FC) reagent was added, after 3 min 2 ml of 20 % Na<sub>2</sub>CO<sub>3</sub> was added and then vertex the samples, tubes were placed in boiling water for 1 min. Finally tubes were cooled and absorbance was measured at 650 nm using spectrophotometer. TPC was calculated by comparing the O.D. at standard with the test sample and expressed as mg/100 g.

### 3.2.3.3.0 Total Antioxidant activity (mg AAE/100 g)

The total Antioxidant activity was estimated by using DPPH free radicle scavenging activity by using the method suggested by Pathirana *et al.* (2005) Sample of 0.5 g was incubated in 5ml methanol for 24 hrs in an incubator shaker. Filter the contents and made to 5 ml with methanol. From this 0.1 ml solution was taken, along with this 0.1ml of standard solution of ascorbic acid was taken as standard and 0.1 ml methanol was taken as control and then 1.9 ml of DPPH working standard solution was added to the samples, standard and control. Samples were kept in dark chamber for 30 min and measured the absorbance at 517 nm. The ability to scavenge was calculated by the following equation:

$$\text{Total antioxidant activity} = \frac{\text{Abs}_{\text{control}} - \text{Abs}_{\text{sample}}}{\text{Abs}_{\text{control}}} \times 100$$

Where Abs<sub>control</sub> is the absorbance of DPPH radical + methanol

Abs<sub>sample</sub> is the absorbance of DPPH radical + sample extract/standard

### 3.2.3.3.1 Zinc and Iron content (ppm)

Zinc and Iron content were estimated by using the energy dispersive X ray fluorescence spectrometry (XRF) at Indian Institute of Rice Research (IIRR), Hyderabad by non-destructive method for all the 26 rice samples were used for estimation of Zn and Fe content of all 26 rice genotypes. The working principle of XRF involves the expulsion of electron from inner most orbit followed by transfer of one of the electrons from the outer most orbit to inner most orbit leading to release of specific energy which is simultaneously identified and quantified by the detector. This instrument is quite useful in non-destructive determination of relative iron and zinc concentrations in rice samples with more ease in comparison with Atomic Absorption Spectrometry (AAS) and Inductively Coupled Plasma Mass Spectrometry (ICP-MS).

### 3.2.3.3.2 Glycemic Index (*in vitro*)

Glycemic Index was determined, following the *in vitro* method as suggested by Goni *et al.* (1997) with slight modifications. A ground sample of 100 mg was incubated with 0.2 ml of solution containing 1 g of pepsin in 10 ml HCL-KCL buffer (p<sup>H</sup> 1.5) and incubated at 40°C for one hour in a shaking water bath. Volume was made to 25 ml with tris-maleate buffer (p<sup>H</sup> 6.9). Then 5 ml of a solution of α-amylase in tris-maleate buffer containing 2.6 UI were added to the sample and incubated at 37 °C in a shaking water bath. An aliquot sample (0.5 ml) was taken every 30 min from 0-3 hours. These aliquots were placed in a test tube at 100°C and were vortexed for 5 min to inactivate the enzyme and refrigerated until the end of the incubation time. Then 3 ml of 0.4 M Sodium acetate buffer (p<sup>H</sup> = 4.75) were added to each aliquot, and 60 µl of amyloglucosidase was used to hydrolyse the digested starch into glucose after 45 min at 60°C in a shaking water bath. Volume was adjusted to one ml with distilled water. Triplicated aliquots of 0.5 ml were incubated with GOD-POD reagent. The areas under hydrolysis curves (AUC, 0-180 min) were calculated, with the equation described below, for all the samples.

$$C=C_{\infty}(1-e^{-kt})$$

Where C is the concentration at t time, C<sub>∞</sub> is the equilibrium concentration, k is the kinetic constant and t is the chosen time.

The HI was calculated as the relation between the AUC of test sample and the AUC for a reference food, white bread, expressed as a percentage. Glycemic index was calculated using the formula given below.

$$GI = 39.71 + 0.549 HI.$$

#### **3.2.3.3.3 Rapidly Digestible Starch (RDS) & Slow Digestible Starch (SDS) (%)**

Rapidly Digestible Starch (RDS) & Slow Digestible Starch (SDS) were determined using the method suggested by Englyst *et al.* (1999) with slight modifications. The amount of total starch hydrolyzed from the above experiment in the first 20 minutes was considered as the RDS and the amount of total starch hydrolyzed from 20<sup>th</sup> minute to 120<sup>th</sup> minute was considered as SDS.

#### **3.2.3.4 Resistant Starch (RS) (%)**

Resistant Starch (RS) content in the sample was measured by Goni *et al.* (1996) method. In brief, the main steps of the procedure are protein removal from samples with pepsin.  $\alpha$ -amylase incubation for 16 hours to hydrolyze digestible starch; treatment of the residue with 2 M KOH to solubilize resistant starch; incubation with amyloglucosidase and determination of glucose using GOD-POD reagent. RS was calculated as glucose (mg) x 0.9.

#### **3.2.3.5 Total Flavonoid Content (TFC) (mg QE/g)**

Total flavonoid content was estimated by Aluminium chloride complex forming assay as suggested by Swain *et al.* (1959). Quercetin was used as standard and a calibration curve for quercetin was drawn by taking the aliquot in the range of 0.1 to 5 mg/ml in methanol. 0.1 ml of each of the quercetin dilution was mixed with 0.5ml of distilled water and then with 0.1 ml of 5% Sodium nitrate and allowed to stand for 6 minutes. Then 0.1 ml of 10% Aluminium chloride solution was added and allowed to stand for 5 minutes after which 0.2 ml solution of 1 M Sodium hydroxide was added sequentially. The absorbance of this reaction mixture was recorded at 510 nm on spectrophotometer. The same procedure was repeated with the methanolic extracts of rice and total flavonoid content was expressed as quercetin equivalents (mg QE/g).

### 3.2.4 Statistical analysis

The mean data in respect of various characters were subjected to the following statistical techniques. All these analysis were carried out by using statistical software OP STAT.

#### 3.2.4.1 Analysis of variance

The analysis of variance for each character was calculated as per the standard statistical procedure given by Panse and Sukhatme (1967).

$$Y_{ij} = \mu + b_i + t_j + e_{ij}$$

Where,

- $Y_{ij}$  = Performance of the  $j^{\text{th}}$  genotype in the  $i^{\text{th}}$  block
- $\mu$  = General mean
- $b_i$  = True effect of  $i^{\text{th}}$  block
- $t_j$  = True effect of  $j^{\text{th}}$  genotype
- $e_{ij}$  = Random error associates with  $j^{\text{th}}$  genotype and  $i^{\text{th}}$  block

The structure of analysis of variance was as follows.

#### ANOVA Table for Randomized Complete Block Design

Source variation	of	d.f.	SS	MSS	Expected MSS	'F' calculated
Replications		(r-1)	RSS	R	$\sigma^2 e + t \sigma^2 r$	$M_r/M_e$
Treatments		(t-1)	TrSS	T	$\sigma^2 e + r \sigma^2 g$	$M_t/M_e$
Error		(r-1) (t-1)	ESS	E	$\sigma^2 e$	
Total		(rt-1)	TSS			

Where,

- r = Number of replications
- g = Number of genotypes
- $M_r$  = Mean sum of square of replication
- $M_t$  = Mean sum of square of treatment
- $M_e$  = Mean sum of square of error

- $\sigma_e^2$  = Environmental variance
- $\sigma_r^2$  = Variance due to replications
- $\sigma_g^2$  = Variance due to genotypes

Test of significance for each character was carried out against the corresponding error degrees of freedom using 'F' table values given by Fisher and Yates (1963).

### 3.2.4.2 Estimation of Genetic Parameters

#### 3.2.4.2.1 Phenotypic and genotypic variance

This was estimated according to the method given by Lush (1940).

$$\text{Genotypic variance } (\sigma_g^2) = \frac{M_t - M_e}{r}$$

$$\text{Phenotypic variance } (\sigma_p^2) = \sigma_g^2 + M_e = \frac{M_t - M_e}{r} + M_e$$

#### 3.2.4.2.2 Coefficient of Variation

Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed according to Burton and Devane (1953).

$$\text{Phenotypic standard deviation } (\sigma_p) = \sqrt{\sigma_p^2} = \sqrt{\sigma_g^2 + \sigma_e^2}$$

$$\text{PCV} = \frac{\text{Phenotypic standard deviation } (\sigma_p)}{\text{General mean } (\bar{X})} \times 100$$

$$\text{GCV} = \frac{\text{Genotypic standard deviation } (\sigma_g)}{\text{General mean } (\bar{X})} \times 100$$

As suggested by Subramanian and Menon (1973), GCV and PCV were categorized into

Low	=	Less than 10%
Moderate	=	10-20%
High	=	More than 20%

### 3.2.4.2.3 Heritability in broad sense [ $h^2(b)$ ]

Heritability in broad sense was estimated as per Allard (1960).

$$h^2(b) = \frac{\text{Genotypic variance } (\sigma_g^2)}{\text{Phenotypic variance } (\sigma_p^2)} \times 100$$

As suggested by Johnson *et al.* (1955),  $h^2(b)$  estimates were categorized

Low	=	0 – 30 %
Moderate	=	31-60 %
High	=	Above 60%

### 3.2.4.2.4 Genetic advance as per cent of mean (GAM)

Genetic advance was estimated as per the formula proposed by Lush (1940) and Johnson *et al.* (1955).

$$\text{Genetic Advance (GA)} = K \times \sigma_p \times h^2(b)$$

Where,

K = Selection differential at 5% selection intensity which accounts to a constant value of 2.06.

$h^2$  (b) = heritability in broad sense.

$\sigma_p^2$  = phenotypic standard deviation.

$$\text{GAM} = \frac{\text{GA}}{\text{Grand mean } (\bar{X})} \times 100$$

The range of genetic advance as per cent of mean was classified as suggested by Johnson *et al.* (1955).

Low	=	Less than 10%
Moderate	=	10-20%
High	=	More than 20%

### 3.2.4.2.5 Correlations

Phenotypic and genotypic correlations were worked out by using the formulae suggested by Falconer (1964).

Phenotypic coefficient of correlation ( $r_p$ )

$$r(x_i, x_j)_P = \frac{\text{Cov}(x_i, x_j)_P}{\sqrt{V(x_i)_P \cdot V(x_j)_P}}$$

$r(x_i, x_j)_P$  = Phenotypic correlation between  $i^{\text{th}}$  and  $j^{\text{th}}$  character

$\text{Cov}(x_i, x_j)_P$  = Phenotypic covariance between  $i^{\text{th}}$  and  $j^{\text{th}}$  character

$V(x_i)_p$  = Phenotypic variance of  $i^{\text{th}}$  character

$V(x_j)_p$  = Phenotypic variance of  $j^{\text{th}}$  character

Genotypic coefficient of correlation ( $r_g$ )

$$r(x_i, x_j)_g = \frac{\text{Cov}(x_i, x_j)_g}{\sqrt{V(x_i)_g \cdot V(x_j)_g}}$$

Where,

$r(x_i, x_j)_g$  = Genotypic correlation between  $i^{\text{th}}$  and  $j^{\text{th}}$  character

$\text{Cov}(x_i, x_j)_g$  = Genotypic covariance between  $i^{\text{th}}$  and  $j^{\text{th}}$  character

$V(x_i)_g$  = Genotypic variance of  $i^{\text{th}}$  character

$V(x_j)_g$  = Genotypic variance of  $j^{\text{th}}$  character

### **Test of significance**

Significance of correlation coefficients was tested by comparing phenotypic correlation coefficients with the table values (Fisher and Yates, 1963) at (n-2) degrees of freedom at 5% and 1% level where 'n' denotes the number of paired observations used in the calculation.

#### **3.2.4.2.6 Path Coefficient Analysis**

Path coefficient analysis suggested by Wright (1921) and elaborated by Dewey and Lu (1959) was used to calculate the direct and indirect contribution of various traits to yield.

For estimation of various direct and indirect effects, a set of simultaneous equations were formed:

$$\begin{aligned}
r_{1y} &= P_{1y} + r_{12} P_{2y} + r_{13} P_{3y} + \dots + r_{1k} P_{ky} \\
r_{2y} &= r_{21} P_{1y} + P_{2y} + r_{23} P_{3y} + \dots + r_{2k} P_{ky} \\
r_{iy} &= r_{i1} P_{1y} + r_{i2} P_{2y} + r_{i3} P_{3y} + \dots + r_{ik} P_{ky} \\
r_{ky} &= r_{k1} P_{1y} + r_{k2} P_{2y} + r_{k3} P_{3y} + \dots + r_{kk} P_{ky}
\end{aligned}$$

Where,

$r_{1y}$  to  $r_{ky}$  = Coefficient of correlations between causal factors 1 to k and dependent character y.

$r_{12}$  to  $r_{k-1,k}$  = Coefficient of correlations among causal factors.

$P_{1y}$  to  $P_{ky}$  = Direct effects of characters 1 to k on character y

The above equations were written in a matrix form as under:

$$\begin{matrix} \text{A} & & \text{C} & & \text{B} \\ \left( \begin{array}{c} r_{1y} \\ r_{2y} \\ - \\ - \\ - \\ r_{iy} \end{array} \right) & = & \left( \begin{array}{ccc} 1 & r_{12} & r_{i1} \\ r_{21} & 1 & r_{i2} \\ - & - & - \\ - & - & - \\ - & - & - \\ r_{i1} & r_{i2} & i \end{array} \right) & \left( \begin{array}{c} p_{1y} \\ p_{2y} \\ - \\ - \\ - \\ p_{iy} \end{array} \right) \end{matrix}$$

Then  $B = [C]^{-1} A$

$$\text{Where } [C]^{-1} = \begin{bmatrix} C_{11} & C_{12} & C_{13} & \cdot & \cdot & C_{1i} \\ C_{21} & C_{22} & C_{23} & \cdot & \cdot & C_{2i} \\ C_{i1} & C_{i2} & C_{i3} & \cdot & \cdot & C_{ii} \end{bmatrix}$$

The direct effects were calculated as follows

$$P_{1Y} = \sum_{i=1}^k = C_{1i} r_{iY}$$

$$P_{2Y} = \sum_{i=1}^k = C_{2i} r_{iY}$$

$$P_{iy} = \sum_{i=1}^k = C_{1i} r_{iy}$$

## Residual effect

The residual effect was estimated with the help of direct effects and simple correlation coefficients using following formula.

$$I = P^2 R_y + \sum P_{iy} r_{iy}$$

Where,  $P^2 R_y$  is the square of the residual effect.

## Chapter – IV

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# Results and Discussion

## Chapter IV

# RESULTS AND DISCUSSION

Rice is a traditional staple food crop consumed by more than half of the world's population. Grain quality has always been an important consideration in rice variety selection and development. It is the primary determinant for market price and consumer acceptability. The kernel appearance, size, shape, nutritional value and cooking characteristics are important for judging the quality and preference of rice from one group of consumer to another (Kanchana *et al.*, 2012). All rice varieties contain higher starch content and hence have a higher glycemic index as compared to other grains. On one hand, where white rice (which is stripped of its fiber and nutrients) is bad for the diabetic health, raw unpolished rice (with intact bran and high amylose content) is beneficial for maintaining the healthy blood sugar levels. Keeping the above points, the present study was taken up to identify some micronutrients dense rice genotypes possessing high antioxidant activity coupled with low glycemic index to recommend for consumption, there by promoting population health and alleviating the public health burden of chronic diseases.

The experimental findings of the present investigation conducted during *khariif* 2017 with 26 rice genotypes are presented and discussed character wise as under:

### ANALYSIS OF VARIANCE

The data collected for all twenty six characters were subjected to statistical analysis as detailed under materials and methods. Analysis of variance was carried out for twenty six characters *viz.*, days to 50% flowering, panicle length (cm), plant height (cm), ear bearing tillers per plant, grain yield per plant (g), test weight (g), number of filled grains per panicle, total number of grains per panicle, fertility %, solid loss, water uptake, volume expansion ratio, alkali spreading value, length/breadth ratio, amylose content (%), protein content (%), total starch content (%), total phenol content (mg/100 g), total antioxidant activity (mg AAE/100 g), flavonoid content (mg QE/100 g), Zn content (ppm), Fe content (ppm), glycemic index, slowly digestible starch (%), rapidly digestible starch (%) and resistant starch (%) and the results were given in Table 4.1. The results revealed significant differences for all characters studied except for solid loss, volume expansion ratio and length/breadth ratio.

The results obtained are presented and discussed under the following headings.

4.1 Mean, variability, heritability and genetic advance as per cent of mean

4.2 Correlation coefficient analysis

4.3 Path coefficient analysis

#### **4.1 MEAN, VARIABILITY, HERITABILITY AND GENETIC ADVANCE (AS PERCENT OF MEAN)**

The mean performance of 26 genotypes for all 26 characters studied is presented in table 4.2. The estimates of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability ( $h^2$  broad sense) and genetic advance as percent of mean (GAM) are presented in table 4.3 and described character wise here under.

**Table 4.1. Analysis of variance for yield, yield components and quality characters among 26 genotypes of rice (*Oryza sativa* L.)**

	Source	Replications	Treatments	Error
	Degree of freedom	2	25	50
MEAN SUM OF SQUARES				
1	Days to 50% flowering	17.58	235.60 <sup>**</sup>	11.16
2	Panicle length (cm)	2.28	22.40 <sup>**</sup>	2.82
3	Plant height (cm)	8.20	176.83 <sup>**</sup>	12.07
4	Ear bearing tillers per plant	2.85	8.2794 <sup>**</sup>	3.045
5	Grain Yield per plant (g)	8.52	142.90 <sup>**</sup>	12.87
6	Test Weight (g)	0.71	49.65 <sup>**</sup>	0.47
7	Number of filled grains per panicle	638.16	12057.005 <sup>**</sup>	1220.16
8	Total number of grains per panicle	727.16	12879.46 <sup>**</sup>	1406.12
9	Fertility %	4.23	18.43 <sup>**</sup>	7.18
10	Solid Loss	0.000015	0.82	0.0021
11	Water Uptake	0.012	2909.06 <sup>**</sup>	11.71
12	Volume Expansion Ratio	0.063	0.50	0.024
13	Alkali Spreading Value	0.89	2.32 <sup>**</sup>	0.29
14	Length/Breadth ratio	0.18	0.34	0.074
15	Amylose Content (%)	1.44	18.66 <sup>**</sup>	0.45
16	Protein Content (%)	0.049	18.57 <sup>**</sup>	0.034
17	Total Starch Content (%)	0.0092	246.80 <sup>**</sup>	0.10
18	Rapidly Digestible Starch (%)	0.0006	59.40 <sup>**</sup>	0.20
19	Slowly Digestible Starch (%)	0.016	44.33 <sup>**</sup>	0.18
20	Resistant Starch (%)	0.0004	2.17 <sup>**</sup>	0.0087
21	Total Phenol Content (mg/100g)	0.0002	5179.64 <sup>**</sup>	0.17
22	Total antioxidant Activity (mg AAE/100g)	0.63	2799.94 <sup>**</sup>	4.77
23	Flavonoid content (mg/100g)	16.85	127866.40 <sup>**</sup>	131.47
24	Zn content (ppm)	3.74	61.93 <sup>**</sup>	2.52
25	Iron content (ppm)	3.66	20.57 <sup>**</sup>	2.43
26	Glycemic Index	0.19	74.25 <sup>**</sup>	0.86

\* Significant at 5% level, \*\* Significant at 1% level

## **4.1.1 Yield Component Characters**

### **4.1.1.1 Days to 50% Flowering**

Among the genotypes under study all brown pericarp colored genotypes had a flowering duration of more than 110 days while the red and black pericarp colored rice genotypes used in the present study flowered early. Among the 26 genotypes studied, days to 50% flowering varied from 103 (Matta Triveni, BPT 3111, BPT 3145, BPT 3143, BPT 3138, BPT 3140 and BPT 2858) to 127 (BPT 2270) with a mean value of 108 days. Low phenotypic (8.704) and genotypic (8.120) coefficients of variation were observed for this trait. These results are in agreement with Sameera *et al.* (2016), Devi *et al.* (2017), Jan *et al.* (2017), Lakshmi *et al.* (2017), Nandini *et al.* (2017) and Mamata *et al.* (2018).

This trait recorded high heritability (87.0) and moderate genetic advance as percent of mean (15.60) indicating the operation of both additive and non additive gene action in the inheritance of this trait. These results are in agreement with Nandan *et al.* (2010), Yadav *et al.* (2010), Prasad *et al.* (2011), Dhanwani *et al.* (2013), Gokulakrishnan *et al.* (2014), Ekka *et al.* (2015), Gampala *et al.* (2015), Patil *et al.* (2015), Umesh *et al.* (2015), Devi *et al.* (2016), Sameera *et al.* (2016), Devi *et al.* (2017), Nandini *et al.* (2017) and Mamata *et al.* (2018).

### **4.1.1.2 Panicle Length (cm)**

Panicle length among all the genotypes varied from 19.89 cm (BPT 5204) to 32.44 cm (BPT 3126) with a mean value of 27.14 cm. The other genotypes which recorded high panicle length include Annapurna (27.44), Harsha (27.23), Samyuktha (28.02), BPT 3139 (28.78), BPT 3145 (30.50), BPT 3138 (29.92), BPT 3139 (28.64), BPT 3191 (27.20), BPT 3143 (28.38), BPT 2848 (30.74), BPT 3144 (30.40), and BPT 2858 (30.53). Among the genotypes studied, red and black pericarp colored rice genotypes had more panicle length when compared with brown pericarp colored genotypes. Low genotypic (9.41) and moderate phenotypic (11.26) coefficients of variation observed for this trait. These findings are in agreement with the results reported by Sanghera *et al.* (2013), Bhati *et al.* (2015), Patil *et al.* (2015), Rukminidevi *et al.* (2016) and Devi *et al.* (2017).

High heritability (69.80) and moderate genetic advance as percent of mean (16.19) observed for this trait indicating the operation of both additive and non additive gene action in the inheritance of this trait. These findings are in agreement with the results reported by Prasad *et al.* (2011), Ekka *et al.* (2015), Devi *et al.* (2016), Mohan *et al.* (2016) and Devi *et al.* (2017).

#### **4.1.1.3 Plant height (cm)**

Plant height exhibited a variation ranging from 88.40 cm (BPT 5204) to 123.53 cm (Jyothi) with mean value of 111.37 cm. Low genotypic (6.65) and phenotypic (7.34) coefficients of variation was observed for this trait. These findings are in agreement with the results reported by Aktar *et al.* (2011), Bhati *et al.* (2015), Gampala *et al.* (2015), Sameera *et al.* (2016), Mohan *et al.* (2016) and Jan *et al.* (2017).

High heritability (82.0) and moderate genetic advance as percent of mean (12.41) observed for this trait indicated the operation of both additive and non-additive gene effects and desired results may not be obtained by direct selection. These findings are in agreement with the results reported by Aktar *et al.* (2011), Rahman *et al.* (2014), Gampala *et al.* (2015), Sameera *et al.* (2016), Jan *et al.* (2017) and Nandini *et al.* (2017).

#### **4.1.1.4 Ear bearing tillers per plant**

The trait ear bearing tillers per plant varied from 12 (Samyuktha, BPT 3125, BPT 3126) to 18 (BPT 2782) with a mean value of 15. More number of ear bearing tillers (EBT) per plant is a desirable trait and in the present study BPT 2270 (16), Aathira (16), BPT 3133 (16), BPT 2295 (17), BPT 2595 (17), BPT 2660 (17), and BPT 2776 (18) also recorded more number of EBT. Low genotypic coefficient of variation (8.99) coupled with moderate phenotypic (14.91) coefficient of variation were observed for this trait which are in agreement with the results reported by Rukminidevi *et al.* (2016), Mohan *et al.* (2016) and Devi *et al.* (2017).

The estimates of heritability (36.4) and genetic advance as percent of mean (11.18) were moderate for this trait suggesting the operation of both additive and non-additive gene effects in governing this trait. Improvement of this trait might be aimed through mass selection, progeny selection or any suitable modified selection procedure to exploit the additive component. These findings are in agreement with the results reported by Prasad *et al.* (2011), Bekele *et al.* (2013), Dhanwani *et al.* (2013), Veni *et*

*al.* (2013), Rahman *et al.* (2014), Bhuvanewari *et al.* (2015), Ekka *et al.* (2015), Patil *et al.* (2015), Umesh *et al.* (2015), Rukminidevi (2016), Sameera *et al.* (2016), Devi *et al.* (2017), Nandini *et al.* (2017) and Mamata *et al.* (2018).

#### **4.1.1.5 Grain yield per plant (g)**

Grain yield per plant exhibited a wide range of variation from 25.0 g (BPT 5204) to 58.33 g (BPT 3142) with a mean value of 41.08 g. From the present study other genotypes with high grain yield include BPT 2858 (41.73), BPT 3145 (41.77), 42.0 (Jyothi), BPT 3111(42.13), Harsha (43.53), Samyuktha (43.67), BPT 3144 (43.93), Annapurna (45.43), BPT 2848 (45.0), BPT 2782 (47.7), BPT 3143 (48.03), BPT 3136 (48.83) and Matta Triveni (50.33). BPT 5204, the variety used as check in the present study recorded low grain yield. All red and black pericarp colored genotypes recorded significantly superior grain yield than the check. Moderate genotypic (16.022) and phenotypic (18.24) coefficients of variation were observed for this trait which are in agreement with the previous findings of Gokulakrishnan *et al.* (2014), Chowdhury *et al.* (2016) and Jan *et al.* (2017)

High heritability (77.10) and high genetic advance as percent of mean (28.98) were observed for this trait indicating the role of additive gene effects in controlling this trait. Hence, direct selection will be highly rewarding for improving this character. These results are in agreement with the previous findings of Prasad *et al.* (2011), Bekele *et al.* (2013), Dhanwani *et al.* (2013), Veni *et al.* (2013), Gokulakrishnan *et al.* (2014), Bhuvanewari *et al.* (2015), Ekka *et al.* (2015), Patil *et al.* (2015), Umesh *et al.* (2015), Chowdhury *et al.* (2016) Devi *et al.* (2016), Sameera *et al.* (2016), Devi *et al.* (2017), Jan *et al.* (2017), Lakshmi *et al.* (2017) and Mamata *et al.* (2018).

#### **4.1.1.6 Test weight (g)**

For test weight, a wide range of variation was observed among the genotypes studied. The minimum value was observed in BPT 2295 (13.49). while the entry Samyuktha recorded maximum value (27.90) with a mean value of 18.51. From the present study other genotypes which recorded high test weight above mean value include BPT 3130 (18.83), BPT 3111 (19.35), BPT 3138 (19.54), BPT 3136 (19.83), Jyothi (21.02), Matha Triveni (21.09), BPT 3145 (21.49), Aathira (22.78), BPT 3142 (24.30), Harsha (24.35) and Annapurna (25.58). All brown pericarp colored genotypes used in the present study are slender type and recorded < 15 g test weight. Among the red pericarp colored genotypes, more test weight was observed in BPT 3111, Jyothi, Matha Triveni, Aathira, Harsha and Annapurna. Among the black pericarp colored

genotypes except BPT 3138 and BPT 3136, all other genotypes are slender. High genotypic (21.87) and phenotypic (22.18) coefficients of variation was observed for this trait. These findings are in agreement with the results reported by Veni *et al.* (2013), Chowdhury *et al.* (2016), Mohan *et al.* (2016) and Lakshmi *et al.* (2017).

High heritability (97.2) coupled with high genetic advance as per cent of mean (44.14) observed for this trait indicated that variation among the genotypes is high and the predominance of additive gene action in the inheritance of this trait. Hence, direct selection will be highly rewarding for improving this character. These findings are in agreement with the results reported by Yadav *et al.* (2010), Prasad *et al.* (2011), Krishnaveni *et al.* (2013), Rahman *et al.* (2014), Bhuvaneswari *et al.* (2015), Devi *et al.* (2015), Patil *et al.* (2015), Devi *et al.* (2016), Devi *et al.* (2017) and Lakshmi *et al.* (2017).

#### **4.1.1.7 Number of filled grains per panicle**

For number of filled grains per panicle a wide range of variation was observed among the genotypes studied. The minimum value observed for this trait was 177 (Harsha) while the entry BPT 2858 recorded maximum value (385) followed by BPT 3138 (376) with a mean value of 274. Among different colored rice genotypes under study, black pericarp colored rice genotypes had more number of filled grains per panicle when compared with brown and red pericarp colored rice genotypes. Among red rice, Aathira, recorded maximum number of filled grains per panicle. All the genetic parameters studied manifested high value for this trait. High genotypic (21.95) and phenotypic (25.39) coefficients of variation was observed. Which are in agreement with the results reported by Dhanwani *et al.* (2013), Sanghera *et al.* (2013), Rahman *et al.* (2014), Bhuvaneswari *et al.* (2015), Umesh *et al.* (2015), Devi *et al.* (2016), Chowdhury *et al.* (2016), Sameera *et al.* (2016), Lakshmi *et al.* (2017) and Mamata *et al.* (2018).

High heritability (74.8) and high genetic advance as per cent of mean (39.10) was observed for this trait, indicating that variation among the genotypes is high and the predominance of additive gene action in the inheritance of this trait. These findings are in agreement with the results reported by Nandan *et al.* (2010), Yadav *et al.* (2010), Dhanwani *et al.* (2013), Sanghera *et al.* (2013), Rahman *et al.* (2014), Ekka *et al.* (2015), Umesh *et al.* (2015), Rukminidevi *et al.* (2016), Sameera *et al.* (2016), Lakshmi *et al.* (2017), Nandini *et al.* (2017), and Mamata *et al.* (2018).

**Table 4.2. Mean performance of 26 genotypes of rice (*Oryza sativa* L.) for yield components, nutritional and biochemical quality parameters**

S. No.	Character	Days to 50% flowering	Panicle length (cm)	Plant height (cm)	Ear bearing tillers per plant	Grain yield per plant (g)	Test weight (g)	No. of filled grains	Total no. of grains	Fertility %	Solid loss	Water uptake	VER	ASV
1	BPT 5204	117.00	19.89	88.40	13.33	25.00	14.84	275.67	304.33	90.52	1.10	80.00	2.56	5.00
2	BPT 2270	127.00	23.39	116.67	15.67	29.33	13.81	260.33	284.00	91.59	2.25	108.00	2.25	4.33
3	BPT 2295	120.00	27.02	114.73	16.67	33.33	13.50	262.67	294.00	89.24	1.35	90.00	2.29	3.33
4	BPT 2595	115.00	25.58	104.47	17.00	37.00	14.90	247.00	267.67	92.08	1.85	55.00	2.00	4.67
5	BPT 2782	112.00	25.39	94.93	18.33	47.70	15.46	274.00	291.00	94.01	1.10	63.00	2.57	4.33
6	BPT 2660	121.00	25.77	110.53	16.67	36.67	15.31	261.00	295.67	88.19	1.70	180.00	2.50	3.67
7	BPT 2776	123.00	25.73	110.47	17.67	40.33	14.84	273.00	295.67	92.31	1.15	73.00	2.67	4.00
8	Matha Triveni	103.00	25.10	112.67	14.67	50.33	21.09	247.33	271.67	90.97	1.70	67.00	2.25	2.00
9	Annapurna	103.00	27.44	110.00	14.33	45.43	25.58	183.67	203.67	90.46	1.70	57.00	2.00	3.00
10	Aathira	108.00	25.19	101.93	15.67	36.13	22.79	312.33	362.67	86.41	0.80	52.00	2.00	2.00
11	Harsha	103.00	27.23	113.13	13.67	43.53	24.36	177.00	191.00	92.68	2.10	50.00	2.00	2.00
12	Jyothi	109.00	24.47	123.53	15.00	42.00	21.02	192.00	209.67	91.43	1.15	73.00	2.14	2.00
13	Samyuktha	104.00	28.03	123.13	12.33	43.67	27.90	187.33	209.33	89.43	0.85	50.00	2.00	2.00
14	BPT 3111	103.00	27.01	109.87	13.33	42.13	19.35	225.33	249.33	90.38	1.20	53.00	1.75	3.83
15	BPT 3139	103.00	28.78	114.67	12.33	34.90	18.12	286.00	312.67	91.45	1.15	85.00	2.29	3.33
16	BPT 3137	104.00	32.44	116.33	12.33	36.93	14.30	361.00	390.00	92.65	1.35	57.00	2.00	4.00
17	BPT 3145	103.00	30.51	114.27	13.33	41.77	21.49	359.00	381.67	94.15	2.30	60.00	1.50	3.67
18	BPT 3138	103.00	29.93	120.87	13.00	39.03	19.54	376.00	393.33	95.59	1.55	55.00	2.00	3.00
19	BPT 3136	104.00	28.64	105.67	14.33	48.83	19.83	195.00	226.00	85.93	1.10	83.33	2.00	4.17
20	BPT 3140	103.00	24.92	116.07	14.67	39.10	18.83	279.33	306.67	90.99	0.60	111.67	3.00	4.00
21	BPT 3141	104.00	27.21	113.87	13.00	37.63	18.10	246.00	268.67	91.46	1.80	57.00	2.25	3.00
22	BPT 3142	104.00	26.07	112.33	14.67	58.33	24.31	349.67	370.67	94.29	1.25	50.00	2.65	3.00
23	BPT 3143	103.00	28.38	110.80	15.67	48.03	16.90	226.67	242.00	93.59	1.90	50.00	3.25	3.17
24	BPT 2848	104.00	30.74	113.40	13.67	45.50	14.78	303.67	345.67	88.34	1.55	140.00	1.50	4.17
25	BPT 3144	106.00	30.40	110.33	15.33	43.93	14.60	370.67	390.67	94.89	2.75	93.00	1.86	4.00
26	BPT 2858	103.00	30.53	112.67	15.00	41.73	15.77	385.00	410.67	93.82	2.20	70.00	2.25	3.33
	Mean	<b>108.52</b>	<b>27.15</b>	<b>111.37</b>	<b>14.68</b>	<b>41.09</b>	<b>18.51</b>	<b>273.72</b>	<b>298.78</b>	<b>91.42</b>	<b>1.52</b>	<b>75.11</b>	<b>2.21</b>	<b>3.42</b>
	C.V	3.14	6.19	3.12	11.89	8.73	3.73	12.76	12.55	2.93	3.08	5.22	7.14	15.85
	C.D. 5%	5.48	2.76	5.70	2.86	5.88	1.13	57.29	61.50	4.40	0.08	5.61	0.26	0.89
	C.D. 1%	7.31	3.68	7.60	3.82	7.84	1.51	76.37	81.99	5.86	0.10	7.48	0.35	1.19
	Range Lowest	103.00	19.89	88.40	12.33	25.00	13.50	177.00	191.00	85.93	0.60	50.00	1.50	2.00
	Range Highest	127.00	32.44	123.53	18.33	58.33	27.90	385.00	410.67	95.59	2.75	180.00	3.25	5.00

VER- volume expansion ratio, ASV= alkali spreading value

Contd...

S. No.	Character	L/B ratio	Amylose content (%)	Protein content (%)	Total Starch content(%)	RDS (%)	SDS (%)	RS (%)	Total Phenol content (mg/100g)	Total Antioxidant Activity (mg AAE/100g)	Flavanoid content (mg/100g)	Zinc content (ppm)	Iron content (pm)	GI
1	BPT 5204	2.85	22.55	8.00	65.39	56.53	41.02	2.45	59.40	28.39	144.41	16.80	8.70	54.44
2	BPT 2270	2.84	20.98	10.14	62.78	54.59	42.84	2.57	67.89	29.94	113.48	15.50	8.80	53.26
3	BPT 2295	2.86	25.45	7.11	63.88	58.49	38.67	2.84	75.59	26.87	128.55	12.00	7.90	56.64
4	BPT 2595	2.87	23.97	10.21	62.52	64.46	32.33	3.21	54.07	28.31	153.92	15.30	7.00	62.08
5	BPT 2782	2.82	21.45	7.14	63.41	60.69	37.05	2.26	69.89	44.90	120.68	17.67	10.53	59.04
6	BPT 2660	2.78	21.11	9.83	64.16	56.64	41.14	2.24	63.39	46.67	145.28	18.60	9.80	54.18
7	BPT 2776	2.87	23.55	6.23	70.80	65.97	32.85	1.18	48.80	30.72	89.69	16.30	8.50	60.00
8	Matha Triveni	2.35	27.44	13.54	79.33	63.88	34.91	1.21	87.33	106.44	434.65	25.90	10.70	60.71
9	Annapurna	2.26	18.86	9.23	71.84	61.74	36.94	1.32	60.25	107.75	296.66	22.00	9.30	59.07
10	Aathira	2.26	24.24	8.21	87.57	58.48	39.40	2.12	56.36	105.13	303.80	25.90	10.70	57.12
11	Harsha	2.68	25.37	13.44	77.11	60.59	36.85	2.56	66.49	106.67	277.63	20.20	12.60	61.09
12	Jyothi	2.75	22.00	12.48	69.42	64.59	34.31	1.10	132.84	111.48	323.63	20.80	9.60	64.00
13	Samyuktha	2.49	26.36	9.07	69.35	62.77	34.34	2.89	65.82	100.91	290.23	18.90	12.50	59.10
14	BPT 3111	2.83	23.02	10.97	68.77	64.20	32.28	3.52	95.50	110.09	410.61	24.20	16.00	62.12
15	BPT 3139	2.82	22.40	7.41	86.65	55.70	40.95	3.35	86.65	105.83	139.65	26.20	11.00	54.13
16	BPT 3137	2.83	16.41	7.26	75.33	60.59	38.16	1.25	93.55	91.05	82.55	24.10	9.30	62.71
17	BPT 3145	2.85	21.70	12.56	81.78	58.69	37.90	3.41	125.47	96.38	444.36	26.10	10.30	56.45
18	BPT 3138	3.08	24.08	9.59	66.61	59.88	37.18	2.94	98.48	74.46	486.98	25.20	8.40	58.90
19	BPT 3136	2.79	21.12	13.55	81.66	65.03	32.43	2.54	81.28	73.55	560.36	27.00	9.10	59.40
20	BPT 3140	3.51	22.17	10.95	66.13	67.55	30.89	1.56	214.34	108.83	590.12	24.30	13.40	69.25
21	BPT 3141	3.64	20.27	13.39	65.23	66.03	32.82	1.15	156.31	105.57	579.54	27.80	9.40	70.12
22	BPT 3142	2.70	22.05	13.35	88.64	60.53	37.15	2.32	88.64	77.07	661.44	21.80	11.10	57.60
23	BPT 3143	2.81	19.11	12.45	71.11	70.20	30.28	1.23	101.67	78.36	364.86	27.90	10.60	70.20
24	BPT 2848	2.82	20.88	13.11	70.49	49.75	43.34	3.97	123.31	86.63	784.54	18.00	12.30	49.05
25	BPT 3144	2.83	22.36	13.52	59.19	60.79	31.45	2.50	150.82	73.01	612.12	19.90	9.60	60.99
26	BPT 2858	2.82	24.18	12.82	53.16	61.32	32.21	2.89	174.48	89.07	548.72	26.80	19.40	61.29
	Mean	<b>2.80</b>	<b>22.42</b>	<b>10.60</b>	<b>70.86</b>	<b>61.15</b>	<b>36.14</b>	<b>2.33</b>	<b>96.10</b>	<b>78.62</b>	<b>349.56</b>	<b>21.74</b>	<b>10.64</b>	<b>59.76</b>
	C.V	9.60	3.03	1.76	0.46	0.73	1.19	4.00	0.44	2.78	3.28	7.31	14.67	1.56
	C.D. 5%	0.45	1.11	0.31	0.53	0.73	0.70	0.15	0.69	3.58	18.80	2.60	2.56	1.53
	C.D. 1%	0.60	1.48	0.41	0.71	0.98	0.94	0.20	0.92	4.78	25.07	3.47	3.41	2.03
	Range Lowest	2.26	16.41	6.23	53.16	49.75	30.28	1.10	48.80	26.87	82.55	12.00	7.00	49.05
	Range Highest	3.64	27.44	13.55	88.64	70.20	43.34	3.97	214.34	111.48	784.54	27.90	19.40	70.20

GI = Glycemic Index , SDS = Slowly Digestible starch, RDS = Rapidly Digestible Starch ,

C.V % = Coefficient of Variation percent C.D. = Critical Difference

Note: Bold figures are maximum and minimum mean values for each character

**Table 4.3. Mean, variability, heritability and genetic advance as per cent of mean for yield, yield components and grain quality parameters in rice (*Oryza sativa* L.).**

S. No.	Character	Mean	Range		Coefficient of variation		Heritability (%) (broad sense)	Genetic advance as per cent of mean (5% level)
			Minimum	Maximum	PCV %	GCV %		
1	Days to 50% flowering	108.52	103.00	127.00	8.70	8.12	87.00	15.60
2	Panicle length (cm)	27.14	19.89	32.44	11.26	9.41	69.80	16.19
3	Plant height (cm)	111.37	88.40	123.53	7.34	6.65	82.00	12.41
4	Ear bearing tillers per plant	14.67	12.33	18.33	14.91	8.99	36.40	11.18
5	Grain Yield per plant (g)	41.09	25.00	58.33	18.24	16.02	77.10	28.98
6	Test Weight (g)	18.51	13.49	27.90	22.18	21.87	97.20	44.41
7	Number of filled grains per panicle	273.71	177.00	385.00	25.39	21.95	74.80	39.10
8	Total number of grains per panicle	298.78	191.00	410.66	24.20	20.69	73.10	36.45
9	Fertility %	91.41	85.93	95.58	3.61	2.11	34.30	2.55
10	Solid Loss	1.51	0.60	2.75	34.59	34.46	99.20	70.70
11	Water Uptake	75.11	50.00	180.00	47.65	47.37	98.80	96.99
12	Volume Expansion Ratio	2.21	1.50	3.25	19.35	17.98	86.40	34.43
13	Alkali Spreading Value	3.42	2.00	5.00	28.77	24.01	69.7	41.29
14	L/B ratio	2.80	2.26	3.64	14.27	10.56	54.80	16.10
15	Amylose Content (%)	22.42	16.41	27.44	11.43	11.02	93.0	21.89
16	Protein Content (%)	10.59	6.23	13.55	6.21	6.18	99.40	48.48
17	Total Starch Content (%)	70.85	53.16	88.64	12.80	12.79	99.90	26.34
18	Rapidly Digestible Starch (%)	61.14	49.75	70.20	7.30	7.26	99.0	14.89
19	Slowly Digestible Starch (%)	36.14	30.28	43.34	14.90	14.71	98.80	21.72
20	Resistant Starch (%)	2.33	1.10	3.97	0.73	0.72	98.80	94.54
21	Total Phenol Content (mg/100 g)	96.10	48.80	214.34	43.23	43.13	99.76	88.85
22	Total Antioxidant Activity (mg AAE/100 g)	78.61	26.87	111.48	38.92	38.82	99.50	79.77
23	Flavonoid Content (mg/100 g)	349.55	82.55	784.54	59.12	59.03	99.70	121.41
24	Zn content (ppm)	21.73	12.00	27.90	21.73	20.47	88.70	39.71
25	Iron content (ppm)	10.63	7.00	19.40	27.38	23.12	71.30	40.21
26	Glycemic Index	59.75	49.75	70.20	8.42	8.27	96.60	16.75

#### **4.1.1.8 Total number of grains per panicle**

Among the 26 genotypes studied, total number of grains per panicle varied from 191 (Harsha) to 411 (BPT 2858) with a mean value of 299. When compared with brown and red pericarp colored genotypes, black pericarp colored genotypes possessed high number of grains per panicle which is a desirable trait to obtain more grain yield. High genotypic (20.69) and phenotypic (24.20) coefficients of variation were observed for this trait. These findings are in agreement with the results reported by Aktar *et al.* (2011), Devi *et al.* (2016) Mohan *et al.* (2016) and Sameera *et al.* (2016)

High heritability (73.10) and genetic advance as percent of mean (36.45) were recorded for this trait indicating that the inheritance of this character is controlled by additive gene action. These findings are in agreement with the results reported by Aktar *et al.* (2011), Gokulakrishnan *et al.* (2014), Gampala *et al.* (2015), Devi *et al.* (2016), Sameera *et al.* (2016), Mohan *et al.* (2016) and Mamata *et al.* (2018).

#### **4.1.1.9 Fertility %**

Among all the genotypes studied, fertility % exhibited a wide range of variation. Minimum value was observed in BPT 3136 (85.93) while BPT 3138 (95.58) recorded maximum value followed by BPT 3144 (94.88) with a mean value of 91.41. Low genotypic (2.11) and phenotypic (3.61) coefficients of variation coupled with moderate heritability (34.30) along with low genetic advance as percent of mean (2.55) were manifested by this trait suggesting the existence of low variation among the genotypes studied for this trait. These findings are in agreement with the results obtained by Umesh *et al.* (2015) and Nandini *et al.* (2017).

#### **4.1.2.0 Solid loss**

Minimum value for solid loss was observed in BPT 3140 (0.60) while BPT 2848 (2.75) recorded maximum value followed by BPT 3137 (2.35) with a mean value of 1.51. If solid loss is more cooking quality of the rice is poor. Hence, the genotypes with less solid loss are preferable. But no significant difference was observed between the treatments for this trait hence all the genotypes had on par cooking quality for this trait.

This trait manifested high estimates for both genotypic (34.46) and phenotypic (34.59) coefficients of variation indicating that variation among the genotypes was high. High heritability (99.2) coupled with high genetic advance as per cent of mean (70.70) was observed for this trait, suggesting the role of additive gene action. Hence direct selection would be effective for improving this character.

#### **4.1.2.1 Water uptake**

Water uptake exhibited a wide range of variation among all the genotypes under study. Minimum value was observed in Harsha, BPT 3111, BPT 3142 and BPT 3143 (50.0) while BPT 2660 (180.0) recorded maximum value followed by BPT 3140 (111.67) with a mean value of 75.11.

High genotypic (47.37) and phenotypic (47.65) coefficients of variation were observed for this trait. High heritability (98.8) coupled with high genetic advance as percent of mean (96.99) recorded for this trait indicating the operation of additive gene action in controlling this trait. Hence for improving this character direct selection would be effective. These findings are in agreement with the results reported by Dhanwani *et al.* (2013), Veni *et al.* (2013) and Devi *et al.* (2015).

#### **4.1.2.2 Volume Expansion Ratio**

Among the 26 genotypes studied, volume expansion ratio varied from 1.50 (BPT 3145 and BPT 2848) to 3.25 (BPT 3143) with a mean value of 2.21. Moderate values were manifested by this trait for genotypic coefficient of variation (17.98) and phenotypic coefficient of variation (19.35) indicating that variation among the genotypes is medium. High heritability (86.4) coupled with high genetic advance as percent of mean (34.43) was observed for this trait suggesting the role of additive gene effects in controlling this trait. These findings are in agreement with the results obtained by Veni *et al.* (2013) and Savitha and Kumari (2015).

#### **4.1.2.3 Alkali Spreading Value**

Cooking quality of rice is mainly depend on amylose content and gelatinization temperature. Gelatinization temperature determines the time required for cooking rice. It directly affects the physical properties of the starch granule which in turn influence the quality of cooked rice. An increase in gelatinization temperature has been observed

with the decrease in alkali spreading value of rice starch. Rice genotypes with intermediate ASV are mostly preferred by Indian consumers. Genotypes for this trait showed wide range of variation ranging from 2.0 (Matta Triveni, Aathira, Harsha, Jyothi, Samyuktha) to 5.0 (BPT 5204) with a mean value of 3.42. This trait observed high estimates for both genotypic (24.01) and phenotypic (28.77) coefficient of variation, indicating that variation among the genotypes are high. These findings are in agreement with the results reported by Sunayana *et al.* (2010), Dhanwani *et al.* (2013), Devi *et al.* (2015), Umesh *et al.* (2015) and Sahu *et al.* (2017). High heritability (69.70) coupled with high genetic advance as per cent of mean (41.29) was observed for this trait suggesting the role of additive gene action in the inheritance of this trait. Hence direct selection would be effective for improving this character. These findings are in agreement with the findings of Sunayana *et al.* (2010), Dhanwani *et al.* (2013) and Umesh *et al.* (2015).

#### **4.1.2.4 Length/Breadth ratio**

Genotypes with L/B ratio between 2.5 to 3.0 are classified as medium slender and those with L/B ratio < 2.5 are classified as short bold and > 3.0 as long slender types. Among the genotypes under study, all brown pericarp colored genotypes are medium slender whereas among red genotypes except Jyothi, Harsha and BPT 3111 all others are short bold type. Among black pericarp colored genotypes, BPT 3138, BPT 3140 and BPT 3141 had long slender grain type and the remaining had medium slender grain type. Genotypes for this trait varied from 2.26 (Annapurna) to 3.64 (BPT 3131) with a mean value of 2.85. Moderate estimates were manifested for genotypic coefficient of variation (10.56) and phenotypic coefficient of variation (14.27) indicating that variation among the genotypes are medium. These findings are in agreement with the results reported by Dhanwani *et al.* (2013), Veni *et al.* (2013), Sanghera *et al.* (2013), Gokulakrishnan *et al.* (2014), Devi *et al.* (2015), Rukminidevi *et al.* (2016), Devi *et al.* (2017) and Sahu *et al.* (2017).

Moderate heritability (54.8) coupled with moderate genetic advance as percent of mean (16.10) was observed for this trait, indicating the predominance of both additive and non additive gene action. These results are in agreement with findings reported by Rafi *et al.* (2014)

#### **4.1.2.5 Amylose content (%)**

Amylose content of milled rice has been found to be positively correlated with hardness values of cooked rice and negatively with stickiness values. Amylose content determines the texture of cooked rice and rice varieties with amylose content between 20-25 are considered as intermediate which cook as fluffy and flaky. Among the genotypes under study, all the brown pericarp colored rice varieties recorded intermediate amylose content where as the genotypes with red pericarp color exhibited low amylose (Annapurna), intermediate (Aathira, Jyothi, BPT 3111 and BPT 3139) and high (Samyuktha, Harsha and Matta Triveni). Among black pericarp colored genotypes, except BPT 3137(16.41) and BPT 3143 (19.11) which recorded low amylose, all other genotypes exhibited intermediate amylose content which is desirable. Among all the 26 genotypes studied, wide range of variation was observed for this trait. Minimum value was exhibited by BPT 3137 (16.41) while Matta Triveni recorded maximum value (27.44) followed by Samyuktha (26.36). Moderate genotypic (11.02) and phenotypic (11.43) coefficients of variation were observed for this trait. These findings are in agreement with the results reported by Sunayana *et al.* (2010), Chowdhury *et al.* (2016), Savitha and Kumari (2015) and Sahu *et al.* (2017).

High heritability (93.0) coupled with high genetic advance as percent of mean (21.89) was observed for this trait, indicating the operation of additive gene action. Hence direct selection would be effective for improving this character. These findings are in agreement with the results reported by Sunayana *et al.* (2010), Veni *et al.* (2013), Devi *et al.* (2015) and Savitha and Kumari (2015).

#### **4.1.2.6 Protein Content (%)**

Among the genotypes studied, minimum value for protein content was recorded in BPT 2776 (6.23), while BPT 3136 (13.55) recorded maximum value followed by Matta Triveni (13.54) with a mean value of 10.59. Highest protein content is a desirable trait, and the varieties with high protein content identified from this study include BPT 3111 (10.97), BPT 3143 (12.45), Jyothi (12.48), BPT 3145 (12.56), BPT 2858 (12.82), BPT 2848 (13.11), BPT 3142 (13.35), BPT 3141 (13.39), Harsha (13.44), BPT 3144 (13.52) and BPT 3136 (13.55). Among the genotypes with brown pericarp, BPT 2595 (10.21%) and BPT 2270 (10.14%) recorded high protein content. When compared with the brown pericarp colored genotypes, red and black pericarp colored genotypes

exhibited very high protein content. Rice protein is the major source in many rice consuming regions of the world. Protein being the second dominant component of rice seed after starch, its content and amino acid composition will determine the nutritional quality of rice (Meijuan and Samuel, 2005). Based on protein content, rice varieties are classified into high ( $\geq 12\%$ ), medium (9 - 11.9%) and low ( $\leq 8.9\%$ ). Based on this, it can be concluded that in this study 11 genotypes were identified for high protein content. As rice protein is one of the highly digestible protein sources, these lines may be useful to improve nutritional quality of rice.

Raghuvanshi *et al* (2017) also reported that red rice genotypes had higher amount of protein content ( $> 10.49\%$ ) when compared with white rice and they suggested that the nutritional quality of red rice was comparable to many millets, fruits and vegetables. Pathak *et al.* (2017) also reported that pigmented rice had higher amount of protein content (10.61%) than non pigmented rice.

This trait manifested high estimates for both genotypic (23.45) and phenotypic (23.52) coefficient of variation indicating that variation among the genotypes are high. High heritability (99.40) coupled with high genetic advance as per cent of mean (48.18) was observed for this trait indicating the operation of additive gene action. Hence for improving this character direct selection would be effective. These results are in agreement with the findings reported by Chakraborty *et al.* (2010) and Raja *et al.* (2013).

#### **4.1.2.7 Total Starch Content (%)**

Starch constitutes a major energy supply for humans worldwide and is produced as a reserve carbohydrate in plants. Chemically, starches are polysaccharides composed of a number of glucose molecules linked together with  $\alpha$ -D-(1-4) and  $\alpha$ -D-(1-6) linkages. For nutritional purposes, starch has been classified as rapidly digestible starch (RDS), slowly digestible starch (SDS) and resistant starch (RS) to differentiate its digestion properties in food products. Genotypes for this trait showed wide range of variation from 53.16 (BPT 2858) to 88.64 (BPT 3142) with a mean value of 70.85.

This trait manifested moderate estimates for both genotypic (12.79) and phenotypic (12.80) coefficient of variation indicating that variation among the genotypes are medium. High heritability (99.9) coupled with high genetic advance as

per cent of mean (26.34) was observed for this trait indicating that this trait is under the control of additive gene action. Hence direct selection would be effective for improving this character.

#### **4.1.2.8 Rapidly Digestible Starch (%)**

It consists mainly of amorphous and dispersed starch which is converted to the constituent glucose molecules within 20 minutes of enzyme digestion. Genotypes for this trait showed wide range of variation from 49.75 (BPT 2848) to 70.20 (BPT 3143) with a mean value of 61.14. RDS is rapidly digested and induces a fast increase in blood glucose and insulin levels, which can induce a series of health complications, such as diabetes and cardiovascular diseases, hence the genotypes with low RDS are desirable. Not much variation was observed between RDS content of different colored genotypes used in the present study. Among the brown pericarp colored genotypes, it ranged from 54.59 (BPT 2270) to 65.97 (BPT 2776). Among the red pericarp colored genotypes, it varied from 55.70 (BPT 3137) to 64.59 (Jyothi) while in black pericarp colored genotypes, BPT 2848 exhibited minimum RDS of 49.75 which is desirable. Patindol *et al.* (2010) reported that RDS was highest for Arborio and HB-1.

Low estimates were manifested by this trait for both genotypic (7.26) and phenotypic (7.30) coefficient of variation indicating that variation among the genotypes are low. High heritability (99.0) coupled with moderate genetic advance as per cent of mean (14.89) was observed for this trait suggesting the predominance of both additive and non-additive gene effects in controlling this trait.

#### **4.1.2.9 Slowly Digestible Starch (%)**

Like RDS, SDS is expected to be completely digested in the small intestine, but for one or other reason, it is digested more slowly, resulting in slow and steady release of blood glucose. Hence, genotypes with high SDS value will have low GI and are desirable for inclusion in diet. Among the brown pericarp colored genotypes, BPT 5204 (41.02), BPT 2270 (42.84) and BPT 2660 (41.14) recorded high SDS value which is very much desirable. Among black pericarp colored genotypes under study BPT 2848 recorded maximum SDS of 43.34 and BPT 3139 (40.95) among red genotypes manifested high SDS. All the above mentioned genotypes also manifested low GI and hence they may be consumed for slow and prolonged release of blood glucose. Among

all the genotypes studied this trait showed wide range of variation from 30.28 (BPT 3143) to 43.34 (BPT 2848) with a mean value of 36.14. SDS is inversely proportional to glycemic index hence genotypes with high SDS manifested low GI which are desirable. Patindol *et al.* (2010) reported high SDS in two brown rice varieties SDS *viz.*, Dixiebelle and Tesanai-2.

This trait manifested moderate estimates for both genotypic (10.61) and phenotypic (10.68) coefficient of variation suggesting that variation among the genotypes are low. High heritability (98.8) coupled with high genetic advance as per cent of mean (21.72) was observed for this trait indicating the preponderance of additive gene action in the inheritance of this trait and direct selection may be practised to improve this trait.

#### **4.1.3.0 Resistant starch (%)**

Resistant starch is defined as the fraction of dietary starch which escapes digestion in the small intestine and after entering large intestine it acts as fibre. The health benefits of resistant starch includes improved blood glucose levels and insulin regulation, lower blood cholesterol and triglyceride levels which reduces the risk of colon cancer hence genotypes with high RS are desirable. Genotypes for this trait showed a wide range of variation from 1.10 (Jyothi) to 3.97 (BPT 2848) with a mean value of 2.32. Among the brown pericarp colored genotypes, the RS content ranged from 1.18 (BPT 2776) to 3.21 (BPT 2595). BPT 2595 recorded high RS content, hence it may be recommended for inclusion in diet to improve the carbohydrate quality of rice. Among the red rice genotypes, it varied from 1.21 (Matta Triveni) to 3.52 (BPT 3111) while in black pericarp colored genotypes it ranged from 1.15 (BPT 3141) to 3.97 (BPT 2848). In addition, BPT 3145 (3.41) along with BPT 2848 also recorded high resistant starch suggesting their suitability in diabetic diets. Deepa *et al.* (2010) reported that RS content was high in pigmented rice varieties than non pigmented varieties which is in confirmation with the present results. This trait observed high estimates for both genotypic (36.40) and phenotypic (36.62) coefficient of variation, indicating that variation among the genotypes are low. High heritability (98.80) coupled with high genetic advance as per cent of mean (74.54) was observed for this trait suggesting the role of additive gene action in the inheritance of this trait.

#### **4.1.3.1 Total Phenol Content (mg/100 g)**

Total Phenol content (TPC) among all the genotypes studied, exhibited wide range of variation. Minimum value was observed (48.8) in brown pericarp colored genotype BPT 2776 while BPT 3140, a black genotype (214.34) recorded maximum value with a mean value of 96.10. The phenolic compounds are mainly associated with the pericarp in rice, and the grains with darker pericarp colour such as red and black contain higher amount of polyphenols (Itani, 2004). The concentration of total phenolics in the grain has been positively associated with antioxidant activity (Itani *et al.*, 2002) with potential beneficial effects on health, such as reduction of oxidative stress (Hu *et al.*, 2003). Hence highest amount of phenolic compounds is a desirable trait and the colored rice genotypes (black & red) in the present study contain high amount of phenolic compounds than brown pericarp colored genotypes. Genotypes with highest amount of TPC include BPT 3138 (98.48), BPT 3143 (101.67), BPT 2848 (123.31), Jyothi (132.84), BPT 3144 (150.82), BPT 3141 (156.31), and BPT 2858 (174.48). Among the brown pericarp colored genotypes, BPT 2295 (75.59) recorded maximum phenol content while in red pericarp colored genotypes, Jyothi recorded the highest phenol content. All the genotypes possessing black pericarp manifested high total phenol content. Irkali *et al.* (2012) also reported that total phenol content was more in black and red rice than non pigmented rice. Pathak *et al.* (2017), Chakuton *et al.* (2012) Saikia *et al.* (2012) also reported that pigmented rice had higher amount of total phenol content (79.88 mg GAE/100g) than non pigmented rice (33.23). Chmiel *et al.* (2017) reported that brown rice had higher amount of total phenol content than white rice.

This trait manifested high estimates for both genotypic (43.13) and phenotypic (43.23) coefficient of variation indicating that variation among the genotypes are high. High heritability (99.76) coupled with high genetic advance as per cent of mean (88.85) was observed for this trait suggesting that this trait is under the control of additive gene action and direct selection can be anticipated for improvement of this trait.

#### **4.1.2.9 Total Antioxidant Activity (mg AAE/100 g)**

The trait total antioxidant activity was ranged from 26.87 (BPT 2295) to 111.48 (Jyothi) with a mean value of 78.61. The total antioxidant activity is high in genotypes with red and black pericarp colour when compared to those with a light brown pericarp

colour (Tian *et al.*, 2004). Colored rice was reported to have a health promoting potential due to its instantial antioxidant activity which inhibits the formation or reduces the concentration of reactive cell damaging free radicals thus protecting the body tissues from oxidative damage. Among the brown pericarp colored genotypes, BPT 2660 exhibited high antioxidant activity (46.67) followed by BPT 2782 (44.9). Among red pericarp colored genotypes, it ranged from 105.13 in Aathira to 111.48 in Jyothi, likewise among black pericarp colored genotypes, BPT 3144 exhibited the minimum value with 73.01 while BPT 3140 recorded the maximum value 108.83. When compared with brown pericarp colored rice genotypes, the red and black colored genotypes exhibited more than double value for antioxidant activity. In a comparative study with red and white rice genotypes, Raghuvanshi *et al.* (2017) reported that red pericarp colored rice genotypes showed excellent antioxidant properties which are in agreement with the present results. Veni *et al.* (2016), Pathak *et al.* (2017) and Chakuton *et al.* (2012) also reported that pigmented rice was found to have highest total antioxidant activity than non pigmented rice. Chmiel *et al.* (2017) reported that brown rice had higher antioxidant activity than white rice.

This trait exhibited high estimates for both genotypic (38.82) and phenotypic (38.92) coefficient of variation indicating that variation among the genotypes are high. High heritability (99.5) coupled with high genetic advance as per cent of mean (79.77) was observed for this trait suggesting the role of additive gene effects in controlling this trait. Thus direct selection will help for improvement of this trait.

#### **4.1.2.10 Flavonoid content (mg QE/100 g)**

Flavonoid content among all the genotypes studied exhibited wide range of variation from 82.55 (BPT 3137) to 784.54 (BPT 2848) with a mean value of 349.55. Like antioxidant activity, flavonoid content also differed drastically among different colored genotypes. In brown pericarp colored genotypes, flavonoid content is less when compared with the red and black pericarp colored genotypes. The normal brown varieties recorded a range of 89.69 (BPT 2776) to 153.92 in (BPT 2595) flavonoid content. Among red pericarp colored genotypes, it varied from 277.63 (Harsha) to 434.65 (Matta Triveni) which is two times higher than the brown genotypes. Among the three colored rice genotypes under study, the black pericarp colored genotypes recorded the maximum flavonoid content in BPT 2848 (784.54) followed by BPT 3142 (661.44), BPT 3144 (612.12), BPT 3140 (590.12) and BPT 3136 (560.36). Kim *et al.*

(2010) reported that black cultivars were higher in flavonoids than the red and white cultivars. Raghuvanshi *et al.* (2017) also reported high flavonoid content (120 mg R.E/100g) for red rice. Pathak *et al.* (2017) and Saikia *et al.* (2012) also reported that pigmented rice (red and black) had higher amount of flavonoids than white rice.

This trait manifested high estimates for both genotypic (59.031) and phenotypic (59.122) coefficient of variation indicating that variation among the genotypes are high. High heritability (99.7) coupled with high genetic advance as per cent of mean (121.41) was observed for this trait hence, it may be concluded that this trait is under the control of additive gene effects and direct selection may be practiced for improvement of flavonoid content in rice.

#### **4.1.2.11 Zn content (ppm)**

The trait Zn content ranged from 12.0 (BPT 2295) to 27.9 (BPT 3143) with a mean value of 21.73. When compared with other cereals, rice contains insufficient levels of the key micronutrients iron, zinc and vitamin A to meet the daily dietary requirements. The vast majority of the rural and urban poor in Asia rely heavily on rice for their major source of energy. Even a small increase in its nutritive value could be highly beneficial for human health. When compared with brown pericarp colored genotypes, the red and black colored genotypes under study are rich in Zinc content. Among brown genotypes the Zinc content ranged between 12.0 (BPT 2295) to 18.6 (BPT 2660) whereas in red rice genotypes it varied from 18.9 (Samyuktha) to 26.2 (BPT 3139). In black rice genotypes, maximum Zinc content was recorded by BPT 3143 (27.9) followed by BPT 3141 (27.8) and BPT 3136 (27.0).

As the red and black colored rice is eaten as a whole grain without polishing, the micronutrient malnutrition may be addressed as these genotypes possess high amount of Zn content than brown rice. Pathak *et al.* (2017) and Laenoia *et al.* (2015) also reported that pigmented rice was found to have high amount of Zn content (39 ppm) than non pigmented rice (25.8 ppm). This trait recorded high estimates for both genotypic (20.47) and phenotypic (21.73) coefficient of variation indicating that variation among the genotypes are high. These findings are in agreement with Devi *et al.* (2016) and Savitha and Kumari (2016). High heritability (88.7) coupled with high genetic advance as per cent of mean (39.71) was observed for this trait which are in agreement with the findings of Devi *et al.* (2016) , Patil *et al.* (2015), Sala *et al.* (2015), Samak *et al.* (2015).

#### **4.1.2.12 Fe content (ppm)**

The trait Fe content ranged from 7.0 ppm(BPT 2595) to 19.40 ppm (BPT 2858) with a mean value of 10.63. Major nutritional problems in rice consuming countries comprise malnutrition and deficiencies of iron and zinc. To combat the risk of anaemia in children and women of rural and urban poor, identification of a genotype with high iron content is very much beneficial. In the present investigation, among the genotypes studied, the brown pericarp colored genotypes recorded less Fe content when compared with red and black pericarp colored genotypes. Among red rice, BPT 3111 recorded 16ppm iron content followed by Harsha (12.6 ppm) and Samyuktha (12.5 ppm). Among the black pericarp colored rice genotypes BPT 2858 recorded the maximum Fe content of 19.5 ppm followed by BPT 3130 13.4 ppm, BPT 2848 (12.3) and BPT 3142 (11.1 ppm ). The micronutrient density of seeds /grains is important not only for human nutrition, but also for the nutrition of the seedlings i.e. for production of more vigorous seedlings in the next generation. A more vigorous crop is established by seeds with high density of micronutrients which confer better resistance to stress and diseases and eventually to higher grain yield. Hence the above identified lines may be useful for reducing the risks of malnutrition among rural poor rice consumers. Laenoi *et al.* (2015) reported that brown rice had higher amount of iron content than white rice. Raghuvanshi *et al.* (2017) and Pathak *et al.* (2017) also reported that pigmented rice was found to have high amount of Fe content (3.67 mg/100g) than non pigmented rice (2.67 mg/100g). This trait observed high estimates for both genotypic (23.12) and phenotypic (27.38) coefficient of variation, indicating that variation among the genotypes are high. These findings are in agreement with Devi *et al.* (2016).

High heritability (71.30) coupled with high genetic advance as per cent of mean (40.21) was observed for this trait. These findings are in agreement with Devi *et al.* (2016) Patil *et al.* (2015), Sala *et al.* (2015), Samak *et al.* (2015).

#### **4.1.2.13 Glycemic Index (%)**

Glycemic index is the classification of food based on the blood glucose response to a food relative to the standard glucose solution and is considered as the therapeutic principle for Diabetes mellitus. For a measurable control of metabolic syndromes, proper choice of food is necessary which offers better satiety, decreased postprandial blood glucose level. Foods with GI lower than 55 are called as low GI

foods. They are safe for diabetic patients, as they result in a gradual and steady rise in blood sugar. Foods with GI between 46 and 69 are low to medium GI foods. These help in slower and smooth rise in blood sugar, hence they are healthy diet options for diabetic diet. Foods with GI above 70 are high GI foods and should be restricted in diabetic diet. In the present study genotypes for this trait showed wide range of variation ranging from 49.75 (BPT 2848) to 70.20 (BPT 3143) with a mean value of 59.75. Among different colored rice genotypes no variation was observed for glycemic index. Majority of the genotypes under study exhibited low to medium GI. BPT 5204, a popular high yielding variety which is most preferred by both consumers as well as traders and farmers in A.P, Telangana, Tamilnadu and Karnataka recorded a low GI value of 54.44. Another popular variety Bhavapuri Sannalu (BPT 2270) with excellent cooking quality traits also recorded low GI value of 53.26. In addition, BPT 2660 a minikit culture developed from ARS, Bapatla also manifested low GI value of 54.18. Among the red pericarp colored genotypes GI ranged from 54.13 (BPT 3139) to 64.0 (Jyothi). Among the black genotypes BPT 2848 exhibited lowest GI value of 49.75. Hence the genotypes which exhibited low GI value will provide better satiety during meals as compared to those which have high GI and give sustained level of blood sugar if consumed.

This trait manifested low estimates for both genotypic (8.27) and phenotypic (8.42) coefficient of variation, indicating that variation among the genotypes are low. High heritability (96.6) coupled with moderate genetic advance as per cent of mean (16.75) was observed for this trait suggesting the predominance of both additive and non-additive gene effects in controlling this character.

Among the brown pericarp colored genotypes, BPT 5204, a popular variety with excellent cooking quality traits manifested all the quality parameters in the desirable range and had a low GI value. Another variety BPT 2270 along with BPT 2660, a minikit culture also recorded low GI coupled with other desirable quality traits. All these genotypes possess medium slender type. BPT 2595 recorded high RS content and flavonoid content among the tested brown rice genotypes which is desirable. Among red pericarp colored genotypes, BPT 3139 manifested low GI coupled with high antioxidant activity, high protein & Zn content. However, Jyothi, Matta Triveni and BPT 3111 recorded high antioxidant activity coupled with high Zn & Iron content coupled with high grain yield. Among black pericarp colored genotypes, BPT 2848

manifested highly desirable quality parameters along with high yield potential. It also recorded high protein content, high flavonoid content, high SDS & RS content coupled with low GI value. Hence, it can be recommended for inclusion in diabetic diet. When compared with BPT 5204, which is highly preferred by consumers for its quality traits BPT 2595 and all red and black colored genotypes recorded high antioxidant activity. Zn, Fe and protein content also high in red and black genotypes. From the present study BPT 2848 (black) and BPT 3139 (red) were identified as promising genotypes with high grain yield, high antioxidant activity and micronutrient content, high protein content coupled with low GI.

Among the yield component traits test weight, total number of grains per panicle, number of filled grains per panicle and grain yield recorded high estimates for all the genetic parameters studied suggesting that inheritance of these traits is controlled by additive gene effects hence these can be improved by direct selection. The remaining traits *viz.*, ear bearing tillers, plant height, panicle length and days to 50% flowering are controlled by both additive and non additive gene effects and the improvement of these traits is not possible by direct selection.

Among physical and cooking quality parameters, the traits *viz.*, solid loss, water uptake, alkali spreading value, volume expansion ratio and amylose content manifested high estimates for all the genetic parameters suggesting that predominance of additive gene effects in controlling these traits while L/B ratio is controlled by both additive and non additive gene effects. Among nutritional and biochemical quality parameters, total phenol content, total antioxidant activity, flavonoid content, zinc content, iron content, protein content, total starch content, slowly digestible starch and resistant starch exhibited high estimates for all the genetic parameters studied suggesting that predominance of additive gene effects. Hence these traits can be improved through direct selection. Glycemic index and rapidly digestible starch manifested high heritability and moderate genetic advance, indicating that inheritance of these traits controlled by both additive and non additive gene effects suggesting that improvement of these traits is not anticipated by direct selection methods.

## 4.2 CORRELATION

Direct selection for yield and quality traits is not effective as they are complex quantitative characters, highly influenced by environment. High genotype and environment interaction will restrict improvement, if selection is based on yield per se. The effective improvement in yield may be brought about through selection on yield component characters. The aim of correlation studies is primarily to know the suitability of various characters for indirect selection because any particular trait may bring about undesirable changes in other associated characters (Singh, 1998).

Yield component characters show associations among themselves and also with yield. Unfavourable associations between the desired attributes under selection may limit genetic advance. Hence, knowledge of relationship between the yield and yield components and also among the yield components is essential for planning a sound selection programme (Falconer, 1964).

In general, the results revealed that the genotypic correlation coefficients were higher than the phenotypic correlation coefficients for almost all the characters under study. This may be due to the relative stability of genotypes as majority of them were subjected to certain amount of selection (Johnson *et al.*, 1955). The phenotypic and genotypic correlation coefficients for different grain yield components and quality parameters are presented in Tables 4.4 and 4.5 and discussed here under.

### 4.2.1 Yield component characters

#### 4.2.1.1 Days to 50% flowering

Days to 50% flowering recorded positive and significant association with ear bearing tillers (0.383<sup>\*\*</sup> and 0.755<sup>\*\*</sup>), water uptake (0.375<sup>\*\*</sup> and 0.407<sup>\*\*</sup>), volume expansion ratio (0.224<sup>\*</sup> and 0.285<sup>\*</sup>), alkali spreading value (0.444<sup>\*\*</sup> and 0.574<sup>\*\*</sup>), length/breadth ratio (0.342<sup>\*\*</sup> and 0.453<sup>\*\*</sup>) and slowly digestible starch (0.269<sup>\*</sup> and 0.296<sup>\*\*</sup>) at both phenotypic and genotypic levels respectively. Suggesting that brown pericarp colored long duration genotypes had more number of ear bearing tillers, more L/B ratio and high SDS content. And also reported significant and positive association of days to 50% flowering with ear bearing tillers. But it had negative significant association with Panicle Length (-0.382<sup>\*\*</sup> and -0.539<sup>\*\*</sup>), Test weight (-0.601<sup>\*\*</sup> and

-0.664\*\*), Protein content (-0.420\*\* and -0.452\*\*), Total starch content (-0.446\*\* and -0.477\*\*), Total phenol content (-0.335\*\* and -0.355\*\*), Total antioxidant activity (-0.837\*\* and -0.900\*\*), Flavonoid content (-0.540\*\* and -0.579\*\*), Zn content (-0.701\*\* and -0.801\*\*), Fe content (-0.305\*\*, -0.396\*\*), GI (-0.314\*\* and -0.343\*\*) and RDS (-0.250\*\* and -0.252\*\*) at phenotypic and genotypic level respectively. These results suggest that red and black pericarp colored genotypes under study in the present investigation that flowered early exhibited more panicle length and test weight. Similar findings were also reported by Sharma & Sharma., (2007). Further it can be concluded that micronutrient concentration, total phenol content, antioxidant activity, flavonoid content, were also more for this red and black colored genotypes when compared with brown pericarp colored rice genotypes.

This trait had significant negative association with plant height (-0.239\*) at genotypic level only. This trait recorded the Significant negative association with the grain yield per plant (-0.469\*\* and -0.582\*\*) at phenotypic and genotypic level respectively suggesting that the genotypes which flowered early recorded high grain yield per plant. Similar findings were previously reported by Pankaj *et al.* (2010) and Lakshmi *et al.* (2017).

#### **4.2.1.2 Panicle Length**

Panicle length manifested positive and significant association with plant height (0.367\*\* and 0.510\*\*), number of filled grains per panicle (0.347\*\* and 0.452\*\*), total number of grains per panicle (0.348\*\* and 0.426\*\*), solid loss (0.362\*\* and 0.366\*\*), total phenol content (0.285\* and 0.342\*\*), total antioxidant activity (0.324\*\* and 0.394\*\*), flavonoid content (0.330\*\* and 0.391\*\*), Zn content (0.334\*\* and 0.445\*\*), Fe content (0.246\* and 0.245\*) and resistant starch (0.240\* and 0.245\*) at both phenotypic and genotypic level respectively. This is an important trait which will directly increase the yield. This trait showed positive significant association with filled grains per panicle, indicating that lengthy panicle will accommodate more number of grains per panicle. Hence, simultaneous improvement of these traits in the breeding programme are anticipated.

It showed positive significant association with fertility % (0.427\*\*) and protein content (0.236\*) only at genotypic level. These results suggest that the red and black colored genotypes which recorded more panicle length also possessed more filled

grains, total grains per panicle and exhibited high Zn, Fe, protein content, total phenol content, antioxidant activity and resistant starch. Panicle length recorded significant and negative relationship with days to 50% flowering (-0.382\*\* and -0.539\*\*), ear bearing tillers per plant (-0.222\* and -0.513\*\*), volume expansion ratio (-0.394\*\* and -0.485\*\*) at both phenotypic and genotypic level respectively, but it had negative significant association with water uptake only at genotypic level.

It had significant positive association with grain yield per plant (0.277\* and 0.358\*\*) at both phenotypic and genotypic level. These results are in agreement with the findings reported by Priya *et al.* (2017), Lakshmi *et al.* (2017), Chowdhury *et al.* (2016b), Bhati *et al.* (2015), Ekka *et al.* (2015), Veni *et al.* (2013), and Sanghera *et al.* (2013).

#### **4.2.1.2 Plant Height**

Plant height showed significant positive correlation with panicle length (0.367\*\* and 0.510\*\*), test weight (0.243\* and 0.294\*\*), protein content (0.226\* and 0.248\*), total phenol content (0.330\*\* and 0.365\*\*), total antioxidant activity (0.407\*\* and 0.448\*\*) at both phenotypic and and genotypic level. But with number of filled grains per panicle (0.347\*\*) it had significant positive association only at phenotypic level, and with fertility % (0.225\*) at genotypic level. On observation of these results, it may be concluded that genotypes which recorded more plant height in the present study manifested more panicle length and bold grains & high protein content also. Positive association of plant height with panicle length and test weight was previously reported by Krishna *et al.* (2009).

This trait showed negative significant association with ear bearing tillers per plant (-0.326\*\* and -0.402\*\*), alkali spreading value (-0.422\*\* and -0.546\*\*) at both phenotypic and genotypic levels and with days to 50% flowering (-0.238\*) at genotypic level. These results are in agreement with the results reported by Sameera *et al.* (2016), Jan *et al.* (2017), and Lakshmi *et al.* (2017). This trait showed positive non significant association at phenotypic (0.161) and genotypic (0.145) levels with grain yield which is in agreement with the results reported by Jan *et al.* (2017), and Sanghera *et al.* (2013),

#### 4.2.1.2 Ear Bearing Tillers per plant

Ear bearing tillers per plant showed positive and significant correlation with days to 50% flowering (0.383<sup>\*\*</sup> and 0.755<sup>\*\*</sup>), volume expansion ratio (0.275<sup>\*\*</sup> and 0.530<sup>\*\*</sup>) at both phenotypic and genotypic levels respectively and with water uptake (0.336<sup>\*\*</sup>) and alkali spreading value (0.355<sup>\*\*</sup>) at genotypic level only.

It had negative and significant association with panicle length (-0.222<sup>\*</sup> and -0.513<sup>\*\*</sup>), plant height (-0.326<sup>\*\*</sup> and -0.402<sup>\*\*</sup>), test weight (-0.311<sup>\*\*</sup> and -0.513<sup>\*\*</sup>), total starch (-0.247<sup>\*\*</sup> and -0.402<sup>\*\*</sup>), total antioxidant activity (-0.476<sup>\*\*</sup> and -0.778<sup>\*\*</sup>), flavanoid content (-0.234<sup>\*</sup> and -0.393<sup>\*\*</sup>), Zn content (-0.367<sup>\*\*</sup> and -0.617<sup>\*\*</sup>) at both phenotypic and genotypic levels respectively, but with total phenol content (-0.295<sup>\*\*</sup>) and Fe content (-0.292<sup>\*\*</sup>) at genotypic level.

This trait showed negative non significant association (-0.03) at phenotypic level and positive non significant association (0.115) at genotypic level with grain yield. These results are in agreement with the findings reported by Nandan *et al.* (2010), Jan *et al.* (2017) and Ekka *et al.* (2015).

#### 4.2.1.3 Test Weight

The trait test weight manifested positive and significant relationship with plant height (0.243<sup>\*</sup> and 0.294<sup>\*\*</sup>), amylose content (0.276<sup>\*</sup> and 0.309<sup>\*\*</sup>), protein content (0.248<sup>\*</sup> and 0.253<sup>\*</sup>), total starch (0.537<sup>\*\*</sup> and 0.546<sup>\*\*</sup>), total antioxidant activity (0.648<sup>\*\*</sup> and 0.661<sup>\*\*</sup>), flavanoid content (0.240<sup>\*</sup> and 0.246<sup>\*</sup>) and Zn content (0.333<sup>\*\*</sup> and 0.367<sup>\*\*</sup>) suggesting that bolder genotypes used in the present investigation had more protein & Zn content coupled with high antioxidant activity and flavonoid content also. It had negative significant association with days to 50% flowering (-0.601<sup>\*\*</sup> and -0.664<sup>\*\*</sup>), ear bearing tillers per plant (-0.311<sup>\*\*</sup> and -0.513<sup>\*\*</sup>), number of filled grains per panicle (-0.321<sup>\*\*</sup> and -0.378<sup>\*\*</sup>), total number of grains per panicle (-0.321<sup>\*\*</sup> and -0.392<sup>\*\*</sup>), solid loss (-0.226<sup>\*</sup> and -0.233<sup>\*</sup>), water uptake (-0.231<sup>\*</sup> and -0.233<sup>\*</sup>), alkali spreading value (-0.647<sup>\*\*</sup> and -0.779<sup>\*\*</sup>) and length/breadth ratio (-0.388<sup>\*\*</sup> and -0.553<sup>\*\*</sup>) at both phenotypic and genotypic levels respectively.

This trait manifested positive and significant association with grain yield (0.424<sup>\*\*</sup> and 0.498<sup>\*\*</sup>) at both phenotypic and genotypic levels respectively indicating that the genotypes with bolder grain will improve the grain yield. These results are in

agreement with the results reported by Nagesh *et al.*(2012), Veni *et al.* (2013), Bhati *et al.* (2015), Naseem *et al.* (2014), Chowdhury *et al.* (2016b), Sameera *et al.* (2016), Priya *et al.* (2017), Sowmiya and Venkatesan (2017).

#### **4.2.1.4 Number of filled grains per panicle**

Number of filled grains per panicle exhibited significant positive association with panicle length (0.347<sup>\*\*</sup> and 0.452<sup>\*\*</sup>), total number of grains per panicle (0.988<sup>\*\*</sup> and 0.996<sup>\*\*</sup>), fertility % (0.388<sup>\*\*</sup> and 0.580<sup>\*\*</sup>), solid loss (0.230<sup>\*</sup> and 0.261<sup>\*</sup>), flavonoid content (0.235<sup>\*</sup> and 0.267<sup>\*</sup>), slowly digestible starch (0.286<sup>\*</sup> and 0.333<sup>\*\*</sup>), resistant starch (0.292<sup>\*\*</sup> and 0.340<sup>\*\*</sup>) at both phenotypic and genotypic levels respectively but with alkali spreading value (0.315<sup>\*\*</sup>) at genotypic level only.

This trait showed significant negative association with test weight (-0.321<sup>\*\*</sup> and -0.378<sup>\*\*</sup>), glycemic index (-0.275<sup>\*</sup> and -0.322<sup>\*\*</sup>) and rapidly digestible starch (-0.418<sup>\*\*</sup> and -0.589<sup>\*\*</sup>) at both phenotypic and genotypic levels respectively. These results suggest that the genotypes which had more filled grains per panicle recorded less test weight *i.e.* they had slender grain type. Hence, it showed negative non significant association with grain yield (-0.037 and -0.079) which are in agreement with the results reported by Jan *et al.* (2017)

#### **4.2.1.4 Total number of grains per panicle**

Total number of grains per panicle showed significant and positive correlation with panicle length (0.348<sup>\*\*</sup> and 0.426<sup>\*\*</sup>), number of filled grains per panicle (0.988<sup>\*\*</sup> and 0.996<sup>\*\*</sup>), fertility % (0.247<sup>\*</sup> and 0.503<sup>\*\*</sup>), flavonoid content (0.233<sup>\*</sup> and 0.269<sup>\*</sup>), slowly digestible starch (0.296<sup>\*\*</sup> and 0.352<sup>\*\*</sup>), resistant starch (0.288<sup>\*</sup> and 0.339<sup>\*\*</sup>) at both phenotypic and genotypic levels respectively but with alkali spreading value (0.322<sup>\*\*</sup>) at genotypic level only.

This trait showed significant negative association with test weight (-0.321<sup>\*\*</sup> and -0.392<sup>\*\*</sup>), glycemic index (-0.295<sup>\*\*</sup> and -0.358<sup>\*\*</sup>) and rapidly digestible starch (-0.433<sup>\*\*</sup> and -0.513<sup>\*\*</sup>) at both phenotypic and genotypic levels respectively indicating that the genotypes possessing more number of total grains per panicle recorded less test weight. Hence, it may be concluded that even though these genotypes had more number of grains they could not improve the grain yield and resulted in negative non significant association with grain yield (-0.068 and -0.114). These results find support by Sowmiya and Venkatesan (2017) and Jan *et al.* (2017).

#### 4.2.1.5 Fertility %

Fertility % showed significant positive association with total number of grains per panicle (0.247<sup>\*</sup>), number of filled grains per panicle (0.388<sup>\*\*</sup>) and solid loss (0.350<sup>\*\*</sup>) at phenotypic level suggesting that the genotypes which had more number of filled grains and total grains per panicle also exhibited high fertility percentage.

It showed significant positive association with panicle length (0.427<sup>\*\*</sup>), plant height (0.225<sup>\*</sup>), number of filled grains per panicle (0.580<sup>\*\*</sup>), total number of grains per panicle (0.503<sup>\*\*</sup>) and solid loss (0.613<sup>\*\*</sup>) and total phenol content (0.350<sup>\*\*</sup>) but it had significant negative association with water uptake (-0.288<sup>\*\*</sup>) and total starch (-0.297<sup>\*\*</sup>) at genotypic level. This trait showed positive non significant association with the grain yield (0.161 and 0.216) at both phenotypic and genotypic levels respectively which is in agreement with the results reported by Kole *et al.* (2008).

### 4.2.2 Quality parameters

#### 4.2.2.1 Solid loss

Solid loss manifested positive significant association with panicle length (0.302<sup>\*\*</sup> and 0.366<sup>\*\*</sup>), number of filled grains per panicle (0.230<sup>\*</sup> and 0.261<sup>\*</sup>), fertility % (0.350<sup>\*\*</sup> and 0.613<sup>\*\*</sup>), protein content (0.475<sup>\*\*</sup> and 0.480<sup>\*\*</sup>), resistant starch (0.242<sup>\*</sup> and 0.245<sup>\*</sup>), but it had significant negative association with test weight (-0.226<sup>\*</sup> and -0.233<sup>\*</sup>), volume expansion ratio (-0.254<sup>\*</sup> and -0.291<sup>\*\*</sup>), total starch (-0.324<sup>\*\*</sup> and -0.327<sup>\*\*</sup>) and rapidly digestible starch (-0.250<sup>\*</sup> and -0.253<sup>\*</sup>) at both phenotypic and genotypic levels. These results suggest that the genotypes with more panicle length, filled grains per panicle coupled with high protein content had more solid loss while those genotypes with more test weight *i.e.* bolder grain types manifested less solid loss.

This trait showed positive non significant association with the grain yield (0.029 and 0.036) at both phenotypic and genotypic levels respectively suggesting that these two traits may be improved independently.

#### 4.2.2.2 Water uptake

Water uptake showed significant positive association with days to 50% flowering (0.375<sup>\*\*</sup> and 0.407<sup>\*\*</sup>), length/breadth ratio (0.290<sup>\*</sup> and 0.393<sup>\*\*</sup>) at phenotypic level suggesting that the genotypes which flowered late manifested more water uptake

and possessed slender grain type. With ear bearing tillers per plant (0.336<sup>\*\*</sup>) and volume expansion ratio (0.231<sup>\*</sup>) it had positive and significant relationship at genotypic level.

At phenotypic level this trait showed negative and significant relationship with test weight (-0.231<sup>\*</sup>) and fertility % (-0.288<sup>\*</sup>), and at genotypic level with panicle length (-0.220<sup>\*</sup>) and test weight (-0.233<sup>\*</sup>) at genotypic level. This trait showed negative and significant association with grain yield per plant (-0.266<sup>\*</sup>) at genotypic level suggesting that the genotypes which produced more grain yield manifested low water uptake.

**Table 4.4. Estimates of phenotypic & genotypic correlation coefficients among yield, yield components and quality traits in rice (*Oryza sativa* L.).**

		1	2	3	4	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	5
1	P	<b>1.000</b>	-0.38**	-0.19	0.38**	-0.60**	-0.03	-0.020	-0.089	0.063	0.37**	0.22*	0.44**	0.34**	0.018	-0.42**	-0.44**	-0.33**	-0.83**	-0.54**	-0.70**	-0.30**	-0.31**	0.26*	-0.23*	0.084	<b>-0.469**</b>
	G	<b>1.000</b>	-0.53**	-0.23*	0.75**	-0.66**	0.014	0.015	0.005	0.070	0.40**	0.28*	0.57**	0.45**	0.025	-0.45**	-0.47**	-0.35**	-0.90**	-0.57**	-0.81**	-0.39**	-0.34**	0.29**	-0.25*	0.095	<b>-0.582**</b>
2	P		<b>1.000</b>	0.36**	-0.22**	0.033	0.34**	0.34**	0.064	0.30**	-0.18	-0.39**	-0.066	0.012	-0.17	0.19	0.059	0.28*	0.32**	0.33**	0.33**	0.24*	0.054	-0.14	-0.039	0.24*	<b>0.277*</b>
	G		<b>1.000</b>	0.51**	-0.51**	0.000	0.45**	0.42**	0.42**	0.36**	-0.22*	-0.48**	-0.091	-0.063	-0.21	0.23*	0.074	0.34**	0.39**	0.39**	0.44**	0.24*	0.070	-0.15	-0.048	0.26*	<b>0.358**</b>
3	P			<b>1.000</b>	-0.32**	0.24*	-0.002	-0.020	0.095	0.11	0.082	-0.16	-0.42**	0.10	0.036	0.22*	0.026	0.33**	0.40**	0.20	0.14	0.10	0.17	-0.10	0.10	-0.059	<b>0.161</b>
	G			<b>1.000</b>	-0.40**	0.29**	-0.004	-0.035	0.22*	0.12	0.090	-0.19	-0.54**	0.09	0.043	0.24*	0.029	0.36**	0.44**	0.23*	0.18	0.15	0.19	-0.13	0.10	-0.059	<b>0.145</b>
4	P				<b>1.000</b>	-0.31**	-0.021	-0.008	-0.065	0.031	0.20	0.27*	0.12	0.11	0.048	-0.15	-0.24*	-0.17	-0.47**	-0.23*	-0.36**	-0.18	-0.056	-0.022	0.042	-0.096	<b>-0.003</b>
	G				<b>1.000</b>	-0.51**	-0.087	-0.097	0.11	0.076	0.33**	0.53**	0.35**	0.14	0.111	-0.28*	-0.40**	-0.29*	-0.77**	-0.59**	-0.61**	-0.29*	-0.094	-0.026	0.090	-0.18	<b>0.115</b>
6	P					<b>1.000</b>	-0.32**	-0.32**	-0.11	-0.22*	-0.23*	-0.17	-0.64**	0.27*	0.24*	0.53**	-0.097	0.64**	0.24*	0.33**	0.18	0.083	-0.10	0.18	-0.070	<b>0.424**</b>	
	G					<b>1.000</b>	-0.37**	-0.39**	-0.10	-0.23*	-0.23*	-0.18	-0.77**	-0.55**	0.30**	0.25*	0.54**	-0.099	0.66**	0.24*	0.36**	0.20	0.083	-0.10	0.18	-0.075	<b>0.498**</b>
7	P						<b>1.000</b>	0.98**	0.38**	0.23*	-0.055	-0.075	0.18	0.13	-0.064	-0.039	-0.052	0.32**	-0.099	0.23*	0.13	0.08	-0.27*	0.28*	-0.41**	0.29**	<b>-0.037</b>
	G						<b>1.000</b>	0.99**	0.58**	0.26*	-0.061	-0.12	0.31**	0.18	-0.10	-0.035	-0.064	0.37**	-0.11	0.26*	0.18	0.15	-0.33**	0.33**	-0.48**	0.34**	<b>-0.079</b>
8	P							<b>1.000</b>	0.24*	0.18	-0.038	-0.099	0.17	0.13	-0.066	-0.060	-0.024	0.30**	-0.097	0.23*	0.13	0.086	-0.29*	0.29**	-0.43**	0.28*	<b>-0.068</b>
	G							<b>1.000</b>	0.50**	0.20	-0.039	-0.14	0.32**	0.15	-0.10	-0.060	-0.032	0.35**	-0.11	0.26*	0.17	0.15	-0.35**	0.35**	-0.51**	0.33**	<b>-0.114</b>
9	P								<b>1.0000</b>	0.35**	-0.152	0.14	0.067	0.040	-0.021	0.082	-0.17	0.20	-0.030	0.047	0.052	-0.012	0.066	0.030	-0.029	0.070	<b>0.161</b>
	G								<b>1.000</b>	0.61**	-0.28*	0.18	0.066	0.36**	-0.11	0.15	-0.30**	0.35**	-0.062	0.074	0.11	0.11	0.10	0.027	-0.058	0.12	<b>0.216</b>
10	P									<b>1.000</b>	0.026	-0.25*	0.072	-0.025	-0.12	0.47**	-0.32**	0.15	-0.10	0.15	0.008	-0.003	-0.12	0.12	-0.25*	0.24*	<b>0.029</b>
	G									<b>1.000</b>	0.034	-0.29**	0.086	-0.032	-0.13	0.48**	-0.32**	0.15	-0.10	0.15	0.010	-0.007	-0.12	0.12	-0.25*	0.24*	<b>0.036</b>
11	P										<b>1.000</b>	0.19	0.15	0.29*	-0.17	-0.060	-0.17	0.049	-0.17	-0.17	-0.11	-0.14	-0.12	0.16	-0.11	-0.12	<b>-0.201</b>
	G										<b>1.000</b>	0.23*	0.19	0.39**	-0.18	-0.061	-0.17	0.050	-0.18	-0.18	-0.12	-0.16	-0.13	0.17	-0.11	-0.12	<b>-0.226*</b>
12	P											<b>1.000</b>	0.080	0.26*	-0.088	-0.18	-0.10	0.051	-0.25*	-0.19	-0.004	-0.042	0.23*	-0.025	0.24*	-0.42**	<b>0.0003</b>
	G											<b>1.000</b>	0.079	0.40**	-0.10	-0.19	-0.11	0.055	-0.28*	-0.21	0.000	-0.048	0.24*	-0.033	0.25*	-0.44**	<b>0.033</b>
13	P												<b>1.000</b>	0.11	-0.38**	-0.21	-0.33**	0.008	-0.56**	-0.12	-0.30**	-0.14	-0.10	-0.004	-0.083	0.20	<b>-0.264*</b>
	G												<b>1.000</b>	0.65**	-0.46**	-0.25*	-0.40**	0.009	-0.68**	-0.14	-0.36**	-0.23*	-0.12	-0.010	-0.10	0.24*	<b>-0.383**</b>
14	P													<b>1.000</b>	-0.15	-0.044	-0.31**	0.33**	-0.22*	0.047	-0.025	-0.060	0.26*	-0.18	0.19	-0.11	<b>-0.224*</b>
	G													<b>1.000</b>	-0.21	-0.062	-0.42**	0.44**	-0.30**	0.63	-0.066	-0.12	0.37**	-0.25*	0.25*	-0.16	<b>-0.306**</b>

\* Significant at 5% level, \*\* Significant at 1% level

contd...

Char acter		1	2	3	4	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	5
15	P														<b>1.000</b>	0.038	0.020	-0.111	0.029	0.045	-0.127	0.184	-0.201	-0.001	-0.069	0.330**	<b>0.064</b>
	G														<b>1.000</b>	0.043	0.017	-0.116	0.033	0.045	-0.154	0.227*	-0.222*	-0.005	-0.078	0.344**	<b>0.075</b>
16	P														<b>1.000</b>	0.047	0.509**	0.422**	0.777**	0.405**	0.282*	0.282*	-0.354**	0.205	0.038	0.490**	
	G														<b>1.000</b>	0.048	0.511**	0.425**	0.780**	0.423**	0.338**	0.288*	-0.359**	0.206	0.038	0.558**	
17	P														<b>1.000</b>	-0.286*	0.411**	0.071	0.378**	-0.104	-0.003	-0.003	0.130	-0.152	0.314**		
	G														<b>1.000</b>	-0.287*	0.412**	0.071	0.405**	-0.130	-0.004	-0.006	0.128	-0.153	0.357**		
18	P														<b>1.000</b>	0.445**	0.663**	0.424**	0.425**	0.363**	-0.262*	0.106	0.007	0.111			
	G														<b>1.000</b>	0.447**	0.664**	0.451**	0.502**	0.369**	-0.264*	0.106	0.006	0.126			
19	P														<b>1.000</b>	0.475**	0.694**	0.456**	0.333**	-0.222*	0.202	-0.134	0.349**				
	G														<b>1.000</b>	0.478**	0.740**	0.532**	0.341**	-0.224*	0.204	-0.134	0.395**				
20	P														<b>1.000</b>	0.447**	0.356**	0.281*	-0.435**	0.199	0.089	0.504**					
	G														<b>1.000</b>	0.478**	0.429**	0.286*	-0.437**	0.201	0.089	0.574**					
21	P														<b>1.000</b>	0.321**	0.243*	-0.120	0.150	-0.100	0.290*						
	G														<b>1.000</b>	0.415**	0.282*	-0.122	0.172	-0.091	0.345**						
22	P														<b>1.000</b>	-0.109	0.068	-0.206	0.343**	0.211							
	G														<b>1.000</b>	-0.135	0.072	-0.257*	0.399**	0.282*							
23	P														<b>1.000</b>	-0.823**	0.888**	-0.586**	0.236*								
	G														<b>1.000</b>	-0.839**	0.904**	-0.602**	0.281*								
24	P														<b>1.000</b>	-0.902**	0.333**	-0.413**									
	G														<b>1.000</b>	-0.919**	0.338**	-0.485**									
25	P														<b>1.000</b>	-0.581**	0.373**										
	G														<b>1.000</b>	-0.588**	0.410**										
26	P														<b>1.000</b>	-0.139											
	G														<b>1.000</b>	-0.160											
5	P																										<b>1.000</b>
	G																										<b>1.000</b>

\* Significant at 5% level, \*\* Significant at 1% level

1 (days to 50%flowering), 2(panicle length), 3(plant height), 4(ear bearing tillers), 5(grain yield per plant), 6(test weight), 7 (number of filled grains per panicle), 8 (total number of grains per panicle), 9 (spikelet %), 10 (solid loss), 11 (water uptake), 12 (volume expansion ratio), 13 (alkali spreading value), 14 (L/B ratio), 15 (amylose content), 16 (protein content), 17 (total starch), 18 (total phenol content), 19 (total antioxidant activity), 20 (flavonoid content), 21 (zinc content ), 22 (iron content), 23(glycemic index), 24 (slowly digestible starch), 25 (rapidly digestible starch) and 26 (resistant starch)

#### 4.2.2.3 Volume expansion ratio

Volume expansion ratio manifested positive and significant association with days to 50 % flowering (0.224<sup>\*</sup> and 0.285<sup>\*</sup>), ear bearing tillers per plant (0.275<sup>\*</sup> and 0.530<sup>\*\*</sup>), length/breadth ratio (0.269<sup>\*</sup> and 0.408<sup>\*\*</sup>), glycemic index (0.231<sup>\*</sup> and 0.243<sup>\*</sup>), and rapidly digestible starch (0.242<sup>\*</sup> and 0.259<sup>\*</sup>) at both phenotypic and genotypic levels but with water uptake (0.231<sup>\*</sup>) at genotypic level only. These results indicate that the slender grain types with more tillers manifested more volume expansion ratio which is a desirable trait.

It had negative and significant relationship with panicle length (-0.394<sup>\*\*</sup> and -0.485<sup>\*\*</sup>), solid loss (-0.254<sup>\*</sup> and -0.291<sup>\*\*</sup>) and total antioxidant activity (-0.258<sup>\*</sup> and -0.281<sup>\*</sup>) at both phenotypic and genotypic levels. It had negative and significant relationship with the grain yield (-0.226<sup>\*</sup>) at genotypic level indicating that the genotypes which recorded high volume expansion ratio manifested low grain yield.

#### 4.2.2.4 Alkali Spreading Value

Alkali spreading value showed positive and significant association with days to 50% flowering (0.574<sup>\*\*</sup>), ear bearing tillers per plant (0.355<sup>\*\*</sup>), number of filled grains per panicle (0.315<sup>\*\*</sup>), total number of grains (0.322<sup>\*\*</sup>), length/breadth ratio (0.653<sup>\*\*</sup>), and resistant starch (0.245<sup>\*</sup>) at genotypic level but with days to 50% flowering at phenotypic level (0.444<sup>\*\*</sup>) suggesting that the slender genotypes which had more tillers, more number of filled grains and total number of grains per panicle, manifested high alkali spreading value.

It had negative and significant relationship with plant height (-0.422<sup>\*\*</sup> and -0.546<sup>\*\*</sup>), test weight (-0.647<sup>\*\*</sup> and -0.779<sup>\*\*</sup>), amylose content (-0.384<sup>\*\*</sup> and -0.469<sup>\*\*</sup>), total starch (-0.337<sup>\*\*</sup> and -0.407<sup>\*\*</sup>), total antioxidant activity (-0.565<sup>\*\*</sup> and -0.683<sup>\*\*</sup>) and Zn content (-0.305<sup>\*\*</sup> and -0.366<sup>\*\*</sup>) at both phenotypic and genotypic level, but with protein content (-0.254<sup>\*</sup>) and Fe content (-0.232<sup>\*</sup>) at genotypic level only. This trait had negative and significant relationship with grain yield (-0.264<sup>\*</sup> and -0.383<sup>\*\*</sup>) at phenotypic and genotypic level indicating that among the genotypes included in the present study, the low yielding genotypes manifested high alkali spreading value which is in agreement with the results reported by Nagajyothi *et al.* (2001).

#### 4.2.2.5 Length/Breadth ratio

Length/breadth ratio manifested positive and significant association with days to 50% flowering (0.342<sup>\*\*</sup> and 0.453<sup>\*\*</sup>), water uptake (0.290<sup>\*</sup> and 0.393<sup>\*\*</sup>), volume expansion ratio (0.269<sup>\*</sup> and 0.408<sup>\*\*</sup>), total phenol content (0.330<sup>\*\*</sup> and 0.446<sup>\*\*</sup>), glycemic index (0.269<sup>\*</sup> and 0.370<sup>\*\*</sup>) at both phenotypic and genotypic level and alkali spreading value (0.653<sup>\*\*</sup>), rapidly digestible starch (0.259<sup>\*</sup>) at genotypic level. These results suggest that the genotypes with slender grain type took more days for flowering and exhibited high water uptake and volume expansion ratio. This trait showed negative and significant association with test weight (-0.388<sup>\*\*</sup> and -0.553<sup>\*\*</sup>), total starch (-0.313<sup>\*\*</sup> and -0.422<sup>\*\*</sup>), total antioxidant activity (-0.222<sup>\*</sup> and -0.302<sup>\*\*</sup>) at both phenotypic and genotypic level, and with slowly digestible starch (-0.254<sup>\*</sup>) at genotypic level. Indicating that the genotypes with slender grains had less test weight resulting in low grain yield and hence this trait showed negative and significant relationship with grain yield (-0.224<sup>\*</sup> and -0.306<sup>\*\*</sup>) at phenotypic and genotypic levels which is in agreement with previous results reported by Nandan *et al.* (2010), and Veni *et al.* (2006).

#### 4.2.2.6 Amylose content

Amylose content exhibited positive and significant association with test weight (0.276<sup>\*</sup> and 0.309<sup>\*\*</sup>) and resistant starch (0.330<sup>\*\*</sup> and 0.344<sup>\*\*</sup>) at phenotypic and genotypic level and with Fe content at genotypic level. It had negative and significant association with alkali spreading value (-0.384<sup>\*\*</sup> and -0.469<sup>\*\*</sup>) at both phenotypic and genotypic level and with glycemic index (-0.222<sup>\*</sup>) at genotypic level. Significant negative association of amylose content with alkali spreading value was previously reported by Veni and Rani (2006), Selvakumar *et al.* (2014a) also reported the significant positive correlation of amylose content on resistant starch in a study using 50 rice accessions.

This trait had positive and non significant relationship with grain yield (0.064 and 0.075) at both phenotypic and genotypic level respectively which are in agreement with the results reported by Chowdhury *et al.* (2016a)

#### 4.2.2.7 Protein content

Protein content manifested positive and significant relationship with test weight (0.248<sup>\*</sup> and 0.253<sup>\*</sup>), solid loss (0.475<sup>\*\*</sup> and 0.480<sup>\*</sup>), total phenol content (0.509<sup>\*\*</sup> and 0.511<sup>\*\*</sup>), total antioxidant activity (0.422<sup>\*\*</sup> and 0.425<sup>\*\*</sup>), Zn content (0.405<sup>\*\*</sup> and 0.423<sup>\*\*</sup>), Fe content (0.282<sup>\*</sup> and 0.338<sup>\*\*</sup>) and glycemic index (0.282<sup>\*</sup> and 0.288<sup>\*</sup>) at both phenotypic and genotypic level respectively and with panicle length (0.236<sup>\*</sup>), and plant height (0.248<sup>\*</sup>) at genotypic level suggesting that the genotypes possessing more panicle length and tall plant stature exhibited high protein content.

It showed negative and significant relationship with days to 50% flowering (-0.420<sup>\*\*</sup> and -0.452<sup>\*\*</sup>), slowly digestible starch (-0.354<sup>\*\*</sup> and -0.254<sup>\*</sup>) at both phenotypic and genotypic level and with alkali spreading value (-0.254<sup>\*</sup>) at genotypic level. This trait had positive and significant association with grain yield (0.490<sup>\*\*</sup> and 0.558<sup>\*\*</sup>) at phenotypic and genotypic level respectively indicating that the genotypes which recorded high grain yield had high protein content, hence simultaneous improvement of both these traits is possible which is agreement with the results reported by Nivedhitha *et al.* (2013).

#### 4.2.2.8 Total starch content

Total starch content showed positive and significant association with test weight (0.537<sup>\*\*</sup> and 0.546<sup>\*\*</sup>), total antioxidant activity (0.411<sup>\*\*</sup> and 0.412<sup>\*\*</sup>), Zn content (0.378<sup>\*\*</sup> and 0.405<sup>\*\*</sup>) at both phenotypic and genotypic level respectively indicating that simultaneous improvement of all these characters is attributed. Similar results were previously reported by Madhuri *et al.* (2015).

It had negative and significant relationship with days to 50% flowering (-0.446<sup>\*\*</sup> and -0.477<sup>\*\*</sup>), ear bearing tillers (-0.247<sup>\*</sup> and -0.402<sup>\*\*</sup>), fertility % (-0.299<sup>\*\*</sup> and -0.324<sup>\*\*</sup>), alkali spreading value (-0.337<sup>\*\*</sup> and -0.407<sup>\*\*</sup>), length/breadth ratio (-0.313<sup>\*\*</sup> and -0.422<sup>\*\*</sup>), total phenol content (-0.286<sup>\*</sup> and -0.287<sup>\*</sup>) at both phenotypic and genotypic level respectively and solid loss (-0.327<sup>\*\*</sup>) at phenotypic level. This trait recorded positive and significant association with grain yield (0.314<sup>\*\*</sup> and 0.357<sup>\*\*</sup>) at both phenotypic and genotypic level respectively suggesting that the genotypes which recorded high starch content also manifested more grain yield and simultaneous improvement of both these traits is anticipated.

#### 4.2.2.8 Total phenol content

Total phenol content manifested positive and significant association with panicle length (0.285\* and 0.342\*\*), plant height (0.330\*\* and 0.365\*\*), length/breadth ratio (0.330\*\* and 0.446\*\*), protein content (0.509\*\* and 0.511\*\*), total antioxidant activity (0.445\*\* and 0.447\*\*), flavonoid content (0.663\*\* and 0.664\*\*), Zn content (0.424\*\* and 0.451\*\*), Fe content (0.425\*\* and 0.502\*\*) and glycemic index (0.363\*\* and 0.369\*) at both phenotypic and genotypic level respectively these results suggest that the genotypes with red and black pericarp colour recorded more panicle length, plant height coupled with desirable biochemical quality traits such as antioxidant activity, flavonoid content, protein content and Zn & Fe content. Previous studies by Saikia *et al.* 2012 also reported that the phenolic compounds are mainly associated with the pericarp colour in rice and the grains with darker pericarp colour such as red and black rice contain higher amounts of polyphenols. It had negative and significant association with days to 50 % flowering (-0.331\*\* and -0.355\*\*), total starch (-0.286\* and -0.287\*), slowly digestible starch (-0.262\* and -0.264\*) at both phenotypic and genotypic level respectively and with ear bearing tillers (-0.295\*) at genotypic level. Whereas it's relationship with grain yield is positive and non significant (0.111 and 0.126) at both phenotypic and genotypic level respectively suggesting that the inheritance of both these traits is independent. Total phenols had high positive & significant association with antioxidant activity and flavonoid content. Pathak *et al.* (2017) also reported the positive and significant association between phenols, antioxidant activity and flavonoid content.

#### 4.2.2.9 Total Antioxidant Activity

Total antioxidant activity exhibited positive and significant association with panicle length (0.324\*\* and 0.394\*\*), plant height (0.407\*\* and 0.448\*\*), test weight (0.648\*\* and 0.661\*\*), protein content (0.422\*\*) and (0.425\*\*), total starch (0.411\*\* and 0.412\*\*), total phenol content (0.445\*\* and 0.447\*\*), flavonoid content (0.475\*\* and 0.478\*\*), Zn content (0.694\*\* and 0.740\*\*), Fe content (0.456\*\* and 0.532\*\*) and glycemic index (0.333\*\* and 0.341\*\*), but it manifested negative and significant association with days to 50% flowering (-0.837\*\* and -0.900\*\*), ear bearing tillers (-0.476\*\* and -0.778\*\*), volume expansion ratio (-0.258\* and -0.281\*), alkali spreading value (-0.565\*\* and -0.683\*\*), length/breadth ratio (-0.222\* and -0.302\*\*) and slowly digestible starch (-0.222\* and -0.224\*) at both phenotypic and genotypic level.

By studying these results, it may be concluded that improvement of antioxidant activity also results in simultaneous improvement of protein, Fe, Zn content, total phenols and flavonoid content which may be useful in the development of a genotype with more micronutrient content and protein, antioxidant properties which will help in reduction of oxidative stress. Pathak *et al.* (2017) in a study of 14 hill rice cultivars along with a non pigmented rice reported positive correlation between phenol content, antioxidant activity and flavonoid content. Chay *et al.* (2017) reported that waxy pigmented rice exhibited a significantly higher total polyphenol content and the increased polyphenol content also improved the antioxidant activity. This trait had positive and significant association with grain yield (0.349\*\* and 0.395\*\*) at both phenotypic and genotypic level suggesting that simultaneous improvement of both the traits is anticipated from the present study.

#### **4.2.2.9 Flavonoid content**

Flavonoid content showed significant and positive relationship with panicle length (0.330\*\* and 0.391\*\*), test weight (0.240\* and 0.246\*), number of filled grains for panicle (0.235\* and 0.267\*), total number of grains per panicle (0.233\* and 0.269\*), protein content (0.777\*\* and 0.780\*\*), total phenol content (0.663\*\* and 0.664\*\*), total antioxidant activity (0.475\*\* and 0.478\*\*), Zn content (0.447\*\* and 0.478\*\*), Fe content (0.356\*\* and 0.429\*\*) and glycemic index (0.281 and 0.286). These results suggest that flavonoid content, total phenol content, antioxidant activity, Zn, Fe and Protein content are positively correlated hence, simultaneous improvement of all these traits is attributed which is highly useful for isolation of genotypes possessing beneficial health effects. Similar results were previously reported by Pathak *et al.* (2017). It showed negative and significant association with days to 50% flowering (-0.540\*\* and -0.579\*\*), ear bearing tillers per plant (-0.234\* and -0.393\*\*) and slowly digestible starch (-0.435\*\* and -0.437\*\*) at both phenotypic and genotypic levels suggesting that the genotypes which possessed more ear bearing tillers had long duration which manifested low flavonoid content in the present study. A positive and significant association of this trait with grain yield (0.504\*\* and 0.574\*\*) was observed at both phenotypic and genotypic levels suggesting the possibility of simultaneous improvement of both these traits.

#### 4.2.2.9 Zn content

Zn content recorded positive and significant association with panicle length (0.334<sup>\*\*</sup> and 0.445<sup>\*\*</sup>), test weight (0.333<sup>\*\*</sup> and 0.367<sup>\*\*</sup>), protein content (0.405<sup>\*\*</sup> and 0.423<sup>\*\*</sup>), total starch (0.378<sup>\*\*</sup> and 0.405<sup>\*\*</sup>), total phenol content (0.424<sup>\*\*</sup> and 0.451<sup>\*\*</sup>), total antioxidant activity (0.694<sup>\*\*</sup> and 0.740<sup>\*\*</sup>), flavonoid content (0.447<sup>\*\*</sup> and 0.478<sup>\*\*</sup>), Fe content (0.321<sup>\*\*</sup> and 0.415<sup>\*\*</sup>) and glycemic index (0.243<sup>\*\*</sup> and 0.282<sup>\*\*</sup>), while it had negative and significant association with days to 50% flowering (-0.701<sup>\*\*</sup> and -0.810<sup>\*\*</sup>), ear bearing tillers (-0.367<sup>\*\*</sup> and -0.617<sup>\*\*</sup>) and alkali spreading value (-0.305<sup>\*\*</sup> and -0.366<sup>\*\*</sup>). This trait showed positive and significant association with grain yield per plant (0.290<sup>\*</sup> and 0.345<sup>\*\*</sup>) at both phenotypic and genotypic level indicating that improvement in Zn content in genotypes also bring improvement in protein content, total phenol content, antioxidant activity, flavonoid content, Fe content which is very much useful in isolation of a high yielding genotype with superior micronutrient density and desirable biochemical traits for improving human health.

#### 4.2.2.9 Fe content

Fe content manifested positive and significant relationship with the panicle length (0.246<sup>\*</sup> and 0.245<sup>\*</sup>), protein content (0.282<sup>\*</sup> and 0.338<sup>\*\*</sup>), total phenol content (0.425<sup>\*\*</sup> and 0.502<sup>\*\*</sup>), total antioxidant activity (0.456<sup>\*\*</sup> and 0.532<sup>\*\*</sup>), flavonoid content (0.356<sup>\*\*</sup> and 0.429<sup>\*\*</sup>), Zn content (0.321<sup>\*\*</sup> and 0.415<sup>\*\*</sup>). Resistant starch (0.343<sup>\*\*</sup> and 0.399<sup>\*\*</sup>) at phenotypic and genotypic level and with amylose content at genotypic level. These results indicate that improvement of Fe content also brings simultaneous improvement in zinc content which is in corroboration of the findings reported by Patil *et al.* (2015) and Chowdhury *et al.* (2016b) also reported the positive correlation between Fe and Zn content.

It had negative and significant relationship with days to 50% flowering (-0.305<sup>\*\*</sup> and -0.396), alkali spreading value (-0.232<sup>\*</sup> and -0.292<sup>\*\*</sup>) at phenotypic and genotypic level and with rapidly digestible starch (-0.257<sup>\*</sup>) at genotypic level suggesting that the genotypes which flowered early *i.e.* red and black rice had more Fe content than brown rice genotypes which are in agreement with the results reported by Raghuvanshi *et al.* (2017).

This trait showed significant and positive association with grain yield (0.282<sup>\*</sup>) at genotypic level only. These results are in agreement with the findings reported by Patil *et al.* (2015).

#### 4.2.3.0 Glycemic Index

This trait exhibited positive and significant relationship with volume expansion ratio (0.231<sup>\*</sup> and 0.243<sup>\*</sup>), length/breadth ratio (0.269<sup>\*</sup> and 0.370<sup>\*\*</sup>), protein content (0.282<sup>\*</sup> and 0.288<sup>\*</sup>), total phenol content (0.363<sup>\*\*</sup> and 0.369<sup>\*\*</sup>), total antioxidant activity (0.333<sup>\*\*</sup> and 0.341<sup>\*\*</sup>), flavonoid content (0.281<sup>\*</sup> and 0.286<sup>\*</sup>), Zn content (0.243<sup>\*</sup> and 0.282<sup>\*</sup>), rapidly digestible starch (0.888<sup>\*\*</sup>, 0.904<sup>\*\*</sup>) while it showed negative and significant relationship with days to 50% flowering (-0.314<sup>\*\*</sup> and -0.343<sup>\*\*</sup>), number of filled grains per panicle (-0.275<sup>\*</sup> and -0.332<sup>\*\*</sup>), total number of grains per panicle (-0.295<sup>\*\*</sup> and -0.358<sup>\*\*</sup>), slowly digestible starch (-0.823<sup>\*\*</sup> and -0.839<sup>\*\*</sup>), resistant starch (-0.586<sup>\*\*</sup> and -0.602<sup>\*\*</sup>) at both phenotypic and genotypic levels respectively and with amylose content (-0.222<sup>\*</sup>) it showed negative and significant association at genotypic level. From these results, it may be concluded that the red and black pericarp colored rice genotypes which flowered early manifested low GI, high SDS, amylose and RS. As low GI diets believed to improve health indices independent of the amount of carbohydrate consumed (Psaltopon *et al.*, 2010), developing a genotype with high SDS & RS will result in low GI rice variety. Inverse relationship of GI with amylose content, SDS and RS was previously reported by Peisong *et al.* (2004) and Odenighbo *et al.* (2013).

This trait recorded significant and positive relationship with grain yield per plant (0.236<sup>\*</sup> and 0.281<sup>\*</sup>) at both phenotypic and genotypic levels respectively indicating that improvement of grain yield of genotypes also increase the GI value which is undesirable.

#### 4.2.3.1 Slowly Digestible Starch

This trait recorded positive and significant relationship with days to 50% flowering (0.269<sup>\*</sup> and 0.296<sup>\*\*</sup>), number of filled grains per panicle (0.286<sup>\*</sup> and 0.333<sup>\*\*</sup>), total number of grains per panicle (0.296<sup>\*\*</sup> and 0.352<sup>\*\*</sup>), resistant starch (0.333<sup>\*\*</sup> and 0.338<sup>\*\*</sup>), but it showed negative and significant association with protein content (-0.354<sup>\*\*</sup> and -0.359<sup>\*\*</sup>), total phenol content (-0.262<sup>\*</sup> and -0.264<sup>\*</sup>), total

antioxidant activity (-0.222<sup>\*</sup> and -0.224<sup>\*</sup>), flavonoid content (-0.434<sup>\*\*</sup> and -0.437<sup>\*\*</sup>), glycemic index (-0.823<sup>\*\*</sup> and -0.839<sup>\*\*</sup>), rapidly digestible starch (-0.902<sup>\*\*</sup> and -0.919<sup>\*\*</sup>) at both phenotypic and genotypic levels. These results suggest that genotypes with more SDS content will also possess more resistant starch. Hence simultaneous improvement of these traits is anticipated which is a highly desirable relationship to develop a low GI variety. As the SDS exhibited a negative correlation with GI and positive association with resistant starch, selecting a genotypes with high SDS and RS will result in low GI variety. Accordingly, lowering the GI of the diet could help in preventing the development and slowing the progression of type II diabetes and thereby lead to an improvement in public health. Inverse relationship of SDS with RDS and GI were previously reported by Odenigbo *et al.* (2013).

This trait showed negative and significant association with grain yield (-0.413<sup>\*\*</sup> and -0.485<sup>\*\*</sup>) at both phenotypic and genotypic levels indicating that the genotypes which had low SDS content manifested high grain yield which is undesirable.

#### **4.2.3.2 Rapidly Digestible Starch**

Rapidly digestible starch exhibited positive and significant association with volume expansion ratio (0.242<sup>\*</sup> and 0.259<sup>\*</sup>) and glycemic index (0.888<sup>\*\*</sup> and 0.904<sup>\*\*</sup>) at both phenotypic and genotypic levels and with length/breadth ratio (0.259<sup>\*</sup>) at genotypic level suggesting that increase of rapidly digestible starch also increases the glycemic index value of rice hence it is a nutritionally undesirable trait. It had negative and significant association with days to 50% flowering (-0.235<sup>\*</sup> and -0.252<sup>\*</sup>), number of filled grains per panicle (-0.418<sup>\*\*</sup> and -0.489<sup>\*\*</sup>), total number of grains per panicle (-0.433<sup>\*\*</sup> and -0.513<sup>\*\*</sup>), solid loss (-0.250<sup>\*</sup> and -0.255<sup>\*</sup>), slowly digestible starch (-0.902<sup>\*\*</sup> and -0.919<sup>\*\*</sup>) and resistant starch (0.581<sup>\*\*</sup> and 0.588<sup>\*\*</sup>) at both phenotypic and genotypic levels and with Fe content at genotypic level. These results indicate that the genotypes possessing more SDS and RS will be isolated if we select against RDS. The inverse relationship of RDS with resistant starch was previously reported by Patindol *et al.* (2010) and Odenigbo *et al.* (2013)

This trait showed positive and significant relationship with grain yield (0.373<sup>\*\*</sup> and 0.410<sup>\*\*</sup>) at both phenotypic and genotypic levels suggesting that the genotypes which recorded more grain yield also manifested high RDS content which is undesirable.

#### 4.2.3.2 Resistant Starch

This trait manifested significant and positive relationship with panicle length (0.240\* and 0.264\*), number of filled grains per panicle (0.292\*\* and 0.340\*\*), total number of grains per panicle (0.288\* and 0.339\*\*), solid loss (0.242\* and 0.245\*), amylose content (0.330\*\* and 0.334\*\*), Fe content (0.343\*\* and 0.399\*\*), slowly digestible starch (0.333\*\* and 0.338\*\*) and it had negative & significant association with glycemic index (-0.586\*\* and -0.602\*\*), rapidly digestible starch (-0.881\*\* and -0.588\*\*) at both phenotypic and genotypic level suggesting that the genotypes with red and black pericarp color had more panicle length, filled and total grains per panicle exhibited more resistant starch, high amylose content and slowly digestible starch. Hence simultaneous improvement of all these traits is anticipated and will help in isolation of healthy rice genotype which improves blood glucose levels and insulin regulation. Patindol *et al.* (2010) in a study involving 16 rice cultivars revealed that apparent amylose content correlated positively with resistant starch and negatively with rapidly digestible starch which support the findings of present investigation. Odenigbo *et al.* (2013) also reported the negative association of resistant starch with rapidly digestible starch in a study to evaluate five improved varieties for nutritionally important starch fractions. Significant positive correlation of resistant starch with amylose content was previously reported by Selvakumar *et al.* (2014a) while Shu *et al.* (2009) reported the negative association of resistant starch with GI in a study involving seven rice mutants.

This trait showed negative and non significant association with grain yield per plant (-0.139 and -0.160) at both phenotypic and genotypic level respectively indicating the independent improvement of these two traits.

In the present study panicle length, fertility %, test weight among yield components, protein content, total starch, total antioxidant activity, flavonoid content, zinc content, iron content, rapidly digestible starch and glycemic index among quality traits showed positive & significant correlation with grain yield suggesting simultaneous improvement of these traits with grain yield. While days to 50% flowering, water uptake, alkali spreading value, L/B ratio and slowly digestible starch manifested negative and significant association with grain yield indicating that selection against these traits will improve the grain yield.

Among nutritional and biochemical quality traits, zinc content, iron content and protein content are positively correlated among themselves suggesting that selection for one trait will improve the other traits also. Likewise a positive and significant relationship between total phenol content, total antioxidant activity and flavonoid content revealed simultaneous improvement of all these traits. Glycemic index had significant negative association with slowly digestible starch and resistant starch and positive association with rapidly digestible starch indicating that selection for high SDS and RS will result in low RDS and GI value of the genotype. All these relationships among these nutritional and biochemical parameters would help in isolation of a genotype with high micronutrient density, high antioxidant activity coupled with low GI which is very much desirable for development of rice variety with potential health benefits.

### **4.3 PATH COEFFICIENT ANALYSIS**

The correlation coefficients between effect and casual factors do not project the complete picture, especially when the casual factors are inter-related. The correlation coefficients between the grain yield per plant and its component characters were partitioned into their corresponding direct and indirect effects through the path coefficient analysis. The path coefficients of different attributes on grain yield are given in Table 4.5.

The observed correlation between yield and its component character is the net result of the direct and indirect effects of the component character through other yield attributes. The total correlation between grain yield and its component characters may sometimes be misleading. Since, it may be over or under estimate of its association with other characters. Hence, direct selection on correlation may not be worthwhile. The correlation coefficient needs to be split into direct and indirect effects, using path coefficient analysis for critical evaluation as many characters affect a given trait. Thus, the correlation and path analysis in combination, can give a better insight, into cause and effect relationship between different pairs of characters.

In the present investigation, path analysis is carried out with 25 yield components and quality parameters as independent variables and grain yield per plot as a dependent variable and results of characters bearing significant association with grain yield are discussed here under.

### 4.3.1 Yield Component Characters

#### 4.3.1.1 Days to 50 %flowering

At phenotypic level, days to 50% flowering exhibited significant and negative correlation (-0.469) with the grain yield and positive direct effect (0.016) on grain yield per plant. Apart from direct effect, it also exhibited prominent positive indirect effects *via* total phenol content (0.083), Zn content (0.076), glycemic index (0.211) and prominent negative indirect effects *via* panicle length (-0.135), protein content (-0.169), flavonoid content (-0.184) and rapidly digestible starch (-0.198).

This trait exhibited significant and negative correlation (-0.582) with grain yield and negative direct effect (-1.158) on grain yield per plant at genotypic level. Apart from direct effect, it also exhibited prominent positive indirect effects *via* total grains per panicle (0.386), water uptake (0.186), alkali spreading value (0.109), total antioxidant activity (4.041), flavonoid content (1.009) and rapidly digestible starch (0.374) and prominent negative indirect effects *via* panicle length (-0.495), ear bearing tillers per plant (-0.101), test weight (-1.549), filled grains per panicle (-0.376), volume expansion ratio (-0.117), protein content (-0.476), total starch (-0.156), total phenol content (-0.416), Zn content (-0.596), Fe content (-0.477), slowly digestible starch (-0.595) and resistant starch (-0.115).

This character showed negative direct effect along with negative correlation with grain yield which is in confirmation with the results reported by Yadav *et al.* (2010), Bekele *et al.* (2013), Bhati *et al.* (2015), Devi *et al.* (2017) and Lakshmi *et al.* (2017).

#### 4.3.1.2 Panicle length

Panicle length recorded positive direct effect (0.351) coupled with positive and significant correlation (0.277) with grain yield at phenotypic level. It also exhibited prominent indirect effect *via* total phenol content (0.296), protein content (0.077) and flavonoid content (0.112) whereas it showed negative and significant indirect effect *via* number of filled grains per panicle (-0.294) and total phenol content (-0.072).

At genotypic level, panicle length recorded positive direct effect (0.920) coupled with positive and significant correlation (0.358) with grain yield. It also exhibited positive indirect effect *via* days to 50% flowering (0.624), number of filled

grains per panicle (12.089), total number of grains per panicle (10.853), fertility % (1.045), VER (0.198), protein content (0.248), total phenol content (0.401), Zn content (0.327), Fe content (0.295), slowly digestible starch (0.301). It showed negative and significant indirect effect *via* water uptake (-0.101) total antioxidant activity (-1.769), flavonoid content (-0.681) and resistant starch (-0.320).

This trait had positive direct effect on grain yield per plant coupled with positive correlation (Yadav *et al.*, 2010, Veni *et al.*, 2013, Bhuvaneshwari *et al.*, 2015, Ekka *et al.*, 2015 and Sowmiya and Venkatesan, 2017). Hence, simultaneous selection would be more effective in improving this trait.

#### **4.3.1.2 Plant height**

This character manifested positive and non significant (0.162) relationship coupled with negative direct effect on grain yield (-0.003) at phenotypic level. This trait had positive indirect effects *via* panicle length (0.129) and negative indirect effects *via* glycemic index (-0.116).

At genotypic level, this trait exhibited positive direct effect (0.153) coupled with positive and non significant association with grain yield (0.0162). It also reported positive indirect affects *via* days to 50% flowering (0.276), panicle length (0.469), test weight (0.687), number of filled grains per panicle (0.103), protein content (0.261), total phenol content (0.428), Zn content (0.134), Fe content (0.189) and slowly digestible starch (0.261). It also exhibited negative indirect effects *via* total number of grains per panicle (-0.902), ASV (-0.103), total antioxidant activity (-2.010), flavonoid content (-0.403) and rapidly digestible starch (-0.157).

The positive direct effect of Plant height on grain yield was previously reported by Nandan *et al.* (2010), Bekele *et al.* (2013), Sanghera *et al.* (2013), Karim *et al.* (2014), Rahman *et al.* (2014), Bhati *et al.* (2015), Sameera *et al.* (2016), Jan *et al.* (2017), Devi *et al.* (2017) and Sowmiya and Venkatesan (2017) indicating direct selection should be practiced for improvement of grain yield.

#### 4.3.1.2 Ear bearing tillers per plant

Ear bearing tillers per plant recorded positive direct effect (0.129) coupled with negative and non significant correlation (-0.003) with grain yield at phenotypic level. It also exhibited prominent indirect effect *via*, total phenol content (0.045). It also exhibited negative indirect effects *via* panicle length (-0.078) and flavonoid content (0.080).

At genotypic level this trait exhibited negative direct effect (-0.134) coupled with positive and non significant association with grain yield (0.115). It also reported positive indirect affects *via* number of filled grains per panicle (2.319), fertility % (0.283), water uptake (0.154), total antioxidant activity (3.494), flavonoid content (0.685) and resistant starch (0.225). It also exhibited negative indirect effects *via* days to 50% flowering (-0.874), panicle length (-0.472), test weight (-1.196), protein content (-0.299), total starch (-0.131) total phenol content (-0.346), Zn content (-0.454), Fe content (-0.352) and rapidly digestible starch (-0.133).

Nandan *et al.* (2010), Yadav *et al.* (2010), Bhati *et al.* (2015) and Jan *et al.* (2017) also reported negative direct effect of this trait on grain yield along with positive correlation. Under such situation indirect effects seem to be cause of positive correlation and indirect causal factors are to be considered simultaneously for selection to improve yield.

#### 4.3.1.2 Test weight

At phenotypic level, test weight exhibited significant and positive correlation (0.425) with the grain yield and positive direct effect (0.068) on grain yield per plant. Apart from direct effect, it also exhibited prominent positive indirect effects *via* number of filled grains per panicle (0.272), protein content (0.100) and rapidly digestible starch (0.155). It also had negative indirect effects *via* total number of grains per panicle (-0.273) and fertility %.

At genotypic level, this trait exhibited positive direct effect (2.333) coupled with positive and significant association with grain yield (0.498). It also reported positive indirect affects *via* days to 50% flowering (0.769), number of filled grains per panicle (10.107), protein content (0.267), total starch (0.178), Fe content (0.252), slowly digestible starch (0.204). It also had negative indirect affects *via* total number of

grains per panicle (-9.988), fertility % (-0.268), water uptake (-0.107), ASV (-0.148), total phenol content (-0.116), total antioxidant activity (-2.968), flavonoid content (-0.428) and rapidly digestible starch (-0.279).

Test weight had positive direct effect coupled with positive correlation on grain yield per plot indicating direct selection for this trait should be practiced to reduce the undesirable indirect effects. These results are in agreement with the findings reported by Yadav *et al.* (2010), Aktar *et al.* (2011), Rahman *et al.* (2014), Karim *et al.* (2014), Bhuvaneswari *et al.* (2015), Sameera *et al.* (2016), Jan *et al.* (2017) and Sowmiya and Venkatesan (2017).

#### **4.3.1.6 Number of filled grains per panicle**

At phenotypic level, number of filled grains per panicle exhibited non significant and negative correlation (-0.038) with the grain yield and negative direct effect (-0.846) on grain yield per plant. Apart from direct effect, it also exhibited prominent positive indirect effects *via* panicle length (0.122), total number of grains per panicle (0.839), fertility % (0.169), flavonoid content (0.680), glycemic index (0.185). It showed negative indirect effect *via* test weight (-0.022) and rapidly digestible starch (-0.352).

At genotypic level number of filled grains per panicle exhibited non significant and negative correlation (-0.079) with the grain yield and negative direct effect (-26.764) on grain yield per plant. Apart from direct effect, it also exhibited prominent positive indirect effects *via* panicle length (0.415), total number of grains per panicle (25.34), fertility % (1.420), total phenol content (0.433), total antioxidant activity (0.505), Zn content (0.134), Fe content (0.187) and rapidly digestible starch (0.727). This trait had negative indirect effect through test weight (-0.881), flavonoid content (-0.466), slowly digestible starch (-0.669) and resistant starch (-0.412). This trait had negative direct effect on grain yield per plant (Nandan *et al.*, 2010, and Jan *et al.*, 2017).

#### **4.3.1.8 Total number of grains per panicle**

Total number of grains per panicle showed non significant and negative correlation (-0.069) coupled with positive direct effect (0.849) with grain yield at phenotypic level. This trait had positive indirect affects through panicle length (0.122) and fertility % (0.108). This trait showed negative indirect effect through number of filled grains per panicle (-0.837) and rapidly digestible starch (-0.365).

This trait exhibited negative and non significant correlation (-0.114) along with positive direct effect (25.46) with grain yield at genotypic level. It showed positive indirect affects through panicle length (0.392), filled grains per panicle (26.643), fertility % (1.232), total phenol content (0.433), total antioxidant activity (0.494), Zn content (0.130), Fe content (0.186) and rapidly digestible starch (0.761). It showed negative indirect effect through test weight (-0.915), flavonoid content (-0.470), slowly digestible starch (-0.706) and resistant starch (-0.410).

This trait showed positive direct effect on grain yield per plant. These results are in agreement with the findings reported by Nandan *et al.* (2010), Naseem *et al.* (2014), Bhati *et al.* (2015) and Jan *et al.* (2017).

#### **4.3.1.9 Fertility %**

Fertility % exhibited high positive direct effect (0.436) along with positive and non significant correlation (0.162) with grain yield at phenotypic level which is in agreement with the results reported by Niveditha *et al.* (2013). Apart from its direct effect, it also showed prominent positive indirect effects *via* total number of grains per panicle (0.210) and it showed negative indirect effect *via* number of filled grains per panicle (-0.329).

At genotypic level fertility % exhibited high positive direct effect (2.448) along with positive and non significant correlation (0.216) with grain yield (Qamar *et al.*, 2005 and Bhuvanewari *et al.*, 2015). It had prominent positive indirect effects through panicle length (0.393), number of filled grains per panicle (15.529), total number of grains per panicle (12.810), protein content (0.159), total phenol content (0.410), total antioxidant activity (0.278) and Fe content (0.144). It showed negative indirect effect through solid loss (-0.161), water uptake (-0.132), flavonoid content (-0.128) and resistant starch (-0.148).

#### **4.3.2.0 Solid loss**

This trait recorded negative direct effect (-0.197) along with positive and non significant correlation (0.029) with grain yield at phenotypic level. Apart from its direct effect, it also showed prominent positive indirect effects through panicle length (0.106), total number of grains per panicle (0.157) and fertility % (0.153) and manifested negative indirect effect through number of filled grains per panicle (-0.195) and rapidly digestible starch (-0.211).

At genotypic level, this trait manifested positive indirect effect through panicle length (0.337), total number of grains per panicle (5.296), fertility % (1.501), volume expansion ratio (0.119), protein content (0.506), total phenol content (0.181), total antioxidant activity (0.466) and rapidly digestible starch (0.379) and showed negative indirect effect through test weight (-0.544), number of filled grains per panicle (-6.995), total starch (-0.107), flavonoid content (-0.271), slowly digestible starch (-0.245) and resistant starch (-0.297).

#### **4.3.2.1 Water Uptake**

Water uptake showed positive direct effect (0.026) along with negative non significant association with grain yield per plant at phenotypic level (Veni *et al.*, 2013). In addition, it also displayed positive indirect effects through glycemic index (0.087) and showed negative indirect effect through rapidly digestible starch (-0.096).

At genotypic level, it showed positive direct effect (0.468) along with negative significant association with grain yield. It exhibited prominent positive indirect effects through number of filled grains per panicle (1.638), total antioxidant activity (0.810), flavonoid content (0.319), rapidly digestible starch (0.165) and resistant starch (0.153) while negative indirect effect was exhibited by slowly digestible starch (-0.347).

#### **4.3.2.2 Volume Expansion Ratio**

Volume expansion ratio manifested positive direct effect (0.117) at phenotypic level. It also showed positive indirect effect through rapidly digestible starch and it showed negative indirect effect through panicle length (-0.139) and glycemic index (-0.155).

At genotypic level, this trait exhibited negative direct effect (-0.409) along with positive and non significant correlation (0.033). It manifested positive indirect effect through number of filled grains per panicle (0.343), fertility % (0.444), water uptake (0.106), total antioxidant activity (1.260), flavonoid content (0.368) and resistant starch (0.544) and it showed negative indirect effect through days to 50% flowering (-0.331), panicle length (-0.446), test weight (-0.438), number of filled grains per panicle (-3.786) and rapidly digestible starch (-0.384).

**Table 4.5. Direct and indirect effects (phenotypic & genotypic) of yield components and quality traits on yield among 26 genotypes of rice (*Oryza sativa* L.).**

Character		1	2	3	4	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26
1	P	<b>0.016</b>	-0.006	-0.003	0.006	-0.009	-0.001	0.000	-0.001	0.001	0.006	0.003	0.007	0.005	0.000	-0.007	-0.007	-0.005	-0.013	-0.008	-0.011	-0.005	-0.005	0.004	-0.004	0.001
	G	<b>-1.158</b>	0.624	0.276	-0.874	0.769	-0.016	-0.018	-0.006	-0.081	-0.471	-0.331	-0.665	-0.525	-0.029	0.524	0.553	0.411	1.043	0.671	0.938	0.459	0.397	-0.343	0.291	-0.110
2	P	-0.135	<b>0.351</b>	0.129	-0.078	0.012	0.122	0.122	0.023	0.106	-0.065	-0.139	-0.023	0.004	-0.063	0.067	0.021	0.100	0.114	0.116	0.117	0.086	0.019	-0.051	-0.014	0.085
	G	-0.495	<b>0.920</b>	0.469	-0.472	0.000	0.415	0.392	0.393	0.337	-0.202	-0.446	-0.084	-0.058	-0.193	0.217	0.068	0.315	0.362	0.360	0.409	0.226	0.065	-0.138	-0.045	0.243
3	P	0.001	-0.001	<b>-0.003</b>	0.001	-0.001	0.000	0.000	0.000	0.000	0.000	0.001	0.001	0.000	0.000	-0.001	0.000	-0.001	-0.001	-0.001	0.000	0.000	-0.001	0.000	0.000	0.000
	G	-0.036	0.078	<b>0.153</b>	-0.062	0.045	-0.001	-0.005	0.034	0.019	0.014	-0.030	-0.084	0.015	0.007	0.038	0.004	0.056	0.069	0.036	0.028	0.024	0.030	-0.020	0.016	-0.009
4	P	0.049	-0.029	-0.042	<b>0.129</b>	-0.040	-0.003	-0.001	-0.008	0.004	0.026	0.035	0.015	0.015	0.006	-0.020	-0.032	-0.023	-0.061	-0.030	-0.047	-0.023	-0.007	-0.003	0.005	-0.012
	G	-0.101	0.069	0.054	<b>-0.134</b>	0.069	0.012	0.013	-0.015	-0.010	-0.045	-0.071	-0.048	-0.019	-0.015	0.038	0.054	0.040	0.104	0.053	0.083	0.039	0.013	0.004	-0.012	0.025
6	P	-0.041	0.002	0.017	-0.021	<b>0.068</b>	-0.022	-0.022	-0.008	-0.016	-0.016	-0.012	-0.044	-0.027	0.019	0.017	0.037	-0.007	0.044	0.016	0.023	0.013	0.006	-0.007	0.013	-0.005
	G	-1.549	-0.001	0.687	-1.196	<b>2.333</b>	-0.881	-0.915	-0.255	-0.544	-0.543	-0.438	-1.816	-1.291	0.720	0.591	1.274	-0.231	1.542	0.573	0.856	0.488	0.193	-0.237	0.438	-0.174
7	P	0.028	-0.294	0.002	0.018	0.272	<b>-0.846</b>	-0.837	-0.329	-0.195	0.047	0.064	-0.156	-0.113	0.055	0.034	0.044	-0.271	0.084	-0.199	-0.115	-0.068	0.234	-0.242	0.354	-0.248
	G	-0.376	-12.089	0.103	2.319	10.107	<b>-26.764</b>	-26.643	-15.529	-6.975	1.638	3.343	-8.428	-4.842	2.861	0.950	1.706	-9.901	3.008	-7.155	-4.869	-4.159	8.883	-8.917	13.100	-9.092
8	P	-0.017	0.296	-0.018	-0.007	-0.273	0.839	<b>0.849</b>	0.210	0.157	-0.033	-0.084	0.152	0.111	-0.057	-0.051	-0.021	0.255	-0.082	0.199	0.111	0.074	-0.251	0.252	-0.368	0.245
	G	0.386	10.853	-0.902	-2.479	-9.988	25.349	<b>25.464</b>	12.814	5.296	-1.003	-3.786	8.202	3.812	-2.587	-1.529	-0.804	8.933	-2.799	6.862	4.479	3.939	-9.114	8.955	-13.055	8.623
9	P	-0.039	0.028	0.042	-0.029	-0.049	0.169	0.108	<b>0.436</b>	0.153	-0.066	0.061	0.029	0.018	-0.009	0.036	-0.074	0.090	-0.013	0.021	0.023	-0.005	0.029	0.013	-0.013	0.031
	G	0.013	1.045	0.550	0.283	-0.268	1.420	1.232	<b>2.448</b>	1.501	-0.705	0.444	0.163	0.894	-0.292	0.370	-0.727	0.857	-0.152	0.180	0.287	0.292	0.249	0.065	-0.141	0.300
10	P	-0.013	-0.060	-0.022	-0.006	0.045	-0.045	-0.036	-0.069	<b>-0.197</b>	-0.005	0.050	-0.014	0.005	0.024	-0.094	0.064	-0.030	0.021	-0.030	-0.002	0.001	0.024	-0.024	0.049	-0.048
	G	-0.018	-0.096	-0.033	-0.020	0.061	-0.068	-0.055	-0.161	<b>-0.263</b>	-0.009	0.076	-0.023	0.008	0.035	-0.126	0.086	-0.041	0.027	-0.041	-0.003	0.002	0.034	-0.032	0.067	-0.064
11	P	0.010	-0.005	0.002	0.005	-0.006	-0.001	-0.001	-0.004	0.001	<b>0.026</b>	0.005	0.004	0.007	-0.005	-0.002	-0.004	0.001	-0.005	-0.005	-0.003	-0.004	-0.003	0.004	-0.003	-0.003
	G	0.186	-0.101	0.041	0.154	-0.107	-0.028	-0.018	-0.132	0.016	<b>0.458</b>	0.106	0.089	0.180	-0.083	-0.028	-0.079	0.023	-0.083	-0.084	-0.057	-0.076	-0.060	0.079	-0.051	-0.058
12	P	0.026	-0.046	-0.019	0.032	-0.020	-0.009	-0.012	0.016	-0.030	0.023	<b>0.117</b>	0.009	0.031	-0.010	-0.021	-0.012	0.006	-0.030	-0.023	-0.001	-0.005	0.027	-0.003	0.028	-0.049
	G	-0.117	0.198	0.080	-0.217	0.077	0.051	0.061	-0.074	0.119	-0.094	<b>-0.409</b>	-0.032	-0.167	0.043	0.079	0.046	-0.022	0.115	0.086	0.000	0.020	-0.099	0.013	-0.106	0.183
13	P	-0.041	0.006	0.039	-0.011	0.059	-0.017	-0.016	-0.006	-0.007	-0.014	-0.007	<b>-0.092</b>	-0.011	0.035	0.019	0.031	-0.001	0.052	0.011	0.028	0.013	0.009	0.000	0.008	-0.019
	G	0.109	-0.017	-0.103	0.067	-0.148	0.060	0.061	0.013	0.016	0.037	0.015	<b>0.190</b>	0.124	-0.089	-0.048	-0.077	0.002	-0.129	-0.027	-0.069	-0.044	-0.024	-0.002	-0.020	0.047
14	P	-0.055	-0.002	-0.018	-0.018	0.063	-0.022	-0.021	-0.007	0.004	-0.047	-0.044	-0.019	<b>-0.162</b>	0.024	0.007	0.051	-0.053	0.036	-0.008	0.004	0.010	-0.044	0.031	-0.031	0.019
	G	-0.037	0.005	-0.008	-0.012	0.046	-0.015	-0.012	-0.030	0.003	-0.032	-0.034	-0.054	<b>-0.082</b>	0.018	0.005	0.035	-0.037	0.025	-0.005	0.005	0.010	-0.030	0.021	-0.021	0.013

Character		1	2	3	4	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26
15	P	-0.002	0.017	-0.003	-0.004	-0.026	0.006	0.006	0.002	0.011	0.016	0.008	0.036	0.014	<b>-0.093</b>	-0.003	-0.002	0.010	-0.003	-0.004	0.012	-0.017	0.019	0.000	0.006	-0.031
	G	0.003	-0.024	0.005	0.013	0.035	-0.012	-0.011	-0.013	-0.015	-0.020	-0.012	-0.053	-0.024	<b>0.113</b>	0.005	0.002	-0.013	0.004	0.005	-0.017	0.026	-0.025	-0.001	-0.009	0.039
16	P	-0.169	0.077	0.091	-0.063	0.100	-0.016	-0.024	0.033	0.191	-0.024	-0.074	-0.085	-0.018	0.015	<b>0.402</b>	0.019	0.205	0.170	0.313	0.163	0.114	0.114	-0.142	0.082	0.015
	G	-0.476	0.248	0.261	-0.299	0.267	-0.037	-0.063	0.159	0.506	-0.065	-0.204	-0.267	-0.065	0.046	<b>1.054</b>	0.050	0.539	0.447	0.822	0.446	0.356	0.304	-0.378	0.217	0.040
17	P	-0.011	0.002	0.001	-0.006	0.014	-0.001	-0.001	-0.004	-0.008	-0.004	-0.003	-0.009	-0.008	0.001	0.001	<b>0.025</b>	-0.007	0.010	0.002	0.010	-0.003	0.000	0.000	0.003	-0.004
	G	-0.156	0.024	0.009	-0.131	0.178	-0.021	-0.010	-0.097	-0.107	-0.056	-0.037	-0.133	-0.138	0.006	0.016	<b>0.326</b>	-0.094	0.134	0.023	0.132	-0.042	-0.001	-0.002	0.042	-0.050
18	P	0.083	-0.072	-0.083	0.045	0.025	-0.081	-0.076	-0.052	-0.039	-0.013	-0.013	-0.002	-0.083	0.028	-0.128	0.072	<b>-0.251</b>	-0.112	-0.167	-0.107	-0.107	-0.091	0.066	-0.027	-0.002
	G	-0.416	0.401	0.428	-0.346	-0.116	0.433	0.411	0.410	0.181	0.059	0.064	0.010	0.523	-0.136	0.599	-0.336	<b>1.172</b>	0.523	0.778	0.529	0.588	0.432	-0.309	0.125	0.007
19	P	-0.011	0.004	0.005	-0.006	0.009	-0.001	-0.001	0.000	-0.001	-0.002	-0.003	-0.008	-0.003	0.000	0.006	0.005	0.006	<b>0.013</b>	0.006	0.009	0.006	0.004	-0.003	0.003	-0.002
	G	4.041	-1.769	-2.010	3.494	-2.968	0.505	0.494	0.278	0.466	0.810	1.260	3.062	1.354	-0.149	-1.906	-1.849	-2.005	<b>-4.490</b>	-2.145	-3.321	-2.388	-1.530	1.007	-0.917	0.603
20	P	-0.184	0.112	0.071	-0.080	0.082	0.080	0.079	0.016	0.052	-0.060	-0.068	-0.041	0.016	0.015	0.264	0.024	0.225	0.161	<b>0.340</b>	0.152	0.121	0.095	-0.148	0.067	0.030
	G	1.009	-0.681	-0.403	0.685	-0.428	-0.466	-0.470	-0.128	-0.271	0.319	0.368	0.246	-0.110	-0.079	-1.360	-0.125	-1.157	-0.833	<b>-1.742</b>	-0.832	-0.747	-0.499	0.762	-0.349	-0.156
21	P	0.076	-0.036	-0.016	0.040	-0.036	-0.015	-0.014	-0.006	-0.001	0.013	0.001	0.033	0.003	0.014	-0.044	-0.041	-0.046	-0.075	-0.048	<b>-0.108</b>	-0.035	-0.026	0.013	-0.016	0.011
	G	-0.596	0.327	0.134	-0.454	0.270	0.134	0.130	0.086	0.007	-0.092	0.000	-0.269	-0.049	-0.114	0.312	0.298	0.332	0.545	0.352	<b>0.736</b>	0.305	0.208	-0.090	0.127	-0.067
22	P	-0.059	0.047	0.020	-0.035	0.036	0.015	0.017	-0.002	-0.001	-0.027	-0.008	-0.027	-0.011	0.035	0.054	-0.020	0.082	0.088	0.068	0.062	<b>0.192</b>	-0.021	0.013	-0.040	0.066
	G	-0.477	0.295	0.189	-0.352	0.252	0.187	0.186	0.144	-0.008	-0.200	-0.058	-0.280	-0.147	0.273	0.407	-0.156	0.605	0.641	0.516	0.499	<b>1.204</b>	-0.162	0.086	-0.310	0.481
23	P	0.211	-0.037	-0.116	0.038	-0.056	0.185	0.198	-0.045	0.081	0.087	-0.155	0.068	-0.181	0.135	-0.189	0.002	-0.243	-0.224	-0.188	-0.163	0.073	<b>-0.671</b>	0.552	-0.596	0.393
	G	0.018	-0.004	-0.010	0.005	-0.004	0.018	0.019	-0.005	0.007	0.007	-0.013	0.007	-0.020	0.012	-0.015	0.000	-0.020	-0.018	-0.015	-0.015	0.007	<b>-0.054</b>	0.045	-0.048	0.032
24	P	0.019	-0.010	-0.008	-0.002	-0.007	0.020	0.021	0.002	0.009	0.012	-0.002	0.000	-0.013	0.000	-0.025	0.000	-0.018	-0.016	-0.030	-0.008	0.005	-0.057	<b>0.070</b>	-0.063	0.023
	G	-0.595	0.301	0.261	0.053	0.204	-0.669	-0.706	-0.053	-0.245	-0.347	0.065	0.021	0.510	0.009	0.720	0.011	0.530	0.450	0.878	0.245	-0.144	1.685	<b>-2.008</b>	1.845	-0.679
25	P	-0.198	-0.033	0.085	0.036	0.155	-0.352	-0.365	-0.025	-0.211	-0.096	0.204	-0.070	0.160	-0.058	0.173	0.109	0.090	0.170	0.167	0.126	-0.173	0.747	-0.759	<b>0.842</b>	-0.489
	G	0.374	0.072	-0.157	-0.133	-0.279	0.727	0.761	0.086	0.379	0.165	-0.384	0.159	-0.385	0.116	-0.306	-0.190	-0.158	-0.303	-0.298	-0.255	0.382	-1.342	1.364	<b>-1.485</b>	0.874
26	P	-0.012	-0.035	0.009	0.014	0.010	-0.043	-0.043	-0.010	-0.036	0.018	0.062	-0.030	0.017	-0.049	-0.006	0.022	-0.001	0.020	-0.013	0.015	-0.050	0.086	-0.049	0.086	<b>-0.147</b>
	G	-0.115	-0.320	0.072	0.225	0.090	-0.412	-0.410	-0.148	-0.297	0.153	0.544	-0.297	0.195	-0.417	-0.046	0.185	-0.008	0.163	-0.108	0.111	-0.484	0.730	-0.410	0.713	<b>-1.212</b>
5	P	<b>-0.469</b>	<b>0.277</b>	<b>0.162</b>	<b>-0.003</b>	<b>0.425</b>	<b>-0.038</b>	<b>-0.069</b>	<b>0.162</b>	<b>0.029</b>	<b>-0.201</b>	<b>0.000</b>	<b>-0.264</b>	<b>-0.224</b>	<b>0.064</b>	<b>0.490</b>	<b>0.314</b>	<b>0.111</b>	<b>0.349</b>	<b>0.504</b>	<b>0.290</b>	<b>0.211</b>	<b>0.236</b>	<b>-0.413</b>	<b>0.373</b>	<b>-0.139</b>
	G	<b>-0.582</b>	<b>0.358</b>	<b>0.145</b>	<b>0.115</b>	<b>0.498</b>	<b>-0.079</b>	<b>-0.114</b>	<b>0.216</b>	<b>0.036</b>	<b>-0.226</b>	<b>0.033</b>	<b>-0.383</b>	<b>-0.306</b>	<b>0.075</b>	<b>0.558</b>	<b>0.357</b>	<b>0.126</b>	<b>0.395</b>	<b>0.574</b>	<b>0.345</b>	<b>0.282</b>	<b>0.281</b>	<b>-0.485</b>	<b>0.410</b>	<b>-0.160</b>
Partial r <sup>2</sup>	P	-0.007	0.097	-0.001	0.000	0.029	0.032	-0.058	0.071	-0.006	-0.005	0.000	0.024	0.036	-0.006	0.197	0.008	-0.028	0.005	0.171	-0.031	0.041	-0.158	-0.029	0.314	0.020
	g	0.674	0.329	0.022	-0.015	1.161	2.114	-2.910	0.528	-0.009	-0.103	-0.013	-0.073	0.025	0.008	0.588	0.117	0.148	-1.772	-0.999	0.254	0.340	-0.015	0.975	-0.609	0.194

Diagonal bold letters indicate direct effect

\* Significant at 5% level, \*\* Significant at 1% level

1- days to 50%flowering, 2-panicle length, 3-plant height, 4-ear bearing tillers, 5-grain yield per plant, 6-test weight, 7-number of filled grains per panicle, 8-total number of grains per panicle, 9-spikelet %, 10-solid loss, 11-water uptake, 12-volume expansion ratio, 13-alkali spreading value, 14-L/B ratio, 15-amylose content, 16-protein content, 17-total starch, 18-total phenol content, 19-total antioxidant activity, 20-flavonoid content, 21-zinc content , 22-iron content, 23-glycemic index, 24-slowly digestible starch, 25-rapidly digestible starch and 26-resistant starch.

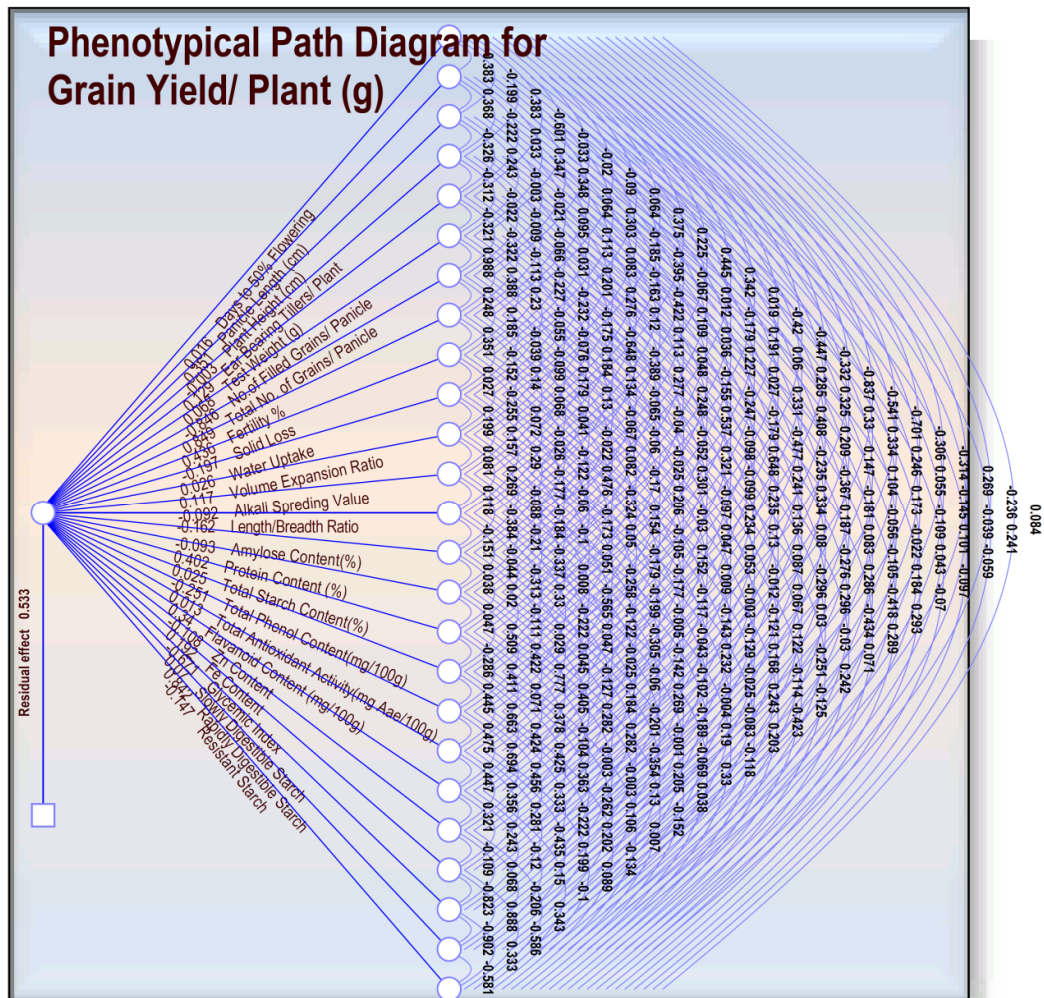


Fig. 4.1 Phenotypic path diagram showing cause-effect relationship in rice (*Oryza sativa* L.)

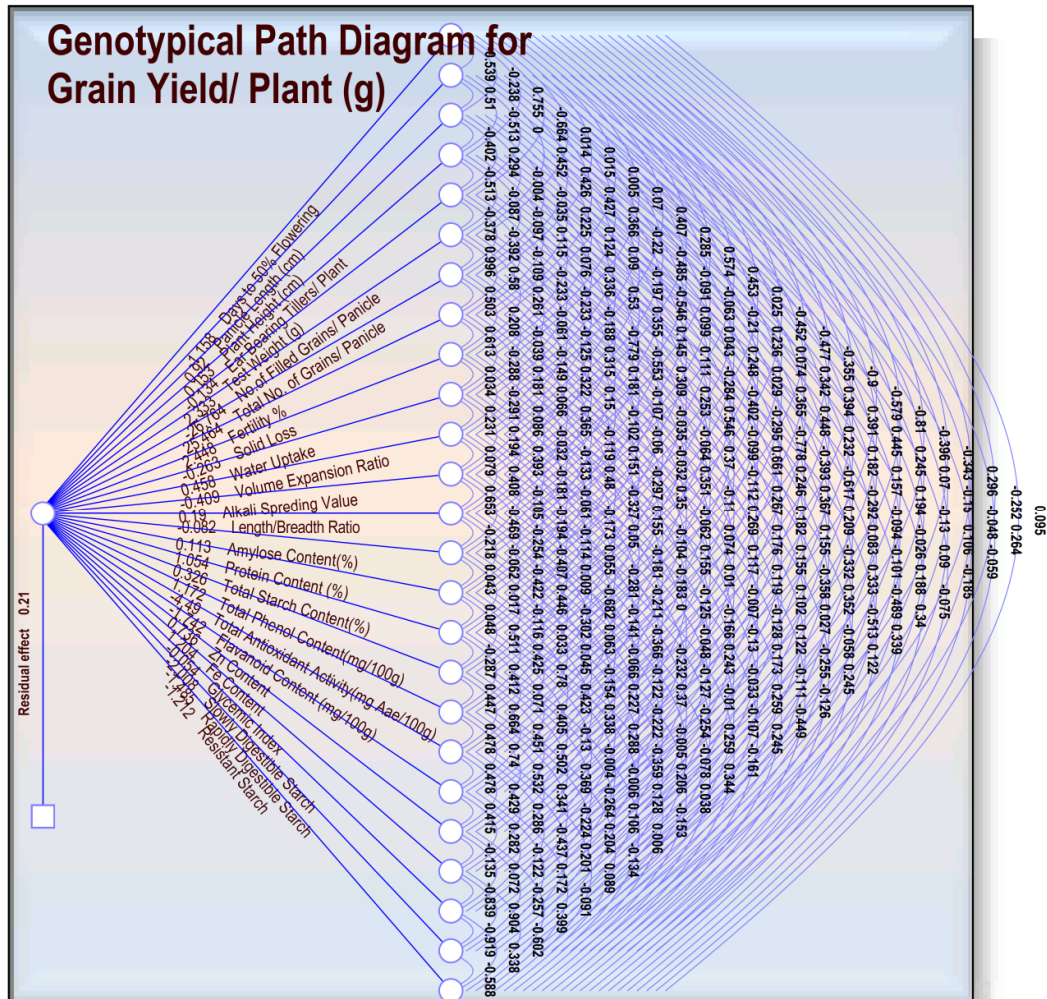


Fig. 4.2 Genotypic path diagram showing cause-effect relationship in rice (*Oryza sativa* L.).

#### 4.3.2.3 Alkali Spreading Value

This trait manifested negative direct effect (-0.092) along with negative and significant correlation (-0.264) with grain yield at phenotypic level. This trait showed indirect positive effect through total number of grains per panicle (0.152) and negative indirect effect through number of filled grains per panicle (-0.156).

At genotypic level, this trait recorded positive direct effect (0.190) along with negative and significant correlation. It showed positive indirect effects *via* total number of grains per panicle (8.202), fertility % (0.163), total antioxidant activity (3.062), flavonoid content (0.246) and rapidly digestible starch (0.159) and it showed negative indirect effects *via* days to 50% flowering (-0.665), test weight (-1.816), number of filled grains per panicle (-8.428), protein content (-0.267), total starch (-0.133), Zn content (-0.269), Fe content (-0.280) and resistant starch (-0.290). Negative direct effects of alkali spreading value was previously reported by Veni *et al.* (2003) and Nivedhitha *et al.* (2013).

#### 4.3.2.4 L/B ratio

This character had negative direct effect (-0.162) on grain yield along with negative correlation (-0.306) at phenotypic level. Similar findings were previously reported by Veni and Rani (2006). Apart from this, it also showed indirect positive effects *via* total number of grains per panicle (0.111) and rapidly digestible starch (0.160) and it had negative indirect effect through number of filled grains per panicle (-0.113) and glycemic index (-0.181).

At genotypic level, this character manifested negative direct effect (-0.082) along with negative correlation (-0.306) (Nandan *et al.*, 2010, Sowmiya & Venkatesan 2017). Prominent positive indirect effects, were exhibited *via* total number of grains per panicle (3.812), fertility % (0.894), water uptake (0.180), alkali spreading value (0.124), total phenol content (0.523), total antioxidant activity (1.354), slowly digestible starch (0.510) and resistant starch (0.195) and it showed negative indirect effects through days to 50% flowering (-0.525), test weight (-1.291), number of filled grains per panicle (-4.84), volume expansion ratio (-0.167) total starch (-0.138), flavonoid content (-0.110), Fe content (-0.147) and rapidly digestible starch (-0.385).

#### 4.3.2.5 Amylose content

Amylose content manifested negative direct effect (-0.093) along with positive correlation (0.064) on grain yield. Apart from this, it also showed indirect positive effects *via* glycemic index (0.135) and negative indirect effect through panicle length (-0.063).

At genotypic level, this trait showed positive direct effect (0.113) which is in agreement with the findings reported by Veni *et al.* (2003), Nivedhitha *et al.* (2013) and Pavan *et al.* (2016). It had positive indirect effects through test weight (0.720), number of filled grains for panicle (2.861), Fe content (0.273) and rapidly digestible starch (0.116) and it had negative indirect effect *via* panicle length (-0.193), total number of grains per panicle (-2.587), fertility % (-0.292), total phenol content (-0.136), total antioxidant activity (-0.149), Zn content (-0.114) and resistant starch (-0.417).

#### 4.3.2.6 Protein content

Protein content recorded highest positive direct effect (0.402) along with positive correlation (0.490) with grain yield at phenotypic level followed by positive indirect effects through flavonoid content (0.264) and rapidly digestible starch (0.173) and it had negative indirect effects through total phenol content (-0.128) and glycemic index (-0.189).

This trait recorded positive direct effect (1.054) coupled with positive correlation (0.558) at genotypic level. It had positive indirect effect through days to 50% flowering (0.524), panicle length (0.217), test weight (0.591), number of filled grains per panicle (0.950), fertility % (0.370), total phenol content (0.599), Zn content (0.312), Fe content (0.407) and slowly digestible starch (0.720) and indirect effect through total number of grains per panicle (-1.529), solid loss (-0.126), total antioxidant activity (-1.906), flavonoid content (-0.360) and rapidly digestible starch (-0.306). Nivedhitha *et al.* (2013) also reported similar findings in a study involving the mutants of Akshaya rice variety.

#### 4.3.2.7 Total starch content

This trait manifested positive direct effect (0.025) along with positive correlation (0.314) with grain yield. Apart from this, it also showed indirect positive effects *via* rapidly digestible starch (0.109) and negative indirect effect through fertility % (-0.727).

At genotypic level this trait recorded positive direct effect (0.326) along with positive correlation (0.357). It had positive indirect effect through days to 50% flowering (0.553), test weight (1.274), number of filled grains per panicle (1.706), Zn content (0.298) and resistant starch (0.185) and negative indirect effect through total number of grains per panicle (-0.804), total phenol content (-0.336), total antioxidant activity (-1.849), flavonoid content (-0.125), Fe content (-0.156) and rapidly digestible starch (-0.190). Nivedhitha *et al.* (2013) also reported positive correlation and positive direct effect of amylose content (a fraction of starch) on grain yield/plant.

#### **4.3.2.7 Total phenol content**

Total phenol content recorded negative direct effect (-0.251) along with positive correlation (0.111) at phenotypic level on grain yield followed by positive indirect effects *via* panicle length (0.100), total number of grains per panicle (0.255), protein content (0.205) and flavonoid content (0.090). It had negative indirect effects *via* number of filled grains per panicle (-0.271) and glycemic index (-0.243).

At genotypic level, this trait exhibited positive direct effect (1.172) along with positive correlation (0.126) and showed positive indirect effect through days to 50% flowering (0.401), panicle length (0.315), number of filled grains per panicle (8.933), fertility % (0.857), protein content (0.539), Zn content (0.332), Fe content (0.605) and slowly digestible starch (0.530) and had negative indirect effects through test weight (-0.231), number of filled grains per panicle (-9.901), total antioxidant activity (-2.005), flavonoid content (-1.157) and rapidly digestible starch (-0.158). As this trait manifested positive correlation along with positive direct effect, simultaneous improvement of both these characters is anticipated.

#### **4.3.2.7 Total antioxidant activity**

This trait showed positive direct effect (0.013) along with positive correlation (0.349) with grain yield at phenotypic level and it had positive indirect effect *via* panicle length (0.114), protein content (0.170), flavonoid content (0.161) and rapidly digestible starch (0.170). It showed negative indirect effects through total phenol content (-0.112) and glycemic index (-0.224).

At genotypic level, this trait exhibited negative direct effect (-4.490) and positive correlation (0.395) with grain yield at phenotypic level. It showed positive indirect effect *via* days to 50% flowering (1.043), panicle length (0.362), ear bearing

tillers per plant (0.104), test weight (1.542), number of filled grains per panicle (3.008), volume expansion ratio (0.115), protein content (0.447), total starch (0.134), total phenol content (0.523), Zn content (0.545), Fe content (0.641), slowly digestible starch (0.450) and resistant starch (0.163). It manifested negative indirect effects through total number of grains per panicle (-2.799), fertility % (-0.152), alkali spreading value (-0.129), flavonoid content (-0.833) and rapidly digestible starch (-0.303). Even though it recorded negative direct effect, the indirect effects seem to be the cause of positive correlation, hence the indirect causal factors have to be considered simultaneously to improve grain yield.

#### **4.3.2.8 Flavonoid content**

Flavonoid content manifested positive direct effect (0.340) along with positive correlation (0.504) at phenotypic level, it showed positive indirect effect through panicle length (0.116), total number of grains per panicle (0.199), protein content (0.313) and rapidly digestible starch (0.167). This trait exhibited negative indirect effects *via* number of filled grains per panicle (-0.199), total phenol content (-0.167) and glycemic index (-0.188).

At genotypic level, this trait exhibited negative direct effect (-1.742) and positive correlation (0.574) with grain yield. It had positive indirect effect through days to 50% flowering (0.671), panicle length (0.360), test weight (0.573), total number of grains per panicle (6.862), fertility % (0.180), protein content (0.822), total phenol content (0.778), Zn content (0.352), Fe content (0.516) and slowly digestible starch (0.878). It showed negative indirect effects through number of filled grains per panicle (-7.155), total antioxidant activity (-2.145), rapidly digestible starch (-0.298) and resistant starch (-0.108).

#### **4.3.2.8 Zinc content**

Zinc content recorded negative direct effect (-0.108) and positive correlation (0.290) with grain yield at phenotypic level. This trait showed positive indirect effects through panicle length (0.117), total number of grains per panicle (0.111), protein content (0.163), flavonoid content (0.152) and rapidly digestible starch (0.126). It had negative indirect effect through number of filled grains per panicle (-0.115), total phenol content (-0.107) and glycemic index (-0.163).

At genotypic level, this trait showed positive direct effect (0.736) along with positive correlation (0.346). It had positive indirect effect *via* days to 50% flowering (0.938), panicle length (0.409), test weight (0.856), total number of grains per panicle (4.479), fertility % (0.287), protein content (0.446), total starch (0.132), total phenol content (0.529), Fe content (0.499), slowly digestible starch (0.245) and resistant starch (0.111), it showed negative indirect effect through number of filled grains per panicle (-4.869), total antioxidant activity (-3.321), flavonoid content (-0.832) and rapidly digestible starch (-0.255).

#### **4.3.2.9 Iron content**

Iron content manifested positive direct effect (0.192) along with positive phenotypic association (0.211) with grain yield per plant. This exhibited prominent positive indirect effects through protein content (0.114) and total antioxidant activity (0.121) it had negative indirect effects through total phenol content (-0.107) and rapidly digestible starch (-0.173).

This trait exhibited positive direct effect (1.204) coupled with positive genotypic correlation (0.282) with grain yield suggesting the simultaneous improvement of both these traits. This character recorded positive indirect effects through panicle length (0.226), test weight (0.488), days to 50% flowering (0.459), total number of grains per panicle (3.939), fertility % (0.292), protein content (0.356), total phenol content (0.588), Zn content (0.305) and rapidly digestible starch (0.382), it had negative indirect effects through number of filled grains per panicle (-4.159), flavonoid content (-2.388), total antioxidant activity (-0.747), slowly digestible starch (-0.144) and resistant starch (-0.484).

#### **4.3.3.0 Glycemic Index**

This trait exhibited negative direct effect (-0.671) along with positive correlation (0.236) with grain yield at phenotypic level followed by positive indirect effects through number of filled grains per panicle (0.234), protein content (0.114) and rapidly digestible starch (0.747), it showed negative indirect effects through fertility % (-0.251)

At genotypic level, this trait exhibited negative indirect effect (-0.054) coupled with positive correlation (0.281) with grain yield and it had positive indirect effects through days to 50% flowering (0.397), test weight (0.193), number of filled grains per panicle (8.863), total number of grains per panicle (0.249), protein content (0.304), total

phenol content (0.432), Zn content (0.208), slowly digestible starch (1.685) and resistant starch (0.730), it had negative indirect effect through (-9.114), total antioxidant activity (-1.530), flavonoid content (-0.499), Fe content (-0.162) and rapidly digestible starch (-1.342).

#### **4.3.3.0 Slowly Digestible Starch**

This character recorded positive direct effect (0.070) along with negative phenotypic correlation (-0.413) on grain yield per plant. This trait showed positive indirect effects *via* total number of grains per panicle (0.252) and it had negative indirect effect through number of filled grains per panicle (-0.242), protein content (-0.142), flavonoid content (-0.148) and rapidly digestible starch (-0.759).

At genotypic level this trait showed negative correlation (-0.485) along with negative direct effect (-2.008) on grain yield per plant. It showed positive indirect effects through total number of grains per panicle (8.955), total antioxidant activity (1.007), flavonoid content (0.762) and rapidly digestible starch (1.364), it showed negative indirect effect through days to 50% flowering (-0.343), panicle length (-0.138), test weight (-0.237), number of filled grains per panicle (-8.917), protein content (-0.378), total phenol content (-0.309) and resistant starch (-0.410).

#### **4.3.3.0 Rapidly Digestible Starch**

Rapidly digestible starch manifested positive phenotypic correlation (0.373) along with positive direct effect (0.842) on grain yield per plant. It showed positive indirect effect through number of filled grains per panicle (0.354) and it had negative indirect effect through total number of grains per panicle (-0.368) and glycemic index (-0.596).

This trait exhibited negative direct effect (-1.485) along with positive genotypic correlation (0.410) with grain yield per plant, it showed positive indirect effects through days to 50% flowering (0.291), test weight (0.438), number of filled grains per panicle (13.100), total number of grains per panicle (13.055), protein content (0.217), total phenol content (0.125), total antioxidant activity (-0.917), rapidly digestible starch (1.845) and resistant starch (0.713) and it had negative indirect effect *via* fertility % (-0.141), volume expansion ratio (-0.106), flavonoid content (-0.349), Zn content (-0.127) and Fe content (-0.310)

#### 4.3.3.1 Resistant Starch

Resistant starch had negative direct effect (-0.147) along with negative phenotypic correlation (-0.139) with grain yield per plant. This trait recorded positive indirect effects through total number of grains per panicle (0.245) and glycemic index (0.393) while it had negative indirect effects through number of filled grains per panicle (-0.248) and rapidly digestible starch (-0.489).

At genotypic level this trait exhibited negative correlation (-0.160) along with negative direct effect (-1.212). It showed positive indirect effect through panicle length (0.243), total number of grains per panicle (8.623), fertility % (0.300), volume expansion ratio (0.183), total antioxidant activity (0.603), Fe content (0.481) and rapidly digestible starch (0.874) while negative indirect effects were manifested through days to 50% flowering (-0.110), test weight (-0.174), number of filled grains per panicle (-9.092), slowly digestible starch (-0.489) and flavonoid content (-0.156).

Among the yield components and quality traits positive and significant correlation coupled with positive direct effect was manifested by panicle length, test weight, protein content, total starch content, zinc and iron content. Moreover, all these characters are inter-related positively. Hence, all these traits would be improved simultaneously through simple selection. Days to 50% flowering, L/B ratio, slowly digestible starch exhibited negative and significant correlation coupled with negative direct effect indicating selection based on these characters will not aid in yield improvement. Traits like total antioxidant activity, flavonoid content, glycemic index and rapidly digestible starch are positively associated with grain yield but manifested negative direct effect suggesting that the positive indirect effects exhibited through other characters seem to be the reason for positive correlation. Whereas water uptake, alkali spreading value had positive direct effects coupled with negative correlation indicating the restricted simultaneous selection to be followed to nullify the undesirable indirect effects in order to make use of the direct effect for yield improvement.

## Chapter – V

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# Summary and Conclusions

## Chapter V

# SUMMARY AND CONCLUSIONS

The present investigation was carried out during *kharif*, 2017 at Agricultural College Farm, Bapatla with 26 genotypes of rice to obtain information on the nature and extent of variability, heritability, genetic advance as per cent of mean, correlation and the magnitude of direct and indirect effects of yield and physicochemical, nutritional and biochemical quality characters on grain yield of different colored rice genotypes (*Oryza sativa* L.).

The analysis of variance revealed significant differences among the genotypes for 23 characters *viz.*, days to 50% flowering, panicle length (cm), plant height (cm), ear bearing tillers per plant, grain yield per plant (g), test weight (g), number of filled grains per panicle, total number of grains per panicle, fertility %, water uptake, alkali spreading value, amylose content (%), protein content (%), total starch content (%), total phenol content (mg/100 g), total antioxidant activity (mg AAE/100 g), flavonoid content (mg QE/100 g), Zn content (ppm), Fe content (ppm), glycemic index, slowly digestible starch (%), rapidly digestible starch (%) and resistant starch (%) except for solid loss, volume expansion ratio and L/B ratio.

When compared to other brown pericarp colored rice genotypes BPT 5204, a popular variety with excellent cooking quality traits manifested all the quality parameters in the desirable range and had a low GI value. Another variety BPT 2270 along with BPT 2660, a minikit culture also recorded low GI coupled with other desirable quality traits. All these genotypes possess medium slender grain type. BPT 2595 had high RS content and flavonoid content among brown rice genotypes. All these brown pericarp colored genotypes are low in total phenol content, antioxidant activity and flavonoid content. Among red pericarp colored genotypes, BPT 3139 manifested high SDS, RS, antioxidant activity, high Zn content and low GI. Whereas Jyothi, Matta Triveni and BPT 3111 recorded high antioxidant activity coupled with high Zn and Iron content and high grain yield. Among black pericarp colored genotypes, BPT 2848 manifested highly desirable quality parameters like slender grain, intermediate amylose content and alkali spreading value along with high yield potential. It also recorded high protein content, high flavonoid content, high SDS and RS content coupled with low GI value. Hence all these genotypes may be recommended for inclusion in diabetic diet.

The results of genetic parameters revealed that among the yield component traits test weight, total number of grains per panicle, number of filled grains per panicle and grain yield recorded high estimates for all the genetic parameters studied suggesting that inheritance of these traits is controlled by additive gene effects hence these can be improved by simple selection. The remaining traits *viz.*, ear bearing tillers, plant height, panicle length and days to 50% flowering are controlled by both additive and non additive gene effects and the improvement of these traits may not be anticipated through simple selection

Among physical and cooking quality parameters, the traits *viz.*, solid loss, water uptake, alkali spreading value, volume expansion ratio and amylose content manifested high estimates for all the genetic parameters suggesting that predominance of additive gene effects in controlling these traits while L/B ratio is controlled by both additive and non additive gene effects.

Among nutritional and biochemical quality parameters, total phenol content, total antioxidant activity, flavonoid content, zinc content, iron content, protein content, total starch content, slowly digestible starch and resistant starch exhibited high estimates for all the genetic parameters studied suggesting that predominance of additive gene effects. Hence these traits can be improved through simple selection. Glycemic index and rapidly digestible starch manifested high heritability and moderate genetic advance indicating that inheritance of these traits controlled by both additive and non additive gene effects and improvement of these traits may not be anticipated through simple selection.

Correlation studies revealed that panicle length, test weight and fertility % among yield components, protein content, total starch, total antioxidant activity, flavonoid content, zinc content, iron content, rapidly digestible starch and glycemic index among quality traits showed positive & significant correlation with grain yield suggesting simultaneous improvement of these traits with grain yield. While days to 50% flowering, water uptake, alkali spreading value, L/B ratio and slowly digestible starch manifested negative and significant association with grain yield indicating that selection against these traits will improve the yield.

Among nutritional and biochemical quality traits, zinc content, iron content and protein content are positively correlated among themselves. Likewise, there is a positive relationship among total phenol content, total antioxidant activity and flavonoid content indicating that simultaneous improvement of these characters is anticipated which is desirable. Glycemic index had negative association with slowly digestible starch and resistant starch and positive association with rapidly digestible starch. Selecting the genotypes with higher SDS & RS, will lower the GI value. Genotypes with low GI value promote the health benefits by reducing the risk of diabetes. All these relationships among these nutritional and biochemical parameters would help in isolation of a genotype with high antioxidant activity coupled with low GI which is very much desired for development of rice variety with potential health benefits.

Studies of path coefficient analysis revealed positive direct effects coupled with positive correlation coefficients of grain yield with panicle length, plant height, test weight, fertility%, amylose content, protein content, total starch content, total phenol content, Zn content and Fe content suggesting that simple selection of all the above traits would bring improvement to grain yield in rice while days to 50% flowering, L/B ratio and slowly digestible starch manifested negative direct effect coupled with negative correlation indicating that selection against these traits will improve the yield. Water uptake and alkali spreading value exhibited positive direct effect coupled with negative correlation suggesting restricted simultaneous selection to nullify the undesirable indirect effects. Solid loss, volume expansion ratio, glycemic index and rapidly digestible starch showed negative direct effect with positive correlation indicating that indirect casual factors are to be considered simultaneously during selection to improve the grain yield.

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**Note:** The pattern of Literature Cited presented above is in accordance with the guidelines for thesis presentation, Acharya N. G. Ranga Agricultural University, Lam, Guntur.