

**CHARACTER ASSOCIATION AND
SCREENING FOR SHEATH BLIGHT AND
BACTERIAL LEAF BLIGHT OF
F₅ FAMILIES IN RICE
(*Oryza sativa* L.)**

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**THESIS SUBMITTED TO THE
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CHAIRPERSON: Dr. B.N.V.S.R. RAVI KUMAR



DEPARTMENT OF GENETICS AND PLANT BREEDING

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2016

DECLARATION

I, **Ms. K.L.Y. TEJASWINI**, hereby declare that the thesis entitled **“CHARACTER ASSOCIATION AND SCREENING FOR SHEATH BLIGHT AND BACTERIAL LEAF BLIGHT OF F₅ FAMILIES IN RICE (*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:

(K.L.Y. TEJASWINI)

I.D. No.: BAM- 13-12

Date:

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LIST OF SYMBOLS AND ABBREVIATIONS

&	:	And
σ_p	:	Phenotypic standard deviation
σ_g	:	Genotypic standard deviation
σ_p^2 (or) V_p	:	Phenotypic variance
σ_g^2 (or) V_g	:	Genotypic variance
σ_e^2 (or) V_e	:	Environmental variance
APRRI	:	Andhra Pradesh Rice Research Institute
ANOVA	:	Analysis of variance
BLB	:	Bacterial leaf blight
$^{\circ}\text{C}$	:	Degree centigrade
CD	:	Critical difference
cm	:	Centimeter
COV	:	Covariance
CV	:	Coefficient of variation
DAS	:	Days after sowing
d.f	:	Degrees of freedom
<i>et al.</i> ,	:	and coworkers
F_5	:	Fifth filial generation of a cross
Fig.	:	Figure
g	:	Gram
GA	:	Genetic advance
GAM	:	Genetic advance as per cent of mean
GCV	:	Genotypic coefficient of variation
ha	:	Hectare
h^2 (bs)	:	Heritability in broad sense
IRRI	:	International Rice Research Institute
K	:	Selection differential
kg ha^{-1}	:	Kilograms per hectare
L	:	Litre
L/B	:	Kernal length to breadth ratio
Max.	:	Maximum
Min.	:	Minimum
ml	:	Milli litre
mm	:	Millimeter
MR	:	Moderately resistant
MS	:	Moderately susceptible
MSS	:	Mean sum of squares
No.	:	Number
NS	:	Non-significant
PCV	:	Phenotypic coefficient of variation
<i>per se</i>	:	As such with mean
r	:	Correlation coefficient
R	:	Resistant

RARS	:	Regional Agricultural Research Station
RBD	:	Randomized Block Design
rpm	:	Revolutions per minute
S	:	Significant
S	:	Susceptible
SES	:	Standard evaluation system
%	:	Per cent
<i>Via</i>	:	Through
<i>viz.,</i>	:	Namely
$\bar{X}$	:	Grand mean
/	:	Per
<	:	Less than
>	:	Greater than

ABSTRACT

Name of the Author	:	K.L.Y. TEJASWINI
Title of the thesis	:	Character association and screening for sheath blight and bacterial leaf blight of F₅ families in rice (<i>Oryza sativa</i> L.)
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The present investigation was carried out during *khariif*, 2015 at Andhra Pradesh Rice Research Institute & Regional Agricultural Research Station, Maruteru, Andhra Pradesh with one hundred and fourteen F₅ families along with their seven parents of rice (*Oryza sativa* L.) in order to study the variability, character association, magnitude of direct and indirect effects and to screen for sheath blight and bacterial leaf blight reaction of the genotypes. The data were recorded on days to 50% flowering, days to maturity, plant height (cm), number of panicles per plant, panicle length (cm), grain yield per plant (g), test weight (g), kernel length (mm), kernel breadth (mm) and L/B ratio.

The analysis of variance revealed significant differences among the genotypes for all the characters indicating the presence of sufficient genetic variability in the studied material.

High PCV and GCV were observed for grain yield per plant and test weight. Difference between PCV and GCV was very low indicating little environmental influence on genotypes. High heritability coupled with high genetic advance as per cent of mean was observed for number of grains per panicle, grain yield per plant and test weight indicating the presence of additive gene action in governing the inheritance of these traits. Hence, direct phenotypic selection is useful with respect to these traits.

The study of character association and path coefficient analysis indicated that panicle length had positive direct effect coupled with positive significant correlation with grain yield per plant and hence direct selection can be made based on this trait for improving yield.

Screening for sheath blight resistance revealed that out of one hundred and fourteen F₅ families, no family was found to be immune or resistant. Forty four families belonging to different crosses were found to be moderately resistant, sixty three were susceptible while seven families recorded were highly susceptible where as in case of bacterial leaf blight thirteen families were found to be moderately resistant, ninety nine were susceptible, two families were highly susceptible while no family was found to be immune or resistant.

The families MTU 2462-1-9-2 (43.75 g), MTU 2462-1-1-1 (32.6 g), MTU 2462-22-3-1 (30.7 g), MTU 2462-2-1-1 (27.1 g), MTU 2463-4-1-2 (16.6 g), MTU 2463-4-2-1 (15.5 g), MTU 2463-14-1-1 (14 g), MTU 2463-15-1-1 (14.6 g), MTU 2465-12-2-2 (27.3 g) and MTU 2468-28-1-1 (28.7 g) recorded higher grain yield than their parents but showed susceptibility to both the diseases and can be selected when grain yield is taken as major criterion for selection where as families MTU 2462-1-9-1 (41.6 g), MTU 2462-15-3-1 (30.3 g), MTU 2462-15-1-1 (28.6 g), MTU 2462-17-2-1 (27.6 g), MTU 2462-1-5-2 (25.9 g) and MTU 2463-8-2-1 (15.4 g) recorded higher yield than their parents along with moderate resistance (score 5) to sheath blight and hence highly preferred.

In addition to them, MTU 2462-1-5-2 (25.9 g), MTU 2462-26-3-1 (25.4 g), MTU 2465-6-2-1 (18.2 g), MTU 2465-11-3-1 (19.4 g), MTU 2466-4-2-2 (15.8 g), MTU 2468-25-2-1 (18.6 g), MTU 2469-6-3-2 (19.8 g), MTU 2469-6-5-1 (18.6 g), MTU 2469-8-1-1 (20.8 g) and MTU 2469-36-1-1 (19.5 g) recorded moderate resistance (score 5) to sheath blight and families MTU 2462-1-8-2 (25.7 g), MTU 2462-35-2-2 (20.3 g), MTU 2462-37-2-1 (19.2 g), MTU 2462-45-2-1 (20.3 g), MTU 2465-6-2-1 (18.2 g), MTU 2468-2-1-1 (18.4 g), MTU 2468-25-2-1 (18.6 g), MTU 2469-6-5-1 (18.6 g) and MTU 2469-10-2-1 (19.7 g) showed moderate resistance to bacterial leaf blight along with moderate to high yield than their parents and hence can also be selected.

The families MTU 2465-6-2-1 (18.2 g), MTU 2468-25-2-1 (18.6 g) and MTU 2469-6-5-1 (18.6 g) showed moderate resistance to both the diseases and hence highly preferred in future breeding programmes.

Chapter - I

INTRODUCTION

Rice (*Oryza sativa*, $2n = 2x = 24$, family: *Graminaea*) is the major food crop grown across all the continents in the world, except Antarctica. As a global food, it has a large influence on human nutrition and food security. It is the staple food for half of the world's population. In Asia alone, more than 2 billion people obtain 60-70% of caloric intake from rice and its derived products and almost a billion households in Asia, Africa and America depends on rice based cropping systems for their livelihood and main source of employment. Rice is therefore on the frontline in the fight against world hunger and poverty. Rice is also a symbol of both cultural identity and global unity. For all of these reasons, it is apt to say that **“Rice is Life”** (Jacques Biouf, 2003).

The demand for rice production is increasing day by day because of expansion of rice consuming people, more specifically for developing countries like Asia and Africa. Globally, it is planted on about 158 million hectares with an annual production of 478 million tons. India ranks first in area (43.85 million hectares) and second in the production (104.78 million tonnes) with a productivity of 2185 kg ha^{-1} . Andhra Pradesh occupies an area of 3.80 million hectares with a production of 11.56 million tones and productivity of 3244 kg ha^{-1} (www.indiaagristat.com, 2014-15). Maintaining stable rice production is extremely important to feed the growing population. At the current rate of population growth of 1.58% in India, the requirement of rice by 2025 is estimated to be around 140.7 million tonnes (Abdullah *et al.*, 2005) and this demand can be met only by enhancing the productivity and production of rice (Hossain, 1996 and Mishra, 2002).

To achieve this target, it is necessary to enhance the production and productivity of existing rice cultivars through pyramiding of high yield alleles into agronomically desirable genotypes. Therefore, keeping in view of the future demand of rice, there is a continuous need to evolve new varieties with higher yields through various genetic approaches and selection of genotypes in early generations would become essential. As yield is a complex character, which is highly influenced by environment, direct selection for yield results in limited success in yield improvement. Hence, indirect approach has to be practiced by selecting yield component characters as they show association among themselves and also with yield and this way is more effective if the components are positively correlated with yield (Surek and Beser, 2005).

Information on nature and magnitude of variability present in a population due to genetic and non-genetic causes is an important prerequisite for systematic breeding programmes to improve yield potential of the crop. Genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are useful in detecting the amount of variability present in the population (Idris *et al.*, 2012).

Broad sense heritability is the relative magnitude of genotypic and phenotypic variances for the traits and has a predictive role in selection procedures (Allard, 1960). This gives an idea of total variation ascribed to genotypic effects, which are exploitable portion of variation (Akinwale *et al.*, 2011). The estimate of heritability alone is not very much useful because it includes the effect of both additive and non additive genes. The genetic advance is a useful indicator of the progress that can be expected as a result of exercising selection on the pertinent population (Aditya and Bhartiya, 2013). Heritability estimates along with genetic advance are more helpful in predicting gain under selection (Sinha *et al.*, 2004 and Johnson *et al.*, 1955).

Correlation is the measure of mutual relationship between two variables and measures the degree of closeness and the linear relationship between them. To know how the improvement of one character will bring simultaneous improvement in other characters, study of correlations is essential for a plant breeder. Information on the correlation co-efficient between grain yield and yield contributing traits is a prerequisite for improving yield. Path analysis facilitates the partitioning of correlation coefficients into direct and indirect effects of various characters on yield. Information on association of characters, direct and indirect effects contributed by each character towards yield will be an added advantage in aiding the selection process. Correlation and path analysis establish the extent of association between yield and its components and also bring out relative importance of their direct and indirect effects, thus giving an obvious understanding of their association with grain yield. Ultimately, this kind of analysis could help the breeder to design his selection strategies to improve grain yield (Ravindrababu *et al.*, 2012).

Rice crop suffers from several biotic and abiotic stresses that seriously affect its production. Bacterial leaf blight, caused by *Xanthomonas oryzae* pv. *Oryzae* is one of the major devastating diseases. Crop loss assessment studies have revealed that this disease reduces grain yield to varying levels, depending on stage of the crop, degree of

cultivar susceptibility and to a great extent, conduciveness of the environment. Bacterial leaf blight can reduce crop yield from 50% to 80% (Singh *et al.*, 1977 and Khush and Ogawa, 1989). The most effective approach to control bacterial leaf blight is using resistant varieties. Sheath blight, caused by *Rhizoctonia solani* (teleomorph: *Thanatephorus cucumeris*) is also one of the major disease of rice in many countries affecting more than 50% of global rice production (Groth *et al.*, 1991 and Marchetti and Bollich, 1991). Many rice cultivars have been identified as moderately resistant to sheath blight, however no resistant cultivar has been found so far (Prasad and Eizenga, 2008). Hence, screening of selected families for tolerance against Bacterial leaf blight and sheath blight will enable us to identify rice genotypes having high yield potential as well as tolerance to these diseases.

With regard to the importance of aforesaid aspects, an attempt has been made in the present investigation to identify the promising rice genotypes with moderate resistance to sheath blight and bacterial leaf blight with the following objectives.

- 1) To study variability for yield and its component characters.
- 2) To study character association between yield and yield component characters.
- 3) To study direct and indirect effects of yield components on seed yield.
- 4) Screening of selected F₄₋₅ families for tolerance to sheath blight and bacterial leaf blight

Chapter II

REVIEW OF LITERATURE

The present investigation in rice was undertaken to study the extent of variability and association among yield and yield component characters and to estimate correlation and path coefficients. In addition to them, screening for sheath blight and bacterial leaf blight was also carried out. The literature available on the main objectives of the present study has been comprehensively reviewed under the following headings.

2.1 Variability, Heritability and Genetic advance

2.2 Character association

2.3 Path analysis

2.4 Screening for Sheath blight and Bacterial leaf blight

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

2.1.1 Variability

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.

Yield is a quantitative character which is polygenic in nature and is highly influenced by environment (Allard, 1960). Hence partitioning of variability into heritable (due to genotype) and non-heritable (due to environment) components is very much needed to get a true indication of the genetic coefficient of variability which represents the true breeding behavior of the phenotype.

The efficiency of selection in plant breeding largely depends upon the amount of heritable variation present in the material. The difference between PCV and GCV estimates is an indication of relative influence of environment on the character. If the difference is low, influence of environment is less indicating high heritability of the trait. Reverse is the case when the difference between PCV and GCV is high. The character wise chronological report of available literature on phenotypic and genotypic coefficient of variability is presented in the Table 2.1.

Table 2.1. Review of literature on genetic variability for yield and its components in rice.

S.No.	Character	Variability	Reference
1	Days to 50% flowering	High PCV, GCV	Anjaneyulu <i>et al.</i> (2010) Anseri <i>et al.</i> (2010) Hasan <i>et al.</i> (2011) Seyoum <i>et al.</i> (2012) Singh <i>et al.</i> (2014) Nitesh Kumar <i>et al.</i> (2015)
		Moderate PCV, GCV	Lal and Chauhan (2011) Kumar and Saravanan (2012) Bekele <i>et al.</i> (2013) Paikhomba <i>et al.</i> (2014)
		Moderate to low PCV, GCV	Akinwale <i>et al.</i> (2011) Sanghera <i>et al.</i> (2013) Idris and Mohammad (2013)
		Low PCV, GCV	Shiva Prasad <i>et al.</i> (2009) Laxuman <i>et al.</i> (2010) Saidaiah <i>et al.</i> (2010) Shiva Parvathi <i>et al.</i> (2011) Shiva Prasad <i>et al.</i> (2011) Sravan <i>et al.</i> (2012) Ghosh and Sharma (2012) Aditya and Bhartiya (2013) Gangashetty <i>et al.</i> (2013) Neha <i>et al.</i> (2014) Khare <i>et al.</i> (2014) Patel <i>et al.</i> (2014) Shrivastava <i>et al.</i> (2014) Suresh <i>et al.</i> (2014) Sameera <i>et al.</i> (2015)
2	Days to Maturity	High PCV, GCV	Shiva Prasad <i>et al.</i> (2011)
		Moderate PCV, GCV	Nitesh Kumar <i>et al.</i> (2015)
		Moderate to low PCV, GCV	Akinwale <i>et al.</i> (2011) Idris and Mohammad (2013) Sanghera <i>et al.</i> (2013)
		Low PCV, GCV	Laxuman <i>et al.</i> (2010) Aditya and Bhartiya (2013) Bekele <i>et al.</i> (2013) Khare <i>et al.</i> (2014) Patel <i>et al.</i> (2014) Shrivastava <i>et al.</i> (2014) Sameera <i>et al.</i> (2015)
3	Plant Height	High PCV, GCV	Selvaraj <i>et al.</i> (2011) Lal and Chauhan (2011) Bhadru <i>et al.</i> (2012) Seyoum <i>et al.</i> (2012) Gangashetty <i>et al.</i> (2013) Jambhulkar and Bose (2014) Neha <i>et al.</i> (2014) Ogunbayo <i>et al.</i> (2014)

Table 2.1 (cont.).

		Moderate to high PCV, GCV	Kumar and Ramesh (2008)
		Moderate PCV, GCV	Shiva Prasad <i>et al.</i> (2009) Saidaiah <i>et al.</i> (2010) Shiva Parvathi <i>et al.</i> (2011) Sravan <i>et al.</i> (2012) Kumar and Saravanan (2012) Ghosh and Sharma (2012) Bekele <i>et al.</i> (2013) Idris and Mohamed (2013) Paikhomba <i>et al.</i> (2014) Nitesh Kumar <i>et al.</i> (2015)
		Moderate to low PCV, GCV	Akinwale <i>et al.</i> (2011) Idris and Mohammad (2013) Sanghera <i>et al.</i> (2013)
		Low PCV, GCV	Aditya and Bhartiya (2013) Paikhomba <i>et al.</i> (2014) Patel <i>et al.</i> (2014) Sameera <i>et al.</i> (2015)
4	Number of panicles per plant	High PCV, GCV	Lal and Chauhan (2011) Selvaraj <i>et al.</i> (2011) Singh <i>et al.</i> (2011) Shiva Prasad <i>et al.</i> (2011) Seyoum <i>et al.</i> (2012) Gangashetty <i>et al.</i> (2013) Idris and Mohammad (2013) Khare <i>et al.</i> (2014) Ogunbayo <i>et al.</i> (2014) Sameera <i>et al.</i> (2015)
		High PCV, Moderate GCV	Saidaiah <i>et al.</i> (2010)
		Moderate PCV, GCV	Saidaiah <i>et al.</i> (2010) Shiva Parvathi <i>et al.</i> (2011) Shiva Prasad <i>et al.</i> (2011) Sravan <i>et al.</i> (2012)
		Moderate PCV, Low GCV	Karthikeyan <i>et al.</i> (2007) Kuchanur <i>et al.</i> (2009)
		High PCV, Low GCV	Paikhomba <i>et al.</i> (2014)
5	Panicle length	High PCV, GCV	Nayudu <i>et al.</i> (2007)
		Moderate PCV, GCV	Saidaiah <i>et al.</i> (2010) Shiva Prasad <i>et al.</i> (2011) Gangashetty <i>et al.</i> (2013) Idris and Mohamed (2013) Nitesh Kumar <i>et al.</i> (2015)
		Moderate to low PCV, GCV	Akinwale <i>et al.</i> (2011) Idris and Mohammad (2013) Sanghera <i>et al.</i> (2013)
		Moderate PCV, Low	Shiva Parvathi <i>et al.</i> (2011)

Table 2.1 (cont.).

		GCV	Ghosh and Sharma (2012)
		Low PCV, GCV	Sravan <i>et al.</i> (2012) Aditya and Bhartiya (2013) Paikhomba <i>et al.</i> (2014) Patel <i>et al.</i> (2014) Suresh <i>et al.</i> (2014) Sameera <i>et al.</i> (2015)
6	Grain yield per plant	High PCV, GCV	Anjaneyulu <i>et al.</i> (2010) Anseri <i>et al.</i> (2010) Sreeparvathy <i>et al.</i> (2010) Hasan <i>et al.</i> (2011) Lal and Chauhan (2011) Shiva Parvthi <i>et al.</i> (2011) Selvaraj <i>et al.</i> (2011) Singh <i>et al.</i> (2011) Subbaiah <i>et al.</i> (2011) Idris <i>et al.</i> (2012) Seyoum <i>et al.</i> (2012) Sravan <i>et al.</i> (2012) Kumar and Saravanan (2012) Ghosh and Sharma (2012) Bhadru <i>et al.</i> (2012) Aditya and Bhartiya (2013) Bekele <i>et al.</i> (2013) Paikhomba <i>et al.</i> (2014) Idris and Mohamed (2013) Bornare <i>et al.</i> (2014) Dhurai <i>et al.</i> (2014) Jambhulkar and Bose (2014) Khare <i>et al.</i> (2014) Patel <i>et al.</i> (2014) Rai <i>et al.</i> (2014) Singh <i>et al.</i> (2014) Suresh <i>et al.</i> (2014) Nitesh Kumar <i>et al.</i> (2015)
		Moderate to high GCV, PCV	Thirumala Rao <i>et al.</i> (2014)
		High PCV, Moderate GCV	Monalisa Manna <i>et al.</i> (2006)
		Moderate PCV, GCV	Saidaiah <i>et al.</i> (2010) Paikhomba <i>et al.</i> (2014) Sameera <i>et al.</i> (2015)
		Low PCV, GCV	Umadevi <i>et al.</i> (2010) Shiva Parvthi <i>et al.</i> (2011) Idris and Mohammad (2013)
7	Test weight	High PCV, GCV	Bhadru <i>et al.</i> (2012) Gangashetty <i>et al.</i> (2013)
		High to moderate PCV, GCV	Thirumala Rao <i>et al.</i> (2014)

Table 2.1 (cont.).

		Moderate PCV, GCV	Saidaiah <i>et al.</i> (2010) Lal and Chauhan (2011) Shiva Prasad <i>et al.</i> (2011) Subbaiah <i>et al.</i> (2011) Kumar and Saravanan (2012) Ghosh and Sharma (2012) Bekele <i>et al.</i> (2013) Patel <i>et al.</i> (2014)
		Moderate PCV, Low GCV	Vijayalakshmi <i>et al.</i> (2008) Kuchanur <i>et al.</i> (2009)
		Low PCV, GCV	Sravan <i>et al.</i> (2012) Aditya and Bhartiya (2013) Idris and Mohamed (2013) Paikhomba <i>et al.</i> (2014)
8	Kernel length	High PCV, GCV	Suresh <i>et al.</i> (2014)
		Moderate PCV, GCV	Subbaiah <i>et al.</i> (2011) Bekele <i>et al.</i> (2013) Nitesh Kumar <i>et al.</i> (2015)
		Low PCV, GCV	Manonmani <i>et al.</i> (2010) Aditya and Bhartiya (2013) Patel <i>et al.</i> (2014)
9	Kernel breadth	Moderate PCV, GCV	Subbaiah <i>et al.</i> (2011) Bekele <i>et al.</i> (2013) Nitesh Kumar <i>et al.</i> (2015)
		Low PCV, GCV	Manonmani <i>et al.</i> (2010) Aditya and Bhartiya (2013) Patel <i>et al.</i> (2014)
10	L/B ratio	High PCV, GCV	Lal and Chauhan (2011)
		Moderate PCV, GCV	Rajeswari <i>et al.</i> (2010) Umadevi <i>et al.</i> (2010) Subbaiah <i>et al.</i> (2011) Kumar and Saravanan (2012) Bekele <i>et al.</i> (2013) Gangashetty <i>et al.</i> (2013) Shejul <i>et al.</i> (2013) Patel <i>et al.</i> (2014) Nitesh Kumar <i>et al.</i> (2015)
		Low PCV, GCV	Aditya and Bhartiya (2013)

2.1.2. Heritability and genetic advance as per cent of mean

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.

Heritability measures the relative amount of heritable portion of variability, while the genetic advance helps to measure the amount of progress that could be expected with selection in a character. High heritability is not always an indication of high genetic gain as it includes both additive and non-additive types of gene action. Hence, heritability along with genetic advance considered together should be used in predicting the ultimate effect for selecting superior varieties (Ali *et al.*, 2002).

The available literature on heritability and genetic advance as per cent of mean in rice was presented here under.

Akinwale *et al.* (2011) observed the pattern of heritability and genetic advance in twenty rice genotypes and revealed that high to medium broad sense heritability estimates was observed on days to heading, days to maturity, plant height, grain yield, number of panicles per m² and panicle length suggests high component of heritable portion of variation. The low broad sense heritability was observed for the number of tillers per plant and 1000 grain weight is indicative of the influence of the environment on these traits. Low heritability of these traits indicates the ineffectiveness of direct selection for these traits. High to medium heritability and genetic advance were recorded for number of grains per panicle, grain yield and the number of panicles per plant. This suggests that these traits are primarily under genetic control and selection for them can be achieved through their phenotypic performance.

Hasan *et al.* (2011) carried out heritability and genetic advance studies in twenty four rice hybrids and reported that high heritability associated with high genetic advance were found in panicle per m² which indicated that the character was simply inherited in nature and possessed additive gene effects.

Subbaiah *et al.* (2011) studied heritability and genetic advance estimates in sixteen parents and forty eight hybrids and reported that high heritability coupled with high genetic advance as per cent of mean were recorded for total number of productive

tillers per plant, kernel length, kernel L/B ratio and grain yield per plant in case of parents and for total number of productive tillers per plant in hybrids indicating the additive gene effects in the genetic control of these traits and can be improved by simple selection in the present breeding material.

Seyoum *et al.* (2012) evaluated fourteen rice genotypes and reported that high to medium heritability and high genetic advance was observed for plant height, days to 50% flowering, panicles per plant, 1000 grain weight and grain yield which suggests that these traits can be directly considered for selection where as panicle length showed high heritability with low genetic advance indicating the predominance of non additive gene action and influence of environment in governing the expression of this trait.

Sravan *et al.* (2012) conducted an investigation on thirty six rice genotypes and observed that heritability and genetic advance as per cent of mean was high for plant height, which indicates the preponderance of additive gene action.

Aditya and Bhartiya (2013) studied heritability and genetic advance in eighteen rainfed upland rice genotypes and reported that high broad sense heritability for plant height and fertile grains per panicle followed by grains per panicle, days to 50 per cent flowering and days to maturity. The estimate of genetic advance was found to be highest for grains per panicle and fertile grains per panicle. The number of grains per panicle and fertile grains per panicle had high heritability as well as high genetic advance. It is suggested that these characters were predominantly controlled by additive gene action. Hence genetic improvement through selection for these traits may be effective.

Bekele *et al.* (2013) evaluated sixty four rice genotypes and observed that high heritability estimates were recorded for all the characters in this study. High heritability coupled with high genetic advance as percent mean were recorded for all the traits in this study except days to maturity indicating that these traits were not much influenced by environmental factors. Hence, these traits are mostly controlled by genetic factors and expected to respond to direct selection for trait improvement. High heritability coupled with moderate genetic advance as percent mean was recorded for days to maturity which means that this trait is controlled by the interaction of genetic and environmental components and hence selection based on phenotypic observations alone may not be very effective for these traits.

Gangashetty *et al.* (2013) carried out an investigation on forty two rice genotypes to know the extent of heritability and genetic advance and found that high heritability coupled with high genetic advance as per cent of mean were recorded for plant height, productive tillers per plant, test weight, L/B ratio, grain length, plant height and grain yield per plant. This indicates that there was low environmental influence on the expression of these characters and hence simple selection can be practiced on these characters.

Idris and Mohammad (2013) evaluated eighteen rice genotypes for their heritability and genetic advance estimates and results revealed that high to medium broad sense heritability was observed for days to 50% flowering, days to 50% maturity, 1000-grain weight, number of panicles per m² and panicle length revealing high component of heritable portion and selection for these traits can be achieved directly based on their phenotypic performance. The low broad sense heritability observed for the plant height, number of tillers per plant and grain yield is indicative of the influence of the environment on these traits. Low heritability of these traits indicates the ineffectiveness of direct selection for these traits. High to medium heritability and genetic advance were recorded for the number of grains per panicle, number of filled grain per panicle, days to 50% flowering, days to 50% maturity and number of panicles/m². This suggests that these traits are primarily under genetic control and selection for them can be achieved through their phenotypic performance. High heritability estimates with low genetic advance observed for panicle length and 1000-grain weight indicates non additive type of gene action and that genotype x environment interaction plays a significant role in the expression of the traits.

Sanghera *et al.* (2013) studied heritability and genetic advance estimates in fourteen red rice genotypes and observed high heritability accompanied by high to moderate genetic advance for panicle density, days to 50% flowering and plant height, indicated the predominance of additive gene action for the expression of these characters while high heritability coupled with moderate genetic advance was exhibited by 100 grain weight indicating the role of non additive gene action in inheritance of this trait.

Jambhulkar and Bose (2014) carried out an investigation on twenty two upland rice genotypes to study their heritability and genetic advance and observed high heritability with moderate to high genetic advance for days to 50% flowering, plant

height, panicle length and test grain weight indicating the presence of additive genetic effects hence selection based on phenotypic performance of these character will be effective.

Khare *et al.* (2014) studied sixty rice genotypes to know their heritability and genetic advance estimates and results revealed that high heritability along with high genetic advance as per cent of mean was recorded for grain yield per plant, plant height and number of effective tillers per plant indicated that the less influence of environmental effect in the inheritance of these traits. High heritability coupled with low genetic advance as per cent mean were observed in days to maturity and days to 50% flowering.

Paikhomba *et al.* (2014) evaluated thirty rice hybrids and observed that characters like grain yield showed high heritability coupled with moderate genetic advance. Number of panicles showed comparatively low heritability and low genetic advance. Characters like days to 50% flowering and plant height reported high heritability with low genetic advance as percent of mean, suggesting preponderance of nonadditive gene action in the inheritance of these traits.

Patel *et al.* (2014) carried out investigation on forty four diverse rice genotypes and studied their heritability and genetic advance. Results revealed that high heritability coupled with high genetic advance as percentage of mean was observed for number of grains per panicle, grain yield per plant, 1000-grain weight and Grain L/B ratio indicating additive gene action controlling these traits. Hence phenotypic selection may be effective for improving these characters. The characters like days to 50% flowering, days to maturity, plant height, grain length, grain breadth and protein content showed moderate genetic advance coupled with high heritability which indicating presence of both additive and non-additive gene action and improvement in this population through cyclic selection method is possible.

Shrivastava *et al.* (2014) studied heritability and genetic advance estimates of 125 diverse parental lines and observed that high heritability accompanied with high genetic advance was recorded for seed yield per plant, effective tillers per plant, length breadth ratio, 1000 seed weight, plant height and panicle length indicating lesser environmental influence and the heritability is due to additive gene effects and selection may be effective. High heritability along with low genetic advance was observed in days to 50 per cent flowering and days to maturity. High heritability accompanied with low genetic advance indicates of non additive gene action.

Suresh *et al.* (2014) evaluated one hundred and eighty nine inbred lines for their heritability and genetic advance estimates and observed that high heritability coupled with high genetic advance as a per cent of mean was recorded for grain yield per plant, panicle weight, L/B ratio, test weight and kernel breadth, indicating the predominance of additive gene effects in controlling these traits and hence simple individual plant selection could be exercised to develop high yielding genotypes.

Thirumala Rao *et al.* (2014) studied forty nine rice cultures and observed that high heritability coupled with high genetic advance as percent of mean was observed in test weight (g) and grain yield per plant (g) indicating the role of additive gene in expressing these traits and revealed better scope for improvement of these traits through direct selection.

Kishore *et al.* (2015) evaluated seventy three rice genotypes to study their extent of heritability and genetic advance and observed that high heritability coupled with high genetic advance as per cent mean was recorded for days to 50 per cent flowering, 1000-grain weight and grain yield per plant indicating that the high heritability observed is due to additive gene effects and selection may be effective for these characters. High heritability coupled with moderate genetic advance in per cent of mean was observed for plant height indicating the role of both additive and non-additive gene effects for control of the characters. Panicle length has recorded high heritability coupled with low genetic advance in per cent of mean in the present investigation.

Nitesh Kumar *et al.* (2015) evaluated one hundred and thirty four rice germplasm accessions to study their heritability and genetic advance and results revealed that high heritability coupled with high genetic advance as per cent of mean was observed for the grain yield per plant, number of effective tillers per plant, panicle weight, test weight, plant height and days to 50% flowering indicating the less influence of environmental variance in the inheritance of these traits, which can be further improved by simple selection.

Sameera *et al.* (2015) evaluated twenty five rice genotypes were to study heritability and genetic advance and observed that high estimates of heritability were recorded for all the characters under study. High heritability coupled with high genetic advance as per cent of mean was also recorded for productive tillers per plant, days to maturity, 1000 seed weight, days to 50 per cent flowering, panicle length, grain yield

per plant and plant height indicating minimum influence of environment on these characters and these traits were more useful for targetted yield improvement programmes in rice.

2.2. CHARACTER ASSOCIATION

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).

The available literature on character association studies in rice were summarized and presented in Tables 2.2 and 2.3.

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.

Table 2.2. Review of literature on association of different components with yield in rice

S.No.	Character	Correlation	S/NS	P/G	Reference
1	Days to 50% flowering	Positive	S	P,G P P,G P,G	Ekka <i>et al.</i> (2011) Aditya and Bhartiya (2013) Tushara <i>et al.</i> (2013) Khare <i>et al.</i> (2014)
			NS	P P,G P,G P,G P,G P,G G	Akinwale <i>et al.</i> (2011) Rangare <i>et al.</i> (2012) Nagaraju <i>et al.</i> (2013) Jambhulkar and Bose (2014) Patel <i>et al.</i> (2014) Venkata Lakshmi <i>et al.</i> (2014) Thirumala Rao <i>et al.</i> (2014)
		Negative	S	P,G P,G G P,G G P,G G	Dey <i>et al.</i> (2010) Hasan <i>et al.</i> (2011) Ravindrababu <i>et al.</i> (2012) Sravan <i>et al.</i> (2012) Arulmozhi and Muthuswamy (2013) Gangashetty <i>et al.</i> (2013) Rai <i>et al.</i> (2014)
			NS	P,G P ----- P P,G P	Seyoum <i>et al.</i> (2012) Bekele <i>et al.</i> (2013) Gopikannan and Ganesh (2013) Idris and Mohammad (2013) Sanghera <i>et al.</i> (2013) Ogunbayo <i>et al.</i> (2014)
		Positive	S	G P P,G P,G	Hasan <i>et al.</i> (2011) Aditya and Bhartiya (2013) Khare <i>et al.</i> (2014) Venkata Lakshmi <i>et al.</i> (2014)
			NS	P P P,G P P,G P,G	Akinwale <i>et al.</i> (2011) Hasan <i>et al.</i> (2011) Nagaraju <i>et al.</i> (2013) Ogunbayo <i>et al.</i> (2014) Patel <i>et al.</i> (2014) Rai <i>et al.</i> (2014)
2	Days to maturity	Negative	S	P,G	Sanghera <i>et al.</i> (2013)
			NS	P,G P P	Hasan <i>et al.</i> (2011) Bekele <i>et al.</i> (2013) Idris and Mohammad (2013)
		Positive	S	P P,G P,G P P P,G	Rani and Reddy (2010) Ekka <i>et al.</i> (2011) Shet <i>et al.</i> (2012) Sravan <i>et al.</i> (2012) Aditya and Bhartiya (2013) Bekele <i>et al.</i> (2013) Idris and Mohamed (2013)
			NS	P,G P P	Hasan <i>et al.</i> (2011) Bekele <i>et al.</i> (2013) Idris and Mohammad (2013)
3	Plant height	Positive	S	P P,G P,G P,G P P P,G	Rani and Reddy (2010) Ekka <i>et al.</i> (2011) Shet <i>et al.</i> (2012) Sravan <i>et al.</i> (2012) Aditya and Bhartiya (2013) Bekele <i>et al.</i> (2013) Idris and Mohamed (2013)

				P,G P,G P,G P,G P,G P,G P,G	Sharifi <i>et al.</i> (2013) Sudharani <i>et al.</i> (2013) Jambhulkar and Bose (2014) Khare <i>et al.</i> (2014) Patel <i>et al.</i> (2014) Rai <i>et al.</i> (2014) Venkata Lakshmi <i>et al.</i> (2014)
			NS	P,G P,G G	Hasan <i>et al.</i> (2011) Rangare <i>et al.</i> (2012) Arulmozhi and Muthuswamy (2013)
		Negative	S	G P,G P	Ravindrababu <i>et al.</i> (2012) Gangashetty <i>et al.</i> (2013) Ogunbayo <i>et al.</i> (2014)
			NS	P,G P P,G P,G P,G G P,G G	Dey <i>et al.</i> (2010) Akinwale <i>et al.</i> (2011) Akhtar <i>et al.</i> (2011) Laxuman <i>et al.</i> (2011) Seyoum <i>et al.</i> (2012) Nagaraju <i>et al.</i> (2013) Sanghera <i>et al.</i> (2013) Thirumala Rao <i>et al.</i> (2014)
4	Number of panicles per plant	Positive	S	P,G P,G P,G P,G P	Hasan <i>et al.</i> (2011) Sanghera and Kashyap (2012) Sravan <i>et al.</i> (2012) Sanghera <i>et al.</i> (2013) Ogunbayo <i>et al.</i> (2014)
			NS	P P P,G	Akinwale <i>et al.</i> (2011) Idris and Mohammad (2013) Sanghera <i>et al.</i> (2013)
		Negative	NS	P,G	Khare <i>et al.</i> (2014)
5	Panicle length	Positive	S	P P,G P,G P,G P,G P,G P,G P,G P,G P,G P G P,G P P,G P,G P,G	Rani and Reddy (2010) Yadav <i>et al.</i> (2010) Akhtar <i>et al.</i> (2011) Ekka <i>et al.</i> (2011) Laxuman <i>et al.</i> (2011) Yadav <i>et al.</i> (2011) Rangare <i>et al.</i> (2012) Sanghera and Kashyap (2012) Seyoum <i>et al.</i> (2012) Sravan <i>et al.</i> (2012) Shet <i>et al.</i> (2012) Aditya and Bhartiya (2013) Arulmozhi and Muthuswamy (2013) Ashim and Ghosh (2013) Gangashetty <i>et al.</i> (2013) Nagaraju <i>et al.</i> (2013) Sanghera <i>et al.</i> (2013) Jambhulkar and Bose (2014)

Table 2.2 (cont.).

				P,G P P,G G	Khare <i>et al.</i> (2014) Ogunbayo <i>et al.</i> (2014) Patel <i>et al.</i> (2014) Thirumala Rao <i>et al.</i> (2014)
			NS	G P P,G P,G G P P,G	Rani and Reddy (2010) Akinwale <i>et al.</i> (2011) Hasan <i>et al.</i> (2011) Seyoum <i>et al.</i> (2012) Nagaraju <i>et al.</i> (2013) Idris and Mohammad (2013) Rai <i>et al.</i> (2014)
		Negative	S	G P,G	Ravinrababu <i>et al.</i> (2012) Rashid <i>et al.</i> (2014)
			NS	P,G	Venkata Lakshmi <i>et al.</i> (2014)
6	Test weight	Positive	S	G P,G P,G P,G P,G P P,G ----- P,G P P,G P,G G	Rani and Reddy (2010) Ekka <i>et al.</i> (2011) Hasan <i>et al.</i> (2011) Seyoum <i>et al.</i> (2012) Sravan <i>et al.</i> (2012) Bekele <i>et al.</i> (2013) Gangashetty <i>et al.</i> (2013) Gopikannan and Ganesh (2013) Sharifi <i>et al.</i> (2013) Ogunbayo <i>et al.</i> (2014) Patel <i>et al.</i> (2014) Rai <i>et al.</i> (2014) Thirumala Rao <i>et al.</i> (2014)
				NS P P,G P P,G P,G P,G P,G	Rani and Reddy (2010) Pankajgarg <i>et al.</i> (2010) Akinwale <i>et al.</i> (2011) Arulmozhi and Muthuswamy (2013) Nagaraju <i>et al.</i> (2013) Sanghera <i>et al.</i> (2013) Jambhulkar and Bose (2014) Venkata Lakshmi <i>et al.</i> (2014)
			Negative	S	P,G Khare <i>et al.</i> (2014)
				NS P,G P,G P	Ravindrababu <i>et al.</i> (2012) Seyoum <i>et al.</i> (2012) Idris and Mohammad (2013)
		Positive	S	P P P,G	Aditya and Bhartiya (2013) Ogunbayo <i>et al.</i> (2014) Venkata Lakshmi <i>et al.</i> (2014)
				NS P,G P G	Ekka <i>et al.</i> (2011) Bekele <i>et al.</i> (2013) Patel <i>et al.</i> (2014)
7	Kernel length	Negative	S	---	Krishnaveni and Sobharani (2006)
			NS	P,G	Sanghera <i>et al.</i> (2013)
8	Kernel breadth	Positive	S	P P	Bekele <i>et al.</i> (2013) Ogunbayo <i>et al.</i> (2014)

Table 2.2 (cont.).

			NS	P,G P,G P,G P,G	Shiva Parvathi (2010) Ekka <i>et al.</i> (2011) Sanghera <i>et al.</i> (2013) Patel <i>et al.</i> (2014)
		Negative	S	P,G P,G	Gyanendrapal <i>et al.</i> (2011) Nagaraju <i>et al.</i> (2013)
			NS	P,G	Venkata Lakshmi <i>et al.</i> (2014)
9	L/B ratio	Positive	S	P	Aditya and Bhartiya (2013)
			NS	P,G G P,G P,G	Parvthi <i>et al.</i> (2011) Nagaraju <i>et al.</i> (2013) Patel <i>et al.</i> (2014) Venkata Lakshmi <i>et al.</i> (2014)
		Negative	S	G	Arulmozhi and Muthuswamy (2013)
			NS	P,G P P,G	Pankajgarg <i>et al.</i> (2010) Bekele <i>et al.</i> (2013) Sanghera <i>et al.</i> (2013)

Table 2.3. Review of literature on association among different components in rice

S.No.	Character	Correlation	S/NS	P/G	Reference
I. Association of Days to 50% flowering with					
1	Days to maturity	Positive	S	P P,G P P P,G P P,G	Akinwale <i>et al.</i> (2011) Hasan <i>et al.</i> (2011) Aditya and Bhartiya (2013) Bekele <i>et al.</i> (2013) Khare <i>et al.</i> (2014) Ogunbayo <i>et al.</i> (2014) Venkata Lakshmi <i>et al.</i> (2014)
			NS	G P,G G	Nagaraju <i>et al.</i> (2013) Sanghera <i>et al.</i> (2013) Patel <i>et al.</i> (2014)
		Negative	NS	P	Idris and Mohammad (2013)
2	Plant height	Positive	S	P,G P,G P G P,G P P,G P,G	Ekka <i>et al.</i> (2011) Ravindrababu <i>et al.</i> (2012) Aditya and Bhartiya (2013) Arulmozhi and Muthuswamy (2013) Khare <i>et al.</i> (2014) Ogunbayo <i>et al.</i> (2014) Patel <i>et al.</i> (2014) Venkata Lakshmi <i>et al.</i> (2014)
			NS	----- P,G P P,G P,G	Dey <i>et al.</i> (2010) Nagaraju <i>et al.</i> (2013) Idris and Mohammad (2013) Sanghera <i>et al.</i> (2013) Jambhulkar and Bose (2014)
		Negative	S	P	Akinwale <i>et al.</i> (2011)
			NS	P,G P,G P G	Hasan <i>et al.</i> (2011) Sravan <i>et al.</i> (2012) Bekele <i>et al.</i> (2013) Thirumala Rao <i>et al.</i> (2014)
3	Number of panicles per plant	Positive	NS	P,G	Sanghera <i>et al.</i> (2013)
		Negative	S	P,G P,G	Hasan <i>et al.</i> (2011) Sravan <i>et al.</i> (2012)
			NS	P P P P	Akinwale <i>et al.</i> (2011) Aditya and Bhartiya (2013) Idris and Mohammad (2013) Ogunbayo <i>et al.</i> (2014)
4	Panicle length	Positive	S	P P,G P,G P G P,G P,G	Akinwale <i>et al.</i> (2011) Ekka <i>et al.</i> (2011) Ravindrababu <i>et al.</i> (2012) Aditya and Bhartiya (2013) Arulmozhi and Muthuswamy (2013) Khare <i>et al.</i> (2014) Venkata Lakshmi <i>et al.</i> (2014)

Table 2.3 (cont.).

			NS	P,G P,G P P,G P P,G	Hasan <i>et al.</i> (2011) Nagaraju <i>et al.</i> (2013) Idris and Mohammad (2013) Sanghera <i>et al.</i> (2013) Ogunbayo <i>et al.</i> (2014) Patel <i>et al.</i> (2014)
			Negative	S	P,G Sravan <i>et al.</i> (2012)
				NS	P,G G Jambhulkar and Bose (2014) Thirumala Rao <i>et al.</i> (2014)
5	Test weight	Positive	S	P,G	Patel <i>et al.</i> (2014)
			NS	P P,G P,G P,G P G P P,G P,G	Akinwale <i>et al.</i> (2011) Hasan <i>et al.</i> (2011) Dwivedi <i>et al.</i> (2012) Sravan <i>et al.</i> (2012) Aditya and Bhartiya (2013) Arulmozhi and Muthuswamy (2013) Idris and Mohammad (2013) Jambhulkar and Bose (2014) Khare <i>et al.</i> (2014)
		Negative	S	P,G	Ekka <i>et al.</i> (2011)
			NS	P,G P G P G	Pankajgarg <i>et al.</i> (2010) Bekele <i>et al.</i> (2013) Nagaraju <i>et al.</i> (2013) Ogunbayo <i>et al.</i> (2014) Thirumala Rao <i>et al.</i> (2014)
6	Kernel length	Positive	S	-----	Krishna <i>et al.</i> (2008)
			NS	P,G P P P,G	Ekka <i>et al.</i> (2011) Aditya and Bhartiya (2013) Bekele <i>et al.</i> (2013) Patel <i>et al.</i> (2014)
		Negative	NS	P,G P	Sanghera <i>et al.</i> (2013) Ogunbayo <i>et al.</i> (2014)
7	Kernel breadth	Positive	S	P	Ogunbayo <i>et al.</i> (2014)
			NS	P	Aditya and Bhartiya (2013)
		Negative	S	P,G	Venkata Lakshmi <i>et al.</i> (2014)
			NS	P,G P P,G P,G	Ekka <i>et al.</i> (2011) Bekele <i>et al.</i> (2013) Sanghera <i>et al.</i> (2013) Patel <i>et al.</i> (2014)
8	L/B ratio	Positive	S	P	Aditya and Bhartiya (2013)
			NS	P P,G P,G	Bekele <i>et al.</i> (2013) Sanghera <i>et al.</i> (2013) Patel <i>et al.</i> (2014)
		Negative	S	G	Arulmozhi and Muthuswamy (2013)
			NS	P,G	Nagaraju <i>et al.</i> (2013)

Table 2.3 (cont.).

II. Association of Days to maturity with					
1	Plant height	Positive	S	P P,G P,G	Aditya and Bhartiya (2013) Patel <i>et al.</i> (2014) Venkata Lakshmi <i>et al.</i> (2014)
			NS	P,G	Sanghera <i>et al.</i> (2013)
		Negative	NS	P P,G P P,G P P,G P	Akinwale <i>et al.</i> (2011) Hasan <i>et al.</i> (2011) Bekele <i>et al.</i> (2013) Nagaraju <i>et al.</i> (2013) Idris and Mohammad (2013) Khare <i>et al.</i> (2014) Ogunbayo <i>et al.</i> (2014)
2	Number of panicles per plant	Positive	NS	P P P,G P	Aditya and Bhartiya (2013) Idris and Mohammad (2013) Sanghera <i>et al.</i> (2013) Ogunbayo <i>et al.</i> (2014)
		Negative	S	P,G	Hasan <i>et al.</i> (2011)
			NS	P	Akinwale <i>et al.</i> (2011)
3	Panicle length	Positive	S	P P P,G P,G P P,G	Akinwale <i>et al.</i> (2011) Aditya and Bhartiya (2013) Sanghera <i>et al.</i> (2013) Khare <i>et al.</i> (2014) Ogunbayo <i>et al.</i> (2014) Venkata Lakshmi <i>et al.</i> (2014)
			NS	P,G P,G	Nagaraju <i>et al.</i> (2013) Patel <i>et al.</i> (2014)
		Negative	NS	P,G P	Hasan <i>et al.</i> (2011) Idris and Mohammad (2013)
4	Test weight	Positive	S	P,G	Patel <i>et al.</i> (2014)
			NS	P P G P,G	Akinwale <i>et al.</i> (2011) Aditya and Bhartiya (2013) Khare <i>et al.</i> (2014) Venkata Lakshmi <i>et al.</i> (2014)
		Negative	S	P P	Bekele <i>et al.</i> (2013) Idris and Mohammad (2013)
			NS	P,G G P P	Hasan <i>et al.</i> (2011) Nagaraju <i>et al.</i> (2013) Khare <i>et al.</i> (2014) Ogunbayo <i>et al.</i> (2014)
5	Kernel length	Positive	NS	P P P,G P,G	Aditya and Bhartiya (2013) Bekele <i>et al.</i> (2013) Patel <i>et al.</i> (2014) Venkata Lakshmi <i>et al.</i> (2014)
		Negative	S	P,G	Sanghera <i>et al.</i> (2013)
			NS	P	Ogunbayo <i>et al.</i> (2014)
6	Kernel breadth	Positive	NS	P P,G	Ogunbayo <i>et al.</i> (2014) Venkata Lakshmi <i>et al.</i> (2014)
		Negative	S	P P,G	Bekele <i>et al.</i> (2013) Sanghera <i>et al.</i> (2013)
			NS	P P,G	Aditya and Bhartiya (2013) Patel <i>et al.</i> (2014)

Table 2.3 (cont.).

7	L/B ratio	Positive	NS	P P P,G P,G P,G P,G	Aditya and Bhartiya (2013) Bekele <i>et al.</i> (2013) Nagaraju <i>et al.</i> (2013) Sanghera <i>et al.</i> (2013) Patel <i>et al.</i> (2014) Venkata Lakshmi <i>et al.</i> (2014)				
III. Association of Plant height with									
1	Number of panicles per plant	Positive	S	G G	Hasan <i>et al.</i> (2011) Sravan <i>et al.</i> (2012)				
			NS	P,G	Kumar and Bapu (2005)				
		Negative	S	P P,G P	Akinwale <i>et al.</i> (2011) Sanghera <i>et al.</i> (2013) Ogunbayo <i>et al.</i> (2014)				
			NS	P,G P	Pankajgarg <i>et al.</i> (2010) Idris and Mohammad (2013)				
2	Panicle length	Positive	S	P,G P P,G P,G P,G P,G P,G P	Pankajgarg <i>et al.</i> (2010) Rani and Reddy (2010) Ekka <i>et al.</i> (2011) Hasan <i>et al.</i> (2011) Sadeghi <i>et al.</i> (2011) Iswardatt <i>et al.</i> (2012) Ravindrababu <i>et al.</i> (2012) Sravan <i>et al.</i> (2012) Aditya and Bhartiya (2013) Manikyaminnie <i>et al.</i> (2013) Sanghera <i>et al.</i> (2013) Patel <i>et al.</i> (2014) Venkata Lakshmi <i>et al.</i> (2014) Thirumala Rao <i>et al.</i> (2014)				
				NS	G G P,G P G	Rani and Reddy (2010) Arulmozhi and Muthuswamy (2013) Nagaraju <i>et al.</i> (2013) Idris and Mohammad (2013) Jambhulkar and Bose (2014)			
					Negative	S	P	Ogunbayo <i>et al.</i> (2014)	
						NS	P	Akinwale <i>et al.</i> (2011)	
					3	Test weight	Positive	S	P G P,G P,G P,G P,G
				NS					G P,G G P G P P,G

Table 2.3 (cont.).

				P,G G	Venkata Lakshmi <i>et al.</i> (2014) Thirumala Rao <i>et al.</i> (2014)
		Negative	S	-----	Krishnaveni and Sobharani (2006)
			NS	P P P,G P,G P	Pankajgarg <i>et al.</i> (2010) Akinwale <i>et al.</i> (2011) Sanghera <i>et al.</i> (2013) Khare <i>et al.</i> (2014) Ogunbayo <i>et al.</i> (2014)
4	Kernel length	Positive	S	P,G	Patel <i>et al.</i> (2014)
			NS	P,G	Venkata Lakshmi <i>et al.</i> (2014)
		Negative	S	P	Ogunbayo <i>et al.</i> (2014)
			NS	P,G P P,G	Ekka <i>et al.</i> (2011) Bekele <i>et al.</i> (2013) Sanghera <i>et al.</i> (2013)
5	Kernel breadth	Positive	S	P P P,G	Bekele <i>et al.</i> (2013) Ogunbayo <i>et al.</i> (2014) Venkata Lakshmi <i>et al.</i> (2014)
			NS	P,G P,G P,G	Ekka <i>et al.</i> (2011) Sanghera <i>et al.</i> (2013) Patel <i>et al.</i> (2014)
		Negative	NS	P,G	Bhattacharyya <i>et al.</i> (2007)
6	L/B ratio	Positive	S	P,G	Patel <i>et al.</i> (2014)
			NS	P,G P,G	Sanghera <i>et al.</i> (2013) Venkata Lakshmi <i>et al.</i> (2014)
		Negative	S	P	Bekele <i>et al.</i> (2013)
			NS	G G	Arulmozhi and Muthuswamy (2013) Nagaraju <i>et al.</i> (2013)
IV. Association of Number of panicles per plant with					
1	Panicle length	Positive	S	G P	Sravan <i>et al.</i> (2012) Aditya and Bhartiya (2013)
			NS	P,G	Hasan <i>et al.</i> (2011)
		Negative	S	P,G	Sanghera <i>et al.</i> (2013)
			NS	P P P	Akinwale <i>et al.</i> (2011) Idris and Mohammad (2013) Ogunbayo <i>et al.</i> (2014)
2	Test weight	Positive	S	P,G G	Hasan <i>et al.</i> (2011) Sravan <i>et al.</i> (2012)
			NS	P P	Akinwale <i>et al.</i> (2011) Aditya and Bhartiya (2013)
		Negative	S	P G P	Idris and Mohammad (2013) Sanghera <i>et al.</i> (2013) Ogunbayo <i>et al.</i> (2014)
			NS	P	Sanghera <i>et al.</i> (2013)
3	Kernel length	Positive	S	G P	Sanghera <i>et al.</i> (2013) Ogunbayo <i>et al.</i> (2014)
			NS	P P	Aditya and Bhartiya (2013) Sanghera <i>et al.</i> (2013)
4	Kernel breadth	Positive	NS	P P	Aditya and Bhartiya (2013) Ogunbayo <i>et al.</i> (2014)

Table 2.3 (cont.).

		Negative	S	P,G	Sanghera <i>et al.</i> (2013)
5	L/B ratio	Positive	S	P	Aditya and Bhartiya (2013)
			NS	P,G	Sanghera <i>et al.</i> (2013)
V. Association of Panicle length with					
2	Kernel length	Positive	S	P,G P,G P,G	Ekka <i>et al.</i> (2011) Patel <i>et al.</i> (2014) Venkata Lakshmi <i>et al.</i> (2014)
					P,G P,G P
		Negative	NS	P	Aditya and Bhartiya (2013)
3	Kernel breadth	Positive	S	-----	Krishna <i>et al.</i> (2008)
			NS	P P,G	Aditya and Bhartiya (2013) Venkata Lakshmi <i>et al.</i> (2014)
		Negative	S	P	Ogunbayo <i>et al.</i> (2014)
			NS	P,G P,G P,G	Ekka <i>et al.</i> (2011) Sanghera <i>et al.</i> (2013) Patel <i>et al.</i> (2014)
4	L/B ratio	Positive	NS	G P,G P,G	Arulmozhi and Muthuswamy (2013) Sanghera <i>et al.</i> (2013) Venkata Lakshmi <i>et al.</i> (2014)
				Negative	NS
VI. Association of Test weight with					
1	Kernel length	Positive	S	P,G P P P,G	Ekka <i>et al.</i> (2011) Aditya and Bhartiya (2013) Bekele <i>et al.</i> (2013) Patel <i>et al.</i> (2014)
			NS	P,G P	Sanghera <i>et al.</i> (2013) Ogunbayo <i>et al.</i> (2014)
		Negative	S	-----	Krishnaveni and Sobharani (2006)
2	Kernel breadth	Positive	S	P,G P,G P P,G P,G	Ekka <i>et al.</i> (2011) Iswardatt <i>et al.</i> (2012) Bekele <i>et al.</i> (2013) Patel <i>et al.</i> (2014) Venkata Lakshmi <i>et al.</i> (2014)
			NS	P P,G	Aditya and Bhartiya (2013) Sanghera <i>et al.</i> (2013)
		Negative	S	P	Ogunbayo <i>et al.</i> (2014)
3	L/B ratio	Positive	S	P	Aditya and Bhartiya (2013)
			NS	G P,G	Nagaraju <i>et al.</i> (2013) Patel <i>et al.</i> (2014)
		Negative	S	P,G P,G	Sanghera <i>et al.</i> (2013) Venkata Lakshmi <i>et al.</i> (2014)
			NS	G P,G	Arulmozhi and Muthuswamy (2013) Bekele <i>et al.</i> (2013)

Table 2.3 (cont.).

VII. Association of Kernel length with					
1	Kernel breadth	Positive	S	P	Aditya and Bhartiya (2013)
				P,G	Sanghera <i>et al.</i> (2013)
			NS	P,G	Iswardatt <i>et al.</i> (2012)
		Negative	S	P,G	Ekka <i>et al.</i> (2011)
				P,G	Sadeghi <i>et al.</i> (2011)
P	Ogunbayo <i>et al.</i> (2014)				
P,G	Patel <i>et al.</i> (2014)				
	P,G	Venkata Lakshmi <i>et al.</i> (2014)			
	NS	P	Bekele <i>et al.</i> (2013)		
2	L/B ratio	Positive	S	P,G	Iswardatt <i>et al.</i> (2012)
				P	Aditya and Bhartiya (2013)
				P	Bekele <i>et al.</i> (2013)
				P,G	Sanghera <i>et al.</i> (2013)
				P,G	Patel <i>et al.</i> (2014)
				P,G	Venkata Lakshmi <i>et al.</i> (2014)
VIII. Association of Kernel breadth with					
1	L/B ratio	Positive	S	P	Aditya and Bhartiya (2013)
			NS	P,G	Sanghera <i>et al.</i> (2013)
		Negative	S	P	Bekele <i>et al.</i> (2013)
				P,G	Patel <i>et al.</i> (2014)
				P,G	Venkata Lakshmi <i>et al.</i> (2014)

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

Pankajgarg *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.

Ekka *et al.* (2011) carried out an investigation on ninety six rice accessions to study direct and indirect effects of various traits on grain yield and reported that there is no common causal factor that directly influence grain yield per plant and head rice recovery percentage. Days to 50% flowering and leaf length could be used as selection criteria for the simultaneous improvement of both the traits.

Hasan *at al.* (2011) carried out path analysis studies in twenty four rice genotypes and reported that spikelet fertility and panicle/m² possessed the highest positive effect on grain yield followed by thousand grain weight and number of effective tillers per hills. Hence, these traits should be given prior attention in rice improvement program because of their major influence on yield. Days to 50% flowering and days to maturity had negative significant effect with yield. Negative direct effect was observed for number of effective tillers/plant, flag leaf length, panicle length and days to maturity. The residual effect of the present study was 0.677, indicating that 32.5 % of the variability in grain yield was contributed by ten characters studied in the path analysis. This result gives an impression that some other major characters than those involved in their present study might also contribute to 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 biological yield per plant, harvest index, number of fertile tiller per plant, days to 50% flowering, test weight, days to maturity and panicle length all had important role in the improvement of grain yield in rice at genotypic and phenotypic levels.

Ravindrababu *et al.* (2012) carried out investigation on forty four diverse genotypes and partitioned the correlation coefficients into direct and indirect effects through path coefficient analysis and results revealed that the number of productive tillers per plant had the maximum positive effect on grain yield followed by panicle length. Hence, selection for this character could bring improvement in yield and yield

components. On the other hand, negative direct effect on grain yield were recorded by number of chaffy grains per panicle, number of filled grains per panicle, 1000 grain weight, days to 50 per cent flowering and plant height.

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) reported high positive direct effect of number of productive tillers per plant, plant height and grain breadth on grain yield per plant in path analysis studies of sixty four rice genotypes.

Nagaraju *et al.* (2013) evaluated six parents and fifteen F₁s to establish the nature of relation between grain yield and yield components by partitioning the correlation coefficients between grain yield and its components into direct and indirect effects by using simple correlation and path analysis and reported that number of grains per panicle exhibited maximum positive direct effect on grain yield followed by total number of productive tillers per plant, plant height and kernel L/B ratio. Hence

selection based on these traits would be effective in increasing the grain yield potential of rice. Conversely, the direct effects of panicle length, harvest index and milling percentage were negative both at phenotypic and genotypic levels on grain yield.

Sanghera *et al.* (2013) conducted path coefficient analysis on fourteen red rice genotypes and results 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 indicating that direct selection based on these traits would be effective.

Jambhulkar and Bose (2014) evaluated twenty two upland rice varieties for eleven characters to know their direct and indirect contribution towards grain yield. Results revealed that plant height has highest direct effect on yield followed by grain per panicle, days to 50% flowering, thousand grain weight and ear bearing tillers. This suggests that these traits can be manoeuvred successfully for breeding high yielding varieties.

Khare *et al.* (2014) studied sixty rice genotypes for path coefficient analysis between yield and yield related traits and results revealed that the traits *via* days to maturity, number of effective tillers per plant and plant height exhibited direct positive effect on grain yield.

Patel *et al.* (2014) carried out investigation on forty four diverse genotypes and partitioned the correlation coefficients into direct and indirect effects through path coefficient analysis and results revealed that straw yield per plant had highest direct effect on grain yield per plant followed by grain length, harvest index, days to maturity, protein content, number of total tillers per plant and number of grains per panicle. This may indicate that direct selection of these characters is likely to be effective in increasing grain yield. Plant height and panicle length has high indirect effect *via* straw yield per plant and grain length while high indirect effect of grain breadth *via* grain L/B ratio. Harvest index was also highly contributed indirectly *via* grain L/B ratio and days to 50% flowering. These indirect effects had not only supported the low magnitude direct effect but also resulted in high significant positive correlation with grain yield. Grain L/B ratio, panicle length, grain breadth, 1000-grain weight and days to 50% flowering exhibited higher negative direct effects on grain yield.

Rai *et al.* (2014) conducted path coefficient analysis among forty four rice genotypes and observed that that number of tillers per plant, biological yield per plant, days to 50 percent flowering, panicle length and plant height had positive direct effect on yield both at the phenotypic and genotypic levels and hence selection for these characters helps in selection of superior fine rice genotypes.

Sandhya *et al.* (2014) carried out path coefficient analysis on thirty two rice genotypes and reported that number of panicles per plant had highest positive direct effect on grain yield per plant, followed by biological yield per plant, days to 50% flowering, panicle length and test weight while days to 50% flowering, number of panicle per plant, and test weight at genotypic level. This may indicate that the direct selection for number of panicles per plant, biological yield per plant, days to 50% flowering, panicle length and test weight would likely be effective in increasing grain yield. The path analysis indicated that there is no common causal factor that directly influences grain yield per plant.

Thirumala Rao *et al.* (2014) studied path coefficient analysis in rice using forty nine rice cultures and reported that highest direct positive effect of number of grains per panicle, test weight and productive tillers per square meter was revealed on grain yield. Hence, a direct selection criterion should be followed for traits to improve the grain yield.

Kishore *et al.* (2015) carried out path coefficient analysis in seventy three rice genotypes and studies on inter-character associations for yield components revealed significant and positive association of plant height with panicle length. However, significant and negative inter-character associations were observed for panicle bearing tillers per hill and number of filled grains per panicle; and number of filled grains per panicle with 1000-seed weight. High positive direct effect of panicle bearing tillers per hill and number of filled grains per panicle on grain yield was reported in the present study. Hence, these traits should be considered as important selection criteria in all rice improvement programmes and direct selection for these traits is recommended for yield improvement. Further, days to 50 percent flowering, plant height and 1000-grain weight had also recorded high positive direct effects on grain yield per plant but non-significant in the present investigation indicating the need for adoption of restricted simultaneous selection model to nullify the undesirable indirect effects and make use of the high direct effects. In contrast, high negative direct effect on grain yield per plant

was recorded by panicle length. However its association with grain yield per plant was observed to be non-significant indicating the indirect effect of the trait on grain yield per plant through other characters.

2.4. SCREENING FOR SHEATH BLIGHT AND BACTERIAL LEAF BLIGHT

2.4.1. Screening for sheath blight resistance

Jia *et al.* (2007) evaluated five rice cultivars against sheath blight by using micro chamber method along with field screening at three locations (Arkansas, Texas, and Colombia) and the results revealed that standard cultivars Jasmine 85 and Lemont produced consistent moderately resistant (index 1.4 to 2.9) and susceptible (index 5.9 to 8.9) reactions, respectively, across the three locations using different *R. solani* isolates in micro-chamber method. In all locations, Pecos was moderately resistant and Rosemont was susceptible. Teqing, known for its moderately resistant reaction in the field, was more resistant in Texas and Colombia than in Arkansas. Cultivars Cocodrie and Cypress, known for their susceptible field reactions, tended to be more susceptible at the Arkansas location than in Texas and Colombia. Field experiments in Arkansas and Texas verified the pathogenicity of *R. solani* isolates used in different locations and also confirmed the results of disease reaction of each test cultivar to *R. solani*. The standard cultivar Jasmine 85 was moderately resistant and Lemont was susceptible. In both locations, Teqing and Pecos were resistant whereas Rosemont and Cocodrie were susceptible. Cypress appeared to be more susceptible in Texas field plots than in Arkansas. Disease reactions determined in the field were consistent with reactions found using micro-chamber method.

Mosaddeque *et al.* (2008) screened forty four test entries of parental lines of rice with one susceptible and one resistant check against sheath blight. 10 lines were resistant, 31 were moderately resistant and three showed moderately susceptible reaction at maximum tillering stage.

Singh *et al.* (2010) screened one hundred and eighty two rice genotypes against six inoculums sources of sheath blight in both nursery and field. The results revealed that five genotypes viz., HKR 99-103, HKR 2000-26, HKRH-1059, HRI 126 and IR 64683-87-2-2-3-3 were found to be moderately resistant to sheath blight in nursery while in field, two genotypes HKR 2000-514 and IR 64683-87-2-2-3-3 proved resistant

and three genotypes HKR 99-103, HKR 2001-537 and HKRH-1059 were moderately resistant. Only three genotypes HKR 99-103, HKRH-1059 and IR 64683-87-2-2-3-3 showed resistant/moderate resistant in both nursery and field conditions.

Latif *et al.* (2011) screened a total of thirty five inbred and thirteen hybrid varieties including susceptible checks against sheath blight. Results showed that all the varieties tested against sheath blight were moderately susceptible in both rainfed and irrigated ecosystem. The inbred varieties BR22, BR25, BRRI dhan31, BRRI dhan32, BRRI dhan33, BRRI dhan34, BRRI dhan38 and BRRI dhan39 demonstrated for moderately resistant reactions.

Ling *et al.* (2011) evaluated one hundred and sixty six indica hybrid rice combinations which were inoculated by using five isolates with different pathogenicities at seedling stage in the greenhouse. No combination was found to be completely immune or highly resistant, and the resistance to sheath blight varied significantly among different combinations. Average disease index of these combinations ranged from 2.84 to 7.64. According to the disease index of each isolate, 166 combinations were classified into five types based on dynamic clustering analysis (DCA), namely resistant (R), moderately resistant (MR), moderately susceptible (MS), susceptible (S), and highly susceptible (HS), accounting for 1.20%, 13.86%, 36.14%, 43.37%, and 5.42%, respectively.

Willocquet *et al.* (2011) screened two hundred accessions obtained from IRRI germplasm bank for their level of susceptibility to sheath blight in field experiment, by inoculating hills at the centre of micro fields and measuring disease intensity. Morphological traits of all accessions were also measured. Analysis of variance indicated significant effects of genetic groups and genotypes on sheath blight intensity, measured by different variables (lesion height, relative lesion height, leaf severity, sheath severity, and disease incidence on tillers). Results from multivariate analyses (canonical correlation, hierarchical cluster analyses, correspondence analysis, and discriminant analysis), and logistic regressions indicated that morphological traits were strongly associated with disease intensity, and that their effect was larger than that of genetic groups. In particular, plant height was associated with low sheath blight intensity. The combination of results suggested a ranking of genetic groups with increasing level of susceptibility to sheath blight as: au < indica < japonica.

Meena *et al.* (2013) studied on identification of resistant genotypes among mutated rice population of the variety Pusa Basmati-1 induced by gamma radiation (15kr). Out of total 8345 mutant lines, 23 lines belong to same class depicting 0 to 20 AULPC (Area Under Lesion Progress Curve) value and 3052 mutant lines come under the class having more than 200 AULPC. Out of 8345 mutated rice population 298 resistant genotypes were identified after screening under field conditions. The selected genotypes depicting very low AULPC value have been advanced to M₂ generation and screened with non-significant deviation for disease score. Thus, these genotypes could be considered a potential source for disease resistance against sheath blight of rice and could be used further in the crossing programme for development of sheath blight resistant rice variety.

Xing *et al.* (2013) screened of nine callus-resistant rice cultivars using pathogenic crude toxins of highly virulent isolates, *R. solani* (Anastomosis Group 1-IA). Lemont and moderate resistant rice cultivar, Kasalath were used for callus screening. The detached leaf and micro-chamber methods were used to evaluate the resistance of regenerated plants (R₀) and their offspring (R₁). The resistance of R₁ was enhanced than their progenitors, the disease index of R₁ of Kasalath was higher than that of IR64, 9311, Teqing and Gan72, while the disease index of R₁ of Lemont higher than that of 9311, Teqing and Gan72. According to the nine-grade disease classification, the R₁ of Lemont was moderately resistant, while R₁ of Kasalath was resistant.

Hossain *et al.* (2014) screened nine rice cultivars in micro chamber and mist chamber methods against sheath blight and observed that severe sheath blight was recorded following inoculation with *R. solani* under micro-chamber conditions. The most resistant cultivar was 'Tetep', followed by 'Teqing'. In mist-chamber screening, 'UKMRC 2' showed the highest level of susceptibility with a disease severity index (DSI) of 6.67, while 'MR 219' produced highest DSI of 7.22 in micro chamber. On the basis of disease reactions, 'Tetep' and 'Teqing' were identified as suitable donors to improve resistance in 'UKMRC 2' and 'MR 219'.

Shamim *et al.* (2014) screened twenty four rice cultivars against sheath blight using detached leaf method. Results showed that none of the tested cultivated rice varieties showed resistance to sheath blight, except wild rice accessions, *Oryza australiensis* and *O. grandiglumis*. Only two rice cultivars IR 42 and TKM 9 showed moderate resistance among the cultivated rice varieties screened.

Suresh Kumar *et al.* (2015) screened six diverse rice genotypes viz., FL 478, IW Ponni, BPT5204, IR64, RNR 57979 and TETEP which were crossed in a diallel mating design in greenhouse. Among the parents, RNR 57979 and TETEP were highly resistant whereas IR 64 was moderately resistant. Remaining three genotypes were susceptible to sheath blight. Among the hybrids 13 were moderately resistant, 7 were moderately susceptible and 10 were susceptible to sheath blight disease.

Yadav *et al.* (2015) screened forty rice germplasm accessions using typha leaf bit inoculation method and found that Tetep and ARC 1053 were moderately resistant to sheath blight. Moderate resistance nature of ARC 1053 was further confirmed by identifying candidate genes conferring sheath blight resistance in ARC 1053 through QTL mapping approach, while moderate resistant nature of Tetep was confirmed earlier by identifying sheath blight resistant QTLs in it by Channamallikarjuna *et al.* (2010) which are in agreement with the results of field screening by typha leaf bit method.

2.4.2. Screening for bacterial leaf blight

Sere *et al.* (2005) carried out a comprehensive disease survey against BLB and selected four isolates of BLB viz., MML-X003, MND-X004, MNG-X001 and MST-X005 for inoculation on four varieties viz., BG 90-2, Bouake 189, NERICA 1 and NERICA 4 in a screen house. The pathogenicity of the selected four BLB isolates were evaluated by their different degree of virulence on rice varieties. MNG-X004 and MST-X005 showed some mild pathogenicity and MML-X003 was highly virulent. NERICA 1 displayed a high level of resistance to BLB across all isolates.

Ahmed Khan *et al.* (2009) screened fifty five rice entries for BLB resistance under artificial field inoculation. No variety was found to be resistant. Only four entries viz., IR-72102-3-107-1-1-2, P-52-9-2, Super-Bas and DM-1-30-3-99 were found moderately resistant.

Ali *et al.* (2009) screened sixteen genotypes against BLB and observed that Kashmir Basmati was highly resistant and showed $\geq 75\%$ resistance to all the four strains tested (LKA4 (i), YR6W14D3, PXO379 and LKA4(i)y). IR-6, Basmati-370, JP-5 and KSK-370 were moderately resistant and showed $\geq 50\%$ resistant to all the tested strains, while remaining genotypes, Basmati-385, Swat-2, NIAB IR-9, KSK-282, Shahkar, GNY-53, KSK-133, Pakhal, Swat-1, Fakhre Malakand, and Dilrosh. were susceptible to all strains/isolates of *Xanthomonas oryzae* pv. *oryzae*.

Latif *et al.* (2011) screened a total of thirty five inbred and thirteen hybrid varieties including susceptible checks against bacterial leaf blight. Results showed that all the varieties tested against BLB were moderately susceptible in both rainfed and irrigated ecosystem. The inbred varieties BR22, BR25, BRRI dhan31, BRRI dhan32, BRRI dhan33, BRRI dhan34, BRRI dhan38 and BRRI dhan39 demonstrated for moderately resistant reactions, but all hybrids were moderately susceptible to BLB in rain-fed ecosystem.

Thimmegowda *et al.* (2011) screened seventy one rice genotypes against bacterial leaf blight and concluded that none of the genotypes are immune to bacterial leaf blight. Three genotypes viz., Ajaya, TKM-6 and IR-8 were found to be resistant, where as six genotypes viz., IR-72, Tetep, PR-111, Zenith, CRMAS-2231-23 and Govind were moderately resistant. 23 genotypes were moderately susceptible, 24 were susceptible and 15 were highly susceptible.

Banito *et al.* (2012) evaluated twenty one rice varieties and near isogenic lines against BLB under screen house and observed that 12 lines, IRBB1, IRBB2, IRBB3, IRBB4, IRBB7, IRBB8, IRBB10, IRBB11, IRBB13, IRBB14, IRBB21 and IR24, were resistant while four lines, NERICA4, NERICA8, NERICA14 and Giganté, were moderately resistant. The susceptible group had also five genotypes, TGR203, IR841, NERICA19, TOG5681 and IRBB5.

Chapter - III

MATERIAL AND METHODS

The present investigation “Character association and screening for sheath blight and bacterial leaf blight of F₅ families in rice (*Oryza sativa* L.)” was taken up during *kharif*, 2015 at Andhra Pradesh Rice Research Institute and Regional Agricultural Research Station, Maruteru, West Godavari district of Andhra Pradesh. Maruteru is located at 81.44° E longitude, 26.38° N latitude and 5 m above mean sea level. Annual rainfall of the location is 1100 mm.

The details of material used, methods adopted and statistical analysis followed, during the course of investigation are described below.

3.1. EXPERIMENTAL MATERIAL

Experimental material for the present investigation comprised of one hundred and fourteen F₅ families and 7 parents obtained from six crosses (Table 3.1) belonging to medium duration group. The list of genotypes is presented in Table 3.2.

Table 3.1. List of crosses studied and number of families studied under each cross

Cross	Number of families studied
MTU 7029/ MTU 1081	45
MTU 7029/ JGL 11118	5
MTU 7029/ NLR 34449	18
MTU 7029/ MTU 1121	3
MTU 7029/ PAU 3116-25-5-1	15
MTU 7029/ PAU 3140-126-1	28
Total - Six crosses	114

3.2. EXPERIMENTAL DESIGN

One hundred and fourteen F₅ families from six crosses of rice were sown in Randomized Block Design with two replications at APRRI & RARS, Maruteru, during *kharif*, 2015 to estimate correlation among the yield and its component characters and direct and indirect contribution of these characters towards yield. Each family was transplanted in two replications each with four rows of three meter length with spacing of 20 cm between rows and 15 cm within row.

Table 3.2. List of F₅ families studied

S.No.	Code	Entry	Cross combination
1	TSM-1	MTU 2462-1-1-1	MTU 7029/ MTU 1081
2	TSM-2	MTU 2462-1-1-2	MTU 7029/ MTU 1081
3	TSM-3	MTU 2462-1-2-1	MTU 7029/ MTU 1081
4	TSM-4	MTU 2462-1-5-1	MTU 7029/ MTU 1081
5	TSM-5	MTU 2462-1-5-2	MTU 7029/ MTU 1081
6	TSM-6	MTU 2462-1-8-1	MTU 7029/ MTU 1081
7	TSM-7	MTU 2462-1-8-2	MTU 7029/ MTU 1081
8	TSM-8	MTU 2462-1-9-1	MTU 7029/ MTU 1081
9	TSM-9	MTU 2462-1-9-2	MTU 7029/ MTU 1081
10	TSM-10	MTU 2462-2-1-1	MTU 7029/ MTU 1081
11	TSM-12	MTU 2462-4-1-1	MTU 7029/ MTU 1081
12	TSM-16	MTU 2462-6-2-1	MTU 7029/ MTU 1081
13	TSM-17	MTU 2462-8-1-1	MTU 7029/ MTU 1081
14	TSM-18	MTU 2462-8-2-1	MTU 7029/ MTU 1081
15	TSM-19	MTU 2462-8-2-2	MTU 7029/ MTU 1081
16	TSM-20	MTU 2462-12-1-1	MTU 7029/ MTU 1081
17	TSM-22	MTU 2462-12-2-1	MTU 7029/ MTU 1081
18	TSM-29	MTU 2462-15-1-1	MTU 7029/ MTU 1081
19	TSM-32	MTU 2462-15-3-1	MTU 7029/ MTU 1081
20	TSM-33	MTU 2462-15-3-2	MTU 7029/ MTU 1081
21	TSM-35	MTU 2462-17-2-1	MTU 7029/ MTU 1081
22	TSM-36	MTU 2462-17-3-1	MTU 7029/ MTU 1081
23	TSM-37	MTU 2462-18-1-1	MTU 7029/ MTU 1081
24	TSM-39	MTU 2462-21-1-1	MTU 7029/ MTU 1081
25	TSM-42	MTU 2462-22-2-1	MTU 7029/ MTU 1081
26	TSM-43	MTU 2462-22-3-1	MTU 7029/ MTU 1081
27	TSM-48	MTU 2462-23-3-1	MTU 7029/ MTU 1081
28	TSM-50	MTU 2462-26-3-1	MTU 7029/ MTU 1081
29	TSM-51	MTU 2462-26-3-2	MTU 7029/ MTU 1081
30	TSM-54	MTU 2462-27-3-1	MTU 7029/ MTU 1081
31	TSM-56	MTU 2462-29-2-1	MTU 7029/ MTU 1081
32	TSM-57	MTU 2462-30-1-1	MTU 7029/ MTU 1081
33	TSM-58	MTU 2462-31-2-1	MTU 7029/ MTU 1081
34	TSM-61	MTU 2462-34-1-1	MTU 7029/ MTU 1081
35	TSM-62	MTU 2462-34-4-1	MTU 7029/ MTU 1081
36	TSM-63	MTU 2462-35-2-1	MTU 7029/ MTU 1081
37	TSM-64	MTU 2462-35-2-2	MTU 7029/ MTU 1081
38	TSM-65	MTU 2462-37-1-1	MTU 7029/ MTU 1081
39	TSM-66	MTU 2462-37-2-1	MTU 7029/ MTU 1081
40	TSM-67	MTU 2462-37-2-2	MTU 7029/ MTU 1081

Table 3.2 (cont.).

S.No	Code	Entry	Cross combination
41	TSM-68	MTU 2462-41-2-1	MTU 7029/ MTU 1081
42	TSM-69	MTU 2462-42-2-1	MTU 7029/ MTU 1081
43	TSM-72	MTU 2462-45-1-2	MTU 7029/ MTU 1081
44	TSM-73	MTU 2462-45-2-1	MTU 7029/ MTU 1081
45	TSM-74	MTU 2462-49-2-1	MTU 7029/ MTU 1081
46	TSM-76	MTU 2463-4-1-2	MTU 7029/ JGL 11118
47	TSM-77	MTU 2463-4-2-1	MTU 7029/ JGL 11118
48	TSM-79	MTU 2463-8-2-1	MTU 7029/ JGL 11118
49	TSM-82	MTU 2463-14-1-1	MTU 7029/ JGL 11118
50	TSM-83	MTU 2463-15-1-1	MTU 7029/ JGL 11118
51	TSM-85	MTU 2465-4-1-1	MTU 7029/ NLR 34449
52	TSM-86	MTU 2465-4-2-1	MTU 7029/ NLR 34449
53	TSM-87	MTU 2465-6-2-1	MTU 7029/ NLR 34449
54	TSM-88	MTU 2465-8-1-1	MTU 7029/ NLR 34449
55	TSM-90	MTU 2465-10-1-1	MTU 7029/ NLR 34449
56	TSM-92	MTU 2465-11-3-1	MTU 7029/ NLR 34449
57	TSM-93	MTU 2465-11-3-2	MTU 7029/ NLR 34449
58	TSM-94	MTU 2465-12-2-1	MTU 7029/ NLR 34449
59	TSM-95	MTU 2465-12-2-2	MTU 7029/ NLR 34449
60	TSM-96	MTU 2465-13-3-1	MTU 7029/ NLR 34449
61	TSM-97	MTU 2465-13-3-2	MTU 7029/ NLR 34449
62	TSM-99	MTU 2465-16-2-1	MTU 7029/ NLR 34449
63	TSM-101	MTU 2465-16-2-3	MTU 7029/ NLR 34449
64	TSM-102	MTU 2465-22-1-1	MTU 7029/ NLR 34449
65	TSM-103	MTU 2465-22-2-1	MTU 7029/ NLR 34449
66	TSM-104	MTU 2465-22-2-2	MTU 7029/ NLR 34449
67	TSM-108	MTU 2465-24-3-2	MTU 7029/ NLR 34449
68	TSM-110	MTU 2465-27-2-1	MTU 7029/ NLR 34449
69	TSM-114	MTU 2466-4-2-1	MTU 7029/ MTU 1121
70	TSM-115	MTU 2466-4-2-2	MTU 7029/ MTU 1121
71	TSM-116	MTU 2466-4-3-1	MTU 7029/ MTU 1121
72	TSM-118	MTU 2468-1-1-1	MTU 7029/ PAU 3116-25-5-1
73	TSM-120	MTU 2468-2-1-1	MTU 7029/ PAU 3116-25-5-1
74	TSM-128	MTU 2468-8-2-1	MTU 7029/ PAU 3116-25-5-1
75	TSM-132	MTU 2468-18-1-1	MTU 7029/ PAU 3116-25-5-1
76	TSM-133	MTU 2468-18-1-2	MTU 7029/ PAU 3116-25-5-1
77	TSM-134	MTU 2468-20-1-1	MTU 7029/ PAU 3116-25-5-1
78	TSM-138	MTU 2468-21-4-1	MTU 7029/ PAU 3116-25-5-1
79	TSM-141	MTU 2468-25-2-1	MTU 7029/ PAU 3116-25-5-1
80	TSM-146	MTU 2468-27-2-1	MTU 7029/ PAU 3116-25-5-1
81	TSM-147	MTU 2468-28-1-1	MTU 7029/ PAU 3116-25-5-1

Table 3.2 (cont.).

S.No	Code	Entry	Cross combination
82	TSM-148	MTU 2468-29-2-1	MTU 7029/ PAU 3116-25-5-1
83	TSM-149	MTU 2468-29-3-1	MTU 7029/ PAU 3116-25-5-1
84	TSM-150	MTU 2468-29-4-1	MTU 7029/ PAU 3116-25-5-1
85	TSM-152	MTU 2468-30-2-2	MTU 7029/ PAU 3116-25-5-1
86	TSM-153	MTU 2468-31-1-1	MTU 7029/ PAU 3116-25-5-1
87	TSM-164	MTU 2469-6-1-2	MTU 7029/ PAU 3140-126-1
88	TSM-165	MTU 2469-6-2-1	MTU 7029/ PAU 3140-126-1
89	TSM-166	MTU 2469-6-3-1	MTU 7029/ PAU 3140-126-1
90	TSM-167	MTU 2469-6-3-2	MTU 7029/ PAU 3140-126-1
91	TSM-168	MTU 2469-6-5-1	MTU 7029/ PAU 3140-126-1
92	TSM-169	MTU 2469-7-1-1	MTU 7029/ PAU 3140-126-1
93	TSM-171	MTU 2469-8-1-1	MTU 7029/ PAU 3140-126-1
94	TSM-174	MTU 2469-10-2-1	MTU 7029/ PAU 3140-126-1
95	TSM-175	MTU 2469-11-1-1	MTU 7029/ PAU 3140-126-1
96	TSM-178	MTU 2469-14-1-1	MTU 7029/ PAU 3140-126-1
97	TSM-183	MTU 2469-23-2-1	MTU 7029/ PAU 3140-126-1
98	TSM-184	MTU 2469-23-2-2	MTU 7029/ PAU 3140-126-1
99	TSM-190	MTU 2469-32-1-1	MTU 7029/ PAU 3140-126-1
100	TSM-191	MTU 2469-32-2-1	MTU 7029/ PAU 3140-126-1
101	TSM-200	MTU 2469-36-1-1	MTU 7029/ PAU 3140-126-1
102	TSM-204	MTU 2469-38-4-1	MTU 7029/ PAU 3140-126-1
103	TSM-211	MTU 2469-41-2-2	MTU 7029/ PAU 3140-126-1
104	TSM-213	MTU 2469-42-1-1	MTU 7029/ PAU 3140-126-1
105	TSM-215	MTU 2469-42-3-1	MTU 7029/ PAU 3140-126-1
106	TSM-216	MTU 2469-42-4-1	MTU 7029/ PAU 3140-126-1
107	TSM-219	MTU 2469-55-1-1	MTU 7029/ PAU 3140-126-1
108	TSM-220	MTU 2469-55-2-1	MTU 7029/ PAU 3140-126-1
109	TSM-221	MTU 2469-55-2-2	MTU 7029/ PAU 3140-126-1
110	TSM-223	MTU 2469-57-1-2	MTU 7029/ PAU 3140-126-1
111	TSM-228	MTU 2469-68-1-1	MTU 7029/ PAU 3140-126-1
112	TSM-229	MTU 2469-68-1-2	MTU 7029/ PAU 3140-126-1
113	TSM-230	MTU 2469-68-2-1	MTU 7029/ PAU 3140-126-1
114	TSM-235	MTU 2469-74-2-1	MTU 7029/ PAU 3140-126-1
		Parents	
115		MTU 7029	
116		MTU 1081	
117		MTU 1121	
118		JGL 11118	
119		NLR 34449	
120		PAU 3116-25-5-1	
121		PAU 3140-126-1	

In addition to this, these one hundred and fourteen F₅ families were planted in separate block in two rows with a spacing of 20 x 15 cm for screening against resistance to sheath blight and bacterial leaf blight to identify promising high yielding lines which are tolerant to these diseases.

Cultural practices such as fertilizer management, weeding, inter cultivation, irrigation and plant protection measures were followed as per the recommendations and observations were recorded on 10 characters viz., days to 50% flowering, days to maturity, plant height (cm), number of panicles per plant, panicle length (cm), grain yield per plant (g), test weight (g), kernel length (mm), kernel breadth (mm) and L/B ratio.

3.3. OBSERVATIONS RECORDED

Observations were recorded on five randomly selected plants as per methodology given in SES, 2014 without border effect of each genotype in each replication and the average values were subjected for statistical analysis. Details of the different characters studied were as follows.

3.3.1. Days to 50% flowering

The total number of days taken from date of sowing to 50 % flowering was recorded.

3.3.2 Days to maturity

Number of days taken from sowing to harvest was recorded.

3.3.3 Plant height (cm)

Height of plant from ground level to the tip of the tallest panicle at the time of maturity was taken as plant height and is measured in centimeters.

3.3.4 Number of panicles per plant

Total number of panicles per plant were counted and recorded.

3.3.5 Panicle length (cm)

Length from the base of panicle (neck node) to the tip of last spikelet was taken as panicle length and is measured in centimeters.

3.3.6 Grain yield per plant (g)

Panicles from a single plant were harvested at maturity, threshed, cleaned and dried to 12-14 per cent moisture content and weight was recorded in grams.

3.3.7 Test weight (g)

Thousand well filled grains were counted at random and weight was recorded in grams

3.3.8 Kernel length (mm)

Ten grains of milled rice were selected by hand randomly and the length in millimeter was recorded using INDOSCAN software of Rice Analyzer version 4.0.

3.3.9 Kernel breadth (mm)

Ten grains of milled rice were selected by hand randomly and the breadth in millimeter was recorded using INDOSCAN software of Rice Analyzer version 4.0.

3.3.10 L/B ratio

The L/B ratio was calculated by using the following formula of Murthy and Govindaswamy (1967)

$$\text{L/B ratio} = \frac{\text{Mean length of the kernel (mm)}}{\text{Mean breadth of the kernel (mm)}}$$

3.4. STATISTICAL PROCEDURE

3.4.1. Analysis of variance

For each character, analysis of variance was computed based on randomized block design separately as per standard statistical procedure (Panse and Sukhatme, 1985) and their significance was tested by referring to the values of 'F' table (Fisher and Yates, 1963).

$$Y_{ij} = \mu + g_i + r_j + e_{ij}$$

Where,

- Y_{ij} = phenotypic observation of i^{th} genotype and j^{th} replication
 μ = general mean
 g_i = effect of i^{th} genotype
 r_j = effect of j^{th} replication
 e_{ij} = random error associated with i^{th} genotype and j^{th} replication

The analysis of variance for each character was carried out as indicated below:

Table 3.3. ANOVA table

Source	Degrees of freedom	Sum of squares	Mean sum of squares	F-ratio
Replications	(r-1)	RSS	M_r	M_s / M_e
Treatments (Genotypes)	(t-1)	TrSS	M_t	M_t / M_e
Error	(r-1)(t-1)	ESS	M_e	
Total	(tr-1)	TSS	TMSS	

Where,

- R = Number of replications
 T = Number of treatments
 M_r = Mean sum of squares due to replications
 M_t = Mean sum of squares due to treatments
 M_e = Mean sum of squares due to error

3.4.2 Estimation of genetic parameters

3.4.2.1 Variance

The genotypic and phenotypic variance was calculated as per the formula given by Burton and Devane (1953).

$$\text{Genotypic variance } (\sigma_g^2) = \frac{(\text{MSS due to treatments} - \text{MSS due to error})}{\text{Number of replications}}$$

$$\text{Phenotypic variance } (\sigma_p^2) = (\sigma_g^2) + (\sigma_e^2) \quad \text{Where, } (\sigma_e^2) = \text{error variance}$$

3.4.2.2. Genotypic and phenotypic coefficients of variation

Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed according to the formula given by Falconer (1964).

$$\text{Genotypic coefficient of variation (GCV)} = \frac{\text{Genotypic standard deviation } (\sigma_g)}{\text{Mean } (\bar{X})} \times 100$$

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\text{Phenotypic standard deviation } (\sigma_p)}{\text{Mean } (\bar{X})} \times 100$$

Categorization of the range of variation was done as proposed by Sivasubramanian and Madhavamenon (1973).

<10%	:	Low
10-20%	:	Moderate
>20%	:	High

3.4.2.3. Heritability

Heritability in the broad sense refers to the proportion of genotypic variance to the total observed variance in the total population. Heritability (h^2) in the broad sense was calculated according to the formula given by Allard (1960).

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

Where,

$h^2 \text{ (bs)}$	=	Heritability in broad sense
σ_g^2	=	Genotypic variance
σ_p^2	=	Phenotypic variance $[(\sigma_g^2) + (\sigma_e^2)]$
σ_e^2	=	Environmental variance

As suggested by Johnson *et al.* (1955) range of heritability (broad sense) estimates were categorized as:

Low	:	0-30%
Medium	:	30-60%
High	:	60% and above

3.4.2.4. Genetic advance (GA)

Genetic advance refers to the expected gain or improvement in the next generation by selecting superior individuals under certain amount of selection pressure. From the heritability estimates the genetic advance was estimated by the following formula given by Burton (1952).

$$GA = K \cdot h^2(b) \cdot \sigma_p$$

Where,

GA = Expected genetic advance

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

$h^2(bs)$ = Heritability in broad sense

σ_p = Phenotypic standard deviation

3.4.2.5. Genetic advance as per cent of mean (GAM)

Genetic advance as percentage of mean was calculated and the range of genetic advance as per cent of mean was classified by using the formulae given by Johnson *et al.* (1955).

$$\text{Genetic advance as per cent of mean} = \frac{\text{Genetic advance (GA)}}{\text{Grand mean } (\bar{X})} \times 100$$

<10% : Low

10-20% : Moderate

>20% : High

3.4.3 Character Association

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

$$\text{Phenotypic coefficient of correlation } (r(X_i, X_j)_p) = \text{Cov}(X_i, X_j)_p / (V(X_i)_p \cdot V(X_j)_p)^{1/2}$$

Where,

$$\begin{aligned} r(X_i, X_j)_p &= \text{Phenotypic correlation between } i^{\text{th}} \text{ and } j^{\text{th}} \text{ characters} \\ \text{Cov}(X_i, X_j)_p &= \text{Phenotypic covariance between } i^{\text{th}} \text{ and } j^{\text{th}} \text{ characters} \\ V(X_i)_p &= \text{Phenotypic variance of } i^{\text{th}} \text{ character} \\ V(X_j)_p &= \text{Phenotypic variance of } j^{\text{th}} \text{ character} \end{aligned}$$

$$\text{Genotypic coefficient of correlation } (r(X_i, X_j)_g) = \text{Cov}(X_i, X_j)_g / (V(X_i)_g \cdot V(X_j)_g)^{1/2}$$

Where,

$$\begin{aligned} r(X_i, X_j)_g &= \text{Genotypic correlation between } i^{\text{th}} \text{ and } j^{\text{th}} \text{ characters} \\ \text{Cov}(X_i, X_j)_g &= \text{Genotypic covariance between } i^{\text{th}} \text{ and } j^{\text{th}} \text{ characters} \\ V(X_i)_g &= \text{Genotypic variance of } i^{\text{th}} \text{ character} \\ V(X_j)_g &= \text{Genotypic variance of } j^{\text{th}} \text{ character} \end{aligned}$$

Significance of correlation coefficients were tested by comparing phenotypic and genotypic correlation coefficients with the table values (Fisher and Yates, 1963) at (n-2) degree of freedom at 5% and 1% level where “n” denotes the number of paired observations tested in the calculations.

3.4.4 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.

Setting up of simultaneous equations

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

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

Where,

- r_{1y} to r_{ky} = Coefficient of correlation between causal factors 1 to k and dependent character Y
 r_{12} to r_{k-k} = Coefficient of correlation among causal factors
 p_{1y} to p_{ky} = Direct effects of characters 1 to k on character y
 $r_{1k} P_{ky}$ to $r_{kk} P_{ky}$ = indirect effects of characters 1 to k on y through k^{th} variable.

Solution of simultaneous equations were derived by matrix method as below

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

$$\begin{matrix} \text{A} & & \text{C} & & \text{B} \\ \begin{pmatrix} r_{1y} \\ r_{2y} \\ . \\ . \\ . \\ r_{ky} \end{pmatrix} & = & \begin{pmatrix} 1 & r_{12} & r_{13} & . & . & . & r_{1k} \\ r_{21} & 1 & r_{23} & . & . & . & r_{2k} \\ . & . & . & . & . & . & . \\ . & . & . & . & . & . & . \\ . & . & . & . & . & . & . \\ r_{k1} & r_{k2} & r_{k3} & . & . & . & 1 \end{pmatrix} & \begin{pmatrix} p_{1y} \\ p_{2y} \\ . \\ . \\ . \\ p_{ky} \end{pmatrix} \end{matrix}$$

or $A = B.C$ and $C = B^{-1} A$

Inverse of matrix 'B' obtained by elimination procedure or through adjoint method.

$$\text{then } (B)^{-1} = \begin{pmatrix} C_{11} & C_{12} & . & . & . & C_{1k} \\ C_{21} & C_{22} & . & . & . & C_{2k} \\ . & . & . & . & . & . \\ . & . & . & . & . & . \\ C_{k1} & C_{k2} & . & . & . & C_{kk} \end{pmatrix}$$

Then direct effects were calculated as follows

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

$$P_{2y} = \sum_{i=1}^k C_{2i} \cdot r_{iy}$$

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

Indirect effects were calculated by solving the simultaneous equations and summation of direct and indirect effects gives correlation co-efficient values.

Residual effect

In plant breeding, it is very difficult to have complete knowledge of all component traits of yield. The residual effect permits precise explanation about the pattern of interaction of other possible components of yield. In other words, residual effect measures the role of other possible independent variables which were not included in the study on the dependent variable. The residual effect is estimated with the help of direct effects and simple correlation coefficients as per following equation

$$1 = P^2 R_y + \Sigma P_{iy} r_{iy}$$

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

3.5. SCREENING FOR BACTERIAL LEAF BLIGHT AND SHEATH BLIGHT

For proper infestation and for getting good reaction of test material to sheath blight and bacterial leaf blight artificial inoculation was carried out along with natural infestation.

3.5.1. Artificial multiplication of sheath blight inoculum

Sheath blight, caused by *Rhizoctonia solani* (teleomorph: *Thanatephorus cucumeris*) is one of the most important fungal disease of rice affecting more than 50% of all global rice production areas (Groth *et al.*, 1991; Marchetti and Bollich, 1991). Symptoms include grayish green lesions which in later stages may enlarge and coalesce with other lesions, mostly on lower leaf sheaths, but occasionally on the leaves also. Due to its devastating nature under severe infection, identifying lines that are tolerant to this disease is essential for which screening of prominent lines is required.

However, field evaluation can only be performed in rice-growing areas with longer growing season, larger space, and higher cost, and is strongly influenced by environmental conditions and plant architectures. During the past decade, significant progress has been made in improving the method for sheath blight inoculation and evaluation under controlled conditions in a growth chamber or a greenhouse.

Typha leaf bit method

This method was first used by Bhaktavastalam *et al.* (1978) for mass multiplication of Sheath blight causing fungus. In this method, uniform sized typha bits were cut and sterilized in autoclave and inoculated with *Rhizoctonia solani*. The material is kept under wet condition for multiplication of the fungus. After complete coverage of the typha bits with fungal mat, the bits were used for artificial inoculation. Two bits per hill were used for artificial inoculation. The bits were inserted in between the tillers at the base of the plant and tied with thread so as to come in contact with the neighbouring tillers. Inoculated hills were observed for the appearance of the symptoms twice, initially at maximum tillering stage and later at panicle initiation stage and scores were recorded as per 0-9 scale of SES, IRRI, 2014 (based on relative lesion height given by Ahn and Mew (1986) in Table 3.4). Highest score among the two was considered as final one.

In the present study, during *kharif* 2015, all the individual plants of one hundred and fourteen F₅ families along with their susceptible check (MTU 7029) were sown in two rows each with a spacing of 20 x 15 cm and were screened against sheath blight by adopting typha leaf bit method of artificial inoculation done at 69 DAS followed by field screening at 125 DAS and later at 149 DAS when 95% of check variety (MTU 7029) was affected (Table 3.5)

Table 3.4. Standard Evaluation System, IRRI (2014) scale for sheath blight

Scale	Rating	Disease symptoms
0	Highly Resistant	No Infection (Immune reaction)
1	Resistant	Lesions limited to lower 20% of the plant height
3	Moderately Resistant	20-30
5	Susceptible	31-45
7	Highly Susceptible	46-65
9	Highly Resistant	>65

3.5.2. Artificial multiplication of bacterial leaf blight inoculum

Bacterial blight caused by *Xanthomonas oryzae* pv. *oryzae* is most important bacterial disease of rice. Lesions usually start near the leaf tips or leaf margins or both and extend down the outer edge(s). Young lesions are pale green to grayish green, later



Plate 3.1. Nursery raised for screening against sheath blight



Plate 3.2. Screening of F_5 families against sheath blight



Plate 3.3 & 3.4. Artificial inoculation with sheath blight fungus



Plate 3.5. Field view showing severity of sheath blight incidence



Plate 3.6. Plant showing typical symptoms of sheath blight

turning yellow to gray (dead) with time. In very susceptible varieties, lesions may extend to entire leaf length into the sheath. Kresek or seedling blight causes wilting and death of plants.

For screening rice germplasm against bacterial leaf blight resistance, artificial inoculation is preferred over natural infection using inoculum prepared from local virulent isolate. In addition, artificial inoculation ensures that the rice plants are properly exposed to right amount of inoculum to cause the disease. The commonly used method for artificial inoculation of screening entries is as given below.

Leaf clipping method

Kauffman *et al.* (1973) reported the leaf clipping method of artificial inoculation for bacterial leaf blight disease. In this method, sterilized surgical scissors dipped in bacterial suspension were used for inoculation. Leaves of all the three plants in a pot were grasped in one hand and the top 1-3 inches of three leaves were clipped off simultaneously. The inoculum should be used within two hours after preparation as *Xanthomonas oryzae* pv. *oryzae* quickly loses its viability. A control of each variety was also maintained, by using scissors dipped in sterile water for clipping off the leaves. This method is very efficient for inoculating large amount of breeding materials in the field and is currently being used at IRRI, Philippines.

One should note that in both seedling and field tests, folded young leaves and old leaves or leaves with symptoms of nutrient deficiency or other diseases should be avoided for inoculation.

In the present study, during *Kharif* 2015, all the individual plants in selected one hundred and fourteen F₅ families along with their susceptible check (TN-1) were sown in two rows each with a spacing of 20 x 15 cm and were screened against bacterial leaf blight by adopting leaf clipping method of artificial inoculation at 80 DAS followed by field screening at 120 DAS and later at 155 DAS when 95% of check variety TN-1 was affected using 0-9 scale of Standard Evaluation System (SES) of IRRI, 2014 (Table 3.5 & 3.6).

Table 3.5. Standard Evaluation System, IRRI (2014) scale for bacterial leaf blight (Based on Green house test, severity, % leaf area diseased)

Scale	% leaf area diseased
1	No disease observed
2	<1
3	1-3
4	4-5
5	11-15
6	16-25
7	26-50
8	51-75
9	76-100

Rating 1 represents immune or highly resistant reaction where as 9 represents highly susceptible reaction.

Table 3.6. Standard Evaluation System, IRRI (2014) scale for bacterial leaf blight (Based on field test, severity, % leaf area diseased)

Scale	Rating	% leaf area diseased
1	Highly Resistant	1-5
3	Resistant	6-12
5	Moderately Resistant	13-25
7	Susceptible	26-50
9	Highly Susceptible	51-100



Plate 3.7. Nursery raised for screening against bacterial leaf blight



Plate 3.8. Artificial inoculation of bacterial leaf blight by leaf clipping method



Plate 3.9. Field view showing severity of bacterial leaf blight incidence

Chapter - IV

RESULTS AND DISCUSSION

The data obtained in the present investigation on one hundred and fourteen F_5 rice families along with seven parents pertaining to 10 characters viz., days to 50% flowering, days to maturity, plant height (cm), number of panicles per plant, panicle length (cm), grain yield per plant (g), test weight (g), kernel length (mm), kernel breadth (mm) and L/B ratio was subjected to statistical analysis and the results are presented here under.

4.1 Analysis of variance

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

4.3 Character association

4.4 Path coefficient analysis

4.5 Screening for sheath blight

4.6 Screening for bacterial leaf blight

4.1. ANALYSIS OF VARIANCE

The ANOVA of one hundred and fourteen F_5 families along with seven parents pertaining to 10 characters revealed the presence of significant differences among the genotypes for all the characters, indicating considerable variation among the genotypes (Table 4.1).

4.2. MEAN, GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE AS PER CENT OF MEAN

Improvement of any crop species depends on the amount of variation present in that population. Greater the variability, higher will be the chances of developing desired form. Estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) will give information regarding non- heritable and heritable portion of variation present in the population.

Heritability refers to the relative index of transmission of a particular character from parents to the off spring. Heritability can be classified as low (0-30%), moderate (30-60%) and high (>60%). Higher the heritability, greater will be the chances for choosing that particular character. Heritability in conjugation with genetic advance gives more reliable index of selection value.

Table 4.1. Analysis of variance (mean sum of squares) for 10 characters for 121 genotypes of rice (*Oryza sativa* L.) during *kharif*, 2015

Source of variations	d. f.	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of panicles per plant	Panicle length (cm)	Grain yield per plant (g)	Test weight (g)	Kernel length (mm)	Kernel breadth (mm)	Kernel L/B ratio
Mean sum of squares											
Replications	1	0.04	0.264	0.051	0.810	3.499	3.380	0.001	0.013	0.000	0.051
Genotypes	120	65.833**	66.903**	122.849**	4.795**	8.045**	52.314**	52.299**	0.336**	0.098**	0.216**
Error	120	2.071	0.981	4.117	0.510	1.250	1.706	1.160	0.025	0.196	0.038

*Significant at 5% level

**Significant at 1% level

In the present investigation, The mean performance of 121 genotypes (114 F₅ families and 7 parents) evaluated during *kharif*, 2015 for 10 characters were presented in Table 4.2 while estimates of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense [h^2 (bs)] and genetic advance as per cent of mean (GAM) for 121 rice genotypes was computed and presented in Table 4.3.

4.2.1. Days to 50% flowering

Days to 50% flowering ranged from 89 days (MTU 1081) to 126 days (MTU 2462-31-2-1 and MTU 2468-25-2-1) with an overall mean of 116 days.

The estimates of PCV and GCV were low (5.03 and 4.87) for days to 50% flowering indicating the presence of low amount of variation. The difference between PCV and GCV was low indicating that influence of environment on this character is low. These results were in conformity with Sameera *et al.* (2015), Suresh *et al.* (2014), Shrivastava *et al.* (2014), Patel *et al.* (2014), Khare *et al.* (2014), Neha *et al.* (2014), Gangashetty *et al.* (2013), Aditya and Bhartiya (2013), Ghosh and Sharma (2012), Sravan *et al.* (2012), Shiva Prasad *et al.* (2011), Shiva Parvathi *et al.* (2011), Saidaiah *et al.* (2010) and Laxuman *et al.* (2010).

High heritability (94%) coupled with low genetic advance as per cent of mean (9.73) was recorded for this trait indicating the presence of non additive gene action and simple selection for such traits may not be effective. Similar findings were reported by Khare *et al.* (2014) and Paikhomba *et al.* (2014).

4.2.2. Days to maturity

Days to maturity ranged from 117 days (MTU 1081) to 151 days (MTU 2462-1-5-2 and MTU 2462-15-1-1) with a general mean of 142 days.

Low estimates of PCV and GCV (4.10 and 4.04) were observed for days to maturity indicating the presence of less variability among these lines for this trait. The difference between PCV and GCV was low indicating that less environmental influence. These results were in conformity with Sameera *et al.* (2015), Shrivastava *et al.* (2014), Patel *et al.* (2014), Khare *et al.* (2014), Bekele *et al.* (2013), Aditya and Bhartiya (2013) and Laxuman *et al.* (2010).

Table 4.2. Mean performance of 121 genotypes of rice (*Oryza sativa* L.) during *kharif*, 2015

S.No.	Entry	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of panicles per plant	Panicle length (cm)	Grain yield per plant (g)	Test weight (g)	Kernel length (mm)	Kernel breadth (mm)	L/B ratio
1	MTU 2462-1-1-1	120	146	108.30	11	26.25	32.60	21.90	6.45	2.45	2.60
2	MTU 2462-1-1-2	108	133	105.00	8	24.00	16.20	23.00	6.20	2.40	2.55
3	MTU 2462-1-2-1	119	145	109.60	9	27.35	17.00	19.75	5.75	2.25	2.55
4	MTU 2462-1-5-1	118	145	121.90	9	24.00	21.60	22.65	6.60	2.15	3.10
5	MTU 2462-1-5-2	124	151	115.00	12	26.25	25.90	18.80	6.80	1.95	3.45
6	MTU 2462-1-8-1	115	144	112.50	8	25.80	21.50	22.80	6.90	2.10	3.35
7	MTU 2462-1-8-2	116	142	114.00	11	24.95	25.70	17.30	6.75	2.05	3.35
8	MTU 2462-1-9-1	120	145	113.10	12	25.60	41.60	21.50	6.90	2.35	2.95
9	MTU 2462-1-9-2	122	149	119.00	11	26.90	43.75	20.35	6.30	2.50	2.50
10	MTU 2462-2-1-1	110	135	109.90	9	24.25	27.10	19.85	6.15	2.40	2.55
11	MTU 2462-4-1-1	111	135	107.40	9	23.40	15.00	19.00	6.00	2.40	2.50
12	MTU 2462-6-2-1	116	135	117.80	9	24.70	21.90	20.15	6.45	2.05	3.15
13	MTU 2462-8-1-1	114	135	112.00	10	24.40	15.60	20.95	5.60	2.55	2.25
14	MTU 2462-8-2-1	110	144	104.80	9	22.35	16.40	21.75	5.80	2.65	2.20
15	MTU 2462-8-2-2	113	144	107.70	12	22.40	21.60	21.10	6.05	2.45	2.50
16	MTU 2462-12-1-1	110	135	106.70	9	24.00	20.30	27.10	6.60	2.60	2.55
17	MTU 2462-12-2-1	111	135	106.70	11	21.45	19.10	23.10	6.95	2.75	2.55
18	MTU 2462-15-1-1	122	151	112.30	11	24.80	28.60	13.80	6.65	2.00	3.30

Table 4.2. (contd.).

S.No.	Entry	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of panicles per plant	Panicle length (cm)	Grain yield per plant (g)	Test weight (g)	Kernel length (mm)	Kernel breadth (mm)	L/B ratio
19	MTU 2462-15-3-1	118	144	117.90	11	25.20	30.30	20.70	6.60	2.25	2.95
20	MTU 2462-15-3-2	110	135	109.30	11	24.20	17.00	17.95	5.85	2.15	2.80
21	MTU 2462-17-2-1	119	145	117.50	12	24.80	27.60	22.35	6.00	2.60	2.35
22	MTU 2462-17-3-1	119	145	113.10	10	23.35	19.00	19.80	5.55	2.35	2.35
23	MTU 2462-18-1-1	119	145	95.30	9	24.95	18.50	22.40	5.85	2.45	2.40
24	MTU 2462-21-1-1	119	145	108.20	12	23.75	17.70	21.35	6.30	2.25	2.80
25	MTU 2462-22-2-1	116	142	110.00	12	25.40	17.20	16.35	6.05	2.05	3.00
26	MTU 2462-22-3-1	113	142	113.40	13	25.10	30.70	18.40	6.20	1.95	3.15
27	MTU 2462-23-3-1	118	143	97.80	12	25.20	15.40	20.70	6.45	2.25	2.85
28	MTU 2462-26-3-1	120	144	120.80	12	27.60	25.40	18.85	6.35	2.35	2.70
29	MTU 2462-26-3-2	120	146	121.90	13	25.00	17.20	19.40	6.95	2.05	3.45
30	MTU 2462-27-3-1	119	146	110.60	11	23.50	17.20	19.00	6.70	2.15	3.05
31	MTU 2462-29-2-1	113	142	114.50	12	21.50	15.50	20.65	5.50	2.40	2.30
32	MTU 2462-30-1-1	119	146	122.50	14	26.80	21.10	20.00	6.65	2.15	3.05
33	MTU 2462-31-2-1	126	150	109.90	14	24.90	20.40	19.45	5.85	2.15	2.75
34	MTU 2462-34-1-1	121	145	106.30	11	24.35	16.70	19.05	6.65	2.50	2.65
35	MTU 2462-34-4-1	115	142	104.70	11	22.35	17.40	19.30	6.85	2.15	3.20
36	MTU 2462-35-2-1	113	143	107.90	13	21.15	19.00	25.50	6.75	2.45	2.80
37	MTU 2462-35-2-2	114	143	114.10	13	25.25	20.30	21.25	6.65	2.45	2.80
38	MTU 2462-37-1-1	122	145	97.20	10	21.70	18.60	17.60	5.50	2.20	2.50
39	MTU 2462-37-2-1	118	145	111.70	12	22.45	19.20	20.05	6.05	2.25	2.75
40	MTU 2462-37-2-2	120	145	108.30	12	24.15	23.40	21.05	6.70	2.20	3.00
41	MTU 2462-41-2-1	119	145	122.70	14	25.85	22.80	30.80	6.60	2.65	2.55

Table 4.2. (contd.).

S.No.	Entry	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of panicles per plant	Panicle length (cm)	Grain yield per plant (g)	Test weight (g)	Kernel length (mm)	Kernel breadth (mm)	L/B ratio
42	MTU 2462-42-2-1	113	143	108.80	11	24.35	18.10	16.65	5.95	2.10	2.80
43	MTU 2462-45-1-2	115	142	109.80	12	25.90	16.30	15.05	5.80	2.00	2.90
44	MTU 2462-45-2-1	108	135	108.70	11	23.30	20.30	16.85	6.25	1.95	3.25
45	MTU 2462-49-2-1	113	142	109.60	13	26.40	16.80	20.00	6.90	2.05	3.30
46	MTU 2463-4-1-2	119	145	110.70	13	22.40	16.60	20.50	5.95	2.10	2.85
47	MTU 2463-4-2-1	120	145	116.90	13	25.40	15.50	14.10	6.00	2.00	3.00
48	MTU 2463-8-2-1	110	135	119.30	12	26.75	15.40	12.80	6.90	2.20	3.15
49	MTU 2463-14-1-1	118	145	120.30	14	26.15	14.00	19.35	6.95	1.75	3.95
50	MTU 2463-15-1-1	119	145	117.70	13	26.10	14.60	19.45	6.15	2.05	2.95
51	MTU 2465-4-1-1	116	144	109.10	12	25.75	22.00	16.85	5.95	2.20	2.65
52	MTU 2465-4-2-1	118	144	110.60	12	27.25	18.80	15.25	6.30	2.05	3.15
53	MTU 2465-6-2-1	115	142	112.00	12	25.35	18.20	15.20	5.75	2.15	2.70
54	MTU 2465-8-1-1	117	144	105.80	9	27.05	18.80	18.25	5.65	2.50	2.25
55	MTU 2465-10-1-1	113	142	119.90	13	26.40	22.40	16.60	5.80	2.30	2.50
56	MTU 2465-11-3-1	113	142	100.20	11	23.25	19.40	19.60	5.90	2.05	2.95
57	MTU 2465-11-3-2	110	135	95.90	9	23.30	17.60	17.85	6.35	2.00	3.20
58	MTU 2465-12-2-1	114	142	111.20	11	21.80	10.00	15.55	6.10	2.20	2.80
59	MTU 2465-12-2-2	116	143	99.30	10	23.40	27.30	20.10	5.40	2.20	2.50
60	MTU 2465-13-3-1	118	145	115.20	12	23.20	19.80	18.70	5.35	2.25	2.40
61	MTU 2465-13-3-2	121	145	115.60	12	25.85	18.80	18.15	5.45	2.30	2.35
62	MTU 2465-16-2-1	113	142	115.20	12	25.25	19.40	11.50	5.70	2.05	2.80
63	MTU 2465-16-2-3	119	145	102.30	9	22.60	22.90	16.00	5.60	2.60	2.15
64	MTU 2465-22-1-1	119	145	100.10	9	24.45	21.25	19.50	6.30	2.25	2.80

Table 4.2. (contd.).

S.No.	Entry	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of panicles per plant	Panicle length (cm)	Grain yield per plant (g)	Test weight (g)	Kernel length (mm)	Kernel breadth (mm)	L/B ratio
65	MTU 2465-22-2-1	120	144	108.80	11	24.00	15.80	21.10	6.50	2.35	2.85
66	MTU 2465-22-2-2	119	144	106.70	11	25.30	16.30	22.75	6.60	2.05	3.20
67	MTU 2465-24-3-2	119	144	104.90	10	23.50	17.20	26.50	6.10	2.10	2.90
68	MTU 2465-27-2-1	117	142	104.60	11	21.90	15.80	25.90	6.00	2.45	2.50
69	MTU 2466-4-2-1	113	142	109.30	12	20.90	12.20	21.90	6.15	2.75	2.25
70	MTU 2466-4-2-2	110	135	111.10	11	23.70	15.85	20.90	6.95	2.15	3.25
71	MTU 2466-4-3-1	110	135	103.90	10	20.80	17.70	15.30	6.40	2.05	3.10
72	MTU 2468-1-1-1	111	135	109.00	10	17.40	17.80	23.70	6.30	2.40	2.55
73	MTU 2468-2-1-1	113	142	97.30	9	23.25	18.40	13.70	6.20	2.60	2.45
74	MTU 2468-8-2-1	120	145	107.40	10	21.60	18.00	20.40	6.10	2.55	2.35
75	MTU 2468-18-1-1	116	144	117.10	13	21.50	17.00	20.55	5.95	2.50	2.35
76	MTU 2468-18-1-2	114	142	110.20	10	20.75	16.40	25.40	6.30	2.45	2.55
77	MTU 2468-20-1-1	119	145	98.00	9	21.15	20.50	22.55	5.80	2.45	2.35
78	MTU 2468-21-4-1	121	146	113.10	11	18.45	17.00	21.75	6.30	2.55	2.50
79	MTU 2468-25-2-1	126	150	99.00	10	22.60	18.60	19.55	5.90	2.35	2.55
80	MTU 2468-27-2-1	118	145	110.10	11	24.20	19.20	21.85	6.05	2.40	2.55
81	MTU 2468-28-1-1	122	150	108.20	12	23.70	28.70	19.60	6.35	2.55	2.50
82	MTU 2468-29-2-1	117	146	111.40	10	23.20	17.60	29.50	6.55	2.50	2.60
83	MTU 2468-29-3-1	122	150	122.60	12	26.05	16.60	23.80	6.50	2.45	2.70
84	MTU 2468-29-4-1	116	142	133.10	16	26.10	15.80	25.35	6.40	2.80	2.30
85	MTU 2468-30-2-2	125	150	111.30	16	22.35	18.60	36.70	6.30	2.50	2.55
86	MTU 2468-31-1-1	120	146	109.80	11	21.60	20.00	34.05	6.45	2.55	2.55
87	MTU 2469-6-1-2	119	146	112.80	11	21.00	15.60	23.10	6.15	2.55	2.40

Table 4.2. (contd.).

S.No.	Entry	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of panicles per plant	Panicle length (cm)	Grain yield per plant (g)	Test weight (g)	Kernel length (mm)	Kernel breadth (mm)	L/B ratio
88	MTU 2469-6-2-1	119	146	99.80	10	20.85	15.50	41.20	6.30	2.55	2.50
89	MTU 2469-6-3-1	118	146	106.50	13	20.95	15.15	27.85	6.50	2.65	2.45
90	MTU 2469-6-3-2	119	146	107.50	11	22.55	19.80	18.40	6.10	2.50	2.45
91	MTU 2469-6-5-1	119	146	104.00	10	23.35	18.60	24.55	6.45	2.55	2.55
92	MTU 2469-7-1-1	116	142	96.40	9	20.45	17.00	20.45	6.20	2.60	2.40
93	MTU 2469-8-1-1	110	135	106.70	10	23.15	20.75	23.05	5.90	2.60	2.25
94	MTU 2469-10-2-1	120	145	100.00	12	21.45	19.70	22.85	6.50	2.55	2.50
95	MTU 2469-11-1-1	118	144	112.60	13	22.05	16.40	22.50	6.50	2.55	2.55
96	MTU 2469-14-1-1	116	144	111.90	11	23.50	15.20	22.50	6.75	2.45	2.80
97	MTU 2469-23-2-1	126	150	110.00	12	23.80	16.40	28.90	6.15	2.05	3.00
98	MTU 2469-23-2-2	124	150	111.50	12	24.80	17.50	22.10	6.20	2.30	2.75
99	MTU 2469-32-1-1	121	145	114.40	11	23.90	17.20	23.25	6.55	2.75	2.40
100	MTU 2469-32-2-1	118	144	112.10	12	22.65	15.70	35.85	6.65	2.40	2.80
101	MTU 2469-36-1-1	118	145	101.20	10	21.55	19.50	41.40	6.30	2.40	2.65
102	MTU 2469-38-4-1	118	145	132.50	12	28.25	18.20	25.40	6.65	2.30	2.90
103	MTU 2469-41-2-2	116	143	113.80	12	24.00	18.20	19.80	6.00	2.10	2.85
104	MTU 2469-42-1-1	120	144	112.50	11	23.35	18.20	33.20	6.15	2.50	2.50
105	MTU 2469-42-3-1	113	142	115.20	12	26.30	15.80	25.65	6.00	2.60	2.30
106	MTU 2469-42-4-1	116	144	109.80	11	23.25	18.60	23.30	6.15	2.40	2.55
107	MTU 2469-55-1-1	122	150	111.50	11	21.30	17.60	18.65	5.70	2.45	2.35
108	MTU 2469-55-2-1	121	145	106.60	11	25.30	18.40	22.70	6.15	2.30	2.75
109	MTU 2469-55-2-2	116	143	136.90	12	25.25	18.40	16.30	5.95	2.45	2.45
110	MTU 2469-57-1-2	115	142	115.20	11	24.95	17.00	31.45	6.10	2.50	2.45

Table 4.2. (contd.).

S.No.	Entry	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of panicles per plant	Panicle length (cm)	Grain yield per plant (g)	Test weight (g)	Kernel length (mm)	Kernel breadth (mm)	L/B ratio
111	MTU 2469-68-1-1	112	142	124.60	10	24.85	16.20	19.60	5.90	2.35	2.50
112	MTU 2469-68-1-2	117	143	127.30	11	25.75	15.60	25.95	6.20	2.50	2.55
113	MTU 2469-68-2-1	119	145	129.60	9	24.70	16.40	21.80	6.25	2.40	2.60
114	MTU 2469-74-2-1	116	142	117.60	13	24.50	21.10	20.70	6.25	2.60	2.40
	Parents										
115	MTU 7029	107	133	116.85	11	25.10	25.85	18.50	5.35	2.20	2.40
116	MTU 1081	89	117	102.00	10	26.05	17.90	15.50	5.55	2.15	2.60
117	MTU 1121	111	133	106.70	10	29.20	33.50	18.60	5.55	2.35	2.35
118	JGL 11118	91	119	97.50	7	23.85	12.85	16.70	6.60	2.25	2.95
119	NLR 34449	95	120	97.70	11	26.20	23.35	15.20	5.30	1.85	3.20
120	PAU 3116-25-5-1	106	129	109.10	9	25.15	27.20	22.00	5.75	2.45	2.80
121	PAU 3140-126-1	108	132	108.10	9	25.55	25.80	22.35	5.55	2.65	2.50
	Mean	116	142	110.73	11	24.02	19.59	21.36	6.20	2.33	2.71
	C.V%	1.24	0.70	1.83	6.59	4.65	6.67	5.04	2.55	6.01	7.18
	F ratio	31.79	68.19	29.84	9.40	6.44	30.66	45.08	13.47	4.98	5.73
	C.D at 5%	2.85	1.96	4.02	1.41	2.21	2.59	2.13	0.31	0.28	0.38
	C.D at 1%	3.77	2.89	5.31	1.87	2.93	3.42	2.82	0.41	0.37	0.51

Table 4.3. Estimates of genetic variability parameters of yield and yield components in rice (*Oryza sativa* L.) during *kharif*, 2015

S.No.	Character	Range		Mean	Variability parameters		h ² (bs)	GAM
		Min.	Max.		PCV	GCV		
1	Days to 50% flowering	89	126	116	5.03	4.87	94.00	9.73
2	Days to maturity	117	151	142	4.10	4.04	97.00	8.20
3	Plant height (cm)	95.3	136.9	110.73	7.20	6.96	94.00	13.86
4	Number of panicles per plant	7	16	11	15.03	13.51	81.00	25.01
5	Panicle length (cm)	17.4	29.2	24.02	8.98	7.68	73.00	13.52
6	Grain yield per plant (cm)	10	43.75	19.59	26.53	25.68	94.00	51.20
7	Test weight (g)	11.5	41.4	21.36	24.20	23.67	96.00	47.69
8	Kernel length (mm)	5.3	6.95	6.2	6.85	6.36	86.00	12.16
9	Kernel breadth (mm)	1.75	2.8	2.33	10.39	8.48	67.00	14.24
10	L/B ratio	2.15	3.95	2.71	13.17	11.04	70.00	19.06

High heritability (97%) coupled with low genetic advance as per cent of mean (8.20) was recorded for this trait indicating the presence of non additive gene action and selection for such traits may not be effective. Similar findings were reported by Khare *et al.* (2014) and Shrivastava *et al.* (2014).

4.2.3. Plant height (cm)

Average plant height recorded was 110.73 cm ranging from 95.3 cm (MTU 2462-18-1-1) to 136.9 cm (MTU 2469-55-2-2).

Both PCV and GCV estimates were low (7.20 and 6.96) for plant height indicating the presence of less variation among the genotypes pertaining to this trait. The difference between PCV and GCV was low indicating less influence of environment on this character. These results were in conformity with Sameera *et al.* (2015), Patel *et al.* (2014), Paikhomba *et al.* (2014) and Aditya and Bhartiya (2013).

High heritability (94%) coupled with moderate genetic advance as per cent of mean (13.86) was recorded for this trait indicating the presence of both additive and non additive gene actions and exploitation of heterosis breeding for such traits will be effective. Similar findings were reported by Patel *et al.* (2014), Paikhomba *et al.* (2014) and Kishore *et al.* (2015).

4.2.4. Number of panicles per plant

Number of panicles per plant ranged from 7 (JGL 11118) to 16 (MTU 2468-29-4-1 and MTU 2468-30-2-2) with an average number of 11 panicles per plant.

Moderate PCV (15.03) and GCV (13.51) were recorded for number of panicles per plant indicating the presence of moderate amount of variability among the genotypes studied. The difference between PCV and GCV was low indicating less influence of environment on this character. These results were in conformity with the findings of Sravan *et al.* (2012), Shiva Prasad *et al.* (2011), Shiva Parvathi *et al.* (2011) and Saidaiah *et al.* (2010).

High heritability (81%) coupled with high genetic advance as percent of mean (25.01) was recorded for this trait indicating the presence of additive gene action and hence simple selection can be practiced for improvement of this trait. Similar findings were reported by Sameera *et al.* (2015), Khare *et al.* (2014), Gangashetty *et al.* (2013) and Hasan *et al.* (2011).

4.2.5. Panicle length (cm)

Panicle length ranged from 17.4 cm (MTU 2468-1-1-1) to 29.2 cm (MTU 1121) with a general mean of 24.02 cm.

The estimates of PCV and GCV were low (8.98 and 7.68) for panicle length indicating the presence of low amount of variation among the genotypes pertaining to this trait. The difference between PCV and GCV was low indicating less influence of environment on this character. These results were in conformity with Sameera *et al.* (2015), Patel *et al.* (2014), Paikhomba *et al.* (2014), Aditya and Bhartiya (2013) and Sravan *et al.* (2012).

High heritability (73%) coupled with moderate genetic advance as per cent of mean (13.52) was recorded for this trait indicating the presence of both additive and non additive gene actions and use of heterosis breeding for exploitation of such traits will be effective. Similar findings were also reported by Jambhulkar and Bose (2014).

4.2.6. Grain yield per plant (g)

Average grain yield per plant was found to be 19.6 g ranging from 10 g (MTU 2465-12-2-1) to 43.75 g (MTU 2462-1-9-2).

High estimates of PCV (26.53) and GCV (25.68) were recorded for grain yield per plant indicating the presence of high variability among the genotypes studied. The difference between PCV and GCV was low indicating less influence of environment on this character. These results were in conformity with the findings of Anjaneyulu *et al.* (2010), Anseri *et al.* (2010), Sreeparvathy *et al.* (2010), Hasan *et al.* (2011), Lal and Chauhan (2011), Shiva Parvathi *et al.* (2011), Selvaraj *et al.* (2011), Singh *et al.* (2011), Subbaiah *et al.* (2011), Idris *et al.* (2012), Seyoum *et al.* (2012), Sravan *et al.* (2012), Kumar and Saravanan (2012), Ghosh and Sharma (2012), Bhadru *et al.* (2012), Aditya and Bhartiya (2013), Bekele *et al.* (2013), Paikhomba *et al.* (2013), Idris and Mohamed (2013), Bornare *et al.* (2014), Dhurai *et al.* (2014), Jambhulkar and Bose (2014), Khare *et al.* (2014), Patel *et al.* (2014), Rai *et al.* (2014), Singh *et al.* (2014), Suresh *et al.* (2014) and Nitesh Kumar *et al.* (2015).

High heritability (94%) coupled with high genetic advance as per cent of mean (51.20) was recorded for this trait indicating the presence of additive gene action and hence simple selection can be practiced for improvement of this trait. Similar findings

were reported by Subbaiah *et al.* (2011), Bekele *et al.* (2013), Gangasetty *et al.* (2013), Khare *et al.* (2014), Patel *et al.* (2014), Suresh *et al.* (2014), Thirumala Rao *et al.* (2014), Nitesh Kumar *et al.* (2015) and Sameera *et al.* (2015).

4.2.7. Test weight (g)

Test weight recorded a general mean of 21.36 g ranging from 11.5 g (MTU 2465-16-2-1) to 41.4 g (MTU 2469-36-1-1).

Both PCV (26.53) and GCV (25.68) were high for test weight indicating the presence of high variability among the lines under study. The difference between PCV and GCV was low indicating less influence of environment on this character. These results were in conformity with the findings of Bhadru *et al.* (2012) and Gangashetty *et al.* (2013).

High heritability (96%) coupled with high genetic advance as per cent of mean (47.69) was recorded for this trait indicating the presence of additive gene action and hence simple selection can be practiced for improvement of this trait. Similar findings were reported by Bekele *et al.* (2013), Gangashetty *et al.* (2013), Patel *et al.* (2014), Shrivastava *et al.* (2014), Suresh *et al.* (2014), Thirumala Rao *et al.* (2014), Nitesh Kumar *et al.* (2015) and Sameera *et al.* (2015).

4.2.8. Kernel length (mm)

Average kernel length was 6.20 mm ranging from 5.30 mm (NLR 34449) to 6.95 mm (MTU 2466-4-2-2).

Low estimates of PCV and GCV (6.85 and 6.36) were observed for kernel length indicating the presence of less variation among the genotypes pertaining to this trait. The difference between PCV and GCV was low indicating less influence of environment on this character. These results were in conformity with Manonmani *et al.* (2010), Aditya and Bhartiya (2013) and Patel *et al.* (2014).

High heritability (86%) coupled with moderate genetic advance as per cent of mean (12.16) was recorded for this trait indicating the presence of both additive and non additive gene actions and heterosis breeding has to be used for exploitation of such traits. Similar findings were reported by Patel *et al.* (2014).

4.2.9. Kernel breadth (mm)

Kernel breadth ranged from 1.75 mm (MTU 2463-14-1-1) to 2.80 mm (MTU 2468-29-4-1) with an overall mean of 2.33 mm.

Moderate PCV (10.39) and low GCV (8.48) for kernel breadth was observed indicating the presence of low amount of heritable variation among the genotypes. The difference between PCV and GCV was low indicating less influence of environment on this character. These results were in conformity with Subbaiah *et al.* (2011), Bekele *et al.* (2013) and Nitesh Kumar *et al.* (2015) for moderate PCV and Manonmani *et al.* (2010), Aditya and Bhartiya (2013) and Patel *et al.* (2014) for low GCV.

High heritability (67%) coupled with moderate genetic advance as per cent of mean (14.24) was recorded for this trait indicating the presence of both additive and non additive gene actions and use of heterosis breeding for improvement such traits. Similar findings were reported by Patel *et al.* (2014).

4.2.10. L/B ratio

L/B ratio recorded a general mean of 2.71 ranging from 2.15 (MTU 2465-16-2-3) to 3.95 (MTU 2463-14-1-1).

Moderate PCV (13.17) and GCV (11.04) were recorded for L/B ratio indicating the presence of moderate amount of variability among the genotypes studied. The difference between PCV and GCV was low indicating less influence of environment on this character. High heritability (70%) coupled with moderate genetic advance as per cent of mean (19.06) was recorded for this trait indicating the presence of both additive and non additive gene actions and hence heterosis breeding can be exploited for improvement of this trait. These results were in conformity with the findings of Rajeswari *et al.* (2010), Umadevi *et al.* (2010), Subbaiah *et al.* (2011), Kumar and Saravanan (2012), Bekele *et al.* (2013), Gangashetty *et al.* (2013), Shejul *et al.* (2013), Patel *et al.* (2014) and Nitesh Kumar *et al.* (2015).

4.3. CHARACTER ASSOCIATION

Yield is the end product of interaction between many interrelated attributes. Selection based on yield is not effective as yield is a complex quantitative trait and considerably affected by environment. Efficiency of selection depends on the magnitude and direction of association between yield and its components and among

themselves. Genetic correlation which is defined as inherent association between two variables will measure the magnitude of relationship between various plant characters that determines the component characters on which selection can be made for improvement in yield (Johnson *et al.*, 1955). This correlation may be either due to pleiotropic action of genes or linkage. If the correlation between grain yield and a character is positive, selection can be practiced in same direction. If the correlation value is negative, selection can be practiced in opposite direction. A great yield response is obtained when the character for which indirect selection is practiced has a high heritability and a positive correlation with yield. Thus, correlation is an important tool helping in deciding the breeding procedure for genetic improvement of grain yield in rice.

In the present investigation, phenotypic and genotypic correlation coefficients between grain yield and other related component characters, among themselves in rice were estimated and presented in Table 4.4.

4.3.1 Days to 50% flowering

This trait showed positive significant association with days to maturity (0.9294**/0.9602), plant height (0.1920**/0.2139**), number of panicles per plant (0.3248**/0.3811), test weight (0.2425**/0.2519) and kernel length (0.1655**/0.2002**) while with kernel breadth (0.0891/0.0929) and grain yield (0.0830/0.0794) it showed positive non significant association at both phenotypic and genotypic levels. Negative non significant association was observed with panicle length (-0.0293/-0.0641) and L/B ratio (-0.0355/-0.0320) at both phenotypic and genotypic levels. Similar findings were reported by Krishna *et al.* (2008), Hasan *et al.* (2011), Ekka *et al.* (2011), Ravindrababu *et al.* (2012), Rangare *et al.* (2012), Nagaraju *et al.* (2013), Jambhulkar and Bose (2014), Khare *et al.* (2014) and Patel *et al.* (2014).

Non significant association of days to 50% flowering with grain yield indicates that this trait has little influence in improving the yield.

4.3.2. Days to maturity

This trait showed significant positive association with plant height (0.2161**/0.2309**), number of panicles per plant (0.3565**/0.3956**), test weight (0.2301**/0.2382**), kernel length (0.1890**/0.2147**) at both genotypic and phenotypic levels where as with kernel breadth (0.1018/0.1116) and grain yield per

Table 4.4. Phenotypic and genotypic correlation coefficient of 121 lines (114 families and 7 parents) of rice (*Oryza sativa* L.) during *kharif*, 2015.

S.No.	Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of panicles per plant	Panicle length (cm)	Test weight (cm)	Kernel length (mm)	Kernel breadth (mm)	L/B ratio	Grain yield / plant(g)
1.	Days to 50% flowering	1.0000	0.9602**	0.2139**	0.3811**	-0.0641	0.2519**	0.2002**	0.0929	-0.0320	0.0794
2.	Days to maturity	0.9294**	1.0000	0.2309**	0.3956**	-0.0902	0.2382**	0.2147**	0.1116	-0.0443	0.0499
3.	Plant height (cm)	0.1920**	0.2161**	1.0000	0.4890**	0.4296**	-0.0045	0.1916**	0.0170	0.0841	0.0475
4.	Number of panicles per plant	0.3248**	0.3565**	0.4577**	1.0000	0.1642*	0.0769	0.2170**	-0.1380	0.2003**	-0.0286
5.	Panicle length (cm)	-0.0293	-0.0708	0.3670**	0.1449*	1.0000	-0.3254**	-0.0117	-0.3990**	0.3281**	0.3543**
6.	Test weight (g)	0.2425**	0.2301**	0.0031	0.0657	-0.2633**	1.0000	0.2383**	0.5120**	-0.2653**	-0.1138
7.	Kernel length (mm)	0.1655**	0.1890**	0.1743**	0.1822**	0.0085	0.2252**	1.0000	-0.0414	0.5847**	-0.0176
8.	Kernel breadth (mm)	0.0891	0.1018	0.0069	-0.0871	-0.2794**	0.4000**	-0.0360	1.0000	-0.8287**	-0.0204
9.	L/B ratio	-0.0355	-0.0486	0.0824	0.1631*	0.2648**	-0.2066**	0.5326**	-0.8083**	1.0000	0.0297
10.	Grain yield per plant (g)	0.0830	0.0380	0.0523	-0.0193	0.3157**	-0.1071	-0.0152	-0.0280	0.0234	1.0000

Below diagonals: Phenotypic correlation coefficient.
Above diagonals: Genotypic correlation coefficient.

*Significant at 5% level
**Significant at 1% level

plant, it showed positive non significant association at both levels. At phenotypic and genotypic level, panicle length (-0.0708/-0.0902) and L/B ratio (-0.0486/-0.0443) showed negative non significant association with days to maturity. These results are in conformity with the findings of Hasan *et al.* (2011), Nagaraju *et al.* (2013), Patel *et al.* (2014), Rai *et al.* (2014) and Venkata Lakshmi *et al.* (2014).

Non significant association of days to maturity with grain yield indicates that this trait has little influence in improving the yield.

4.3.3. Plant height (cm)

This trait showed positive significant association with number of panicles per plant (0.4577**/0.4890**), panicle length (0.3670**/0.4296**) and kernel length (0.1743**/0.1916**) at both genotypic and phenotypic levels. Positive non significant association was observed for test weight (0.0031) at phenotypic level and for kernel breadth (0.0069/0.0170), L/B ratio (0.0824/0.0841) and grain yield (0.0523/0.0475) at both genotypic and phenotypic levels. These results were in similarity with Pankajgarg *et al.* (2010), Rani and Reddy (2010), Ekka *et al.* (2011), Hasan *et al.* (2011), Sadeghi *et al.* (2011), Sravan *et al.* (2012), Rangare *et al.* (2012), Iswardatt *et al.* (2012), Ravindrababu *et al.* (2012), Manikyaminnie *et al.* (2013), Sanghera *et al.* (2013), Patel *et al.* (2014) and Venkata Lakshmi *et al.* (2014).

This shows that increase in plant height will leads to increase in number of panicles per plant, panicle length and kernel length while in our present investigation plant height has little influence on improving grain yield per plant.

4.3.4. Number of panicles per plant

This trait showed positive significant correlation with panicle length (0.1449*/0.1642*), kernel length (0.1822**/0.2170**) and L/B ratio (0.1631*/0.2003**) at both genotypic and phenotypic levels while it showed positive non significant association with test weight (0.0657/0.0769) at both the levels. Kernel breadth (-0.1380*) showed negative significant association at genotypic level where as grain yield per plant (-0.0193/-0.0286) showed negative non significant correlation with number of panicles per plant at both genotypic and phenotypic levels. Similar findings were reported by Khare *et al.* (2014) for grain yield per plant, Akinwale *et al.* (2011), Sravan *et al.* (2012), Aditya and Bhartiya (2013), Sanghera *et al.* (2013) and Ogunbayo *et al.* (2014).

These results indicate that increase in number of panicles per plant will result in increase of panicle length, kernel length and L/B ratio while kernel breadth will be reduced.

4.3.5. Panicle length (cm)

Panicle length showed significant positive association with grain yield per plant ($0.3157^{**}/0.3543^{**}$) and L/B ratio ($0.2648^{**}/0.3281^{**}$) while with test weight ($-0.2633^{**}/-0.3254^{**}$) and kernel breadth ($-0.2794^{**}/-0.3990^{**}$) it showed significant negative association at both the levels. Kernel length (0.0085) recorded positive non significant association with panicle length at phenotypic level only. These results are in conformity with Yadav *et al.* (2010), Akhtar *et al.* (2011), Ekka *et al.* (2011), Laxuman *et al.* (2011), Yadav *et al.* (2011), Rangare *et al.* (2012), Sanghera and Kashyap (2012), Seyoum *et al.* (2012), Sravan *et al.* (2012), Shet *et al.* (2012). Ashim and Ghosh (2013), Nagaraju *et al.* (2013), Sanghera *et al.* (2013), Sudharani *et al.* (2013), Jambhulkar and Bose (2014), Khare *et al.* (2014), Ogunbayo *et al.* (2014) and Patel *et al.* (2014).

These results showed that increase in panicle length will increase grain yield and L/B ratio. Hence selection of plants with higher panicle length will improve yield.

4.3.6. Test weight (g)

This trait recorded positive significant correlation with kernel length ($0.2252^{**}/0.2383^{**}$) and kernel breadth ($0.4^{**}/0.5120^{**}$) where as with L/B ratio it recorded significant negative correlation ($-0.2066^{**}/-0.2653^{**}$) at both genotypic and phenotypic levels. Negative non significant association was recorded with grain yield per plant ($-0.1071/-0.1138$) at both the levels. These results are in conformity with Ekka *et al.* (2011), Iswardatt *et al.* (2012), Ravindrababu *et al.* (2012), Seyoum *et al.* (2012), Bekele *et al.* (2013), Patel *et al.* (2014) and Venkata Lakshmi *et al.* (2014).

Results showed that increase in test weight will increase kernel length and kernel breadth while L/B ratio will be reduced where as its influence on grain yield is not significant.

4.3.7. Kernel length (mm)

This trait showed positive significant association with L/B ratio ($0.5326^{**}/0.5847^{**}$) while negative non significant association with kernel breadth ($-0.0360/-0.0414$) and grain yield per plant ($-0.0152/-0.0176$) at both the levels. Similar findings were reported by Iswardatt *et al.* (2012), Bekele *et al.* (2013), Sanghera *et al.* (2013), Patel *et al.* (2014) and Venkata Lakshmi *et al.* (2014).

These results indicates that increase in kernel length will increase L/B ratio while it recorded non significant association with grain yield.

4.3.8. Kernel breadth (mm)

This trait showed significant negative correlation with kernel L/B ratio (-0.8083**/-0.8287**) and negative non significant association with grain yield per plant (-0.0204/-0.0280) at both the levels. The results are similar with the reports of Aditya and Bhartiya (2013) and Venkata Lakshmi *et al.* (2014).

This shows that increase in kernel breadth results in reduction of kernel length and L/B ratio but it has no significant impact on grain yield.

4.3.9. L/B ratio

L/B ratio recorded positive non significant association with grain yield per plant (0.0234/0.0297) and the results are in support with the findings of Parvthi *et al.* (2011), Patel *et al.* (2014) and Venkata Lakshmi *et al.* (2014). This shows that L/B ratio has no direct role in improving grain yield per plant.

4.4. PATH COEFFICIENT ANALYSIS

The information on the extent of association between the yield and its component factors is important to bring the simultaneous improvement in correlated traits. Increase in number of variables necessitates measurement of contribution of each variable towards the observed correlation. Therefore, partitioning the observed correlation coefficients into unidirectional pathways (direct effects) and alternate pathways (indirect effects) facilitates the characterization of more complex traits devised by Wright (1921) and utilized by Dewey and Lu (1959) in selection programmes. In light of the above inferences, path coefficient analysis splits the correlation coefficients and provides precise information on the direct and indirect effects in order to perceive the most influencing characters to be utilized as selection criteria in rice breeding programme.

As per the guidelines for the interpretation of path analysis results, the following broad points are kept in view (Singh and Chaudhary, 1977).

- If the correlation coefficient between a causal factor and the effect is almost equal to its direct effect, then correlation explains the true relationship and a direct selection through this trait will be effective.
- If the correlation coefficient is positive, but the direct effect is negative or negligible, the indirect effects seem to be the cause of positive correlation. In such situations, the indirect causal factors are to be considered simultaneously for selection.
- Correlation coefficient may be negative but the direct effect is positive and high. Under these circumstances, a restricted simultaneous selection model is to be followed *i.e.*, restrictions are to be imposed to nullify the undesirable indirect effects in order to make use of the direct effect.
- If both correlation coefficient is negative and direct effects are also negative, then we have to drop the selection based on that character.

The residual effect determines how best the causal factors account for the variability of the dependent factor. If the residual effect is high, some other factors which had not been considered in the study, need to be included in the analysis to account fully for the variation in yield.

Hence, in the present study, direct and indirect effects of different yield component traits on grain yield per plant were estimated through path analysis at phenotypic and genotypic levels and are presented in Table 4.5. The genotypic and phenotypic path diagrams are given in Fig. 4.1 and 4.2 respectively.

4.4.1. Days to 50% flowering

The direct contribution of this character on yield was positive (0.2658/0.2303) at phenotypic and genotypic levels while it showed positive non significant correlation (0.0830/0.0794) with the grain yield per plant at both the levels.

The trait, days to 50% flowering, manifested positive indirect effects *via* days to maturity (0.4715) and number of panicles per plant (0.0130) at genotypic level only while for kernel breadth (0.0126/0.5519) at both genotypic and phenotypic levels. Negative indirect effects at both the levels were recorded *via* plant height (-0.0138/-0.0540), panicle length (-0.0103/-0.0256), test weight (-0.0204/-0.1037), kernel length

Table 4.5. Path coefficients of yield and yield components of rice (*Oryza sativa* L.) during *kharif*, 2015

S.No.	Characters		Days to 50% flowering	Days to maturity	Plant height (cm)	Number of panicles per plant	Panicle length (cm)	Test weight (g)	Kernel length (mm)	Kernel breadth (mm)	L/B ratio
1.	Days to 50% flowering	P	0.2658	0.2471	0.0510	0.0864	-0.0078	0.0645	0.0440	0.0237	-0.0094
		G	0.2303	0.2211	0.0493	0.0878	-0.0148	0.0580	0.0461	0.0214	-0.0074
2.	Days to maturity	P	-0.1252	-0.1347	-0.0291	-0.0480	0.0095	-0.0310	-0.0255	-0.0137	0.0065
		G	0.4715	0.4910	0.1134	0.1942	-0.0443	0.1169	0.1054	0.0548	-0.0217
3.	Plant height (cm)	P	-0.0138	-0.0155	0.0719	-0.0329	-0.0264	-0.0002	-0.0125	-0.0005	-0.0059
		G	-0.0540	-0.0583	-0.2523	-0.1234	-0.1084	0.0011	-0.0483	-0.0043	-0.0212
4.	Number of panicles per plant	P	-0.0207	-0.0227	-0.0291	-0.0637	-0.0092	-0.0042	-0.0116	0.0055	-0.0104
		G	0.0130	0.0135	0.0167	0.0342	0.0056	0.0026	0.0074	-0.0047	0.0069
5.	Panicle length (cm)	P	-0.0103	-0.0249	0.1293	0.0511	0.3523	-0.0927	0.0030	-0.0984	0.0933
		G	-0.0256	-0.0360	0.1716	0.0656	0.3994	-0.1300	-0.0047	-0.1593	0.1310
6.	Test weight (g)	P	-0.0204	-0.0194	-0.0003	-0.0055	0.0222	-0.0843	-0.0190	-0.0337	0.0174
		G	-0.1037	-0.0981	0.0018	-0.0317	0.1340	-0.4117	-0.0981	-0.2108	0.1092
7.	Kernel length (mm)	P	-0.0030	-0.0034	-0.0032	-0.0033	-0.0002	-0.0041	-0.0181	0.0007	-0.0097
		G	-0.7790	-0.8353	-0.7455	-0.8441	0.0457	-0.9271	-3.8904	0.1611	-2.2749
8.	Kernel breadth (mm)	P	0.0126	0.0144	0.0010	-0.0123	-0.0394	0.0564	-0.0051	0.1410	-0.1140
		G	0.5519	0.6631	0.1011	-0.8197	-2.3699	3.0410	-0.2460	5.9399	4.9225
9.	L/B ratio	P	-0.0020	-0.0027	0.0046	0.0091	0.0147	-0.0115	0.0296	-0.0450	0.0556
		G	-0.2250	-0.3114	0.5914	1.4085	2.3069	-1.8648	4.1110	-5.8261	7.0303
10.	Grain yield per plant (g)	P	0.0830	0.0380	0.0523	-0.0193	0.3157	-0.1071	-0.0152	-0.0204	0.0234
		G	0.0794	0.0499	0.0475	-0.0286	0.3543	-0.1138	-0.0176	-0.0280	0.0297

Bold are direct effects.

P: Phenotypic path coefficient

G: Genotypic path coefficient

Residual effect(P): R= 0.9309

(G): R= 0.8191

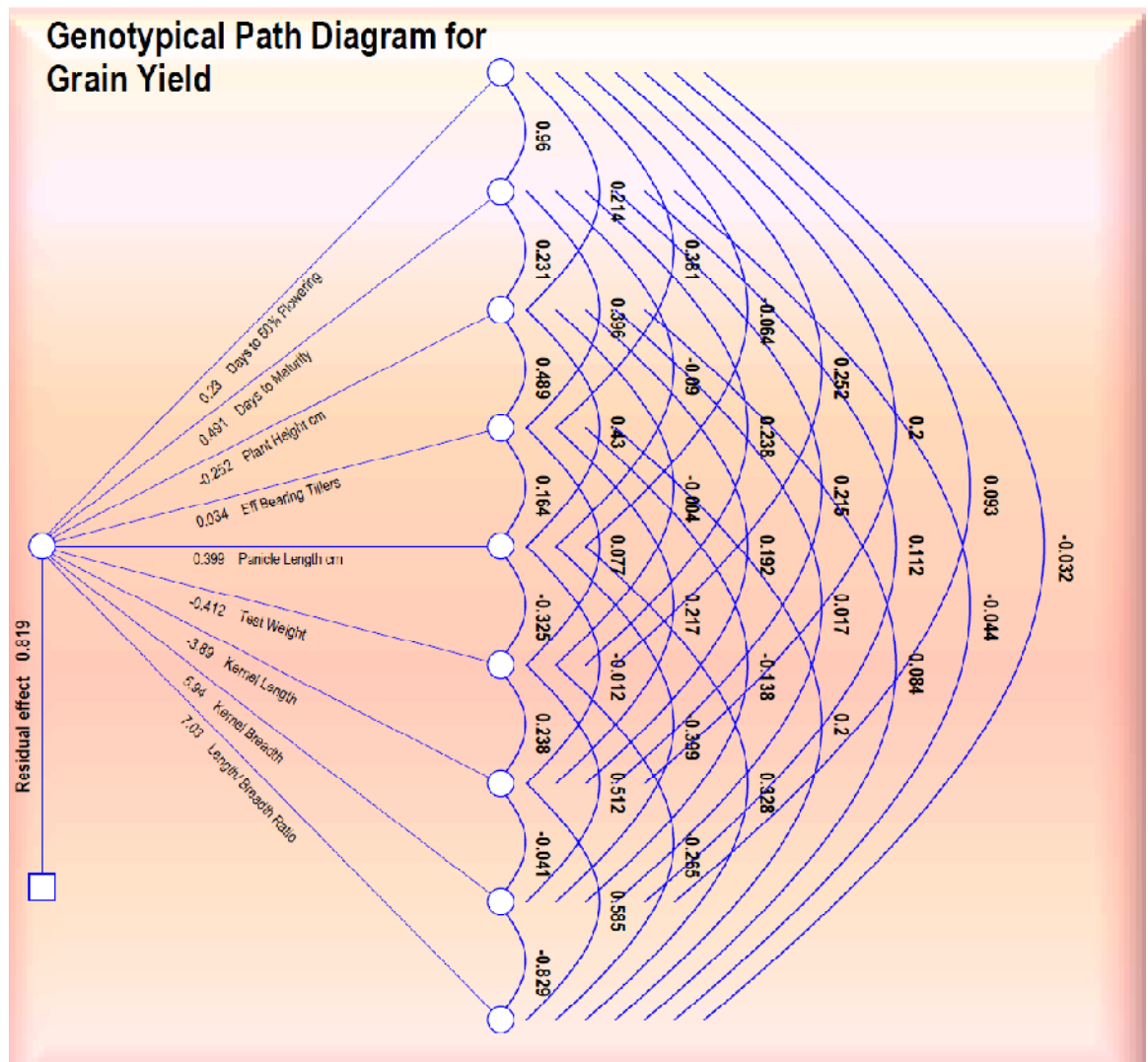


Fig. 4.1. Genotypical path diagram for grain yield per plant

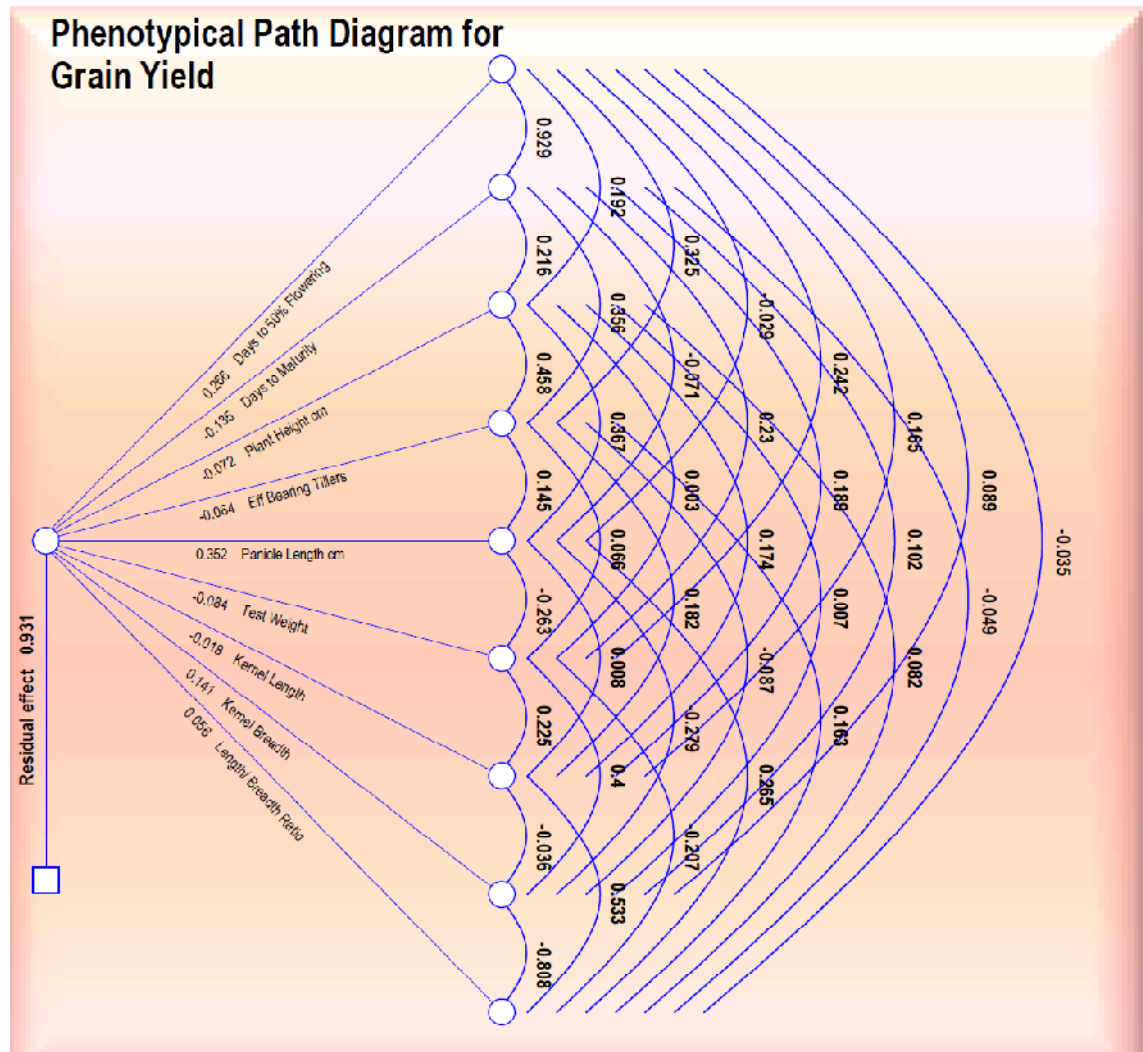


Fig. 4.2. Phenotypical path diagram for grain yield per plant

(-0.0030/-0.7790) and L/B ratio (-0.0020/-0.2250). These results suggest that indirect casual factors are to be considered for improvement of yield. Similar findings were reported by Hasan *et al.* (2011), Rangare *et al.* (2012), Sanghera *et al.* (2013), Aditya and Bhartiya (2013) and Jambhulkar and Bose (2014).

4.4.2. Days to maturity

The direct contribution of this character on yield was positive (0.4910) at genotypic level only while it showed positive non significant correlation (0.0380/0.0499) with the grain yield per plant at both the levels.

Days to maturity manifested positive indirect effects *via* days to 50% flowering (0.2471/0.2211) and kernel breadth (0.0144/0.6631) at both the levels and *via* number of panicles per plant (0.0135) at genotypic level only. While it recorded negative indirect effect *via* plant height (-0.0155/-0.0583), panicle length (-0.0249/-0.0360), test weight (-0.0194/-0.0981), kernel length (-0.0034/-0.8353) and L/B ratio (-0.0027/-0.3114) at both genotypic and phenotypic levels. These results suggest that indirect casual factors are to be considered for improvement of yield. These results are in agreement with the findings of Hasan *et al.* (2011), Sanghera *et al.* (2013), Khare *et al.* (2014), Patel *et al.* (2014) and Rai *et al.* (2014).

4.4.3. Plant height (cm)

The direct contribution of this character on yield was positive (0.4910) at phenotypic level only while it showed positive non significant correlation (0.0523/0.0475) with the grain yield per plant at both the levels.

Plant height recorded positive indirect effects *via* days to 50% flowering (0.0510/0.0493), panicle length (0.1293/0.1716), kernel breadth (0.0010/0.1011) and L/B ratio (0.0046/0.5914) at both the levels and *via* number of panicles per plant (0.0167), days to maturity (0.1134) and test weight (0.0018) at genotypic level only. These results suggest that indirect casual factors are to be considered for improvement of yield. These results are similar with the findings of Pankajgarg *et al.* (2010), Sravan *et al.* (2012), Aditya and Bhartiya (2013), Bekele *et al.* (2013), Nagaraju *et al.* (2013), Sanghera *et al.* (2013), Khare *et al.* (2014) and Patel *et al.* (2014).

4.4.4. Number of panicles per plant

The direct contribution of this character on yield was positive (0.0342) at phenotypic level only while it showed negative non significant correlation (-0.0193/-0.0286) with the grain yield per plant at both the levels. Here, correlation coefficient is negative and non significant while direct effect was positive. Hence, a restricted simultaneous selection model is to be followed *i.e.*, restrictions are to be imposed to nullify the undesirable indirect effects in order to make use of the direct effect.

Number of panicles per plant recorded positive indirect effects *via* days to 50% flowering (0.0864/0.0878), panicle length (0.0511/0.0656) and L/B ratio (0.0091/1.4085) at both the levels and *via* days to maturity (0.1942) at genotypic level only. While it recorded negative indirect effect *via* plant height (-0.0329/-0.1234), test weight (-0.0055/-0.0317), kernel length (-0.0033/-0.8441) and kernel breadth (-0.0123/-0.8917) at both the levels. Similar findings were reported by Hasan *et al.* (2011), Aditya and Bhartiya (2013) and Khare *et al.* (2014).

4.4.5. Panicle length (cm)

The direct contribution of this character on yield was positive (0.3523/0.3994) at phenotypic and genotypic levels while it showed significant positive correlation (0.3157**/0.3543**) with the grain yield per plant at both the levels. Here as the correlation coefficient between a causal factor and the effect is almost equal to its direct effect, correlation explains the true relationship and a direct selection through this trait will be effective.

Panicle length manifested positive indirect effects *via* days to maturity (0.0095) at phenotypic level and number of panicles per plant (0.0056) at genotypic level only while for test weight (0.0222/0.1340) and L/B ratio (0.0147/2.3069) at both genotypic and phenotypic levels. Negative indirect effects at both the levels were recorded *via* days to 50% flowering (-0.0078/-0.0148), plant height (-0.0264/-0.1084) and kernel breadth (-0.0394/-2.3699). These results are in agreement with the findings of Ekka *et al.* (2011), Rangare *et al.* (2012), Ravindrababu *et al.* (2012), Seyoum *et al.* (2012), Sravan *et al.* (2012), Nagaraju *et al.* (2013), Sanghera *et al.* (2013), Jambhulkar and Bose (2014), Khare *et al.* (2014) and Patel *et al.* (2014).

4.4.6. Test weight (g)

The direct contribution of this character on yield was negative (-0.0843/-0.4117) at phenotypic and genotypic levels while it showed negative non significant correlation (-1.8648/-0.1071) with the grain yield per plant at both the levels. As both correlation coefficient and direct effect was negative at both the levels, selection should be dropped based on this character.

Test weight manifested positive indirect effects *via* days to maturity (0.1169), plant height (0.0011) and number of panicles per plant (0.0026) at genotypic level only while for days to 50% flowering (0.0645/0.0580) and kernel breadth (0.0564/3.0410) at both genotypic and phenotypic levels. Negative indirect effects at both the levels were recorded *via* panicle length (-0.0927/-0.1300), kernel length (-0.0041/-0.9271) and L/B ratio (-0.0115/-1.8648). Similar results were reported in the findings of Ravindrababu *et al.* (2012), Khare *et al.* (2014) and Patel *et al.* (2014).

4.4.7. Kernel length (mm)

The direct contribution of this character on yield was negative (-0.0181/-3.8904) at phenotypic and genotypic levels while it showed negative non significant correlation (-0.0152/-0.0176) with the grain yield per plant at both the levels. As both correlation coefficient and direct effect was negative at both the levels, selection should be dropped based on this character.

The trait kernel length manifested positive indirect effects *via* panicle length (0.0030) at phenotypic level where as days to maturity (0.1054) and number of panicles per plant (0.0074) at genotypic level only while for days to 50% flowering (0.0440/0.0461) and L/B ratio (0.0296/4.1110) at both genotypic and phenotypic levels. Negative indirect effects at both the levels were recorded *via* plant height (-0.0125/-0.0483), test weight (-0.0190/-0.0981) and kernel breadth (-0.0051/-0.2460). These results are in agreement with the findings of Sanghera *et al.* (2013) and Patel *et al.* (2014).

4.4.8. Kernel breadth (mm)

The direct contribution of this character on yield was positive (0.1410/5.9399) at phenotypic and genotypic levels while it showed negative non significant correlation (-0.0204/-0.0280) with the grain yield per plant at both the levels. Here as the

correlation coefficient was negative but the direct effect was positive and high, a restricted simultaneous selection model is to be followed *i.e.*, restrictions are to be imposed to nullify the undesirable indirect effects in order to make use of the direct effect.

Kernel breadth manifested positive indirect effects *via* number of panicles per plant (0.0055) at phenotypic level where as days to maturity (0.0548) at genotypic level only while for days to 50% flowering (0.0237/0.0214) and kernel length (0.0007/0.1611) at both genotypic and phenotypic levels. Negative indirect effects at both the levels were recorded *via* plant height (-0.0005/-0.0043), panicle length (-0.0984/-0.1593), test weight (-0.0337/-0.2108) and L/B ratio (-0.0450/-5.8261). Similar findings were reported by Sanghera *et al.* (2013).

4.4.9. L/B ratio

The direct contribution of this character on yield was positive (0.0556/7.0303) at phenotypic and genotypic levels while it showed positive non significant correlation (0.0234/0.0297) with the grain yield per plant at both the levels. These results suggested that indirect casual factors are to be considered for improvement of yield.

The trait L/B ratio manifested positive indirect effects *via* days to maturity (0.0030) at phenotypic level where as with number of panicles per plant (0.0069) and kernel breadth (4.9225) at genotypic level only while for panicle length (0.0933/0.1310) and test weight (0.0174/0.1092) at both genotypic and phenotypic levels. Negative indirect effects at both the levels were recorded *via* days to 50% flowering (-0.0094/-0.0074), plant height (-0.0059/-0.0212) and kernel length (-0.0097/-2.2749). These results are in agreement with the findings of Nagaraju *et al.* (2013), Sanghera *et al.* (2013) and Patel *et al.* (2014).

4.4.10. Residual effect

Residual effect was high (81.9%) indicating that some other factors which were not been considered in the study, need to be included in the analysis to explain total variation in yield.

4.5. SCREENING FOR SHEATH BLIGHT RESISTANCE

One hundred and fourteen F₅ families along with susceptible check MTU 7029 were screened under field conditions against sheath blight by adopting typha leaf bit method of artificial inoculation by following 0-9 scale of Standard Evaluation System (SES) of IRRI, 2014. Entries were scored when susceptible check recorded 9 score under SES and the details were given in Table 4.6. Damage scores were recorded twice (125 DAS and 149 DAS respectively) and highest among the two scores were taken as final score.

Out of one hundred and fourteen F₅ families, no family was found to be immune (score 1) or resistant (score 3). Forty four families in different crosses were found to be moderately resistant with a score 5, sixty three families were susceptible (score 7) while seven families recorded a score of 9 which are highly susceptible to sheath blight. These results are in agreement with Ling *et al.* (2011), Shamim *et al.* (2014) and Yadav *et al.* (2015).

Among the forty five F₅ families screened from the cross MTU 7029/ MTU 1081, seventeen families recorded moderate resistance to sheath blight while twenty four families showed susceptibility in addition to four families which were highly susceptible. In the five F₅ families derived from the cross MTU 7029/JGL 11118, two recorded moderate resistance while three were susceptible. Out of eighteen F₅ families of the cross MTU 7029/ NLR 34449, fourteen families showed susceptibility while two families were highly susceptible and two families were moderately resistant.

Among three F₅ families studied from the cross MTU 7029/ MTU 1121, two families recorded moderate resistance to sheath blight and one family is highly susceptible. In the F₅ population obtained from the cross MTU 7029/ PAU 3116-25-5-1, among the fifteen F₅ families, six recorded moderate resistance while nine were susceptible. Out of twenty eight F₅ families obtained from the cross MTU 7029/ PAU 3140-126-1, fifteen families recorded moderate resistance while thirteen families showed susceptibility (Table 4.7).

Table 4.6. Screening of F₅ families for sheath blight resistance

S.No.	Lines	Score	Total no. of families studied
1	TSM-5, TSM-8, TSM-12, TSM-16, TSM-19, TSM-20, TSM-22, TSM-29, TSM-32, TSM-35, TSM-37, TSM-50, TSM-54, TSM-58, TSM-61, TSM-68, TSM-74, TSM-79, TSM-82, TSM-87, TSM-92, TSM-114, TSM-115, TSM-118, TSM-133, TSM-141, TSM-148, TSM-149, TSM-152, TSM-164, TSM-167, TSM-168, TSM-169, TSM-171, TSM-175, TSM-183, TSM-184, TSM-190, TSM-200, TSM-204, TSM-213, TSM-221, TSM-228, TSM-229	5	44
2	TSM-1, TSM-3, TSM-4, TSM-6, TSM-7, TSM-9, TSM-10, TSM-17, TSM-18, TSM-33, TSM-36, TSM-39, TSM-42, TSM-43, TSM-48, TSM-56, TSM-57, TSM-63, TSM-64, TSM-66, TSM-67, TSM-69, TSM-72, TSM-73, TSM-76, TSM-77, TSM-83, TSM-85, TSM-86, TSM-88, TSM-90, TSM-94, TSM-95, TSM-96, TSM-97, TSM-99, TSM-102, TSM-103, TSM-104, TSM-108, TSM-110, TSM-120, TSM-128, TSM-132, TSM-134, TSM-138, TSM-146, TSM-147, TSM-150, TSM-153, TSM-165, TSM-166, TSM-174, TSM-178, TSM-191, TSM-211, TSM-215, TSM-216, TSM-219, TSM-220, TSM-223, TSM-230, TSM-235	7	63
3	TSM-2, TSM-51, TSM-62, TSM-65, TSM-93, TSM-101, TSM-116,	9	7

Table 4.7. Summary of sheath blight screening scores

S.No.	Cross	Number of families screened	Number of families with score		
			5	7	9
1	MTU 7029/ MTU 1081	45	17	24	4
2	MTU 7029/ JGL 11118	5	2	3	-
3	MTU 7029/ NLR 34449	18	2	14	2
4	MTU 7029/ MTU 1121	3	2	-	1
5	MTU 7029/ PAU 3116-25-5-1	15	6	9	-
6	MTU 7029/ PAU 3140-126-1	28	15	13	-
	Total	114	44	63	7

In addition to this, families MTU 2462-1-5-2 (25.9 g), MTU 2462-1-9-1 (41.6 g), MTU 2462-15-1-1 (28.6 g), MTU 2462-15-3-1 (30.3 g), MTU 2462-17-2-1 (27.6 g), MTU 2462-26-3-1 (25.4 g), MTU 2463-8-2-1 (15.4 g), MTU 2465-6-2-1 (18.2 g), MTU 2465-11-3-1 (19.4 g), MTU 2466-4-2-2 (15.8 g), MTU 2468-25-2-1 (18.6 g), MTU 2469-6-3-2 (19.8 g), MTU 2469-6-5-1 (18.6 g), MTU 2469-8-1-1 (20.8 g) and MTU 2469-36-1-1 (19.5 g) shown moderate resistance to sheath blight with moderate to high yield and hence can be selected.

4.6. Screening for bacterial leaf blight resistance

Leaf clipping method was followed for artificial inoculation of F₅ lines along with susceptible check, TN-1. The lines were scored based on 0-9 scale of Standard Evaluation System (SES) given by IRRI, 2014. The lines were scored at 120 DAS and were given below in Table 4.8.

Out of one hundred and fourteen F₅ families, none was found immune (score 1) or resistant (score 3). Thirteen families belonging to different crosses were found to be moderately resistant with a score 5, nineteen families were susceptible showing 7 score, two families were highly susceptible with score of 9. Similar results were observed in the findings of Ahmed Khan *et al.* (2009) and Thimmegowda *et al.* (2011).

Among the forty five F₅ families obtained from the cross MTU 7029/ MTU 1081, five families recorded moderate resistance to bacterial leaf blight while thirty nine families showed susceptibility. All the five F₅ families obtained from the cross MTU 7029/MTU 1121 showed susceptibility to bacterial leaf blight. Out of eighteen F₅ families obtained from the cross MTU 7029/ NLR 34449, seventeen families showed susceptibility while one family recorded moderate resistance.

Table 4.8. Screening of F₅ families for bacterial leaf blight resistance

S.No.	Lines	Score	Total no. of families studied
1	TSM-7, TSM-33, TSM-64, TSM-66, TSM-73, TSM-87, TSM-120, TSM-141, TSM-164, TSM-166, TSM-168, TSM-174	5	12
2	TSM-1, TSM-2, TSM-3, TSM-4, TSM-5, TSM-6, TSM-8, TSM-9, TSM-10, TSM-12, TSM-16, TSM-17, TSM-18, TSM-19, TSM-20, TSM-22, TSM-29, TSM-32, TSM-35, TSM-36, TSM-37, TSM-39, TSM-43, TSM-48, TSM-50, TSM-51, TSM-54, TSM-56, TSM-57, TSM-58, TSM-61, TSM-62, TSM-63, TSM-65, TSM-67, TSM-68, TSM-69, TSM-72, TSM-74, TSM-76, TSM-77, TSM-79, TSM-82, TSM-83, TSM-85, TSM-86, TSM-88, TSM-90, TSM-92, TSM-93, TSM-94, TSM-95, TSM-96, TSM-97, TSM-99, TSM-101, TSM-102, TSM-103, TSM-104, TSM-108, TSM-110, TSM-114, TSM-115, TSM-116, TSM-118, TSM-128, TSM-132, TSM-133, TSM-134, TSM-138, TSM-146, TSM-147, TSM-148, TSM-149, TSM-150, TSM-152, TSM-153, TSM-165, TSM-167, TSM-169, TSM-171, TSM-175, TSM-178, TSM-190, TSM-191, TSM-200, TSM-204, TSM-211, TSM-213, TSM-215, TSM-216, TSM-219, TSM-220, TSM-221, TSM-223, TSM-228, TSM-229, TSM-230, TSM-235	7	99
3	TSM-183, TSM-184	9	2
4	TSM-42	NG	1

All the 3 F₅ families obtained from the cross MTU 7029/MTU 1121 showed susceptibility to bacterial leaf blight. Among the fifteen F₅ families obtained from the cross MTU 7029/ PAU 3116-25-5-1, two families recorded moderate resistance while thirteen are susceptible. Out of twenty eight F₅ families obtained from the cross MTU 7029/ PAU 3140-126-1, four families recorded moderate resistance while twenty two families showed susceptibility in addition to two highly susceptible families (Table 4.9).

Table 4.9. Summary of bacterial leaf blight screening scores.

S.No.	Cross	Number of families screened	Number of families with score		
			5	7	9
1	MTU 7029/ MTU 1081	45	5	39	-
2	MTU 7029/ JGL 11118	5	-	5	-
3	MTU 7029/ NLR 34449	18	1	17	-
4	MTU 7029/ MTU 1121	3	-	3	-
5	MTU 7029/ PAU 3116-25-5-1	15	2	13	-
6	MTU 7029/ PAU 3140-126-1	28	4	22	2
	Total	114	12	99	2

In addition to this, families MTU 2462-1-8-2 (25.7 g), MTU 2462-35-2-2 (20.3 g), MTU 2462-37-2-1 (19.2 g), MTU 2462-45-2-1 (20.3 g), MTU 2465-6-2-1 (18.2 g), MTU 2468-2-1-1 (18.4 g), MTU 2468-25-2-1 (18.6 g), MTU 2469-6-5-1 (18.6 g) and MTU 2469-10-2-1 (19.7 g) showed moderate resistance to bacterial leaf blight with moderate to high yield and hence can be selected.

In summary, families MTU 2462-1-9-2 (43.75 g), MTU 2462-1-1-1 (32.6 g), MTU 2462-22-3-1 (30.7 g), MTU 2462-2-1-1 (27.1 g), MTU 2463-4-1-2 (16.6 g), MTU 2463-4-2-1 (15.5 g), MTU 2463-14-1-1 (14 g), MTU 2463-15-1-1 (14.6 g), MTU 2465-12-2-2 (27.3 g) and MTU 2468-28-1-1 (28.7 g) recorded higher grain yield than their parents but showed susceptibility to both the diseases and can be selected when grain yield is taken as major criterion where as families MTU 2462-1-9-1 (41.6 g), MTU 2462-15-3-1 (30.3 g), MTU 2462-15-1-1 (28.6 g), MTU 2462-17-2-1 (27.6 g), MTU 2462-1-5-2 (25.9 g) and MTU 2463-8-2-1 (15.4 g) recorded higher yield than their parents along with moderate resistance to sheath blight and hence highly preferred. MTU 2465-6-2-1 (18.2 g), MTU 2468-25-2-1 (18.6 g) and MTU 2469-6-5-1 (18.6 g) showed moderate resistance to both the diseases along with moderate to high yield and hence can be selected (Table 4.10).

Table 4.10. Grain yield of selected genotypes under each cross

S.No.	Cross	Family	Grain yield per plant (g)	Score	
				Sheath blight	Bacterial leaf blight
1	MTU 7029/MTU 1081	MTU 2462-1-9-2	43.8	7	7
2	MTU 7029/MTU 1081	MTU 2462-1-9-1	41.6	5	7
3	MTU 7029/MTU 1081	MTU 2462-1-1-1	32.6	7	7
4	MTU 7029/MTU 1081	MTU 2462-22-3-1	30.7	7	7
5	MTU 7029/MTU 1081	MTU 2462-15-3-1	30.3	5	7
6	MTU 7029/MTU 1081	MTU 2462-15-1-1	28.6	5	7
7	MTU 7029/MTU 1081	MTU 2462-17-2-1	27.6	5	7
8	MTU 7029/MTU 1081	MTU 2462-2-1-1	27.1	7	7
9	MTU 7029/MTU 1081	MTU 2462-1-5-2	25.9	5	7
10	MTU 7029/MTU 1081	MTU 2462-1-8-2	25.7	7	5
11	MTU 7029/MTU 1081	MTU 2462-26-3-1	25.4	5	7
12	MTU 7029/PAU 3140-126-1	MTU 2469-8-1-1	20.8	5	7
13	MTU 7029/MTU 1081	MTU 2462-35-2-2	20.3	7	5
14	MTU 7029/MTU 1081	MTU 2462-45-2-1	20.3	7	5
15	MTU 7029/PAU 3140-126-1	MTU 2469-6-3-2	19.8	5	7
16	MTU 7029/PAU 3140-126-1	MTU 2469-10-2-1	19.7	7	5
17	MTU 7029/PAU 3140-126-1	MTU 2469-36-1-1	19.5	5	7
18	MTU 7029/NLR 34449	MTU 2465-11-3-1	19.4	5	7
19	MTU 7029/MTU 1081	MTU 2462-37-2-1	19.2	7	5
20	MTU 7029/PAU 3116-25-5-1	MTU 2468-25-2-1	18.6	5	5
21	MTU 7029/PAU 3140-126-1	MTU 2469-6-5-1	18.6	5	5
22	MTU 7029/PAU 3116-25-5-1	MTU 2468-2-1-1	18.4	7	5
23	MTU 7029/NLR 34449	MTU 2465-6-2-1	18.2	5	5
24	MTU 7029/JGL 11118	MTU 2463-4-1-2	16.6	7	7
25	MTU 7029/MTU 1121	MTU 2466-4-2-2	15.8	5	7
26	MTU 7029/JGL 11118	MTU 2463-4-2-1	15.5	7	7
27	MTU 7029/JGL 11118	MTU 2463-8-2-1	15.4	5	7
28	MTU 7029/JGL 11118	MTU 2463-15-1-1	14.6	7	7
29	MTU 7029/JGL 11118	MTU 2463-14-1-1	14	7	7

Chapter - V

SUMMARY AND CONCLUSIONS

The present investigation was carried out during *kharif*, 2015 at the APRRI & RARS, Maruteru, Andhra Pradesh with one hundred and fourteen F₅ families obtained from six crosses and their parents to study the mean, genetic variability, heritability, genetic advance as per cent of mean, character association, the magnitude of direct and indirect effects of yield component traits on grain yield, along with screening for two major devastating diseases, sheath blight and bacterial leaf blight of rice.

Observations were recorded on five randomly selected plants in each replication for ten quantitative characters viz., days to 50% flowering, days to maturity, plant height (cm), number of panicles per plant, panicle length (cm), grain yield per plant (g), test weight (g), kernel length (mm), kernel breadth (mm) and L/B ratio. Screening for the two diseases was also carried out using 0-9 scale of SES, IRRI (2014).

The analysis of variance revealed significant differences among the genotypes for all the characters indicating the presence of sufficient genetic variability in the studied material.

The genotypic coefficients of variation for all the characters studied were lesser than the phenotypic coefficients of variation but the difference is very less indicating that low environmental influence. High PCV and GCV was observed for grain yield per plant and test weight. High heritability coupled with high genetic advance as per cent of mean was observed for number of grains per panicle, grain yield per plant and test weight indicating the importance of additive gene action in governing the inheritance of these traits. Hence, direct phenotypic selection is useful with respect to these traits. The high estimates of heritability coupled with moderate genetic advance as per cent of mean was observed for plant height, panicle length, kernel length, kernel breadth and L/B ratio indicating the presence of both additive and non additive gene actions and hence, heterosis breeding for such traits will be effective. High heritability coupled with low genetic advance was observed for traits days to 50% flowering and days to maturity indicating the presence of non additive gene action and simple selection for these traits may not be effective.

The study on character association revealed that the character panicle length showed significant positive association with grain yield per plant indicating that direct selection can be practiced for this character. Other traits viz., days to 50% flowering, days to maturity, plant height and L/B ratio recorded positive non significant correlation with grain yield. Test weight, kernel length and kernel breadth reported negative non significant association with grain yield per plant indicating that they have little influence on yield.

The study of path coefficient analysis indicated that panicle length had positive direct effect coupled with positive significant correlation with grain yield per plant. Therefore, simultaneous improvement of grain yield is possible through selection of this trait. Days to 50% flowering and L/B ratio also recorded direct positive effects but have positive non significant correlation. Hence indirect factors are to be considered for improving the yield.

Screening for sheath blight revealed that out of one hundred and fourteen F₅ families, 44 families belonging to different crosses were found to be moderately resistant, 63 lines were susceptible while 7 lines recorded highly susceptible reaction while in case of bacterial leaf blight, 13 families were found to be moderately resistant 99 families were susceptible and two lines were highly susceptible.

MTU 2462-1-9-2 (43.75 g), MTU 2462-1-1-1 (32.6 g), MTU 2462-22-3-1 (30.7 g), MTU 2462-2-1-1 (27.1 g), MTU 2463-4-1-2 (16.6 g), MTU 2463-4-2-1 (15.5 g), MTU 2463-14-1-1 (14 g), MTU 2463-15-1-1 (14.6 g), MTU 2465-12-2-2 (27.3 g) and MTU 2468-28-1-1 (28.7 g) recorded higher grain yield than their parents but showed susceptibility to both the diseases and can be selected when grain yield is taken as major criterion for selection where as families MTU 2462-1-9-1 (41.6 g), MTU 2462-15-3-1 (30.3 g), MTU 2462-15-1-1 (28.6 g), MTU 2462-17-2-1 (27.6 g), MTU 2462-1-5-2 (25.9 g) and MTU 2463-8-2-1 (15.4 g) recorded higher yield than their parents along with moderate resistance to sheath blight and hence highly preferred.

In addition to them, MTU 2462-1-5-2 (25.9 g), MTU 2462-26-3-1 (25.4 g), MTU 2465-6-2-1 (18.2 g), MTU 2465-11-3-1 (19.4 g), MTU 2466-4-2-2 (15.8 g), MTU 2468-25-2-1 (18.6 g), MTU 2469-6-3-2 (19.8 g), MTU 2469-6-5-1 (18.6 g), MTU 2469-8-1-1 (20.8 g) and MTU 2469-36-1-1 (19.5 g) recorded moderate resistance (score 5) to sheath blight and families MTU 2462-1-8-2 (25.7 g), MTU 2462-35-2-2 (20.3 g), MTU 2462-37-2-1 (19.2 g), MTU 2462-45-2-1 (20.3 g), MTU 2465-6-2-1

(18.2 g), MTU 2468-2-1-1 (18.4 g), MTU 2468-25-2-1 (18.6 g), MTU 2469-6-5-1 (18.6 g) and MTU 2469-10-2-1 (19.7 g) showed moderate resistance to bacterial leaf blight along with moderate to high yield than their parents and hence can also be selected.

MTU 2465-6-2-1 (18.2 g), MTU 2468-25-2-1 (18.6 g) and MTU 2469-6-5-1 (18.6 g) showed moderate resistance to both the diseases and hence highly preferred.

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