

**GENETIC AND MOLECULAR ANALYSIS OF LEAF BLAST
RESISTANCE IN RICE (*Oryza sativa* L.)**

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**SHESHAIAH
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COLLEGE OF AGRICULTURE, SHIVAMOGGA
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C E R T I F I C A T E

This is to certify that the thesis entitled “**GENETIC AND MOLECULAR ANALYSIS OF LEAF BLAST RESISTANCE IN RICE (*Oryza sativa* L.)**” submitted in partial fulfillment of the requirements for the award of the degree of **DOCTOR OF PHILOSOPHY** in **GENETICS AND PLANT BREEDING** to the College of Agriculture, Shivamogga, University of Agricultural and Horticultural Sciences, Shivamogga is a bonafide record of research work carried out by **Mr. SHESHAIAH, ID. No. PA1TAD023** (shesha228@gmail.com) during the period of study in this university under my guidance and supervision and no part of this thesis has previously formed the basis for the award of any other degree, diploma, associateship, fellowship or any other similar titles.

Shivamogga
August, 2018



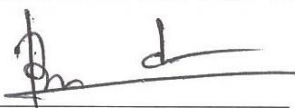

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(SHESHAIAH)

GENETIC AND MOLECULAR ANALYSIS OF LEAF BLAST RESISTANCE IN RICE (*Oryza sativa* L.)

(SHESHIAH)

ABSTRACT

Rice is one of the world's major staple food crop but its production is severely affected by blast. The present study evaluated 35 rice germplasm lines for leaf blast resistance at AHRS, Ponnampet during *Kharif 2014*. Germplasm lines, Tadukan and Tetep showed highly resistant reaction, KPR-1, KPR-2, Kiruwana and IR-64 recorded resistant reaction and whereas, CO-39, HR-12, Jaya, Intan, Ambemori, Bheemasaali, Chittiga and FR-13A showed high susceptibility to leaf blast. The analysis of variance showed significant differences among the germplasm lines and Kiruwana has recorded highest yield per plant under blast hot spot condition. Grain yield per plant recorded highest GCV and PCV and most of the traits recorded high heritability coupled with high GAM. Mahalanobis D^2 statistics grouped total germplasm into six clusters and maximum number of germplasm observed in cluster-I. Among studied characters leaf blast and grain length major contributing traits to the total divergence. Based on leaf blast screening, *per se* performance and diversity studies, Kiruwana was chosen as a donor parent to the most popular blast susceptible cultivar, Jyothi. The F_1 's developed and true F_1 identified at both phenotypic and molecular level. The F_2 population showed positively and negatively skewed platykurtic distribution for studied traits. High heritability coupled with high GAM observed for days to flowering, days to maturity, plant height, number of tillers and productive tillers per plant. The selfed F_2 's were advanced to F_3 and were scored for leaf blast reaction. Among 226 F_3 families, 178 showed resistant and 48 showed susceptible reactions and fit to the expected ratio of 3:1. The marker RM 1337 showed goodness of fit to the expected ratio of 1:2:1 and significantly associated with phenotypic evaluation. The present investigation revealed that germplasm used in the study are diverse and leaf blast resistance in Kiruwana is governed by single dominant gene and RM 1337 has associated with that gene [*Pi-20(t)*].

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ಭತ್ತದ ಎಲೆ ಬೆಂಕಿರೋಗ ನಿರೋಧಕತೆಗೆ ಅನುವಂಶಿಕ ಮತ್ತು ಅಣ್ವಿಕ ಅಧ್ಯಯನ

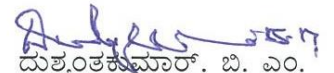
ಶೇಷಯ್ಯ

ಅಮೂರ್ತ್

ಭತ್ತವು ಪ್ರಪಂಚದ ಪ್ರಮುಖ ಸ್ಥಿರ ಆಹಾರ ಬೆಳೆಗಳಲ್ಲಿ ಒಂದಾಗಿದೆ ಆದರೆ ಬೆಂಕಿರೋಗವು ಭತ್ತದ ಉತ್ಪಾದನೆಯ ಮೇಲೆ ತೀವ್ರವಾಗಿ ಪರಿಣಾಮ ಬೀರುತ್ತದೆ. ಪ್ರಸ್ತುತ ಅಧ್ಯಯನವು ೩೫ ಪ್ರಜನನ ದ್ರವ್ಯ ಸಾಲುಗಳನ್ನು ಬೆಂಕಿರೋಗದ ಪ್ರತಿರೋಧಕ್ಕಾಗಿ ೨೦೧೪ರ ಮುಂಗಾರಿನಲ್ಲಿ ಕೃಷಿ ಮತ್ತು ತೋಟಗಾರಿಕೆ ಸಂಶೋಧನಾ ಕೇಂದ್ರ, ಪೊನ್ನಂಪೇಟೆಯಲ್ಲಿ ಮೌಲಿಕರೀಸಲಾಯಿತು. ಪ್ರಜನನ ದ್ರವ್ಯ ಸಾಲುಗಳಲ್ಲಿ ತದುಕನ್ ಮತ್ತು ಟೆಟಪ್ ಹೆಚ್ಚಿನ ನಿರೋಧಕ ಪ್ರತಿಕ್ರಿಯೆಯನ್ನು ತೋರಿಸಿದವು, ಕೆಪಿಆರ್-೧, ಕೆಪಿಆರ್-೨, ಕಿರುವಾಣ ಮತ್ತು ಐಆರ್-೬೪ ನಿರೋಧಕ ಪ್ರತಿಕ್ರಿಯೆಯನ್ನು ದಾಖಲಿಸಿದ್ದು ಆದರೆ, ಸಿಒ-೨೯, ಎಚ್‌ಆರ್-೧೨, ಇಂಟಾನ್, ಅಂಬೆಮೋರಿ, ಭೀಮಸಾಲಿ, ಚಿತ್ತಿಗಾ ಮತ್ತು ಎಫ್‌ಆರ್-೧೩ಎ ಎಲೆ ಬೆಂಕಿರೋಗಕ್ಕೆ ಹೆಚ್ಚು ಒಳಗಾಗುವ ಪ್ರತಿಕ್ರಿಯೆಯನ್ನು ತೋರಿಸಿದವು. ಅನೋವಾ ಪರೀಕ್ಷೆಯು ಪ್ರಜನನ ದ್ರವ್ಯ ಸಾಲುಗಳ ನಡುವೆ ಗಮನಾರ್ಹ ವ್ಯತ್ಯಾಸವನ್ನು ತೋರಿಸಿದೆ ಮತ್ತು ಪ್ರತಿ ಪ್ರದರ್ಶನದಲ್ಲಿ ಕಿರುವಾಣ ಅತಿಹೆಚ್ಚು ಪ್ರತಿ ಸಸ್ಯದ ದಾನ್ಯದ ಇಳುವರಿಯನ್ನು ದಾಖಲಿಸಿದೆ. ಅತ್ಯಧಿಕ ಜಿಸಿವಿ ಮತ್ತು ಪಿಸಿವಿ ಯನ್ನು ಪ್ರತಿ ಸಸ್ಯದ ಇಳುವರಿಯು ದಾಖಲಿಸಿದೆ ಮತ್ತು ಹೆಚ್ಚಿನ ಗುಣಲಕ್ಷಣಗಳು ಜೊತೆಗೂಡಿದ ಹೆಚ್ಚಿನ ಅನುವಂಶಿಕತೆ ಮತ್ತು ಹೆಚ್ಚಿನ ಅನುವಂಶೀಯ ಮುಂಚಿತತೆಯನ್ನು ದಾಖಲಿಸಿವೆ. ಮಹಾಲನೋಬಿಸ್ ಡಿ ಒಟ್ಟಾರೆ ಪ್ರಜನನ ದ್ರವ್ಯ ಸಾಲುಗಳನ್ನು ಆರು ಸಮೂಹಗಳಾಗಿ ವರ್ಗೀಕರಿಸಿದೆ ಮತ್ತು ಗರಿಷ್ಠ ಸಂಖ್ಯೆಯ ಪ್ರಜನನ ದ್ರವ್ಯ ಸಾಲುಗಳನ್ನು ಗುಂಪು-೧ರಲ್ಲಿ ಗಮನಿಸಲಾಗಿದೆ. ಅಧ್ಯಯನ ಮಾಡಿದ ಗುಣಲಕ್ಷಣಗಳಲ್ಲಿ, ಬೆಂಕಿರೋಗ ಮತ್ತು ಧಾನ್ಯದ ಉದ್ದ ಒಟ್ಟು ವೈವಿಧ್ಯತೆಗೆ ಪ್ರಮುಖವಾದ ಗುಣಲಕ್ಷಣಗಳಾಗಿವೆ. ಎಲೆ ಬೆಂಕಿರೋಗದ ನಿರೋಧಕತೆ, ಪ್ರತಿ ಪ್ರದರ್ಶನ ಮತ್ತು ವೈವಿಧ್ಯತೆಯ ಆಧಾರದ ಮೇಲೆ ಕಿರುವಾಣವನ್ನು ಹೆಚ್ಚು ಜನಪ್ರಿಯಗೊಂಡಿರುವ ಬೆಂಕಿರೋಗಕ್ಕೆ ಒಳಗಾಗುವ ತಳಿ ಜ್ಯೋತಿಯ ಜೊತೆಗೆ ಸಂಕರಣ ಮಾಡಲು ಆಯ್ಕೆ ಮಾಡಲಾಯಿತು. ಅಭಿವೃದ್ಧಿಪಡಿಸಿದ ಸಂಕರಣಗಳಲ್ಲಿ ನಿಜವಾದ ಸಂಕರಣವನ್ನು ಭೌತಿಕಗುಣಲಕ್ಷಣಗಳ ಮತ್ತು ಅಣ್ವಿಕ ಮಟ್ಟದಲ್ಲಿಗುರುತಿಸಲಾಯಿತು. ಎಫ್-೨ ಪೀಳಿಗೆಯು ಅಧ್ಯಯನ ಮಾಡಿದ ಗುಣಲಕ್ಷಣಗಳಿಗೆ ಧನಾತ್ಮಕ ಮತ್ತು ಋಣಾತ್ಮಕವಾಗಿ ತಿರುಚಿದ ಪ್ಲಾಟಿಕರ್ಟಿಕ್ ವಿತರಣೆಯನ್ನು ತೋರಿಸಿದೆ. ಹೂ ಬಿಡುವ ದಿನಗಳಿಗೆ, ಪ್ರಬುದ್ಧತೆಯ ದಿನಗಳಿಗೆ, ಸಸ್ಯದ ಎತ್ತರಕ್ಕೆ, ತೆಂಡೆಗಳ ಸಂಖ್ಯೆಗೆ ಮತ್ತು ಉತ್ಪಾದಕ ತೆಂಡೆಗಳ ಸಂಖ್ಯೆಗೆ ಜೊತೆಗೂಡಿದ ಹೆಚ್ಚಿನ ಅನುವಂಶಿಕತೆ ಮತ್ತು ಹೆಚ್ಚಿನ ಅನುವಂಶೀಯ ಮುಂಚಿತತೆಯನ್ನು ಗಮನಿಸಿದೆ. ಎಫ್-೨ ಪೀಳಿಗೆಯನ್ನು ಎಫ್-೩ ಪೀಳಿಗೆಗೆ ಮುಂದುವರಿಸಿ ಮತ್ತು ಎಫ್-೩ ಪೀಳಿಗೆಯ ಕುಟುಂಬಗಳನ್ನು ಎಲೆ ಬೆಂಕಿರೋಗದ ಪ್ರತಿಕ್ರಿಯೆಗಾಗಿ ಮೌಲಿಕರೀಸಲಾಯಿತು. ೨೨೬ ಕುಟುಂಬಗಳಲ್ಲಿ, ೧೭೮ ನಿರೋಧಕ ಪ್ರತಿಕ್ರಿಯೆ ಮತ್ತು ೪೮ ಕುಟುಂಬಗಳು ಬೆಂಕಿರೋಗಕ್ಕೆ ಒಳಗಾಗುವ ಪ್ರತಿಕ್ರಿಯೆಗಳನ್ನು ತೋರಿಸಿದೆ ಮತ್ತು ನಿರೀಕ್ಷಿತ ಅನುಪಾತ ೩:೧ ಕ್ಕೆ ಸರಿಹೊಂದುತ್ತದೆ. ಅಣ್ವಿಕ ಗುರುತುಕಾರಕ ಆರ್‌ಎಮ್-೧೩೩೭ ಯು ನಿರೀಕ್ಷಿತ 'ಅನುಪಾತ ೧:೨:೧ ಕ್ಕೆ ಹೊಂದಿ ಭೌತಿಕ ಮೌಲ್ಯಮಾಪನಕ್ಕೆ ಗಮನಾರ್ಹವಾಗಿ ಸಂಬಂಧಿಸಿದೆ. ಪ್ರಸ್ತುತ ಅಧ್ಯಯನಕ್ಕೆ ಬಳಸಿದ ಪ್ರಜನನ ದ್ರವ್ಯ ಸಾಲುಗಳು ವೈವಿಧ್ಯಮಯವಾಗಿದೆ ಎಂದು ಮತ್ತು ಕಿರುವಾಣದಲ್ಲಿರುವ ನಿರೋಧಕತೆವು ಏಕೈಕ ಪ್ರಬಲ ವಂಶವಾಹಿನಿಂದ ನಿರ್ವಹಿಸುತ್ತದೆ ಮತ್ತು ಆರ್‌ಎಮ್-೧೩೩೭ವು ಆ ವಂಶವಾಹಿನೊಂದಿಗೆ [ಪಿಐ-೨೦(ಟಿ)] ಸಂಬಂಧಿಸಿದೆ ಎಂದು ಬಹಿರಂಗಪಡಿಸಿದೆ.

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Introduction

I INTRODUCTION

Rice (*Oryza sativa* L.) is the annual cereal crop with diploid chromosomes ($2n = 24$) and classified under the genus *Oryzae* and the family *Poaceae*. Asian rice (*Oryza sativa*) and African rice (*Oryza glaberrima*) are the two major distinct cultivated rice types. Asian cultivated rice is an economically important than African rice. It was the first sequenced crop genome with estimated genome size of 430 Mb (Jackson, 2016). It is one of the world's most stable food crop for over half of the world's population (Khush, 2005) and serves as a pillar for food security in many developing countries. More than 90 per cent of rice is grown and consumed in Asia where about 60 per cent of the world's population lives, reflecting the value of rice in daily human life. The year, 2004 was declared as International Year of Rice by the United Nations Food and Agriculture Organization by considering its importance.

Rice is cultivated globally in an area of about 161.40 million hectares with production of about 506.30 million tonnes and productivity of 3.14 tonnes per hectare. India is an important center of rice cultivation and it was cultivated over an area of 44.11 million hectare with an annual production of 105.48 million tonnes and an average productivity of 2.39 tonnes per hectare. In India, rice is grown in almost all the states. Whereas in Karnataka, occupied over an area 13.26 lakh hectares with annual production of 3.54 million tons and its average productivity was 2.67 tonnes per hectare (Anon, 2016). Based on the trend of consumption in our country, it is estimated that requirement of rice will be 137.30 million tonnes by 2050 (Anon, 2013).

Rice contains carbohydrates (70-80 %), proteins (6-12 %), mineral matter (1.2-2.0 %) and significant content of fats and vitamins. It supplies 23 per cent of global human per capita energy and 16 per cent of per capita protein requirements (Ghosh and Sharma, 2012).

The green revolution in the 1960's increased world rice production. On contrary the production potential of modern cultivars of rice is currently declining, because of several biotic, abiotic stresses (Keneni *et al.*, 2012) and narrow genetic base in modern cultivars of rice (Wouw *et al.*, 2010).

Rice has been under cultivation over thousands of years, also it served as a host for a number of diseases and insect-pests. Diseases are considered to be the major limiting factors in rice production around the globe because they are most badly affecting rice production (Song and Goodman 2001). Among the major diseases, rice blast ranks first in reducing yield because of its wide distribution and high destructiveness under favorable conditions (Ou, 1985). Blast is caused by fungi, *Magnaporthe grisea* (Herbert) Borr. (anamorph = *Pyricularia grisea*), is a

haploid filamentous ascomycete with a relatively small genome size of about 40 Mb with seven chromosomes (Dean *et al.*, 2005).

Pathogen, *Magnaporthe grisea* occurs in different environments and causing significant problem in temperate regions. This can also cause problem in areas such as irrigated lowland and upland (Kuyek, 2000). Conditions conducive for rice blast include long periods of free moisture where leaf wetness is required for infection and high humidity is common.

Initially blast symptoms appear as small necrotic lesions in rice seedlings later become larger and under humid conditions aerial hyphae emerge from these lesions and spread their conidia through wind. As the time progresses, the disease spreads to other parts of the plant (Galhano and Talbot, 2011) at any growth stage and can cause severe leaf necrosis and impede grain filling, resulting in decreased grain number and weight and it causing yield loss from 1 to 50 per cent. The fungus causes partial to complete sterility when the last node is attacked. Realizing the economic yield losses caused by them, it is prime importance to breed resistant varieties to blast. The loss caused by this disease should be minimized by directing the efforts towards understanding the genetic basis of resistance.

There are various methods used for managing rice blast viz., use of resistant varieties, cultural practices, biological and chemical control. Chemical control practiced in various parts of the world has been proved to be expensive, less effective and harmful to environment. However, the development of different disease resistant cultivars is considered to be the most eco-friendly and practical approach to manage the disease. Even though many resistant varieties have been developed, due to genetic plasticity in the pathogen genome, there is a continuous threat to the effectiveness of the developed cultivars (Hittalmani *et al.*, 2000). The best management of disease is to bring durable wide spectrum resistance in rice cultivars. This can be accomplished by accumulating both qualitative and quantitative resistance genes in to rice cultivars (Joshi *et al.*, 2009). Introducing these resistance genes from the wild relatives of rice in to commercial cultivars has greatly helped the breeders to accomplish this task. Therefore, exploitation of resistance gene resources or wild relatives of rice are undoubtedly very valuable and have been used in rice breeding programs worldwide.

Compared to conventional breeding, molecular breeding especially using marker assisted selection is extremely valuable in resolving the issues the breeders faced with traditional breeding (Khan, 2015). During the past few decades, marker-assisted selection (MAS) has been proven as a highly efficient breeding method in improving the cultivars/lines for various biotic stresses in various crop breeding

programmes, because of its efficacy in selecting plants with appropriate gene combinations in segregating populations (Collard and Mackill, 2008).

The present investigation was carried out to search the donor sources in the germplasm for blast resistance by screening under natural epiphytotic conditions and utilizing resistant genotypes in crossing programme and to study the nature of blast inheritance and identifying the potential segregants for blast at field and molecular level using co-dominant SSR markers. In this point of view, the following objectives are aimed to carry out the present investigation

1. Screening of rice germplasm lines for leaf blast resistance and assessment of genetic variability and diversity for yield and yield related traits
2. Identification of leaf blast resistant lines in segregating population and
3. Molecular analysis of leaf blast resistance in segregating population

Review of Literature

II REVIEW OF LITERATURE

The present investigation is briefly reviewed under this chapter by the following headings

2.1 Screening of rice germplasm lines for leaf blast reaction

2.2 Assessing the genetic diversity for yield and yield attributing traits

2.3 Descriptive statistics and variability studies of segregating population for yield and yield attributing traits

2.4 Genetic analysis of blast resistance and molecular analysis in segregating population

2.1 Screening of rice germplasm for leaf blast reaction

The rapid genetic evolution of the fungus often overcomes the resistance conferred by major genes after a few years of intensive agricultural use. Therefore, resistance breeding requires continuous efforts of enriching the reservoir of resistance genes /alleles to effectively tackle the disease. Seed banks represent a rich stock of genetic diversity; however, they are still under-explored for identifying novel genes and /or their functional alleles.

Rice blast (*Pyricularia oryzae* L.) can affect all above ground parts of a rice plant viz., leaf, collar, node, neck, parts of panicle and sometimes leaf sheath. The goal of plant breeder is to assemble more desirable combinations of genes for disease resistance in new varieties. To assemble genes, donor or resistant or tolerant sources need to be identified to select superior plants either in artificial or natural screening for the traits of interest.

Mohanta *et al.* (2003) screened 28 restorer lines and four standard checks, for blast disease reaction in two seasons. On the basis of disease intensity, the lines classified into three highly resistant, 12 resistant, 16 moderately resistant and one was moderately susceptible at *T. aman* season and at *boro* season three highly resistant, eight resistant, 17 moderately resistant and four were moderately susceptible to blast. Considering both seasons, the accession numbers 56, 57, 64, 66, 71 and 73 showed comparatively better performance for the blast disease.

Chandrashekara *et al.* (2007) screened 265 germplasm under natural epiphytotic condition and revealed that, none of the germplasm was found immune to *Pyricularia oryzae*. The number of genotypes were found resistant to leaf blast and neck blasts were eight and 18, respectively. 138 genotypes were moderately

resistant to leaf blast and 82 genotypes were moderately resistant to neck blast. The only one entry, Sasyashree was found resistant to both leaf and neck blast.

Ghazanfaret *et al.* (2009) established a disease screening nursery of rice germplasm by artificial inoculum with aqueous spore suspension of *Pyricularia oryzae* to determine the source of resistance in rice germplasm. The screening revealed that none of the test lines were immune or highly resistant. One line IR-70181-1-1-1 of course type was found to be resistant. Nine lines of the course type displayed moderately resistant response, 77 lines of both course and fine rice were found to be moderately susceptible. Twenty four lines of fine rice showed susceptible to highly susceptible response.

Puri *et al.* (2009) assessed leaf and neck blast resistance of 182 rice breeding lines in greenhouse. Among 182 lines, 77 were identified as resistant, 43 as moderately resistant, 39 as moderately susceptible and 23 as susceptible for leaf blast. The selected 31 rice lines evaluated for neck blast, among them four lines were resistant, four were moderately resistant, 16 were moderately susceptible and seven were susceptible and noticed significant and positive correlation between leaf and neck blast infection.

Selvaraj *et al.* (2011a) screened 21 rice genotypes under artificially controlled conditions and identified 16 genotypes which were already reported to have resistance genes reacted negatively to the blast disease and four genotypes were susceptible. The genotypes Moroberekan followed by Columbia 2 and ARBN 142 reported highly significant, lower mean disease reaction score and mean PDI per cent (potential disease incidence).

Idowu *et al.* (2013) screened 34 rice genotypes for blast resistance at two sites at Ibadan and Ikenne under natural infection for two years. Results revealed, 34 varieties responded differently to blast infection and the two sites were significantly different from each other. The genotype main effect plus genotype by environment biplot revealed that only Moroberekan was resistant to blast fungus across years and sites and concluded Ibadan is a better site for screening rice genotypes for blast resistance than Ikenne.

Naveenkumar *et al.* (2013) evaluated 122 genotypes of basmati and non-basmati *Indica* rice genotypes against blast disease under induced epiphytotic conditions and reported 13 genotypes as resistant to blast. Nine genotypes carried blast resistance genes but, were susceptible under induced epiphytotic conditions. The rice genotype, VLD-61 had no resistance genes; however, it expressed strong resistance against blast.

Feng *et al.* (2014) evaluated a total of 200 lines for resistance to 11 isolates of *Magnaporthe oryzae*. The isolate, IB33, was the most virulent isolate, with only six varieties being resistant to this isolate. Isolates 49D and TM2 were also highly virulent with only 20 per cent and 26 per cent lines being resistant to these isolates, respectively. Over 70 per cent of the lines were resistant to isolates A264, isolate #24 and isolate IB54. Line RU1401182 was resistant to all tested isolates, five lines were resistant to 10 isolates, 36 lines were resistant to nine isolates and 19 lines were resistant to eight isolates.

Imam *et al.* (2014) determined reaction of blast in 32 accessions of rice germplasm in UBN and analysis showed that out of 32, six germplasm were resistant, ten moderately resistant and 16 germplasm were susceptible. Presence of *Piz-t*, *Pita/Pita-2* and *Pi-9* gene ensured a resistant reaction in outdoor blast nursery whereas germplasm carrying *Pib* was susceptible when present alone.

Jayawardana *et al.* (2014) evaluated 34 rice varieties including Sri Lankan and IRRI recommended rice varieties for blast resistance. Varieties like Tetep, Bg359, Bg304, IR64, Bg352 and Bg357 were found to be highly resistant, 17 were resistant and 17 were susceptible to the fungal infection. Varieties like LD125, Bg94/1, Bw267-3, Bw451, Bw400, H7, Bg34-6, H10 and IRRI119 were highly susceptible to blast. In marker genotyping, most of the highly resistant and resistant varieties demonstrated the presence of blast resistant *Pita* gene of variety Tetep and *Pita* gene was absent in the highly susceptible varieties.

Vasudevan *et al.* (2014) screened 4246 geographically diverse rice accessions of 13 major rice-growing countries for blast resistance sources in uniform blast nursery and recorded 74.80 per cent of the rice genotypes were exhibited complete resistance with scores between 0 and 3. Although each country had a high number of resistant accessions, the percentages of blast resistant genotypes from different countries varied, Brazil containing the highest number of resistant accessions while, Japan had the lowest number.

Dar *et al.* (2015) conducted a field trial for disease screening of rice germplasm consisting of nine parents, 27 crosses and one local check under natural epiphytotic conditions and the results revealed that none of the test lines was immune or highly resistant. Four crosses namely, K-08-60 × IR-68888A, K-08-61 × SKAU-11A, K-08-61 × IR-68888A, PS-5 × SKAU-11A and one parent PS-5 were found to be resistant. Seven hybrids and four parents displayed moderately resistant response. Three crosses and equal number of parents were found to be moderately susceptible. Rest of the crosses and parents showed susceptible to highly susceptible response.

Thippeswamy *et al.* (2015) investigated 312 indigenous and 65 exotic germplasm lines against blast resistance. More percentage (83%) of exotic germplasm showed resistance to rice blast disease compared to indigenous germplasm (46%). Three genotypes (JGL23710, JGL23713 and JGL23714) in indigenous germplasm and two genotypes (IR09N500 and IR12M101) in exotic germplasm were immune to rice blast disease.

Hossain and Hegde (2016) screened the rice germplasm under natural conditions against rice blast. Results showed that none of the germplasm were immune to blast, 17 genotypes were resistant to leaf blast but none of them were resistant to neck blast. Eight genotypes were moderately resistant to both leaf blast and neck blast. Eighteen genotypes showed highly susceptible reaction to leaf blast.

Pandey (2016) investigated the apparent infection rates of leaf blast on 12 cultivars of rice and showed significant variations of apparent infection rate in all the tested cultivars. The highly susceptible traditional cultivar Gurnatia, Dehula and Indrajal shows high degree of incidence, apparent infection rates and severities. The leaf blast infections were also observed, even though not significantly higher in all improved cultivars. Among the improved cultivars basmati shows high level of susceptibility and other cultivars show slow blasting.

Sabin *et al.* (2016) conducted an experiment to screen 50 rice genotypes under natural epidemic condition against seedling blast (*Pyricularia grisea*). The genotype, Sabitri identified as most resistant among genotypes and recorded the lowest percentage of incidence and severity. The genotypes Taichung-176 and Sankharika showed the highest percentage of disease incidence and severity for seedling blast.

Hassan *et al.* (2017) selected eleven rice mutants from irradiated populations of three Egyptian cultivars. These mutants were evaluated for resistance to blast (*Magnaporthe grisea*) under natural and artificial infection conditions in M₃ and M₄ generations. Out of eleven mutants, nine resistant mutants were obtained from susceptible parents (Sakha 101 and Sakha 104). The results revealed that the blast resistant mutants have a combination of partial resistance genes and complete resistance genes that confer durable resistance to all blast races.

Qudsia *et al.* (2017) assessed diversity of the 52 genotypes based on blast symptoms caused by *P. oryzae* and observed moderately resistant reactions for the genotypes, KSK-470, KSK-463, KSK-460, PK 8685-5-1-1-1, KSK-462, KSK-474, PK 3810-30-1, KSK-471 and KSK-472. The 52 genotypes were grouped in four clusters. The grouping of some genotypes in same cluster is based on their similar reaction against leaf blast.

Yadav *et al.* (2017) screened 80 released rice varieties at National Rice Research Institute, Cuttack. Among them, 19 varieties (23.75 %) showed resistance, 21 were moderately resistant (26.25 %) and 40 varieties (50 %) showed susceptible in uniform blast nursery.

Zewdu *et al.* (2017) screened 46 introduced Korean rice accessions and two checks, IR-64 (resistant) and NERICA-1 (susceptible) under natural field infestation and in the screen house. Results indicated the highly significant among genotypes for final leaf blast severity, lesion size, area under disease progress curve (AUDPC) values, panicle blast and grain yield. Genotypes SRHB-133, SRHB-93 and SRHB-78 were resistant to rice blast in both field and screen house conditions and showed a lower lesion size.

2.2 Assessing the genetic diversity for yield and yield attributing traits

Genetic improvement of any crop mainly depends upon the amount of genetic variation present among genetic resources for various agronomic traits (Hausmann *et al.*, 2004). The estimation of genetic diversity among genotypes of any crop of interest is the first and foremost process in any plant breeding programme. The most potent technique for quantifying the degree of genetic diversity among the genotypes is the D^2 technique developed by Mahalanobis (1928). Genetic divergence analysis, suggests the plant breeder in choosing the right parents for the breeding programme (Vivekananda and Subramaniam, 1993).

Vanaja and Babu (2003) grouped 56 rice genotypes into nine clusters based on genetic distance and concluded that there was no relationship between clustering pattern and geographic distribution and at the same time the relationship exists to some extent between genetic divergence and geographic distribution.

Nayak *et al.* (2004) assessed genetic divergence in 200 scented rice genotypes for 10 morphological characters and revealed that there was no relationship between clustering pattern and geographic distribution. The grain length (31.50 %) followed by days to 50 per cent flowering (31.20 %) contributed maximum towards total genetic diversity.

Senapati and Sarkar (2005) studied 40 tall indica rice genotypes and results revealed that majority of genotypes (30) were included in cluster I only. The characters viz., panicle number per hill, panicle length, sterility parentage, yield per plot and 1000 grain weight were the principal contributors towards genetic divergence and suggested that these characters have to be given importance while selecting parents in crossing programme and in selection of segregants in succeeding generations.

Singh *et al.* (2006) investigated genetic divergence of 52 traditional lowland rice using Mahalanobis D^2 statistic. Based on 15 agro-morphological characters, these genotypes were grouped into six clusters. Genotypes from more than one state were grouped in one cluster, and genotypes from one state were grouped in more than one cluster and concluded that geographical origin was not found to be a good parameter of genetic divergence. Plant height followed by leaf angle and leaf area, highly contributed (32.43 %) to the formation of clusters.

Prasad *et al.* (2009) evaluated 52 traditional aromatic rice genotypes to study genetic diversity in them. Based on D^2 analysis with respect to grain yield and 14 other related traits, genotypes were classified in to four clusters and four ungrouped genotypes. The maximum inter-cluster distance was observed between ungrouped clusters VI and VII followed by between clusters III and VIII. The genotypes having higher mean performance for various traits and diversity exhibited in distant cluster could be considered for their inclusion of parents to obtain desirable segregants after hybridization.

Banumathy *et al.* (2010) studied diversity pattern of 53 rice genotypes for yield and yield attributing characters using D^2 analysis and grouped the genotypes into 11 clusters. Maximum number genotypes were grouped under cluster XI and I, while clusters II, IV, V, VI, VIII, IX and X had only two genotypes each and observed maximum inter cluster distance between cluster I and X. The maximum intra cluster distance was observed in cluster VII followed by cluster XI. Among the eight traits studied, the grain yield, days to 50 per cent flowering, total grains per panicle and plant height together contribute 86.62 per cent towards total divergence.

Garg *et al.* (2011) grouped 48 genotypes into five clusters based on Euclidean cluster analysis with cluster I containing the maximum of 18 genotypes. Maximum intra-cluster distance was observed in cluster I indicating greater genetic divergence between the genotypes. Days to maturity, gel consistency and days to 50 per cent flowering contributed 74.55 per cent of total divergence. Maximum inter-cluster distance was recorded between clusters II and III followed by clusters III and IV indicating wide genetic diversity.

Lal and Chauhan (2012) grouped 48 rice genotypes into seven clusters based on Mahalanobis D^2 multivariate analysis and observed maximum number of genotypes in cluster I, followed by Cluster V. Cluster II and IV comprised only three genotypes in each cluster. Maximum cluster distance was recorded between Cluster II and VI, whereas minimum distance between Clusters I and III. Maximum intra cluster distance was observed in clusters VII and minimum in cluster VI. Cluster III comprised all of tall, long seeded and super fine genotypes with comparatively higher seed weight, while cluster IV comprises semi dwarf and fine genotypes with

minimum seed weight. The cluster VI consisted of coarse seeded and dwarf with comparatively little higher seed weight.

Ramanjaneyulu *et al.* (2014) evaluated ten popular low land rice genotypes and grouped into 4 clusters based on the relative magnitude of the D² values. The yield attribute, 1000-grain weight exhibited the maximum contribution to total genetic divergence (57.78 %), followed by grain yield (15.56 %), number of grains/spikelet (11.11 %), straw yield (6.67 %) and spikelet length (4.44 %).

Khatun *et al.* (2015) obtained five major groups for 43 upland rice genotypes and observed the maximum number of genotypes in Cluster II (20), which consisted of 46.51 per cent of all genotypes, mostly originating from the Philippines. The second highest was cluster III, which consisted of 14 members. Clusters I, IV, and V consisted of seven, one, and one genotypes, respectively.

Tejaswini *et al.* (2016) grouped rice genotypes into 12 clusters and reported that cluster V constituted maximum number of genotypes. The genotypes falling in cluster XII had the maximum divergence, which was closely followed by cluster IX and the maximum inter cluster Euclidean² values was observed between cluster II and XII followed by cluster IX and XII suggesting that the genotypes constituted in these clusters may be used as parents for future hybridization programme.

Sarawgi *et al.* (2017) grouped rice germplasm accessions into 8 clusters and reported cluster VIII had highest mean value for 100 grain weight, Cluster II had highest mean value for panicle length, effective tillers/plant and L:B ratio. On the basis of mean performance suggested selecting better genotypes from different clusters for most of the characters.

2.3 Descriptive statistics and variability studies of segregating population for yield and yield attributing traits

2.3.1 Descriptive statistics studies of segregating population for yield and yield attributing traits

The distribution properties of segregating population studied by third order statistics (skewness) and fourth order statistics (kurtosis), which provides insight about the nature of gene action and number of genes controlling the traits respectively. They are more powerful than first and second degree statistics which reveal interaction genetic effects. Generally, skewed distribution of the characters implies that the control of non-additive type of gene effects and influenced by environmental variables. Positive skewness explained the complementary gene action whereas, negative skewness related to duplicate (additive × additive) gene effects. Kurtosis or near to zero leads the absence of gene interactions (Kotch *et al.*,

1992). The leptokurtic and platykurtic distribution of the characters are controlled by fewer and large number of genes, respectively.

Kiran (2012) studied distribution pattern of two F_2 populations based on skewness and kurtosis and noticed dominance based complementary gene interaction for total tillers per plant, days to panicle emergence, productive tillers per plant, grains per panicle and grain yield in both the crosses, whereas, duplicate interaction was noticed for panicle length in both the crosses.

Mallikarjuna (2013) studied the F_2 population of IR-64 $\times$ IET-16348 and recorded positive skewness for the inheritance of panicle length, productive tillers per plant, filled spikelets per panicle, 1000-grain weight, straw yield, grain yield and SLA indicating the involvement of relatively large number of segregating genes with majority of them having decreasing effects and dominance based complementary type of interaction. However, negatively skewed distribution indicating the involvement of a large number of dominant genes having increasing effects and duplicate type of epistasis was noticed in the inheritance of plant height and harvest index.

Govintharaj *et al.* (2016) studied three back cross population and showed complementary gene interaction in all backcross population for plant height, number of productive tillers and number of grains. Panicle length in two crosses and thousand grain weight and single plant yield in one cross showed duplicate gene interaction suggests that selection would be effective to gain higher genetic advance than expected. Kurtosis for plant height and panicle length was influenced by only few genes for all crosses, whereas number of productive tillers and number of grains were controlled by few genes for at least two crosses.

Rani *et al.* (2016) studied the distribution properties of skewness and kurtosis in two crosses of F_2 population and indicated plant height and flag leaf length was negatively skewed and platykurtic whereas, the total number of tillers, total number of productive tillers, flag leaf width and total filled grains recorded positive skewness and platykurtic.

2.3.2 Variability studies of segregating population for yield and yield attributing traits

Suresh and Reddy (2002) reported moderate to high GCV and PCV values for productive tillers per plant and grain yield per plant and high heritability coupled with high genetic advance was observed for plant height in study of 10 parents and their nine F_2 populations.

Agrawal (2003) studied seven parents and 21 F₂ populations of rice and observed highest GCV and PCV for yield per plant. High heritability with high genetic advance was reported for yield per plant. The days to flowering, days to maturity, tillers per plant and panicle length recorded high heritability.

Sanjeev *et al.* (2005) studied F₁ and F₂ generation of rice cross and reported moderate genotypic coefficient of variation but high heritability in broad sense and genetic advance for 100 grain weight.

Vaithiyalingan and Nandarajan (2006) evaluated seven F₂ populations of rice and reported high GCV for grain yield followed by productive tillers per plant. The grain yield per plant and productive tillers possessed high genetic advance with high heritability.

Bharadwaj *et al.* (2007) reported high heritability estimates coupled with high genetic advance as per cent mean in F₂ generations of three rice crosses for days to fifty per cent flowering, days to maturity, plant height, panicle length and 1000 grain weight. Productive tillers per plant and grain yield per plant had low to moderate heritability coupled with low to moderate genetic advance as per cent mean.

Panwar and Mathur (2007) reported high heritability coupled with high genetic advance for number of productive tillers per plant in 13 parental lines and 30 F₂ populations. High heritability with moderate to low genetic advance for days to 50 per cent flowering, panicle length and 1000 grain weight suggested the predominant role of non-additive gene action in their inheritance.

Habib (2008) reported high PCV and GCV for number of productive tillers, grain weight per plant and test weight per plant in F₂ generation of BPT 5204 × HPR 14. Days to 50 per cent flowering, days to maturity, length of paddy grain, rice kernel length and rice kernel breadth were recorded low PCV and GCV with high heritability and genetic advance.

Hasib and Kole (2008) studied F₂ populations of six cross combinations of rice and reported low genetic gain with high heritability for grain yield per panicle and noticed predominant role of non-additive gene action.

Anjali (2009) investigated the F₂ generation of three rice crosses and recorded high PCV and GCV estimates, high heritability and high genetic advance as per cent mean for grain yield per plant and productive tillers per plant. Moderate PCV and GCV, high heritability and high genetic advance were observed for plant height. Low PCV and GCV, high heritability and low genetic advance were observed for days to 50 per cent flowering. Low PCV and GCV, high heritability

and moderate genetic advance were observed for panicle length and 1000grain weight.

Anilkumar *et al.* (2009) studied the two cross combination of F_2 and F_3 segregants of rice and recorded moderate variability for grain quality traits viz., L:B ratio of grain and grain breadth. All the above mentioned characters showed high heritability coupled with high genetic advance.

Nandeshwar *et al.* (2010) reported high GCV and PCV for grain yield per plant and panicle number per plant in 25 F_2 progenies. High heritability was observed against all the characters studied except panicle weight, grain number per panicle and grain breadth. Grain yield per plant showed maximum genetic advance as per cent mean followed by panicle number per plant, plant height and panicle weight, respectively.

Kiran (2012) investigated the variability parameters in F_2 populations of IR 64 $\times$ BPHR-1 and Jaya $\times$ BPHR-1 crosses of rice. He noticed higher value of genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV) with high heritability coupled with high genetic advance for total tillers per plant, productive tillers per plant, grains per panicle and grain yield per plant in both the crosses and indicated additive gene action in their genetic control.

Shet *et al.* (2012) evaluated the F_2 segregating populations of two crosses of rice. The results revealed that crosses registered high PCV and GCV values for almost all traits except days to 50 per cent flowering and panicle length. However, all traits registered high broad sense heritability accompanied with high genetic advance.

Rajendare *et al.* (2013) studied seven parents, seven F_1 hybrids and their corresponding F_2 populations and reported high heritability in broad sense and genetic advance for grain yield per plant and kernel length; whereas, the estimates were relatively low to moderate for the other characters.

Sadimantara *et al.* (2014) reported high heritability accompanied with high genetic advance for plant height indicating that it is simply inherited trait and the heritability is most likely due to additive gene effects. On the other hand, panicle length, number of productive tillers and 1000grain weight had high heritability coupled with low genetic advance indicating non-additive gene effects.

Shantavva *et al.* (2014) studied the variability parameters in F_2 and F_3 population of rice genotypes derived from the cross Jyothi $\times$ BR 2655 and recorded moderate to high heritability and genetic advance for panicles per plant, panicle weight and the number of grains per panicle.

Shilpaet *et al.* (2014) evaluated 33 leaf blast resistant BC₁F₂ rice plants and revealed significant differences among the genotypes for most of the traits and observed PCV higher than GCV for all the traits. High heritability was recorded number of panicles per plant and number of tillers per plant. Genetic advance as percentage of mean ranged from 4.50per cent (days to flowering) to 56.10per cent (number of filled grains per panicle).

Venkanna *et al.* (2014) studied F₂ population of 36 crosses for variability parameters and recorded low to moderate GCV and PCV with low heritability and genetic advance for harvest index indicating that the character is highly influenced by non-additive genetic effects and thus the selection would be ineffective. The moderate heritability and genetic advance were recorded for grain quality characters viz., kernel length, kernel breadth and L: B ratio.

Bhuvaneswari *et al.* (2015) evaluated the F₂ segregating populations of two black rice crosses and recorded moderate to high PCV and GCV in both populations for all traits except panicle length and days to first flowering. Heritability was moderate to high for all the traits coupled with high genetic advance as per cent mean except for panicle length and days to first flowering.

Kahani and Hittalmani (2015) estimated variability parameters in F₂ segregating populations of 15 crosses for 14 characters. The estimates of PCV were high and moderate for days to flowering and maturity, number of tillers per plant, number of panicles per plant, 100 grain weight, panicle length and grain yield in different crosses. High heritability coupled with high and moderate genetic advance was observed for all the studied traits.

Mallimar *et al.* (2015) reported moderate to high variability for grain length, L:B ratio in 1st cross and for plant height and grains per panicle in 2nd cross of F₃ generation. The high GCV and PCV were noticed for grain yield (kg ha⁻¹) in Swarna × Ranbir basmati and Swarna × BR2655 for number of panicles per plant, panicle weight and grain yield. High heritability coupled with high genetic advance as per cent mean were recorded for plant height, number of panicle per plant, panicle weight, number of grains per panicle, L:B ratio and grain yield (kg ha⁻¹) in Swarna × Ranbir basmati and Swarna × BR2655 for number of panicle per plant.

Patroti *et al.* (2015) evaluated thirty five leaf blast resistant BC₁F₂ rice plants and recorded higher phenotypic coefficients of variability than genotypic coefficients of variability for all the traits. High heritability was recorded in number of productive tillers per plant. Genetic advance as per cent of mean ranged from 4.50per cent (days to flowering) to 56.10per cent (number of filled grains /panicle).

Rahman *et al.* (2015) assessed genetic variation among four parents and their 12 F₂ populations. The F₂ populations, K-Bas × Dilrosh, Dilrosh × K-27 and K-Bas × TN-1 had the highest broad sense heritability for panicle length. On the basis of superior performance, high heritability and genetic advance for maturity and panicle related traits.

Savitha and Ushakumari (2015) studied six crosses of rice, among them, the crosses IR 72 × Veeradangan and ADT39 × Kavuni exhibited superior *per se* performance in both F₂ and F₃ generations for almost all the biometrical characters. The F₂ and F₃ populations of the cross IR 72 × Veeradangan and ADT 39 × Kavuni showed moderate PCV and GCV with high heritability estimates and high genetic advance as per cent of mean for number of productive tillers per plant, number of filled grains per panicle and single plant yield.

Ali *et al.* (2016b) studied the variability in F₂ populations and observed higher PCV than GCV for all the traits in all the crosses. High heritability reported for 1000 grain weight in all crosses and revealed selection of plants on the basis of these traits would lead to improvement in grain yield.

El-Badri *et al.* (2016) studied the variability in six F₂ populations and reported low GCV and PCV for days to heading, plant height and test weight. While, for number of tillers per plant, number of panicles per plant and grain yield per plant recorded high GCV and PCV coupled with high heritability with high GAM.

Hefena *et al.* (2016) studied the variability in eight F₂ populations and observed wide range of variation for grain yield per plant, number of panicles per plant, 1000 grain weight and panicle weight. The high heritability was recorded for all the studied traits, indicated that additive genetic variance play an important role in selection of genotypes for these traits.

Govintharaj *et al.* (2016) studied blast resistance gene introgressed segregating population of three crosses in rice and reported high GCV and PCV was found in the cross, CB 174 R × Zenith for the number of productive tillers per plant. For single plant yield, CB 174 R × Zenith cross was showed high heritability coupled with high genetic advance, whereas, moderate heritability conjugated with high genetic advance was found in the cross, TNAU CMS 2B × Zenith. However in the cross, CB 87 R × Zenith showed moderate heritability joined with moderate low genetic advance as per cent of mean.

Rani *et al.* (2016) studied two populations of F₂ generation and recorded highest PCV and GCV for productive tiller in Swarna *Sub 1* × Kavuni. Difference between GCV and PCV was low in most of the characters studied. Both positive and

negative skewness was observed for different traits, while platykurtic distribution was observed for most of the traits in F₂ populations of two crosses.

Sala and Shanthi (2016) reported high PCV and GCV values for single plant yield followed by number of productive tillers per plant and low PCV and GCV for plant height and panicle length were studied in F₂ population of eight crosses.

Vijaya and Shailaja (2016) studied the variability in F₂ population of KRH-4 and reported high variability in the form of phenotypic coefficient of variability (PCV), genotypic coefficient of variability (GCV) values and these were coupled with high heritability and high genetic advance as per cent of mean for 1000 grain weight. High heritability was observed in plant height at 40 days, plant height at maturity, days to 50 per cent flowering, 1000 grain weight.

Prabhu *et al.* (2017) assessed the genetic variability parameters in two crosses and recorded higher mean performance for plant height, number of productive tillers, 1000 grain weight, seed yield per plant, grain length, grain width and L:B ratios in cross, BPT 5204 × ADT 45 compared with the cross BPT 5204 × JGL-1798. High PCV and GCV along with high heritability values were recorded for productive tillers per plant and grain yield per panicle in both the crosses.

2.4 Genetic analysis for blast resistance and molecular analysis in segregating population

Genetic analysis of segregating population will be very effective if the population size is very large. The larger population size that may be varied from few hundreds to thousand individual plants which helps in identification of specific gene combination precisely in the segregating population and this kind of breeding programme will end up with the selection of desirable individuals and it is further helpful in efficient marker analysis studies of segregating population.

Once tightly linked markers that reliably predict a trait phenotype have been identified, they may be used for Marker assisted selection (MAS). The fundamental advantages of MAS over conventional phenotypic selection are, which can save time, resources and effort. MAS can be carried out at the seedling stage. Therefore, undesirable plant genotypes can be quickly eliminated and individual plants can be selected based on their genotype (Morris *et al.*, 2003). So that target genotypes can be more effectively selected, which may enable certain traits to be ‘fast-tracked’, resulting in quicker line development and variety release.

Pan *et al.* (1999) crossed Aus-373 with a series of Japanese differential cultivars and the Chinese susceptible cultivar Lijiangxintuanheigu (LTH). Ten F₂ populations were tested with one to two races of *P. grisea*. The F₂ population from

the cross between LTH and Aus373 segregated in a 3R: 1S ratio with 433.5 and a 15R: 1S ratio with 007.0 indicating that Aus-373 carries two genes, one of which probably confers resistance to both races, one at the *Pi-k* locus and the second apparently at a new locus linked to an isozyme gene *Amp-1*.

Ahnet *et al.* (2000) evaluated the F₁ of the Suweon 365 and Chucheongbyeon cross and shown resistant to the isolate KI-313, indicating that the resistance is under dominant gene control. Segregation analysis based on evaluation of the 69 F₃ families showed a 1:2:1 ratio for homozygous resistant, heterozygous resistant and susceptible individuals, thereby confirming that a single dominant gene governs the resistance in Suweon 365.

Padmavathi *et al.* (2005) crossed the donors with unknown genes (Carreon and CNM4140) with the donors of known gene (Dular, Tetep, Zenith and Tadukan) and with susceptible check (CO-39). The inheritance pattern of resistance genes in donors when crossed with CO-39 indicated the presence of monogenic dominant gene. CNM 4140 when crossed with Dular, Tetep, Zenith and Tadukan segregated in 15:1 (resistant: susceptible) in F₂ generation, indicating the involvement of different genes governing resistance against the DRR isolate. The allelic test revealed that Carreon, Dular and Tetep possessed the same gene (*Pi-k*), while Zenith, CNM 4140 and Tadukan had different genes.

Sharma *et al.* (2007) studied parents (Mahsuri × Laxmi) and their F₁, F₂, backcross, F₃ and F₄ progeny to determine the inheritance of blast resistance. The F₁ plants were blast-resistant. The F₂ population segregated into 3R:1S ratio. The F₃ and F₄ progeny showed a segregation ratio of 1R:2Sg (segregating):1S. RM25 and RM310 markers showed association with resistant and susceptible progeny and concluded that blast resistance in Laxmi is governed by a single dominant gene.

Prasad *et al.* (2009) analysed near isogenic lines and indicated the presence of a resistance gene, *Pi-1(t)* in the donor cultivar C101LAC which is highly resistant to the rice blast fungus *Magnaporthe grisea*. C101LAC was crossed with susceptible BPT5204 to generate the mapping population. A segregation ratio of 3:1 for resistant to susceptible F₂ plants using bulk segregation analysis confirmed the presence of a major gene *Pi-1(t)* by SSR marker RM224 to the highly virulent blast isolate DRR 001.

Sreewongchai *et al.* (2010) employed MAS to identify F₂ and F₃ plants carrying a combination of four resistance QTLs in a homozygous fusion in a cross of IR64 and JaoHom. Flanking markers RM212/ RM319 and RM144/RM139 to blast resistant QTLs on chromosome 1 and 11 in JHN rice and tightly-linked markers

RM208 and RM179 to blast resistant QTLs on chromosome 2 and 12 in IR64 rice variety were used for MAS.

Ashkani *et al.* (2011) used 23 polymorphic markers for the identification of segregation ratios for blast resistance alleles in F₂ population of Pongsu Seribu 2 (resistant) and Mahsuri (susceptible). Chi-square analyses of 11 SSR markers showed an expected segregation ratio of 1:2:1, inherited in simple Mendelian fashion. Phenotypic data of F₂ population segregated in a 3:1 (R: S) ratio. Therefore, resistance to blast pathotypeP7.2 in donor is more likely controlled by a single nuclear gene. The plants resistant to blast pathotypeP7.2 from F₂ lines had genotypes with SSR markers RM168, RM8225, RM1233, RM6836, RM5961 and RM413.

Rahman *et al.* (2011) tested 112 F₃ lines for the degree of blast field resistance by inoculating the two Korean blast isolates (KI 209 and KI307) at 21 days after seeding by spray method. Disease incidence was evaluated at 8 days after inoculation, using a 0 to 5 scale and analyzed frequency distribution of 112 F_{2:3} segregating progenies for resistance levels and exhibited continuous distribution, which indicated that blast resistance in IR71033-121-15 against two isolates (KI307 and KI209) was controlled by QTLs.

Selvaraj *et al.* (2011b) phenotyped 220 F₃ families of White Ponni × Moroberekan for blast resistance under artificial condition. Bulk segregant analysis revealed 12 leaf blast resistant phenotype specific RAPD markers. Twelve RAPD markers were scored in the F₂ mapping population, out of which, 11 marker loci fitted into the expected segregation ratio of 3:1. One way ANOVA was performed to identify the marker phenotype association and resulted in the identification of seven RAPD markers linked to three traits viz., leaf blast resistance (OPBB 5258, OPBB 5194, OPAL 16940 and OPBD 12680), five markers for GPT and one marker for grain yield per plant.

Kumbhar *et al.* (2013) investigated F₂ population from a cross EK 70 (highly susceptible to blast) and RDN 98-2-3-5-14 (resistant to blast). The F₂ population segregated in 3:1 ratio for resistance: susceptible under hot spot conditions for blast suggesting monogenic control of resistance in this population. Out of two polymorphic marker, one SSR markers RM 204 showed expected segregation ratio (1:2:1) for single gene model in the F₂ population. This marker was found significantly associated with blast resistance on regression analysis.

Rahim *et al.* (2013) made crosses between Pongsu Seribu 2 (resistant) and Mahsuri (susceptible) and confirmed 19 F₁ hybrids using SSR marker, RM168. A total of 2560 F₂ plants of normal crosses and 3182 plants of reciprocal crosses were

challenged with pathotype *P7.2* and observed 3:1 (R:S) segregation ratio in both types of crosses using the chi-square test, indicating the maternal effect which showed resistance to the blast disease caused by pathotype *P7.2* is most likely controlled by a single nuclear gene.

Mizobuchi *et al.* (2014) conducted QTL analysis using SSR markers in F_3 progenies of Inngoppor-Tinawon (IT) with a susceptible lowland variety, Koshihikari. A QTL for blast field resistance (*qBFR4*) was identified on chromosome 4 and the resistance allele was derived from IT. The QTL explained 73.5 per cent of the phenotypic variation for blast resistance. The QTL *qBFR4* mapped to almost the same position as that of the blast field-resistance gene *Pi-39*. Inoculation assays revealed that IT (containing *qBFR4*) showed resistance characteristics. IT showed broad resistance to Japanese isolates and race-specific resistance to some Philippine isolates.

Liang *et al.* (2016) showed blast resistance genes present in cultivar AS20-1, by an analysis of segregation in the F_2 generation bred from a cross with the highly blast susceptible cultivar, Aichi Asahi, due to the action of a single recessive gene *Pi-66(t)*. The presence of *Pi-66(t)* gave an intermediate level control to plants infected with the blast pathogen isolate EHL0635. A bulked segregant analysis indicated that four SSR loci mapping to chromosome 3 were probably linked to *Pi-66(t)*. The F_2 progeny segregated as 101 R, 282 MR, 254 MS and 883 S, fitting a monogenic 1R:3S ratio when the R/MR and MS/S classes were combined. Together, these results indicated that the blast resistance expressed by cv. AS20-1 relied on homozygosity for the recessive allele of a single gene.

Material and Methods

III MATERIAL AND METHODS

The present investigation was carried out to achieve different objectives. The plant materials used, the methodology followed, the protocols and statistical tools employed for analysis during the course of investigation are presented in this chapter under the following sub headings. The details of experiments conducted are described in Table 1.

3.1 Screening of rice germplasm lines for leaf blast resistance and assessment of genetic variability and diversity

3.2 Assessment of parental polymorphism

3.3 Development of F₁'s and segregating populations for blast resistance

3.4 Identification of leaf blast resistant lines in segregating population

3.5 Molecular analysis of leaf blast resistance in segregating population

3.1 Screening of rice germplasm lines for leaf blast resistance and assessment of genetic variability and diversity

3.1.1 Screening of rice germplasm lines for leaf blast resistance

3.1.1.1 Site selection

The environmental conditions prevailing at Agricultural and Horticultural Research Station (AHRs), Ponnampet, during *Kharif* season favors the blast disease development, since Ponnampet is identified as hot spot (Ram *et al.*, 2007) for the blast disease. Hence, all materials of present investigation were carried out at this location in order to study the reaction of rice germplasm to leaf blast disease and identification of potential lines.

3.1.1.2 Genetic material

Totally 35 rice germplasm lines comprising, 15 landraces, 16 popular varieties, two susceptible (CO-39 and HR-12) and two resistant national checks (Tadukan and Tetep) were utilized to screen for leaf blast resistance at Ponnampet during *Kharif* 2014. Rice germplasm lines were sown in two replications for blast disease reaction using Uniform Blast Nursery (UBN). The details of experimental material used for screening of leaf blast resistance are presented in Table 2.

Table 1. The details of experiments conducted during the course of investigation

Sl. No.	Experiments	Season/Year	Location of work
1	a) Screening of germplasm lines for leaf blast resistance and assessment of variability and diversity b) <i>Per se</i> performance evaluation for yield and blast resistance	<i>Kharif</i> 2014	AHRS, Ponnampet, Karnataka
2	a) Developments of F ₁ 's b) Selfing of F ₁ 's	Summer 2015 <i>Kharif</i> 2015	ZAHRS, Shivamogga,
3	a) Descriptive statistics and variability of F ₂ segregating population b) Screening of F ₃ segregating population under natural epiphytotic conditions for leaf blast resistance	Summer 2016 <i>Kharif</i> 2016	ZAHRS, Shivamogga AHRS, Ponnampet
4	a) Molecular analysis of leaf blast resistance in segregating population	<i>Kharif</i> 2016	Department of Biotechnology, UAS, GKVK, Bengaluru.

Table 2. List of germplasm lines screened for leaf blast resistance under natural epiphytotic conditions during *Kharif* 2014 at AHRS, Ponnampet

Sl. No.	Germplasm	Pedigree
1	Kiruwana	Landrace
2	Puttabatta	Landrace
3	Biliya	Landrace
4	Akkalu	Landrace
5	Kesari	Landrace
6	Ambemori	Landrace
7	Bheemsali	Landrace
8	Chamundi	Landrace
9	Gandasaali	Landrace
10	Amruth	Landrace
11	Chittiga	Landrace
12	Doddaabhilasha	Landrace
13	Jeerigesanna	Landrace
14	Kempu madras	Landrace
15	Mysuru mallige	Landrace
16	IET sanna (KHP-11)	Selected from IET 8116
17	Jaya (IET-723)	TN1 × T 141
18	MTU-1001	Vajram × MTU 7014
19	Jyothi	Ptb-10 × IR-8 (HS)
20	MO-4	IR 8 × Ptb 20 (HS)
21	JGL-1798	Samba Mahsuri × Kavya
22	BPT-5204	(GEB 24 × TN 1) × Mahsuri
23	Hemavathi	Introduction from Bangladesh
24	Intan	Introduction from Indonesia
25	Tunga	Progeny of (Pankaj × Mahsuri) × TKM 6
26	IR-64	IR 5657-3-3-3-1 × IR 2061-465-1
27	Tadukan	Philippine indica cultivar (Luzon)
28	Tetep	Vietnamese indica cultivar
29	CO-39	Culture 340 × Kannagi
30	HR-12	Indica cultivar
31	CO-45	Rathu Heenathi × IR 3403 - 261 – 1
32	FR-43B	Sister line of FR-13A
33	KPR-1	Selected from DRR entries
34	KPR-2	Selected from DRR entries
35	FR-13A	Cultivated variety

3.1.1.3 Uniform Blast Nursery (UBN)

It is a mixture of naturally existing blast strains in the hotspot locality. The screening procedure of UBN for leaf blast resistance (Ou, 1965) is presented as follows.

- Nursery beds were raised of 0.50 m width with 50.00 m length under upland conditions
- Two rows of most susceptible checks (CO-39 and HR-12) were sown all along the borders to serve as a source of inoculums for spreading the disease
- Each germplasm line was planted in single row of 50 cm length with a row spacing of 10 cm
- The susceptible and resistant checks were sown after every 10 rows of test material
- Infected leaves, nodes and panicles were chopped and spread in spreader rows
- The proper management practices were followed to establish to spread the disease in the nursery

3.1.1.4 Scoring for leaf blast resistance

Disease scoring in germplasm lines was carried out after 30 to 35 days after sowing according to the standard evaluation system with 0 to 9 scale (SES, IRRI, 1996) after observing disease symptoms on most susceptible checks (Co-39 and HR-12). The detail descriptions of scores were presented in the Table 3.

The germplasm line exhibiting reactions of score 0 to 1 were considered as highly resistant, 2 as resistant, 3 to 4 as moderately resistant, 5 to 6 as moderately susceptible, 7 as susceptible and while those showing reactions that scored 8 to 9 were highly susceptible.

3.1.1.5 Scoring for neck blast resistance

Neck blast disease scoring was done after maturity stage using 0-9 scale of IRRI, 1996 by observing lesions on the neck, which are grayish brown and cause girdling, finally making the neck and the panicle fall over. The detail descriptions of scores were presented in the Table 4.

The germplasm line exhibiting reactions of score 0 considered as highly resistant, 1 as resistant, 3 as moderately resistant, 5 as moderately susceptible, 7 as susceptible and while those showing reactions that scored 9 were highly susceptible.

Table 3. Standard scale for screening rice germplasm lines for leaf blast disease resistance

Disease scale	Symptoms description
0	No lesions observed
1	Small brown specks of pin-point size or larger brown specks without sporulating center
2	Small roundish to slightly elongated, necrotic grey spots, about 1-2 mm in diameter, with a distinct brown margin
3	Lesion type is the same as in scale 2, but a significant number of lesions are on the upper leaves
4	Typical susceptible blast lesions 3 mm or longer, infecting less than 4 <i>per cent</i> of the leaf area
5	Typical blast lesions infecting 4-10 per cent of the leaf area
6	Typical blast lesions infection 11-25 per cent of the leaf area
7	Typical blast lesions infection 26-50 per cent of the leaf area
8	Typical blast lesions infection 51-75 per cent of the leaf area and many leaves are dead
9	More than 75 <i>per cent</i> leaf area affected

Table 4. Standard scale for screening rice germplasm lines for neck blast disease resistance

Disease scale	Symptoms description
0	No incidence
1	Less than 5 per cent infected panicles
3	5-10 per cent infected panicles
5	11-25 per cent infected panicles
7	26-50 per cent infected panicles
9	More than 50 per cent infected panicles

3.1.2. Recording of observations for agro-morphological characters

Observations on randomly five plants were selected in each genotype per replication. The selected plants were tagged for recording observations on various agro-morphological characters. The selected plants were harvested separately.

3.1.2.1. Days to 50 per cent flowering

The total number of days taken from sowing to opening of first flower in 50 per cent of the plants in each row was recorded.

3.1.2.2 Days to maturity

Days taken to complete physiological maturity were recorded from the day of sowing.

3.1.2.3 Plant height (cm)

Plant height was measured in centimeters from the base of the plant to the apex of the panicles excluding awns was measured at maturity.

3.1.2.4 Panicle length (cm)

Length of the panicle was measured in centimeters from flag leaf node to the tip of panicle.

3.1.2.5 Number of tillers per plant

Total number of tillers per hill was recorded by counting both the productive and unproductive tillers.

3.1.2.6 Number of productive tillers per plant

The number of productive tillers bearing panicles per plant was recorded by excluding the tillers which did not bear panicles.

3.1.2.7 Grain yield per plant (g)

Total weight of all the filled grains threshed from harvested labeled plants in each germplasm line was measured in grams.

3.1.2.8 Test weight (g)

Weight in grams of one thousand randomly selected grains was measured using electronic balance.

3.1.2.9 Grain length (mm)

Average grain length of randomly selected handful of grains was used for recording grain length and breadth using INDOSAW grain analyzer.

3.1.2.10 Grain width (mm)

Average grain width of randomly selected handful of grains was used for recording grain length and breadth using INDOSAW grain analyzer.

3.1.2.11 L: B Ratio

Average of the ratio of the length to the breadth was used for recording grain length and breadth using INDOSAW grain analyzer.

3.1.3 Per se performance of rice germplasm lines for yield and its related traits

The performance of germplasm lines were evaluated and compared over KPR-2 (recently released blast resistant variety) for yield and its related traits viz., days to 50 per cent flowering, days to maturity, plant height, total number of tillers per plant, number of productive tillers per plant, panicle length, grain yield per plant, grain length, grain breadth, L:B ratio and test weight.

3.1.4 Statistical analysis

3.1.4.1 Analysis of the design of experiment

The collected data on individual trait was subjected to analysis of variance by adopting randomized block design to test the null hypothesis that there are no genotypic differences for the characters studied. The analysis of variance was done according to Panse and Sukhatme (1985) in the following form.

Analysis of variance

Source	D.f.	Sum of squares	Mean sum of squares	F-cal
Replications	r-1	RSS	RMS	
Treatments	t-1	Tr. SS	Tr.MS	Tr. MS/ ESS
Error	(r-1) (t-1)	ESS	EMS	
Total	n-1	TSS		

3.1.4.2 Estimation of mean, range, standard error of mean, standard error of difference and critical difference

3.1.4.2.1 Mean

Mean was the sum of all observations in a sample divided by the total number of observations (n).

$$\text{Mean} = \frac{\sum_{i=1}^n X_i}{n}$$

Where,

x_i = i^{th} observation of a population

n = Number of observations

3.1.4.2.2 Range

Range was the minimum and maximum values of the observations in a sample of genotypes.

3.1.4.2.3 Standard error

It was the measure of uncontrolled variation present in a sample which was estimated by dividing the standard deviation (SD) by the square root of number of observations (n) in the sample and was denoted by SE.

$$SE = \frac{SD}{\sqrt{n}}$$

3.1.4.2.4 Variance

Variance is defined as average squared difference of each observation from the mean data. It is expressed as the sum of squares of the deviations of all observations of a sample from its mean and divided by (n-1), where n is the number of observations. It is estimated by the following formula,

$$\text{Variance } (\sigma^2) = \frac{\sum x^2 - \frac{(\sum x)^2}{n}}{n - 1}$$

Where,

X_i = i^{th} observation of a population

n = Number of observations

3.1.4.2.5 S.E. of mean

The S.E. of mean difference was calculated as

$$\text{S. E. of mean} = \sqrt{\sigma^2 e} / r$$

3.1.4.2.6 S. E. of difference

The standard error of difference between two means was calculated as

$$\text{S. E. of difference [S.E. (d)]} = \text{S. E (m)} \times \sqrt{2}$$

3.1.4.2.7 Critical difference

The critical difference between any two means was calculated as

$$\text{C. D.} = \text{S.E.(d)} \times \text{table 't' at error d.f.}$$

3.1.4.3 Estimation of Variability components

3.1.4.3.1 Estimation of components of variation

The phenotypic and genotypic variances were calculated by utilizing the respective mean square values from the variance table (Johnson *et al.*, 1955).

- i. Environmental variance = $\sigma^2 e = \text{EMS}$
- ii. Genotypic variance = $\sigma^2 g = (\text{GMS} - \text{EMS}) / r$
- iii. Phenotypic variance = $\sigma^2 p = \sigma^2 g + \sigma^2 e$

Where,

GMS = Genotypic mean sum of squares

EMS = Error mean sum of squares

r = Number of replications

3.1.4.3.2 Estimation of coefficients of variation

The genotypic and phenotypic coefficients of variation were calculated by the formula suggested by Burton (1952).

- i. Genotypic coefficient of variation (GCV)

$$\text{GCV (\%)} = \frac{\sqrt{\sigma^2 g}}{\bar{X}} \times 100$$

Where,

$$\sigma^2 g = \frac{\text{Mean sum of square due to genotypes} - \text{Mean sum of square due to error}}{r}$$

Here,

$\sigma^2g = Vg$ = Genotypic variance

$\bar{X}$ = General mean of the character

r = Number of replications

ii. Phenotypic coefficient of variation (PCV)

$$PCV (\%) = \frac{\sqrt{\sigma^2p}}{\bar{X}} \times 100$$

Where,

σ^2p = Genotypic variance + Mean sum of square due to error

Here,

$\sigma^2p = Vp$ = Phenotypic variance

PCV and GCV were classified as suggested by Shivasubramanian and Menon (1973) into low (0 – 10 %), Moderate (10 – 20 %) and High (>20 %).

3.1.4.3.3 Estimation of heritability (broad sense)

Heritability in broad sense was estimated for various characters as per the formula suggested by Hanson *et al.* (1956).

$$h^2(\text{b.s.}) = \left(\frac{\sigma^2g}{\sigma^2p} \right) \times 100$$

Where,

h^2 = Heritability percentage in broad sense

σ^2g = Genotypic variance

σ^2p = Phenotypic variance

Heritability per cent was classified as suggested by Robinson *et al.* (1949) into low (0 – 30 %), moderate (30 – 60 %) and high (> 60 %).

3.1.4.3.4 Estimation of genetic advance (G.A.)

The extent of genetic advance expected through selection for each character was calculated as per the formula suggested by Johnson *et al.* (1955).

$$G.A. = \left(\frac{\sigma^2g}{\sigma^2p} \right) \times \sigma p \times K$$

OR

$$G.A. = h^2 \times \sigma p \times K$$

Where,

h^2 = Heritability percentage in broad sense

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

K = Selection differential (2.06 at 5 % selection intensity, Lush, 1949)

σ_p = Phenotypic standard deviation

3.1.4.3.5 Genetic advance as per cent of mean

$$\text{G.A. as per cent mean} = \left(\frac{\text{G.A.}}{\bar{X}} \right) \times 100$$

Where,

G.A. = Genetic advance

$\bar{X}$ = Mean of the character

The genetic advance as per cent of mean was categorized as suggested by Johnson *et al.* (1955) as low (0 – 10 %), moderate (10 – 20 %) and high (>20 %).

3.1.4.4 Genetic diversity study

Genetic divergence is an efficient and effective tool to select the genetically divergent parents for choosing of parents for hybridization programme and helps to obtain desirable combinations in the segregating generations.

The genetic divergence between genotypes was estimated using Mahalanobis's D^2 statistic (1936). The genetic distance between any two genotypes was computed using the formula.

$$D^2 = \sum \lambda_{ij} \sigma a_i \sigma a_j$$

Where,

D^2 = Square of generalized distance

λ_{ij} = Reciprocal of the common disposal matrix

$\sigma a_i = (\mu_{i1} - \mu_{i2})$

$\sigma a_j = (\mu_{j1} - \mu_{j2})$

μ = General mean

Since the formula for computation requires inversion of higher order determinant, transformation of the original correlated unstandardized character mean (Xs) to standardize uncorrelated variable (Ys) was done to simplify the

computational procedure. The D^2 values were obtained as the corresponding uncorrelated (Ys) values of any two uncorrelated families (Rao, 1952).

3.1.4.4.1 Clustering genotypes

All the $n(n-1)/2$ values were clustered using Tocher's method as described by Rao (1952).

3.1.4.4.2 Intra cluster distance

The intra cluster distances were calculated by formula given by Singh and Chowdhary (1977).

$$\text{Square of the intra cluster distance} = \frac{\sum D_i^2}{n}$$

Where,

$\sum D_i^2$ = sum of distance between all possible combinations of the entries included in a cluster.

n = number of possible combinations of the entries included in the cluster.

3.1.4.4.3 Inter cluster distance

The inter cluster distances were calculated by the formula described by Singh and Chowdhary (1977).

$$\text{Square of the inter cluster distance} = \frac{\sum D_i^2}{n_i n_j}$$

Where,

$\sum D_i^2$ is the sum of distance between all possible combinations ($n_i n_j$) of the entries included in clusters (i and j).

n_i = Number of entries in cluster i

n_j = Number of entries in cluster j

3.1.4.4.3 Contribution of individual characters towards genetic divergence

The character contribution towards genetic divergence was computed using the method given by Singh and Chowdhary (1977). In all the combinations, each character was ranked on the basis of $d_i = y_i^j - y_i^k$ values.

Where,

d_i = Mean deviation

y_i^j = Mean value of the j^{th} genotype for the i^{th} character and

y_i^k = Mean value of the k^{th} genotype for the i^{th} character.

Rank 'I' is given to the highest mean difference and rank 'P' is given to the lowest mean difference Where, P is the total number of characters. Finally, the number of times that each character appeared in the first rank is computed and per cent contribution of characters towards divergence was estimated.

3.2 Assessment of parental polymorphism

Among the screened germplasm lines (Table 2), the selected parents (Jyothi × Kiruwana) discussed in the section 4.2.1 were analyzed for polymorphism using SSR marker after isolating DNA from the leaf samples of 21 days old seedlings using CTAB (Cetyl Trimethyl Ammonium Bromide) method (Doyle and Doyle, 1990).

3.2.1 DNA isolation

3.2.1.1 Requirements:

- Leaf samples were collected from field and stored immediately at -70°C.
- Cetyl Trimethyl Ammonium Bromide (CTAB) extraction buffer (100ml)
 - CTAB 2 per cent (w/v) Tris HCl (pH 8.0) 100 mM
 - Sodium Chloride 4 M
 - EDTA 20 mM

(Autoclave ris, Sodium Chloride and EDTA and add 2 % CTAB was after autoclaving and preheat the buffer before using).

- 0.2 per cent β – Mercapto ethanol (added freshly)
- Tris EDTA (TE) buffer
- TrisHCl (pH 8.0) 10 mM
- EDTA (pH 8.0) 1 mM

(Dissolved and made up to 100 ml, autoclave and store at 4°C)

- 2 per cent Polyvinyl Poly Pyrrolidone (PVP)
- Ice cold Isopropanol

- Chloroform: Isoamyl alcohol 24:1 (v/v)
- Sodium acetate (3.0 M, pH 7.0) (pH adjusted using glacial acetic acid)
- Absolute ethanol and 76 % ethanol (stored at -20°C)
- RNase A: 10 mg/ml (RNase A was dissolved in TE buffer and stored at -20°C).

3.2.1.2 Protocol for DNA extraction

- Leaf samples (Approximately 2 g) were cut into small bits with sterile scissors and transferred to prechilled mortar
- The leaf tissues were frozen using liquid nitrogen and ground to fine powder
- The fine powder was allowed to thaw in 10 ml of preheated extraction buffer in polypropylene centrifuge tubes and incubated for 30 minutes at 65°C in water bath with occasional mixing
- The tubes were removed from the water bath and equal volume of chloroform: Isoamyl alcohol mixture (24:1) v/v was added and mixed by inversions for 15 minutes
- The contents of polypropylene centrifuge tubes were centrifuged at 10000 rpm for 10 minutes at room temperature
- The clear aqueous phase was transferred to a new sterile tube and equal volume of ice cold isopropanol was added and mixed gently by inversion and then kept in the freezer at 4°C for the precipitation of DNA
- Using blunt end tips, the precipitate was pooled out into a micro centrifuge tube and air dried after removing the supernatant by brief spin
- 500 µl of chloroform: Isoamyl alcohol mixture was added and centrifuged at 10000 rpm for 10 minutes at room temperature
- Aqueous phase was transferred to another micro centrifuge tube without disturbing the inner phase
- To this, 2.5 volume of absolute alcohol and 1/10 volume of sodium acetate were added and kept for incubation overnight
- It was centrifuged and the supernatant was discarded. To this 500 µl of each 70 per cent and 100 per cent ethanol was used subsequently to wash the DNA by centrifugation

- The alcohol was discarded and DNA was completely air dried and DNA pellet was dissolved in 250 µl of TE and stored at 4°C

3.2.1.3 DNA quality assay using agarose gel electrophoresis

Materials

3X loading dye

- 5 M NaOH 200 µl
- 95 per cent Formamide (v/v) 95 ml
- 50 per cent Bromophenol blue (w/v) 50 g
- 0.5 per cent Xylene cyanol (w/v) 50 mg

(Dissolved in sterile double distilled water and made up the volume to 100ml)

10X Tris Borate EDTA buffer (TBE)

- Tris base 107.8 g
- Boric acid 55.2 g
- EDTA (Na₂.2H₂O) 9.2 g

(Dissolved in 800 ml of sterile double distilled water and made up to 1000 ml)

100bp Ladder

- 40 µl Loading dye
- 10 µl 100 bp Ladder
- 120 µl Sterilized double distilled water

(Total volume made up to 170 µl)

3.2.1.4 Protocol:

- The Pyrex gel casting plate's open ends were sealed with cello tape and the comb was placed properly in casting plate kept on a perfectly horizontal platform
- 0.8 per cent(0.8 g/100 ml) agarose was added to 1X TBE, boiled until the agarose dissolved completely and then allowed to cool. Ethidium bromide (DNA intercalating agent) was added when temperature reaches to 55 to 60°C as the staining agent

- Then it was poured into the gel mould with combs placed and allowed to solidify. The comb and the cello tape were removed after solidification of the agarose
- The casted gel was placed in the electrophoresis unit with wells towards the cathode and submerged with 1X TBE to a depth of about 1 cm

3.2.1.5 Loading the DNA samples

- 1 µl of the crude DNA sample was pipetted onto a parafilm and mixed well with 3 µl of 3X loading dye by pipetting up and down gently several times
- The mixed contents were transferred to the wells of agarose gel placed inside the 1X TBE buffer

3.2.2 Quantification of DNA

The genomic DNA was quantified spectrophotometrically both at 260 nm and 280 nm wavelengths. The absorbance at 260 nm allows the calculation of DNA concentration in the sample. An OD of 1 at 260 nm corresponds to 50 ng of double stranded DNA. A pure sample of DNA shows the ratio of OD 260/280 as 1.8. Ratio less than 1.8 indicated contamination in the isolation either with phenol or with proteins. The values higher than this indicate the presence of RNA in the isolation.

3.1.2.3 Normalization of the DNA concentration

Normalization of the DNA concentration was done to bring all the DNA concentrations to a relatively equal level (25ng µl⁻¹) by appropriate dilutions for PCR reaction. Dilution was done with double distilled sterile water.

3.1.2.4 PCR reaction mixture

PCR for SSR markers was performed in a total volume of 10µl containing 1X PCR buffer, 0.25 µM of each forward and reverse primers, 50 ng rice genomic DNA, 0.5 mM dNTPs mix and 1.2 units of *Taq* polymerase (Bangalore Genei, India). The PCR amplification conditions of the present study are mentioned below.

PCR amplification conditions

Steps	Temperature (°C)	Time (min)	No. of cycles
Initial denaturation	95	5	1
Denaturation	94	0.5	35
Primer annealing	*	0.5	
Primer extension	72	2	
Complete primer extension	72	8	1
Hold	4	Till removal	

*annealing temperature differs with primers.

3.1.2.5 Agarose gel electrophoresis

Agarose gel (3.00 %) was prepared using electrophoresis grade agarose (Bangalore Genei, India) in a volume of electrophoresis buffer (1X TBE) sufficient for casting a gel (220 ml for 20× 20 cm gel). Ethidium bromide was added at concentration of 10 mg/ml of gel. The gel was allowed to solidify fully before removing the combs and loading the sample. 7 µl of 3X loading dye was added to 20 µl of PCR products and mixed well before loading into the well. Care was taken to prevent mixing of samples between the wells. A voltage of 5 V/cm was given for a time period of three hours for separation of PCR fragments. The gel was viewed under UV trans-illuminator and the DNA banding pattern was recorded directly and later with Alpha Inno tech gel documentation instrument.

3.1.2.6 Selection of primers

Primers were linked to blast resistance used for present investigation was selected from Gramene.org. and from previous researchers data. Twenty two simple sequence repeats (SSR) markers were used for polymorphism between the parents and details of the primers are mentioned in the Table 5. Primers were synthesized from Indus Biosolutions, Bangalore.

3.3 Development of F₁'s and segregating population for reaction to blast disease

3.3.1 Development of F₁'s progeny

The parental lines selection for the development of F₁'s is discussed in the section 4.2.1. The selected parents (Jyothi and Kiruwana) were staggered sown for its synchronous flowering. The crossing was initiated during Summer2015 at ZAHRS, Shivamogga by hand emasculation and pollination technique as discussed below

Table 5. List of the SSR primers linked to blast resistance used in the present investigation

Sl. No.	Gene	Primers	Chr. no.	Forward sequence	Reverse sequence	Annealing temp. (°C)	Reference
1	<i>Pi 1</i>	RM 5926	11	ATATACTGTAGGTCCATCCA	AGATAGTATAGCGTAGCAGC	54	Fuentes <i>et al.</i> (2003)
2	<i>Pi 1</i>	RM 1233	11	GTGTAATCATGGGCACGTG	AGATTGGCTCTGAAGAAGG	58	Fuentes <i>et al.</i> (2008)
3	<i>Pi 1</i>	RM 224	11	ATCGATCGATCTTCACGAGG	TGCTATAAAAGGCATTCCGG	59	Fjellstrom <i>et al.</i> (2004)
4	<i>Pi 1</i>	RM 1223	4	CAGCGTCTCCAAGAACTCC	GCTACCAAGGTCAGAGTTGCC	56	Fuentes <i>et al.</i> (2008)
5	<i>Pi 1</i>	MRG 4766	11	ATTGCTGCAAGTGGGAGAC	AAGTGGAGGCAGTTCACCAC	59	Li <i>et al.</i> (2012)
6	<i>Pi 2</i>	AP-5930	6	CATGAAAGAAAGGAGTGCAG	ACAGAAATTGACAGCCAAAG	62	Fjellstrom <i>et al.</i> (2006)
7	<i>Pi 2</i>	RM 527	6	GGCTCGATCTAGAAAATCCG	TTGCACAGGTTGCGATAGAG	52	Jeung <i>et al.</i> (2007)
8	<i>Pi 2</i>	RM 6836	6	TGTTGCATATGGTGCTATTGA	GATACGGCTTCTAGGCCAAA	55	Eizenga <i>et al.</i> (2006)
9	<i>Pi 5</i>	RM 21	11	ACAGTATTCCGTAGGCACGG	GCTCCATGAGGGTGGTAGAG	54	Singh (2015) and Cuong <i>et al.</i> (2006)
10	<i>Pi 5</i>	RM 219	9	CGTCGGATGATGTAAAGCCT	CATATCGGCATTGCGCTG	64	Gramene.org
11	<i>Pi 5</i>	RM 524	9	TGAAGAGCAGGAACCGTAGG	TCTGATATCGGTTCTTCGG	65	Gramene.org
12	<i>Pi 20 (i)</i>	RM 7012	7	ATGATTTCTGCTCAGAGGGG	GGCCCAAAACAAAAGTCACTC	59	McCouch <i>et al.</i> (2002)
13	<i>Pi 20 (i)</i>	RM 1337	12	GTGCAATGCTGAGGAGTATC	CTGAGAAATCTGGAGTGCTTG	54	McCouch <i>et al.</i> (2002)
14	<i>Pi 20 (i)</i>	RM 28050	12	GATAAGACTTGGGTGGACATCACG	CTTCTATGGTCGCAATTCAAGATGC	58	IRGSP (2005)
15	<i>Pi 20 (i) / Pi 48</i>	RM 111	6	CACAAACCTTTGAGCACCGGGTC	ACGCCTGCAAGCTTGATCACCGG	58	Gramene.org
16	<i>Pi 39</i>	RM 492	2	CCAAAAATAGCGCGAGAGAG	AAGACGTACATGGGTCAGGC	58	Gramene.org
17	<i>Pi 2</i>	RM 3	6	ACACTGTAGCGGCCACTG	CCTCCACTGCTCCACATCTT	58	Gramene.org
18	<i>Pi 33</i>	RM 44	8	ACGGGCAATCCGAACAACC	TCGGGAAAACCTACCCCTACC	59	Gramene.org
19	<i>Pi 27 (i)</i>	RM 144	11	TGCCCTGGCGCAAAATTGATCC	GCTAGAGGAGATCAGATGGTAGTGCATG	59	Gramene.org
20	<i>Pi 35 (i)</i>	RM 1216	1	TTCCCCAATGGAACAGTGAC	AGGGTCTACCAACCCGATCTC	60	Nguyen <i>et al.</i> (2006) and Fukuoka <i>et al.</i> (2014)
21	<i>Pi 39</i>	RM 5757	4	CCTGAGACCATATGCTGCTG	GAGGGAGCATCATTAGCTGG	60	Gramene.org
22	<i>Pi 39</i>	RM 451	4	GATCCCTCCGTCAAACAC	CCCTTCTCTCTTCTCCTCAACC	55	Gramene.org

3.3.1.1 Hand emasculation

- The spikelets which are about to open in one or two days were selected for hand emasculation in the female parent (Jyothi).
- After selection, thinning of spikelets was carried out to keep 20 to 30 spikelets per panicle.
- The spikelets were made to open by slightly separating lemma and palea and anthers were removed with help of forceps during early morning hours (6.30 to 7.30 AM).
- The emasculated panicles covered with butter paper and labeled using price tags.

3.3.1.2 Pollination

- From the male parent (Kiruwana), anthers that are about to shed the pollen are collected on watch glass using forceps between 7.30 to 7.45 AM.
- The collected anthers were transferred to the emasculated spikelets with the help of camel brush after removing the cover.
- After pollination, again butter cover was placed and labeled and 35 days after crossing, F_1 's seeds were harvested.

3.3.2 Identification of true F_1 's progenies

The parents and their F_1 's were sown during *Kharif* 2015 at ZAHRS, Shivamogga in pro trays and after well establishment (21 days after sowing) they were transplanted at main field. Few days after transplantation, the leaf samples were collected from each parent and their F_1 's for DNA isolation using CTAB method (Doyle and Doyle 1990) to check the true hybridity of F_1 's. The SSR markers which were linked to blast resistance and polymorphic between parents were used to test true F_1 's, at the Department of Biotechnology, University of Agricultural Sciences, Bengaluru. The plants which exhibited both types of the parental bands are considered as true hybrid plants.

3.3.3 Development of segregating population for reaction to blast disease

The true F_1 plants were selfed and advanced to F_2 generation after recording observations on days to flowering, plant height, total number of tillers, productive tillers, days to maturity, grain yield per plant, grain length, grain width, test weight and husk color were recorded on the parents and the hybrid plants as explained in the section 3.1.2.

F_2 seeds were harvested from true F_1 hybrids. The harvested seeds were sown in nursery and seedlings were transplanted (21 days old) to the main field during Summer 2016 at Zonal Agricultural and Horticultural Research Station (ZAHRS),

Shivamogga. Observations were recorded on parents and in the F₂ population consisting of 226 individuals, as explained in the section 3.1.2. In addition to that husk color of F₂ individuals recorded based on the visual observation of parents, those were Jyothi type were considered as brown and Kiruwana type considered as black.

3.3.4 Statistical analysis

The details of statistical procedure adopted for analysis of F₂ segregating generation of cross as follows.

3.3.4.1 Descriptive statistics

The following descriptive statistics were calculated using SPSS (Ver.16.0) software.

3.3.4.1.1 Skewness and Kurtosis

Skewness, the third degree statistics and kurtosis, the fourth degree statistics were estimated as per Snedecor and Cochran (1994) to understand the nature of distribution of progenies for growth and yield related traits. The mean values of F₂ generation were used for estimation of coefficients of skewness and kurtosis using ‘SPSS’ software program. Kurtosis indicates the relative number of genes controlling the traits (Robson, 1956). Three types of kurtosis were recognized based on the kurtosis value which depends on distribution curve.

If kurtosis value = 3 = Normal curve = Mesokurtic

If kurtosis value > 3 = Leaping curve = Leptokurtic

If kurtosis value < 3 = Flat curve = Platykurtic

Similarly, the lack of symmetry *i.e.*, skewness was recognized based on the co-efficient of skewness values which range from -3 to +3. The type of distribution based on the skewness values are as follows.

If skewness value zero = Symmetrical distribution

If skewness value negative = Negatively skewed distribution

If skewness value positive = Positively skewed distribution

3.3.4.2 Estimation of variability parameters

Genotypic and phenotypic variances were estimated using the formula given by Weber and Moorthy (1952).

Genotypic variance (σ^2_g) = Phenotypic variance – Environmental variance

Phenotypic variance (σ^2_p) = Variance of F_2

Environmental variance = Variance of P_1 + Variance of P_2 + Variance of F_1

The estimation of coefficients of variation, heritability (broad sense), genetic advance (G.A.) and genetic advance as per cent of mean were discussed in the section 3.1.3.3

3.4 Identification of leaf blast resistant lines in segregating population

A total of 226 F_3 families were used for identification of leaf blast resistant lines under natural epiphytotic conditions during *Khari* 2016 using Uniform Blast Nursery (UBN) technique at AHRS, Ponnampet. The screening procedure and disease reactions followed as described in section 3.1.1.

In nursery, all F_3 families were screened and disease reactions were recorded using 0 to 9 scale of IRRI, 1996. Thirty days after sowing each family was transplanted to the main field by randomly selecting 10 individuals.

3.4.1 Observation recorded

The observations were recorded on 10 plants of each F_3 family on morphological, yield and yield related traits discussed in the section 3.1.2 and mean values presented in appendix II.

3.5 Molecular analysis of blast resistance in segregating population

The molecular analyses of F_3 families were carried out in the Department of Biotechnology, UAS, GKVK, Bengaluru. For DNA isolation the leaf samples were collected by mixing the equal quantities of leaf of all transplanted individuals within the family. The DNA isolation protocol, quantification and PCR amplification conditions followed were mentioned in the section 3.2.

3.5.1 Genotyping of F_3 population

The SSR markers which are polymorphic between parents and between the resistant and susceptible parents were used for genotyping the F_3 families. The markers alleles in all F_3 families scored based on the amplicon sizes of parents. The allele of female parent was always scored as “0”. Similarly the allele of male parent

was always scored as “1” and the progenies having the alleles from the parent were designated as “2”. Therefore, the allele scoring was carried out as follows:

‘0’- Allele of female parent Jyothi

‘1’- Allele of male parent Kiruwana

‘2’- Heterozygous (presence of both parental alleles)

3.5.2 Statistical analysis

3.5.2.1 Chi-square test

To test the goodness of fit of the F₃ segregating population to blast reaction, the phenotyping data as well as genotyping data were used. The Chi-square (χ^2) test was performed by comparing an observed frequency distribution with an expected one. The χ^2 value was calculated by the formula

$$\chi^2 = \sum \frac{(O - E)^2}{E}$$

Where,

O = Observed frequency

E = Expected frequency

The calculated (χ^2) value was tested against standard (χ^2) values at (n-1) degrees of freedom.

3.5.2.2 Simple linear regression

The genotypic and phenotypic data obtained in F₃ families were analyzed by simple linear regression method to know the association between the markers and the blast score. For each of the F₃ family, molecular data (0, 1 and 2) was considered as an independent variable (X) and phenotypic data for a particular character under consideration was considered as a dependent variable (Y). The linear regression model (Fisher, 1922) was used to study regression of linked polymorphic markers on blast score.

Regression model $Y = \alpha + \beta X + \varepsilon$

Where,

Y = Dependent variable

X = Independent variable

α = Y-intercept of regression line

β = Slope of the line (linear regression coefficient)

It is the amount of change in Y for each unit change in X

ε = Error / unexplained variance.

The means (X and Y), corrected sum of squares $\Sigma (X_i - \bar{X})^2$ and $\Sigma (Y_i - \bar{Y})^2$ and the corrected sum of products $\Sigma (X_i - \bar{X})(Y_i - \bar{Y})$ of variables X and Y were computed.

Where,

$i = 1$ to n and

$n = F_3$ families and the two parents showing association with the SSR primer under consideration.

Experimental Results and Discussion

IV EXPERIMENTAL RESULTS AND DISCUSSION

The biotic and abiotic stress is adversely affects the rice production; especially rice blast is one of the critical limiting factors responsible for reduction in rice production. In present study, germplasm lines were screened for leaf blast reaction and selected lines were utilized in production of segregating population with an aim of drawing information on reaction of blast disease resistance in field and laboratory conditions. The results obtained in the present study and its related discussions are presented under following headings

- 4.1 Screening of rice germplasm lines for blast resistance and assessment of genetic variability and diversity for yield and yield related traits
- 4.2 Selection of germplasm lines as parents and development of segregating population for blast resistance
- 4.3 Identification of leaf blast resistant lines in segregating population
- 4.4 Molecular analysis of leaf blast resistance in segregating population

4.1 Screening of rice germplasm lines for blast resistance and assessment of genetic variability and diversity for yield and yield related traits

4.1.1 Screening of rice germplasm lines for blast resistance

A total of 35 germplasm lines were screened during *Kharif* 2014 for blast resistance under field conditions by UBN technique at AHRS, Ponnampet (Plate 1) as this location was considered as hot spot for blast (Ram *et al.*, 2007). Disease reaction were scored after observing disease symptoms on most susceptible checks (CO-39 and HR-12) according to the standard evaluation system with 0 to 9 scale (IRRI, 1996). The response of germplasm lines to leaf blast reactions in UBN was presented in Table 6 and percentage was presented in Fig. 1.

Screening study revealed that, out of 35 germplasm, none of them recorded immune to the blast reaction. The resistant checks (Tadukan and Tetep), scored one and shown highly resistant response (5.71%), KPR-1, KPR-2, Kiruwana and IR-64 recorded resistant response (11.43%), whereas, Biliya recorded moderately resistant (2.86%). On contrary, Kesari, KHP-11, Hemavathi, Tunga, Jeerige sanna, Mysuru mallige, Gandasaali, Doddaabhilasha, Akkalu, MTU-1001, MO-4 and Kempu madras were shown moderate susceptibility (34.29 %). Puttabatta, Jyothi, JGL-1798, BPT-5204, CO-45, Amruth, Chamundi and FR-43B were shown are susceptible reaction (22.86 %), whereas Jaya, Intan, Ambemori, Bheemasaali, Chittiga and FR-13A were recorded highly susceptible (22.86%) to the leaf blast along with susceptible checks (CO-39 and HR-12).

Table 6. Reaction of germplasm lines to leaf blast disease under natural epidemic conditions

Sl. No.	Germplasm	Recorded scores	Description
1	Tadukan (C)	1	Highly Resistant
2	Tetep (C)	1	
3	KPR-1	2	Resistant
4	KPR-2	2	
5	Kiruwana	2	
6	IR-64	2	
7	Biliya	4	Moderately resistant
8	Kesari	5	Moderately susceptible
9	KHP-11	5	
10	Hemavathi	5	
11	Tunga	5	
12	Mysuru mallige	5	
13	Jeerige sanna	5	
14	Gandasaali	5	
15	Doddaabhilasha	6	
16	Akkalu	6	
17	MTU-1001	6	
18	MO-4	6	
19	Kempu madras	6	Susceptible
20	Puttabatta	7	
21	Jyothi	7	
22	JGL 1798	7	
23	BPT-5204	7	
24	CO-45	7	
25	Amruth	7	
26	Chamundi	7	
27	FR-43B	7	Highly susceptible
28	Jaya	8	
29	Intan	8	
30	CO-39 (C)	9	
31	HR-12 (C)	9	
32	Ambemori	9	
33	Bheemsali	9	
34	Chittiga	9	
35	FR-13A	9	

C-checks

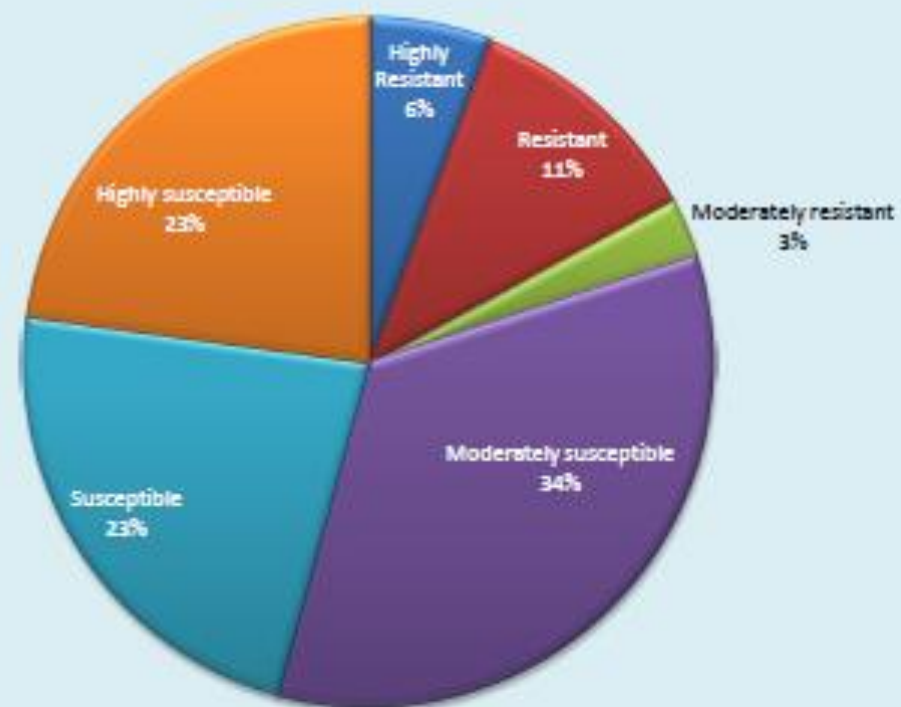


Fig. 1: Distribution of rice germplasm for reaction to leaf blast under uniform blast nursery



Plate 1. General view of germplasm lines for the leaf blast reaction at AHRS, Ponnampet

The responses of germplasm lines to leaf blast reaction, used in screening were varied from highly resistant to highly susceptible, indicating the germplasm used in the study were diverse in nature. The significant variations for leaf blast disease in rice were also noticed Chandrashekara *et al.* (2007), Idowu *et al.* (2013), Naveenkumar *et al.* (2013), Vasudevan *et al.* (2014), Dar *et al.* (2015), Hossain and Hegde (2016) and Sabin *et al.* (2016) under natural conditions. Whereas, Puri *et al.* (2009), Feng *et al.* (2014), Selvaraj *et al.* (2011a) and Ghazanfar *et al.* (2009) under artificial conditions noticed significant variations for blast. Hassan *et al.* (2017) and Zewdu *et al.* (2017) reported variations among genotypes under both natural and artificial conditions for leaf blast.

4.1.2 Per se performance of rice germplasm for yield and its related traits under blast hot spot region, Ponnampet.

The analysis of variance revealed significant differences among the genotypes for all the studied characters (Table 7) indicating the presence of substantial amount of variability among the genotypes. The significant differences for all studied traits were also noticed by Garg *et al.* (2011), Bekele *et al.* (2013), Vijaykumar *et al.* (2015), Chandramohan *et al.* (2016) and Srujana *et al.* (2017).

Germplasm lines were evaluated and compared over KPR-2 (recently released blast resistant variety) for agronomical traits viz., days to 50 per cent flowering, days to maturity, plant height, total number of tillers per plant, number of productive tillers per plant, panicle length, grain yield per plant, grain length, grain breadth, L:B ratio and test weight. The *per se* performance of 35 rice germplasm for yield and its related traits under blast hot spot region, Ponnampet is presented in Table 8.

4.1.2.1 Days to 50 per cent flowering

The significant variation was observed for days to 50 per cent flowering and it ranged from 100.50 to 126.50 days with an average of 114.51 days. The genotype Mysuru mallige was earliest among all the genotypes (100.50 days) followed by HR-12 (102 days) and Jyothi (102.50 days). The germplasm lines, Gandasaali and Chittiga has recorded maximum days to 50 per cent flowering (126.50 days) followed by Kesari and FR-43B (124.50 days). The *per se* performance indicated that among germplasm lines 16 lines were earlier than KPR-2 for days to 50 per cent flowering.

Table 7. Analysis of variance in rice germplasm lines under hot spot conditions for growth, yield and blast resistance reaction

		Mean sums of squares													
S. V.	d. f	DFF	DM	PH (cm)	TT	PT	PL (cm)	GY (g)	GL (mm)	GB (mm)	LB ratio	TW (g)	LB	NB	
Replications	1	2.06	13.73	162.37	0.20	0.86	0.26	0.54	0.0001	0.01	0.02	0.04	0.51	2.80	
Treatments	34	121.01**	193.24**	716.47**	21.40**	18.81**	11.58**	41.87**	0.99**	0.19**	0.26**	31.44**	10.86**	5.86**	
Error	34	3.50	3.73	22.24	2.90	2.12	2.36	1.70	0.02	0.02	0.03	2.87	0.13	1.27	

** - Significant at 1 % probability

DFF- Days to fifty percent flowering
 PT- Productive tillers per plant
 GB-Grain breadth (mm)
 NB- Neck blast
 DM- Days to maturity
 PH-Plant height (cm)
 GY-Grain yield per plant (g)
 TT- Total tillers per plant
 PL- Panicle length (cm)
 LB ratio: Length: Breadth ratio
 TW- Test weight (g)
 GL-Grain length (mm)
 LB-Leaf blast

Table 8. *Per se* performance of rice germplasm lines for yield and its related traits under hot spot conditions of rice blast at AHRS, Ponnampet during *Kharif*-2014.

Sl. No.	Germplasm lines	Days to 50% flowering	Days to maturity	Plant height (cm)	Total tillers/pl.	Productive tillers/pl.	Panicle length (cm)	Grain yield/pl. (g)	Test weight (g)	Grain length (mm)	Grain breadth (mm)	L: B ratio	LB	NB
1	Kiruwana	117.00	165.00	114.05	10.52	9.56	20.35**	22.54**	23.00*	9.12*	2.28	4.06**	2	3
2	Puttabatta	120.00	168.50	110.99	4.90	4.20	20.40**	11.53	25.00**	9.42**	3.07**	3.07	6	5
3	Biliya	116.50	144.00*	108.14	7.87	7.20	16.50	4.62	25.50**	9.80**	2.96**	3.32	4	9
4	Akkalu	112.00**	154.50	61.58	13.25	11.20	13.32	8.77	23.50**	8.71	2.47	3.53*	6	7
5	Kesari	124.50	150.50	55.03	17.64	15.72	11.30	6.92	20.50	9.33**	3.00**	3.11	5	5
6	KHP-11	118.00	153.50	91.61	11.60	10.00	19.45*	8.88	28.00**	9.72**	2.60	3.74**	5	7
7	Jaya	116.50	154.00	67.42	18.90	16.80	16.53	4.55	35.00**	9.46**	3.32**	2.85	8	7
8	MTU-1001	103.50**	139.00**	67.68	9.00	7.90	15.67	6.01	27.50**	9.27**	3.00**	3.09	6	5
9	Jyothi	102.50**	135.00**	71.17	9.85	8.14	19.11*	10.42	31.70**	9.04**	2.85	3.17	7	7
10	MO-4	104.00**	138.00**	59.15	12.01	10.08	15.47	9.75	30.00**	7.20	2.80	2.57	6	7
11	JGL -1798	108.00**	143.00**	57.24	15.65	14.53	17.02	5.50	16.50	8.81	2.67	3.31	7	9
12	BPT 5204	109.00**	146.50	94.28	8.88	8.46	16.93	8.17	19.50	9.88**	3.47**	2.85	7	5
13	Hemavathi	119.00	147.00	104.04	12.93	10.91	19.54*	12.64	22.00	9.10*	2.85*	3.19	5	6
14	Intan	121.50	151.00	100.25	13.39	11.58	18.61	7.50	23.50*	9.81**	2.69	3.65**	8	7
15	Tunga	121.00	168.00	91.84	19.68	17.86	19.38*	17.15	25.50**	10.41**	3.01**	3.46	5	5
16	IR-64	106.00**	143.50*	59.84	12.18	11.60	17.00	13.37	25.50**	9.59**	2.40	4.01	2	3
17	Ambemori	125.00	151.50	58.56	10.23	9.17	15.86	5.50	21.50	8.96**	3.08**	2.92	9	5
18	Bheemsali	119.00	145.00	71.94	9.70	8.50	20.17**	5.50	17.00	10.19**	3.13**	3.25	9	7
19	CO-45	114.00*	146.00	69.53	9.96	8.66	19.43*	9.20	27.50**	9.90**	3.18**	3.12	7	3
20	Chamundi	109.00**	141.50**	76.27	13.50	11.00	16.33	5.70	21.50	10.79**	2.90**	3.72**	7	5
21	FR-43B	124.50	163.50	61.31	12.50	11.55	16.70	6.00	23.50*	9.58**	3.24**	2.96	7	5

Contd....

22	Gandasaali	126.50	160.00	76.64	12.00	11.70	19.72*	5.50	24.50**	9.48**	2.79	3.40	5	3
23	Amruth	109.50**	149.00	69.60	11.65	9.83	16.07	8.80	18.00	10.24**	3.25**	3.15	7	5
24	Chittiga	126.50	166.00	80.73	12.54	11.11	19.93*	4.15	24.50**	9.36**	3.03**	3.09	9	7
25	Doddaabhilasha	119.00	162.50	63.41	12.50	10.60	16.88	4.50	24.00**	9.48**	2.53	3.76**	6	5
26	Jeerige sanna	114.00*	148.50	103.60	12.53	9.54	19.89*	3.38	28.00**	9.70**	3.14**	3.09	5	7
27	Kempu madras	108.00**	141.00**	99.56	14.00	11.50	18.06	3.50	24.50**	9.31**	3.33**	2.80	6	7
28	Mysuru mallige	100.50**	141.00**	58.02	16.53	14.17	14.26	7.13	28.00**	8.26	2.58	3.20	5	5
29	KPR1	117.00	148.00	81.25	14.50	12.50	16.40	15.00	20.00	8.83**	2.57	3.43	2	3
30	KPR2	118.00	148.50	63.95	18.50	17.20	15.90	15.90	19.00	8.25	2.61	3.17	2	3
31	FR13A	104.50**	143.00**	74.81	11.98	9.97	16.57	5.45	26.50**	8.89	3.21**	2.77	9	7
32	Tadukan (C)	122.50	166.00	96.05	15.00	13.75	20.09**	13.30	25.50**	9.40**	2.99**	3.14	1	3
33	Tetep (C)	121.50	171.00	99.01	13.45	12.70	20.68**	12.95	19.50	9.09**	2.60	3.50*	1	3
34	CO-39 (C)	108.00**	148.50	50.64*	10.46	9.10	14.42	4.00	24.00**	8.13	3.00**	2.71	9	8
35	HR-12 (C)	102.00**	146.00	53.95*	7.47	5.60	12.66	2.50	22.50	8.51**	2.38	3.60	9	9
Mean		114.51	151.07	77.80	12.49	10.97	17.33	8.46	24.43	9.28	2.88	3.25		
SEm±		1.32	1.37	3.34	1.20	1.03	1.09	0.92	1.20	0.09	0.07	0.11		
C.V.		1.64	1.27	6.06	13.61	13.28	8.86	15.39	6.94	1.32	3.56	4.86		
C.D. @ 5%		3.80	3.92	9.58	3.46	2.96	3.12	3.56	3.44	0.25	0.21	0.32		
C.D. @ 1%		5.10	5.22	12.87	4.64	3.97	4.19	3.55	4.62	0.34	0.28	0.43		

*- Significant at 5 % probability

**-. Significant at 1 % probability

LB-Leaf blast scores

NB- Neck blast scores

4.1.2.2 Days to maturity

The genotypes recorded an average 151.07 days for days to maturity and it ranged between 135.00 to 171.00 days. The line, Jyothi (135.00 days) matured earliest among the germplasm lines followed by MO-4 (138.00 days) and MTU-1001 (139.00 days). Maximum of 171.00 and 168.50 days maturity were recorded for Tetep and Puttabatta, respectively. Among 35 genotypes studied, ten genotypes were found earlier in maturity over KPR-2.

4.1.2.3 Plant height (cm)

The plant height varied 50.64 cm to 114.05 cm with an average value of 77.80 cm recorded in the rice germplasm lines studied. The genotype Kiruwana (114.05 cm) was tallest followed by Puttabatta (110.99cm), whereas the line CO-39 (50.64 cm) was dwarfest followed by HR-12 (53.95 cm) and these two lines were significantly dwarfer than KPR-2.

4.1.2.4 Total number of tillers per plant

The rice germplasm lines varied in number of total tillers per plant from 4.90 to 19.68 with the mean of 12.49. The genotype Tunga recorded highest number of total tillers per plant (19.68) followed by Jaya (18.90), while Puttabatta produced least number of tillers per plant (4.90) followed by HR-12 (7.47). None of the germplasm lines recorded significantly higher number total tillers per plant over KPR-2.

4.1.2.5 Productive tillers per plant

The germplasm lines have recorded an average of 10.97 productive tillers per plant and it ranged from 4.20 to 17.86. Tunga (17.86) has recorded highest productive tillers per plant followed by KPR-2 (17.20) and the germplasm line Puttabatta has recorded least number of productive tillers per plant (4.20). Among the studied 35 germplasm lines, none of them were found significantly higher number of productive tillers per plant than KPR-2.

4.1.2.6 Panicle length (cm)

The variation in the panicle length among 35 germplasm lines ranged from 11.30 to 20.68 cm with the mean value of 17.33 cm. The genotype Tetep had longest panicle length (20.68) followed by Puttabatta (20.40 cm), whereas Kesari (11.30 cm) and HR-12 (12.66 cm) showed lowest panicle length among the germplasm lines studied. Thirteen germplasm lines recorded significantly higher panicle length than KPR-2.

4.1.2.7 Grain yield per plant (g)

The results revealed that seed yield per plant for 35 genotypes ranged between 2.50 and 22.54 g, with the population mean of 8.46 g. The landrace Kiruwana (22.54 g) recorded highest seed yield per plant followed by Tunga (17.15 g), whereas the check entry HR-12 (2.50 g) recorded lowest seed yield per plant followed by Jeerige sanna (3.38 g) and Kiruwana recorded significantly higher grain yield per plant over KPR-2.

4.1.2.8 Test weight (g)

The variability for test weight in the studied germplasm material was ranged from 17.00 to 35.00 (g). The highest test weight recorded by Jaya (35.00) and lowest test recorded by JGL-1798 among the studied germplasm lines. Twenty three germplasm lines had significantly higher test weight than the KPR-2.

4.1.2.9 Grain length (mm)

The wide range for grain length was observed in the germplasm lines and it was ranged between 7.20 and 10.79 mm with mean value of 9.28 mm. The germplasm Chamundi recorded longest grain length (10.79 mm) followed by Tunga (10.41 mm). MO-4 (7.20 mm) recorded shortest grain length among germplasm lines studied.

4.1.2.10 Grain breadth (mm)

The *per se* performance for grain breadth among 35 genotypes ranged from 2.28 to 3.47 mm, with the mean of 2.88 mm. The genotypes, BPT-5204 reported broader grain breadth (3.47 mm) followed by FR-43B (3.24 mm). The germplasm line, Kiruwana narrower grain breadth (2.28 mm) followed by Akkalu (2.47 mm). There were 18 genotypes recorded significantly broader grain breadth than the KPR-2.

4.1.2.11 Length : Breadth ratio

The mean performance for length: breadth ratio of grain indicated wide variation between genotypes studied. The average L:B ratio of 3.25 was observed and it ranged from 2.57 to 4.06. The genotype Kiruwana showed highest L:B ratio of 4.06 while MO-4 showed 2.57 L:B ratio. There were seven germplasm lines recorded significantly higher than KPR-2 for L:B ratio.

4.1.2.12 Leaf blast

The leaf blast scores ranged from 1 to 9. The resistant checks Tadukan and Tetep recorded least scores over other germplasm lines, whereas the Ambemori, Bheemasali, Chittiga and FR-13 along with susceptible checks CO-39 and HR-12 recorded highest scores for leaf blast disease.

4.1.2.13 Neck blast

The neck blast scores ranged from 3 to 9. The genotype KPR-1, KPR-2, Kiruwana, IR-64, Tadukan, Tetep and CO-45 recorded least scores over other germplasm lines, whereas the Biliya and JGL-1798 along with susceptible check HR-12 recorded highest scores for neck blast disease.

4.1.3 Assessment of genetic variability in rice germplasm

The components of genetic variation viz. phenotypic co-efficient of variation (PCV), genotypic co-efficient of variation (GCV), broad sense heritability, genetic advance (GA) and genetic advance under selection expressed as per cent mean (GAM) were estimated for different quantitative characters studied in rice germplasm are presented in Table 9.

4.1.3.1 Days to 50 per cent flowering

The low GCV (6.69) and low PCV (6.89) values were recorded for this trait. The high heritability of 94.40 per cent, moderate genetic advance of 15.34 and moderate genetic advance expressed as per cent mean of 13.40 were recorded.

4.1.3.2 Days to maturity

The low GCV (6.44) and low PCV (6.60) were recorded for this trait. The high heritability for this trait was 96.20 per cent. The moderate genetic advance (19.67) and moderate genetic advance expressed as per cent mean (13.02) were recorded for this trait.

4.1.3.3 Plant height (cm)

The GCV (23.95) and PCV (24.70) values were high. The high heritability (94.00) coupled with high genetic advance (37.21) with high genetic advance expressed as per cent mean (47.82) were recorded for this trait.

4.1.3.4 Total number of tillers per plant

The high GCV of 24.35 per cent and high PCV of 24.70 per cent were recorded. The high heritability of 76.20 per cent, low genetic advance of 5.47 and high genetic advance expressed as per cent mean of 43.79 were recorded for this trait.

Table 9. Variability parameters for yield and its related traits in rice germplasm lines studied under hot spot conditions for blast

Sl. No.	Characters	Mean	Range		GCV (%)	PCV (%)	h ² (%)	GA	GAM
			Minimum	Maximum					
1	Days to 50% flowering	114.51	100.50	126.50	6.69	6.89	94.40	15.34	13.40
2	Days to maturity	151.07	135.00	171.00	6.44	6.60	96.20	19.67	13.02
3	Plant height (cm)	77.80	50.64	114.05	23.95	24.70	94.00	37.21	47.82
4	Total tillers per plant	12.49	4.90	19.86	24.35	27.90	76.20	5.47	43.79
5	Productive tillers per plant	10.97	4.20	17.86	26.34	29.50	79.70	5.31	48.44
6	Panicle length (cm)	17.33	11.30	20.68	12.39	15.23	66.20	3.60	20.76
7	Yield per plant (g)	8.46	2.50	22.54	52.95	55.14	92.20	8.87	104.75
8	Grain length (mm)	9.28	7.20	10.80	7.52	7.63	97.00	1.42	15.25
9	Grain breadth (mm)	2.88	2.28	3.47	10.27	10.87	89.30	0.58	20.00
10	L:B ratio	3.25	2.57	4.06	10.46	11.53	82.30	0.63	19.54
11	Test weight (g)	24.43	17.00	35.00	15.47	16.95	83.30	7.10	29.07
12	Leaf blast	5.77	1.00	9.00	40.14	40.63	97.60	4.71	81.68
13	Neck blast	5.31	3.00	9.00	28.49	35.52	64.30	2.50	47.08

4.1.3.5 Productive tillers per plant

The high values of GCV (26.34 %) and PCV (29.50 %) were recorded. The high heritability (79.70 %), low genetic advance (5.31) and high genetic advance expressed as per cent mean (48.44) were observed for this trait.

4.1.3.6 Panicle length (cm)

The moderate GCV (12.39 %) and moderate PCV (15.23 %) values were recorded. The heritability for this trait was high (66.20 %). Low genetic advance (3.60) and high genetic advance expressed as *per cent* mean (20.76) were recorded for this trait.

4.1.3.7 Grain yield per plant (g)

The GCV (52.95 %) and PCV (55.14 %) values were high. The heritability for this trait was high (92.20 %). The low genetic advance of 8.87 and high genetic advance expressed as per cent mean of 104.75 were recorded for this trait.

4.1.3.8 Grain length (mm)

The low GCV of 7.52 per cent and low PCV of 7.63 per cent were recorded. The high heritability of 97.00 per cent and low genetic advance (1.42) with moderate GAM (15.25) were recorded.

4.1.3.9 Grain breadth (mm)

The GCV and PCV values were moderate and its values are 10.27 and 10.87 per cent respectively. The high heritability of 89.30 per cent, low genetic advance (0.58) and high genetic advance expressed as per cent mean of 20.00 were recorded for this trait.

4.1.3.10 L:B ratio

The moderate GCV (10.46 %) and PCV (11.53 %) were recorded. The high heritability of 82.30 per cent and low genetic advance of 0.63 with moderate GAM of 19.54 was recorded.

4.1.3.11 Test weight (g)

The moderate GCV and PCV values were 15.47 and 16.95 per cent respectively and were moderate. The heritability for this trait was 83.30 per cent. The Low genetic advance of 7.10 and high genetic advance expressed as per cent mean of 29.07 were recorded for this trait.

4.1.3.12 Leaf blast scores

The high GCV and PCV values were recorded 40.14 and 40.63 per cent respectively and high heritability (97.60 %) also recorded. The low genetic advance of 4.71 and high genetic advance expressed as per cent of 81.68 were recorded for this trait.

4.1.3.13 Neck blast scores

The high GCV of 28.49 per cent and high PCV of 35.52 per cent were recorded. The high heritability of 64.30 per cent and low genetic advance of 2.50 with high GAM of 47.08 were recorded.

The high GCV and PCV were recorded for plant height, total number of tillers per plant, number of productive tillers per plant, grain yield per plant, leaf blast and neck blast scores. High PCV, GCV and further the differences between PCV and GCV values for most of the traits were small values indicates character under the influence of genetic control and less influenced by environmental conditions, indicating that these characters could be used as selection for crop improvement. These results are in accordance with reports of Vanishree *et al.* (2013), Madhubabu *et al.* (2017) for plant height; Selvaraj *et al.* (2011a) and Bekele *et al.*, (2013) for total number of tillers per plant; Selvaraj *et al.* (2011a), Bekele *et al.*, (2013) and Hosagoudar *et al.*, (2017) for number of productive tillers per plant; Selvaraj *et al.* (2011a), Bekele *et al.*, (2013), Shaikh *et al.*, (2017), Srujana *et al.* (2017) and Yugandhar *et al.* (2017) for grain yield per plant.

The moderate GCV and PCV recorded for panicle length, grain breadth, LB ratio, and test weight indicated that considerable amount of variability for these characters. The moderate GCV and PCV also recorded for panicle length and grain breadth by Bekele *et al.*, (2013); for LB ratio by Pratap *et al.*, (2012), Ravindra Babu *et al.*, (2012), Bekele *et al.*, (2013), Bhinda *et al.* (2017) and Madhubabu *et al.* (2017) and for test weight by Selvaraj *et al.* (2011a), Bekele *et al.*, (2013), Vanishree *et al.* (2013), Tandekar and Koshta (2014), Madhubabu *et al.* (2017), Shaikh *et al.* (2017) and Yugandhar *et al.* (2017).

The low GCV and low PCV were observed for days to 50% flowering, days to maturity and grain length (mm) indicates lower amount of variability for these characters. These findings are similar with the Ravindra Babu *et al.*, (2012), Paikhomba *et al.* (2014), Vijaykumar *et al.* (2015), Chandramohan *et al.* (2016), Bhinda *et al.* (2017), Madhubabu *et al.* (2017), Srujana *et al.* (2017), Shaikh *et al.*, (2017), Sangare *et al.* (2017) and Yugandhar *et al.* (2017) for days to 50 per cent flowering, Selvaraj *et al.* (2011a), Bekele *et al.* (2013), Tandekar and Koshta (2014) Vijaykumar *et al.* (2015), Bhinda *et al.* (2017), Madhubabu *et al.* (2017),

Shaikh *et al.* (2017) and Yugandhar *et al.* (2017) for days to maturity; Pratap *et al.* (2012), Ravindra Babu *et al.* (2012), Vanishree *et al.* (2013), Perera *et al.* (2014) and Bhinda *et al.* (2017) for grain length.

The knowledge of heritability of a character is important as it indicates the possibility and extent to which improvement is possible through selection. High heritability recorded for all the characters in this study. High heritability does not always indicate high genetic gain. Burton (1952) pointed out that the heritability in combination with intensity of selection and amount of variability present in the population influences gains to be obtained from selection. Therefore, heritability and genetic advance should be considered together in selection process for obtaining best segregants.

High heritability coupled with high genetic advance as percent mean were recorded for plant height, total number of tillers per plant, number of productive tillers per plant, panicle length, grain yield per plant, grain breadth, L: B ratio, test weight, leaf blast and neck blast scores indicates that these traits were not much influenced by environmental factors, Hence, these traits are mostly controlled by genetic factors and expected to respond to the direct selection for trait improvement. These observations are in accordance with Selvaraj *et al.* (2011a), Pratap *et al.* (2012), Vijaykumar *et al.* (2015), Srujana *et al.* (2017), Hosagoudar *et al.* (2017) and Shaikh *et al.* (2017) for plant height; Selvaraj *et al.* (2011a), Vijaykumar *et al.* (2015) and Srujana *et al.* (2017) for total number of tillers per plant; Selvaraj *et al.* (2011a), Vanishree *et al.* (2013), Perera *et al.* (2014), Hosagoudar *et al.* (2017) and Shaikh *et al.* (2017) for number productive tillers per plant; Pratap *et al.* (2012) for panicle length; Vijaykumar *et al.* (2015), Paikhomba *et al.* (2014), Vanishree *et al.* (2013), Srujana *et al.* (2017), Shaikh *et al.* (2017) and Yugandhar *et al.* (2017) for grain yield per plant; for grain breadth; Selvaraj *et al.* (2011a), Pratap *et al.* (2012), Chandramohan *et al.* (2016), Vanishree *et al.* (2013) and Yugandhar *et al.* (2017) for test weight; for leaf blast and for neck blast scores.

High heritability coupled with moderate genetic advance as percent mean were recorded for days to 50 per cent flowering, days to maturity, grain length and L:B ratio indicates that these traits controlled by the interaction of genetic and environmental components. The selection based on phenotypic observations may not be very effective and it is the role of both additive and non-additive gene effects in their inheritance, therefore, adoption of breeding procedures which could exploit both the gene actions would be a prospective approach (Krishna *et al.*, 2008 and Patil and Sarawgi, 2005). High heritability coupled with moderate genetic advance as percent mean were recorded for days to 50 per cent flowering by Ravindra Babu *et al.* (2012), Paikhomba *et al.* (2014) and Bhinda *et al.* (2017); for days to maturity

by Bekele *et al.*(2013), Bhinda *et al.* (2017), and Srujana *et al.* (2017);for grain length by Pratap *et al.* (2012), Bhinda *et al.* (2017) and Ravindra Babu *et al.*(2012), and for L:B ratio by Vanishree *et al.* (2013).

4.1.4 Assessment of genetic diversity in rice germplasm

4.1.4.1 Genetic diversity based on Mahalanobis generalized distance (D^2)

The genetic diversity among 35 rice germplasm was measured by employing D^2 statistics. Based on D^2 values, 35 germplasm lines were grouped into six clusters (Table 10) using Tocher's method given by Rao (1952). The dendrogram of germplasm into different clusters are presented in Fig. 2. Maximum number of germplasm lines (16) were grouped in cluster I followed by Cluster III (10). Cluster II had 6 genotypes and remaining Cluster IV, V and VI had solitary germplasm in each cluster. The genotypes within each cluster were closer to each other than the genotypes in different clusters. The overall composition of the clustering pattern showed that genotypes having leaf blast resistance are grouped in the same cluster.

4.1.4.2 Inter cluster distances

The intra and inter cluster distance are presented in Table 11 and the nearest and farthest clusters from each cluster based on D^2 values are given in Table 12. Inter cluster distance was higher than intra cluster distance indicating wider genetic diversity among the genotypes. The maximum inter cluster distance was observed between cluster II and IV (990.00) followed by between cluster IV and VI (767.97) and between cluster I and II (651.00) indicating wider genetic diversity among the genotypes between these groups (Subudhi *et al.*, 2009, Garg *et al.*, 2011). The F_1 's developed from the selected members of these clusters would produce maximum heterosis and highly variable population in the segregating generations (Souroush *et al.*, 2004). The minimum inter cluster distance was found between cluster I and III (250.58) followed by between cluster I and IV (252.15). The genotypes in these clusters are genetically very close and hence, hybridization among the varieties will not give successful genotypes (Garg *et al.*, 2011).

4.1.4.3 Intra cluster distances

The maximum intra cluster distance was recorded in clusters III (202.08) followed by cluster II (170.78) and cluster I (145.09). Hence, selection within these clusters may be exercised based on the highest area for the desirable traits, which would be made useful in improvement through inter varietal hybridization (Joshi *et al.*, 2008).

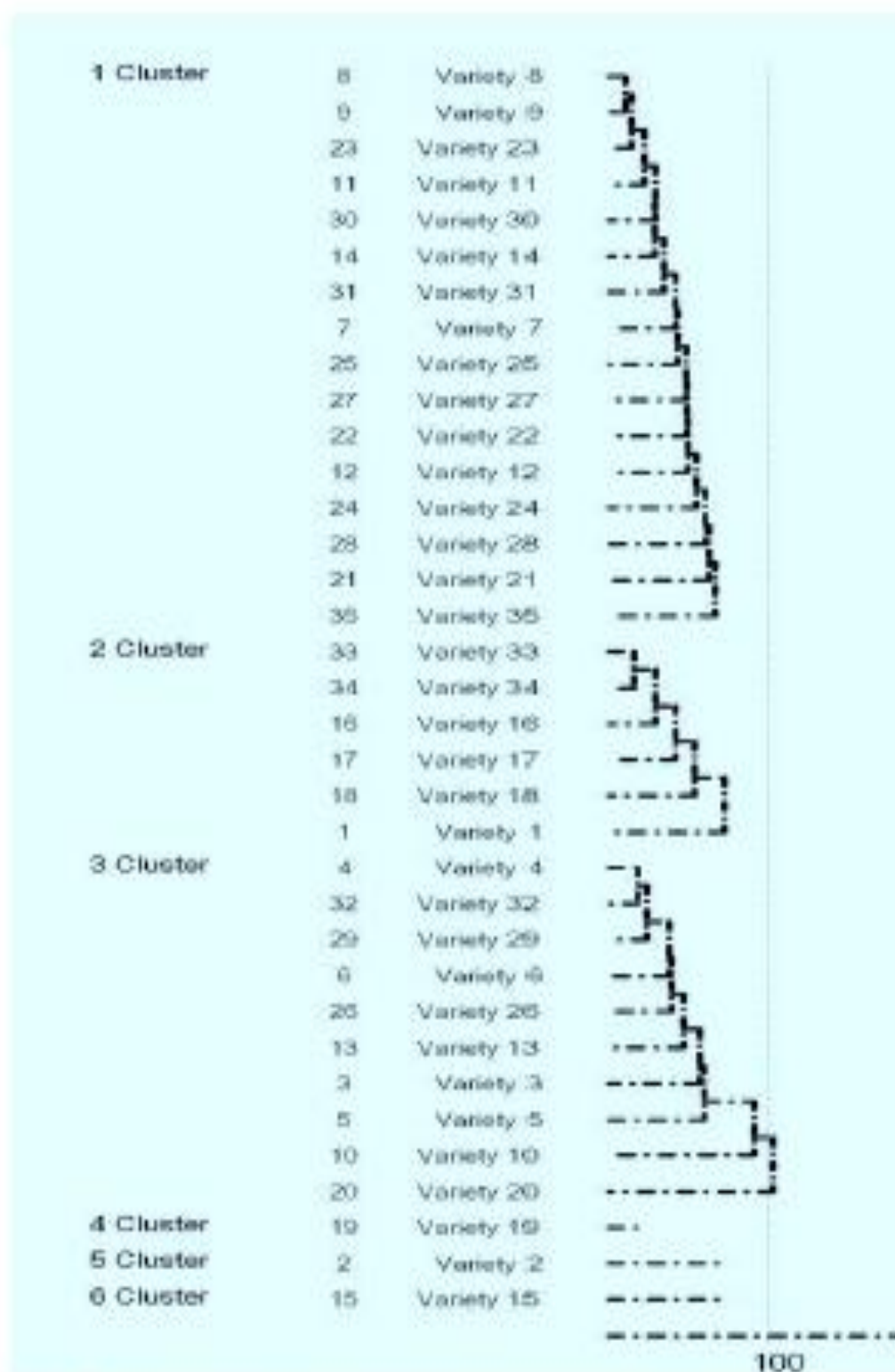


Fig.2: Dendrogram of 35 rice germplasm lines grouped into six different clusters

Table 10. Grouping of 35 rice germplasm lines based on D² values under hot spot conditions of blast

Clusters	Number of germplasm	Germplasm number	Germplasm lines	Characters
I	16	8, 9, 23, 11, 30, 14, 31, 7, 25, 27, 22, 12, 24, 28, 21 and 35	MTU-1001, Jyothi, CO-45, JGL-1798, Jeerige Sanna, Intan, Kempu madras, Jaya , FR-43B, Amruth, Bheemsali, BPT-5204, Chamundi, Chittiga, Ambemori and FR-13A	Susceptible to highly susceptible
II	6	33, 34, 16, 17, 18 and 1	KPR-1, KPR-2, IR-64, Tadukan, Tetep and Kiruwana	Resistant to highly resistant leaf blast
III	10	4, 32, 29, 6, 26, 13, 3, 5, 10 and 20	Akkalu, Mysuru mallige, Doddaabhilasha, KHP-11, Gandasaali, Hemavathi, Biliya, Kesari, MO-4 and HR-12	Moderately resistant to moderately susceptible
IV	1	19	CO-39	Highly susceptible
V	1	2	Puttabatta	Susceptible
VI	1	15	Tunga	Moderately susceptible

Table 11. Average intra and inter cluster distances in rice germplasm lines

Clusters	I	II	III	IV	V	VI
I	145.09	651.90	250.58	252.15	275.59	420.23
II		170.78	374.08	990.00	566.58	426.66
III			202.08	397.68	332.21	420.70
IV				0.00	396.60	767.97
V					0.00	196.57
VI						0.00

Table 12. The nearest and farthest clusters from each cluster based on D² values in rice germplasm lines

Sl. No.	Clusters	Nearest Cluster	Farthest cluster
1	I	III (250.58)	II (651.90)
2	II	III (374.08)	IV (990.00)
3	III	I (250.58)	VI (420.70)
4	IV	I (252.15)	II (990.00)
5	V	VI (196.57)	II (566.58)
6	VI	V (196.57)	IV (767.97)

4.1.4.4 Cluster mean analysis

The results of cluster means of yield and yield related characters are presented in the Table 13. Maximum mean for days to 50 per cent flowering (121.00) was observed in cluster VI followed by cluster V (120.00), while minimum cluster mean of 108.00 was observed in cluster IV. The maximum mean for days to maturity (168.50) was observed in cluster V followed by cluster VI (168.00) and minimum mean (147.72) was observed in cluster I.

The highest mean for plant height was recorded in cluster V (110.99 cm) followed by cluster VI (91.84 cm) while, lowest mean of 50.64 cm was shown by clusters IV. Maximum mean of number of tillers recorded in cluster VI (19.68) followed by III (12.38). While, minimum mean of 4.90 was observed in cluster V. The number of productive tillers had a highest mean of 17.86 in cluster VI followed by 12.89 in cluster II and lowest mean of 4.20 in cluster V.

The highest cluster mean of panicle length was observed in cluster V (20.40 cm) and it was lowest for families under cluster IV (14.42 cm). Grain yield per plant recorded highest mean of 17.15 g in cluster VI and lowest mean of 4.00g in cluster IV. The cluster mean of grain length was recorded highest for cluster VI (10.41 mm) and it was lowest under cluster IV (8.13 mm). Cluster I had a maximum mean of 3.09 mm for grain breadth and cluster II recorded minimum mean of 2.57mm. L:B ratio recorded maximum mean in cluster II (3.55), while minimum mean of 2.71 was observed in cluster IV. Test weight, maximum mean was recorded in the cluster VI (25.50 g), while clusters II depicted minimum mean of 22.02 g. Clusters V recorded a maximum mean of 9.00 for leaf blast score whereas minimum mean of 1.67 was observed in under cluster II. The cluster mean of neck blast score was recorded highest for cluster IV (8.00) and it was lowest under cluster II (3.00).

4.1.4.5 Contribution of each trait to total divergence

The contribution of each trait to total divergence is presented in Table 14. Among the traits studied, reaction to the leaf blast contributed maximum divergence of 46.89 per cent followed by grain length (16.30 %), days to maturity (12.44 %), days to 50 per cent flowering (6.72 %), yield per plant (4.87 %) and plant height (4.71 %). The least contribution of trait to total divergence was by neck blast (0.67 %), grain breadth (1.34 %), test weight (2.35 %) and L: B ratio (3.70 %). The traits viz., reaction to leaf blast, grain length (mm), days to maturity and days to 50 per cent flowering themselves contributed 82.35 per cent towards total divergence. Hence, these characters should be given importance during hybridization and selection in the segregating population. Remaining traits had very little or no contribution towards genetic divergence and hence, they were of less importance.

Table 13. Cluster mean values for yield and yield related traits in rice germplasm lines evaluated at AHRs, Ponnampet during *Kharif*-2014

Sl. No.	Clusters	No. of genotypes	Days to 50 % flowering	Days to maturity	Plant height (cm)	Total tillers/pl.	Productive tillers/pl.	Panicle length (cm)	Grain yield/pl. (g)	Grain length (mm)	Grain width (mm)	L: B ratio	Test weight (g)	LB	NB
1	I	16	113.44	147.72	76.50	12.14	10.51	17.68	6.21	9.57	3.09	3.11	24.98	7.31	5.63
2	II	6	117.00	157.00	85.69	14.02	12.89	18.40	15.51	9.04	2.57	3.55	22.02	1.67	3.00
3	III	10	114.20	149.70	73.16	12.38	10.72	15.91	7.12	8.96	2.69	3.34	24.85	5.50	6.10
4	IV	1	108.00	148.50	50.64	10.46	9.10	14.42	4.00	8.13	3.00	2.71	24.00	9.00	8.00
5	V	1	120.00	168.50	110.99	4.90	4.20	20.40	11.53	9.42	3.07	3.07	25.00	6.00	5.00
6	VI	1	121.00	168.00	91.84	19.68	17.86	19.38	17.15	10.41	3.01	3.46	25.50	5.00	4.00

LB: Leaf blast

NB: Neck blast

Table 14. Per cent contribution of characters for the diversity of rice germplasm lines

Sl. No.	Character	Percent contribution (%)
1	Leaf blast	46.89
2	Grain length (mm)	16.30
3	Days to maturity	12.44
4	Days to 50 per cent flowering	06.72
5	Per plant yield (g)	04.87
6	Plant height (cm)	04.71
7	L:B ratio	03.70
8	Test weight (g)	02.35
9	Grain breadth (mm)	1.34
10	Neck blast	0.67

Since varieties with narrow genetic base are increasingly vulnerable to diseases and adverse climatic changes, availability of the genetically diverse genotypes for hybridization programme become more important (Garg *et al.*, 2011).

Genetic diversity has a massive amount of significance in the way of survival and adaptation to varying environments (Gao, 2003; Rao and Hodgkin, 2002); it has a role in collection and conservation of germplasm and crop improvement (Duran *et al.*, 2009). Moreover, the information in turn helps to study heterosis as genetic diversity between parents is generally related to the magnitude of heterosis (Virk *et al.*, 2003). This shows the requirement of divergent parents in any crossing program in order to be benefited from the hybrid vigor in the F₁ and from the variability created in the subsequent segregating population. Whether the objective is hybrid or pure-line variety development, the availability and access to diverse genetic material is crucial to be successful in any plant breeding effort (Hoisington *et al.*, 1999; Naik *et al.*, 2006; Maxted *et al.*, 2002 and Rohman *et al.*, 2004).

4.2 Selection of germplasm lines as parents and development of segregating population for blast resistance

4.2.1 Selection of parents

Selection of parents was one of the most important steps in any breeding programme in order to develop superior segregants, so emphasis was given to choose appropriate parents. Breeders have different approach to choose parents and have achieved in different ways. In common, inclusion of at least one locally adapted, popular cultivar as parent will largely help to ensure the recovery of a high proportion of progenies with adaptation and quality that are acceptable to farmers. The selection of parents would be in such a way that each parent should have the ability to complement the weakness of the other (Selvaraj *et al.*, 2011b).

The female parent, Jyothi was chosen because it is cultivated in larger area and most widely adapted red rice variety of southern parts of Karnataka, having grain acceptable qualities, most preferred variety for consumption and fetches more price compared to white rice variety. However, this variety is vulnerable to blast disease causing yield losses ranging from 50-60 per cent annually especially in southern, transitional and coastal zones of Karnataka and Kerala. Hence, for this female parent, the only red rice donor identified in the screening is the landrace Kiruwana, which is a multiple disease resistant landrace and recorded resistant response to the blast (Scored 2) under UBN (Plate 2.), which might favour for improvement of leaf blast resistance in the variety Jyothi to sustain yield losses.

The diversity analysis clustered the Jyothi (cluster I) and Kiruwana (cluster II) in different clusters, indicating both the parents are diverse in nature. Hence, the union of genetically dissimilar parents like Kiruwana and Jyothi would give better recombinants in the segregating progenies. The details of characteristic features of parents are presented in Table 15. The two parents were red grain type rice varieties known to be rich in Fe and Zn content and they are also part and parcel of livelihood of people of especially in some southern, transitional and coastal zones of Karnataka and Kerala.

4.2.2 Identification of polymorphism between parents and true F_1 s

The resistant (Kiruwana) and susceptible parent (Jyothi) were assessed for polymorphism by SSR primers. Twenty-two SSR markers were tested for amplification quality and polymorphism among the parents. The sequence information of the primer pairs used for present investigation is presented in Table 5. Among 22 primers, RM5926 and RM1337 were found polymorphic between two parents (Plate 3) the remaining markers represented monomorphism. Polymorphism results from either chromosomal changes in the amplified regions or base changes that alter primer binding. Out of three F_1 plants, one F_1 plant showed polymorphism for both the parents (Plate 4) hence, it is true F_1 plant. The true F_1 plant again confirmed with phenotypic observations as these plants showed plant type of Kiruwana i.e. the F_1 plant taller than Jyothi with pigmented and producing black colour seeds.

The F_1 plant recorded 115 days for days to flowering, 145 days for days to maturity, 130 cm plant height, 16 total tillers, 15 productive tillers, 24.80 of panicle length, 47.33 g of plant yield, 32.85 g of test weight, 8.33 mm of average grain length, 2.50 mm of average grain width and with L: B ratio of 4.39. The identified true F_1 plant was advanced to F_2 segregating generation for blast resistance genes.

4.2.3 Descriptive statistics and variability studies in F_2 segregating population

Totally 226 F_2 individuals were raised during summer 2016 and observations on days to flowering, plant height, total number of tillers, productive tillers, days to maturity, grain yield, grain length, grain width, test weight and colour of husk were recorded on individual plant (Appendix I) of F_2 and randomly selected five plants of both the parents.

The observations recorded in F_2 populations on yield and its attributing traits was used to analyze the descriptive statistics and compute the extent of genetic variation available for grain yield and yield components in the segregating generations of the cross Jyothi $\times$ Kiruwana. The distribution properties of skewness



Parent Jyothi



Parent Kiruwana

**Plate 2. Response of parents Jyothi and Kiruwana to leaf blast reaction under
UBN, AHRS, Ponnampet**

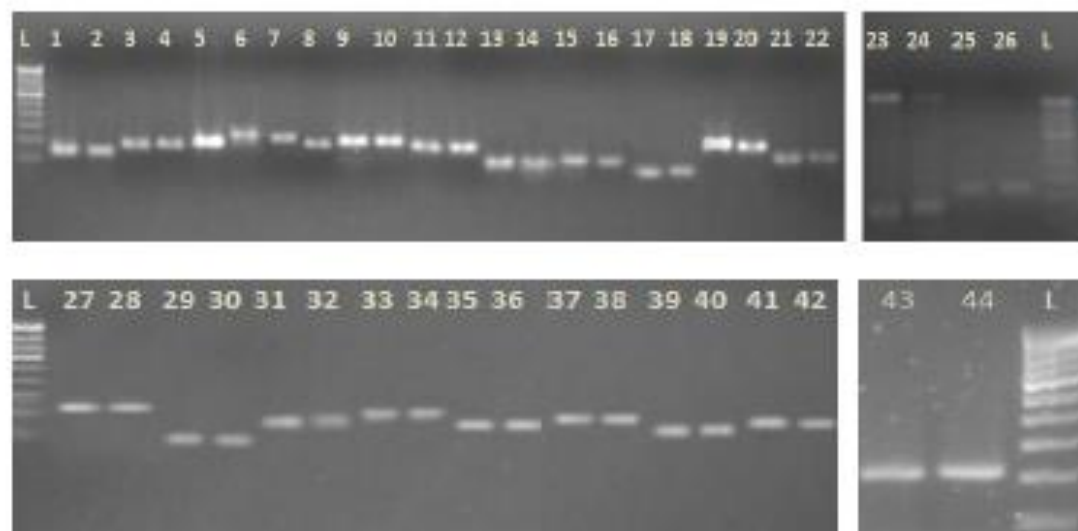
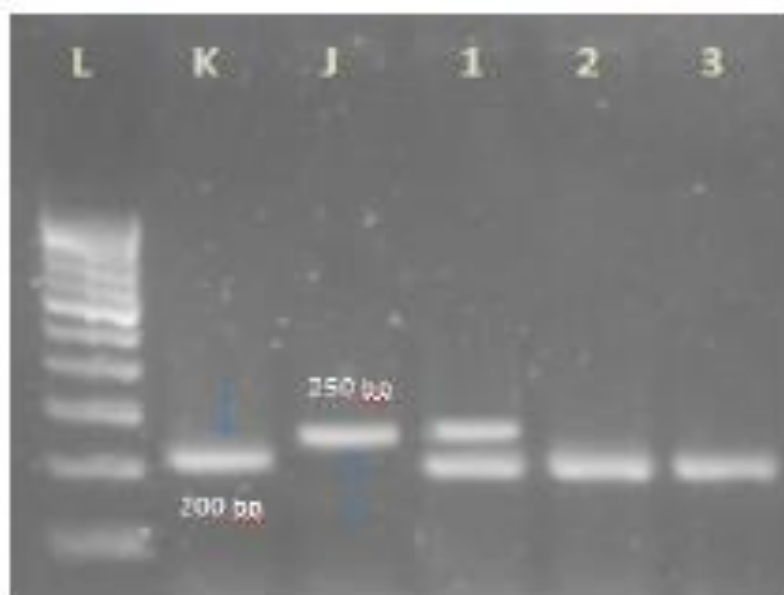


Plate 3. Identification of parental polymorphism using SSR markers linked to blast

RM 21 (1-2), RM 1233 (3-4), RM1337(5-6), RM 5926 (7-8), RM451 (9-10), RM7012 (11-12), MrG-4766 (13-14), RM 44 (15-16), RM 144 (17-18), RM 28050 (19-20), RM 111(21-22), RM 3 (23-24) and RM 492 (25-26), RM 6836 (27-28), RM 1216 (29-30), RM5757(31-32), RM 219 (33-34), RM224 (35-36), RM524 (37-38), RM 1233(39-40), AP-5630(41-42) andRM 527 (43-44) Odd no: Kiruwana, Even No: Jyothi, L-Ladder (100bp)



RM 5926, J-Jyothi (150 bp), K-Kiruwana (190 bp)



RM 1337, J-Jyothi (250 bp), K-Kiruwana (200 bp)

Plate 4. Identification of true F_1 plants by using polymorphic markers for leaf blast resistance

Table 15. The detailed morphological characteristics features of parental lines

Sl. No.	Description	Kiruwana	Jyothi
1	Reaction to blast	Resistant	Susceptible
2	Flowering	Late	Early
3	Plant stature	Tall	Semi dwarf
4	Tillering ability	Moderate	Good
5	Plant type	Non-spreading	Spreading
6	Colour of stigma	White	Black
7	Pigmentation of stem	Yes	No
8	Husk colour	Black	Brown
9	Grain yield (qha ⁻¹)	32	48
10	Rice colour	Red rice	Red rice
11	Test weight	Low	Very high

and kurtosis represent the insight about the nature of gene action and number of genes controlling for each trait, respectively. They are more powerful than first and second degree statistics which reveal interaction genetic effects.

The frequency distributions of segregating population were estimated and their skewness and kurtosis were represented in the Fig. 3 and 4. The descriptive statistics of mean, range, skewness and kurtosis for all characters in F₂ generation of cross, Jyothi × Kiruwana were tabulated in Table 16.

4.2.3.1 Days to flowering

The average days recorded for flowering was 109.69 days and it ranged from 86.00 to 136.00 days. The parent Jyothi and Kiruwana recorded 104.20 and 118.60 days, respectively (Appendix-I). The platykurtic (-0.89) and positively skewed (0.43) distribution were recorded for this trait. The similar findings were also observed by Rani *et al.* (2016) and platykurtic distribution reported by Vijaya and Shailaja (2016).

4.2.3.2 Plant height (cm)

Plant height varied from 60.00 to 148.00 cm with a mean value of 102.09 cm. The parental means were 95.40 (Jyothi) and 123.20 cm (Kiruwana). The platykurtic (-0.33) and negatively skewed (-0.26) distribution was observed for this trait. These results agree with the findings of Rani *et al.* (2016) and Vijaya and Shailaja (2016).

4.2.3.3 Number of tillers per plant

The minimum and maximum number of tillers per plant recorded was 04.00 and 36.00 respectively, with a mean value of 16.17. The parental means were 19.40 (Jyothi) and 10.20 (Kiruwana). The platykurtic (-0.13) and positively skewed (0.86) distribution for this trait was noticed, these results are in accordance with the findings of Kiran *et al.* (2012), Vijaya and Shailaja (2016) and Rani *et al.* (2016).

4.2.3.4 Productive tillers per plant

Number of productive tillers per plant varied from 04.00 to 35.00 with a mean value of 15.61. The parental means were 18.60 (Jyothi) and 9.80 (Kiruwana). The frequency distribution for this trait was platykurtic (-0.17) and positively skewed (0.82). These findings are in accordance with earlier reports of Kiran *et al.* (2012), Rani *et al.* (2016) and Vijaya and Shailaja (2016).

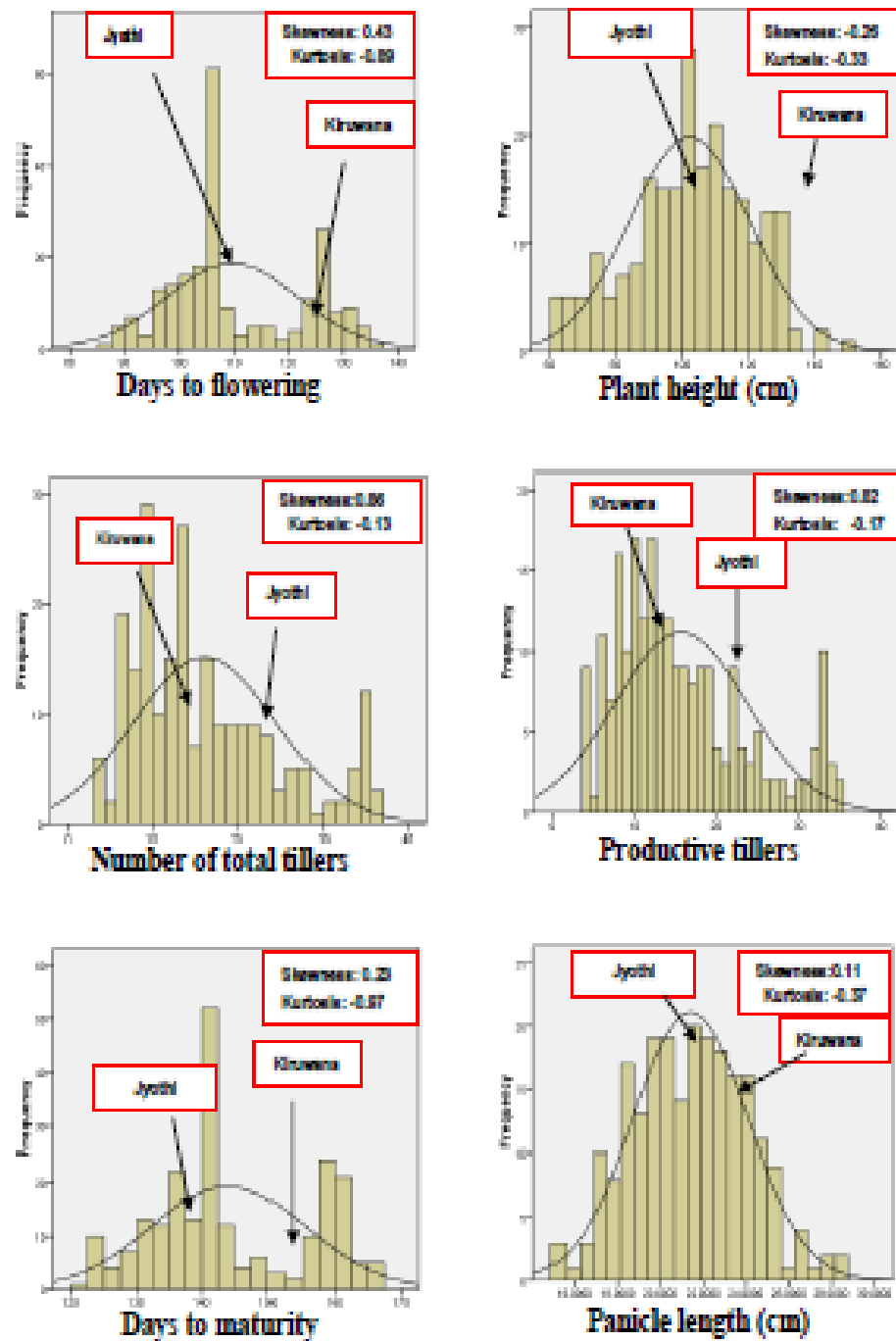


Fig. 3: Frequency distribution of F₂ population of cross Jyothi × Kuruwara for days to flowering, plant height, number of total tillers, productive tillers, days to maturity and panicle length

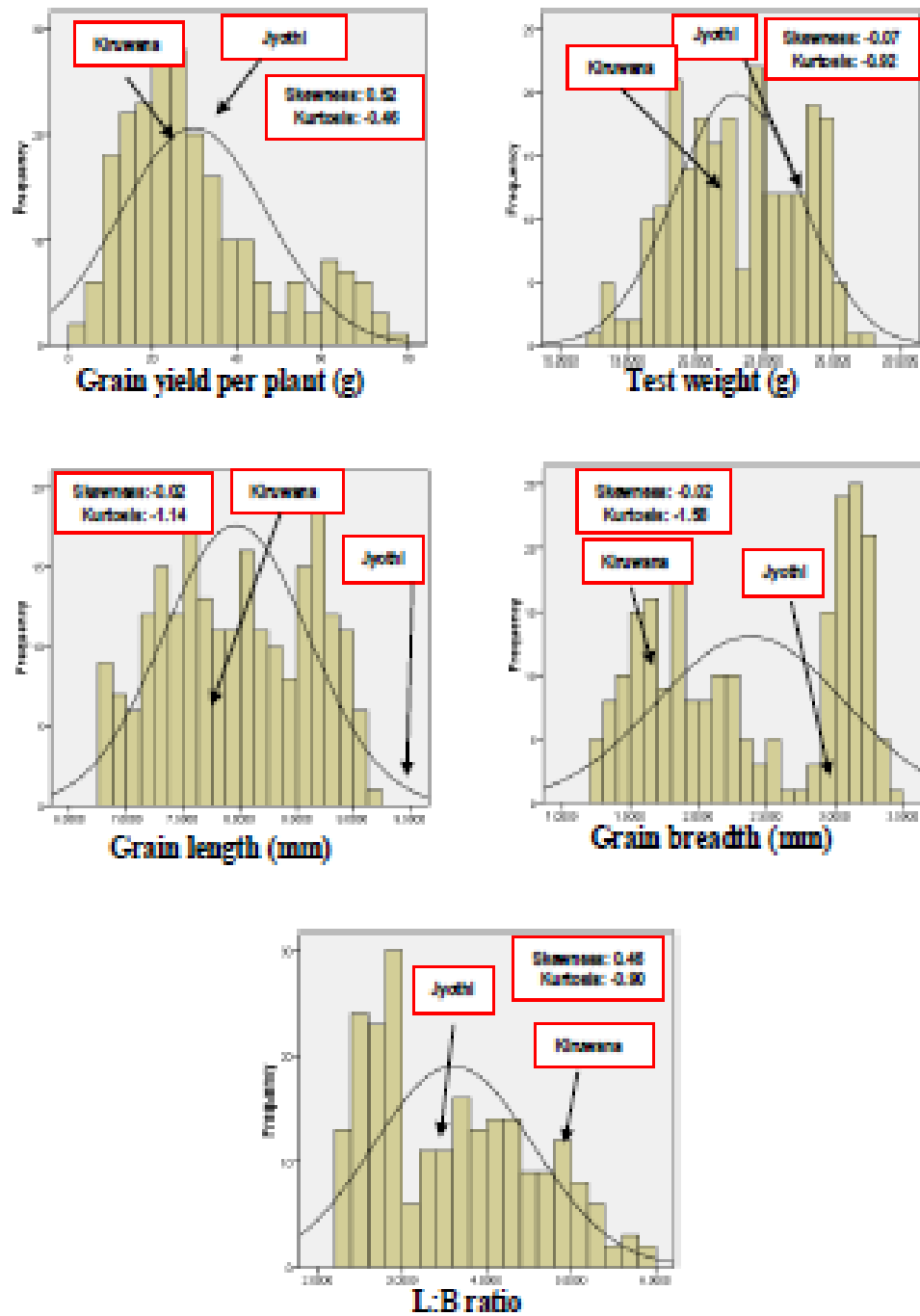


Fig. 4: Frequency distribution of F₂ population of cross Jyothi × Kiruwana for yield per plant, test weight, grain length, grain breadth and L:B ratio

Table 16. Descriptive statistics for yield and yield related traits in F₂ segregating population of cross Jyothi × Kiruwana

Sl No.	Characters	Mean± SE	Range		Skewness	Kurtosis	Kurtosis type
			Min.	Max.			
1	Days to flowering	109.69 ± 0.81	86.00	136.00	0.43	-0.89	Platykurtic
2	Plant height (cm)	102.09 ± 1.21	60.00	148.00	-0.26	-0.33	Platykurtic
3	Number of tillers per plant	16.17 ± 0.57	04.00	36.00	0.86	-0.13	Platykurtic
4	Productive tillers per plant	15.61 ± 0.54	04.00	35.00	0.82	-0.17	Platykurtic
5	Days to maturity	143.88 ± 0.78	120.00	167.00	0.23	-0.97	Platykurtic
6	Panicle length (cm)	21.39 ± 0.18	15.06	28.52	0.11	-0.37	Platykurtic
7	Grain yield per plant (g)	27.65 ± 0.94	03.00	63.00	0.52	-0.46	Platykurtic
8	Test weight (g)	23.01 ± 0.30	12.64	32.97	-0.07	-0.92	Platykurtic
9	Grain length (mm)	07.96 ± 0.04	06.76	09.23	-0.02	-1.14	Platykurtic
10	Grain breadth (mm)	02.38 ± 0.05	01.20	03.42	-0.02	-1.58	Platykurtic
11	L:B ratio	03.61 ± 0.06	02.27	05.96	0.46	-0.90	Platykurtic

4.2.3.5 Days to maturity

The average days to maturity attained in 143.88 days and it was ranged from 120 to 167 days in the population. The parental means were 135.60 (Jyothi) and 149.60 days (Kiruwana). The frequency distribution for this trait was platykurtic (-0.97) and positively skewed (0.23).

4.2.3.6 Panicle length (cm)

The panicle length varied from 15.06 to 28.52 cm with an average of 21.39 cm. The parental means were 20.98 cm (Jyothi) and 22.42 cm (Kiruwana). The platykurtic (-0.37) and positively skewed (0.11) distribution was observed for this trait. These results coincide with the findings of Kiran *et al.* (2012), Rani *et al.* (2016) and Vijaya and Shailaja (2016).

4.2.3.7 Grain yield per plant (g)

Grain yield per plant varied from 03.00 to 63.00 g with a mean value of 27.65 g. The parental means were 26.80 (Jyothi) and 19.60 g (Kiruwana). The frequency distribution for this trait was platykurtic (-0.46) and positively skewed (0.52). These findings are in accordance with earlier reports of Kiran *et al.* (2012) and Rani *et al.* (2016) for the cross ASD 16 × Kavuni.

4.2.3.8 Test weight (g)

The average test weight of the population was 23.01 g and it ranged from 12.64 to 32.97 g. The parental means were 29.70 g (Jyothi) and 19.79 g (Kiruwana). The negatively skewed (-0.07) platykurtic (-0.92) distribution was observed for this trait. These findings also observed by Kiran *et al.* (2012) and Rani *et al.* (2016) for the crosses Jaya × BPHR-1 and Swarna *Sub1* × Kavuni, respectively. The platykurtic distribution also observed by Vijaya and Shailaja (2016). But, the negative skewness and leptokurtic distribution also reported by Rani *et al.* (2016) for the cross ASD 16 × Kavuni.

4.2.3.9 Grain length (mm)

Grain length ranged from 6.76 to 9.23 mm with a mean value of 7.96 mm. The parental means were 9.23 mm (Jyothi) and 7.50 mm (Kiruwana). The frequency distribution for this trait was platykurtic (-1.14) and negatively skewed (-0.02), these findings, which was in accordance with the Rani *et al.* (2016) in the cross ASD 16 × Kavuni for this trait.

4.2.3.10 Grain breadth (mm)

Grain breadth varied from 1.20 to 3.42 mm with a mean value of 2.38 mm. The parental means were 2.86 (Jyothi) and 1.50 mm (Kiruwana). The negatively skewed (-0.02) platykurtic (-1.58) distribution was noticed for this trait. Similar findings were also observed by Rani *et al.* (2016) for the cross ASD 16 × Kavuni.

4.2.3.11 L:B ratio (mm)

L:B ratio varied from 2.27 to 5.96 mm with a mean value of 3.61 mm. The parental means were 3.23 mm (Jyothi) and 4.99 mm (Kiruwana). The frequency distribution for this trait was platykurtic (-0.90) and positively skewed (0.46). These results similar with the findings of Rani *et al.* (2016) for Swarna *Sub1* × Kavuni.

The present study revealed that the skewed distribution of the traits indicated both duplicate and non-additive gene interactions involved in governing the traits. A positively skewed distribution shows non-additive complementary gene interactions. Whereas, negatively skewed associated with additive × additive duplicate gene interactions. The kurtosis value less than three was observed for all the studied traits and they are platykurtic, indicating characters are controlled by large number of genes.

The positively skewed platykurtic distribution recorded for days to flowering, number of tillers per plant, productive tillers per plant, days to maturity, panicle length, grain yield per plant and L: B ratio indicated that, these traits are governed by large number of segregating genes and majority of them having decreasing effects displaying dominant and dominant based complementary epistasis. Hence, intense selection is required for immense genetic gain in these traits.

Whereas, negatively skewed platykurtic distribution recorded for plant height, test weight, grain length and grain breadth indicated that these traits are governed by large number of genes and majority of them have increasing effects displaying dominant and dominant based duplicate epistasis. Hence, mild selection is expected to result in rapid genetic gain for those traits.

4.2.4 Genetic variability studies in F_2 generation of cross, Jyothi × Kiruwana

Genetic variability is a necessity for successful selection of superior progenies from segregating generations for further selection and F_2 is perfect generation for imposing selection where, segregation and recombination are maximum. The magnitude of recombination potential depends on the genetic diversity of the parents. Genetic variability studies provide basic information on genetic properties of the population, based on which breeding methods could be formulated for further improvement of the crop.

Genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are helpful tools in detecting the amount of variability present in the germplasm. The estimates of heritability act as measure in predicting the expression of reliability of phenotypic value. Therefore, high heritability is useful in effective selection of particular character. The genetic advance is also helpful indicator of the progress that can be expected as result of exercising selection on the pertinent population. Heritability in conjunction with genetic advance would give a more reliable index of selection value.

Variability parameters viz., PCV, GCV, broad sense heritability (h^2) and genetic advance as per cent of mean (GAM) for grain yield and its attributing characters in F_2 generation of cross Jyothi $\times$ Kiruwana were tabulated in Table 17.

In the present study, the estimates of PCV were slightly higher than the corresponding GCV estimates for most of the studied characters indicating that the portion of PCV was more contributed by the genotypic component and less influenced by the environment. Therefore, selection on the basis of phenotype alone can be effective for the improvement of these traits. These type of results also noticed for the studied traits by Shet *et al.* (2012), Savitha and Ushakumari (2015), El-Badri *et al.* (2016), Hefena *et al.* (2016) and Rani *et al.* (2016).

4.2.4.1 Days to flowering

The moderate GCV (10.99 %) and PCV (11.05 %) were recorded for days to flowering whereas, the high heritability (98.87 %) coupled with genetic advance as per cent of mean (33.42 %) were recorded for days to flowering. Bhuvaneswari *et al.* (2015) reported similar results in F_2 population of RCM 14 $\times$ RCM 23. Moderate PCV and low GCV, high heritability with moderate GAM noticed by Rani *et al.* (2016) in the F_2 population of Swarna *Sub1* $\times$ Kavuni. The high heritability with high GAM also reported in the studies of Hefena *et al.* (2016) for this trait.

4.2.4.2 Plant height (cm)

The moderate GCV (17.21 %) and PCV (17.87 %) values were recorded for plant height whereas, high of broad sense heritability (92.69 %) coupled with high genetic advance as per cent of mean (122.22 %) were recorded for this trait. These results coincide with the findings of Sadimantara *et al.* (2014), Bhuvaneswari *et al.* (2015), Kahani and Hittalamani (2015) and Rani *et al.* (2016). However, Shantavva *et al.* (2014) reported moderate PCV, GCV and high heritability and Hefena *et al.* (2016) reported high heritability with high GAM. Shilpa *et al.* (2014) and Patroti *et al.* (2015) reported moderate PCV and GCV in the BC_1F_2 of blast resistant plants

Table 17. Variability parameters for yield and yield related traits in F₂ segregating population of cross Jyothi × Kiruwana

Sl. No.	Characters	Mean	Range		GCV (%)	PCV (%)	h ² (%)	GAM
			Min.	Max.				
1	Days to flowering	109.69	86.00	136.00	10.99	11.05	98.87	33.42
2	Plant height (cm)	102.09	60.00	148.00	17.21	17.87	92.69	122.22
3	Number of tillers	16.17	04.00	36.00	53.18	54.01	96.94	82.57
4	Number of productive tillers	15.61	04.00	35.00	53.04	53.98	96.56	75.45
5	Days to maturity	143.88	120.00	167.00	08.02	08.13	97.33	22.87
6	Panicle length (cm)	21.39	15.06	28.52	10.97	12.52	76.86	01.85
7	Grain yield per plant (g)	27.65	03.00	63.00	38.47	51.16	56.54	210.81
8	Test weight (g)	23.01	12.64	32.97	20.99	21.49	95.36	09.93
9	Grain length (mm)	07.96	06.76	09.23	07.38	08.04	84.32	00.07
10	Grain breadth (mm)	02.38	01.20	03.42	28.67	28.97	97.94	00.28
11	L:B ratio	03.61	02.27	05.96	25.37	26.24	93.46	00.48

4.2.4.3 Number of tillers per plant

The high GCV of 53.18 per cent and high PCV of 54.01 per cent were observed for this trait. The high heritability estimate of 96.94 per cent and the high GAM of 82.57 per cent were recorded for this trait. The similar findings also noticed in their studies of El-Badri *et al.* (2016), Hefena *et al.* (2016), Rani *et al.* (2016) and Kiran *et al.* (2012) reported same kind of results in cross IR 64 × BPHR-1. Kahani and Hittalamani (2015) reported high heritability with high GAM. Shilpa *et al.* (2014) and Patroti *et al.* (2015) reported high PCV and GCV in the BC₁F₂ of blast resistant plants for this trait.

4.2.4.4 Number of productive tillers per plant

The high GCV (53.04 %) and PCV (53.98 %) values were recorded for number of productive tillers per plant. Estimates of broad sense heritability (96.56 %) and genetic advance as per cent of mean (75.45 %) were also high for this trait. These results coincide with the findings of Kiran *et al.* (2012), Shantavva *et al.* (2014), Kahani and Hittalamani (2015), Rani *et al.* (2016), Hefena *et al.* (2016), El-Badri *et al.* (2016), Savitha and Ushakumari (2015) (in three F₂ and F₃ crosses) and Bhuvaneswari *et al.* (2015) in F₂ population of RCM 14×RCM 23. Similar results were also obtained in BC₁F₂ of blast resistant plants by Shilpa *et al.* (2014) and Patroti *et al.* (2015). High PCV and GCV and high heritability also reported by Sadimantara *et al.* (2014) for this trait.

4.2.4.5 Days to maturity

The low values of GCV (08.02 %) and PCV(08.13 %) and high values of broad sense heritability (97.33 %) and genetic advance as per cent of mean (22.87 %) were recorded for number of productive tillers per plant. The low GCV and PCV were also reported by Vijaya and Shailaja (2016) for this trait.

4.2.4.6 Panicle length (cm)

Panicle length showed moderate GCV (10.97 %) and PCV (12.52 %) whereas, the estimates of broad sense heritability (76.86 %) and genetic advance as per cent of mean (1.85 %) were recorded high and low, respectively. These findings are in accordance with earlier reports of Sadimantara *et al.* (2014) and Rani *et al.* (2016). The Moderate values of PCV and GCV and high heritability also reported by Shantavva *et al.* (2014) and Kahani and Hittalamani (2015). High heritability with low GAM reported in two crosses of F₂ and F₃ generations by Savitha and Ushakumari (2015). High heritability with high GAM reported by Hefena *et al.* (2016) and low heritability with low GAM reported by Vijaya and Shailaja (2016) for this trait.

4.2.4.7 Grain yield per plant (g)

The high values of GCV and PCV (38.47 and 51.16 %) with a moderate heritability (56.54 %) and high GAM (210.81 %) were recorded for grain yield per plant. These results coincide with the findings of Shantavva *et al.* (2014), Bhuvaneswari *et al.* (2015), Kahani and Hittalamani (2015), Rani *et al.* (2016), Shilpa *et al.* (2014) and by Patroti *et al.* (2015). The High values of GCV and PCV were reported by Kiran *et al.* (2012). Moderate to high heritability and GAM reported by Savitha and Ushakumari (2015). High PCV and GCV also reported by El-Badri *et al.* (2016) and high GAM reported by El-Badri *et al.* (2016).

4.2.4.8 Test weight (g)

High GCV (20.99 %) and PCV (21.49%) coupled with high heritability (95.36 %) and low GAM (09.93 %) was observed for test weight. The high GCV, PCV and high heritability found by Kahani and Hittalamani (2015) and high heritability with low GAM reported by Sadimantara *et al.* (2014). El-Badri *et al.* (2016) found high heritability with moderate GAM and Rani *et al.* (2016) reported the same in the F₂ population of cross ASD 16 × Kavuni.

4.2.4.9 Grain length (mm)

The low values of GCV (7.38 %) and PCV (8.04 %) were recorded with a high heritability of 84.32 per cent and low GAM of 0.07 per cent for this trait. These results coincide with the findings of Rani *et al.* (2016) in F₂ cross of Swarna Sub1 × Kavuni. Low values of GCV and PCV reported by Venkanna *et al.* (2014) and high heritability by Kahani and Hittalamani (2015) for this trait.

4.2.4.10 Grain breadth (mm)

The high GCV (28.67 %) and PCV (28.97 %) values were observed for grain breadth. Estimates of broad sense heritability (97.94 %) and genetic advance as per cent of mean (0.28 %) were high and low, respectively for this trait. The high heritability with low GAM was also found by Kahani and Hittalamani (2015). The high heritability with moderate GAM reported by Rani *et al.* (2016) in their studies.

4.2.4.11 L:B ratio

The GCV and PCV recorded were high (25.37 and 26.24 %, respectively) for L:B ratio. High broad sense heritability (93.46 %) and low genetic advance as per cent of mean (0.48 %) were observed for this trait. Rani *et al.* (2016) reported the high heritability with moderate GAM type but low GCV and PCV for this trait.

The traits like number of tillers per plant, number of productive tillers per plant, grain yield per plant, test weight, grain breadth and L: B ratio showed high GCV and PCV indicating prominent variation or substantial amount of genetic variability in the population for the concerned trait and hence, there is scope for selection. Thus, these traits might be controlled by additive gene action, which could be improved through simple selection methods.

Estimated heritability value alone is less reliable because as these values are prone to alter with change in the environment and experimental material (Swarup and Changale, 1962). Hence, heritability values coupled with genetic advance would be more reliable than heritability alone. In the present investigation, high heritability coupled with high GAM observed for days to flowering, plant height, number of tillers per plant, number of productive tillers per plant and days to maturity. Thus, these traits are most probably controlled by additive gene action and hence these traits can be fixed by selection.

Some traits like panicle length, test weight, grain length, grain breadth and L: B ratio recorded the high heritability coupled with low GAM. The high heritability was exhibited due to the influence of favorable environment rather than genotype. So, selection for such trait might not be rewarding. Hence, these traits may not be useful as a criterion for selection for increased grain yield.

Moderate GCV and PCV, high heritability and high GAM recorded for plant height indicated that although the variation is not so perceptible still there is an opportunity to improve this trait through selection.

4.2.5 Transgressive segregants identified in F₂ population for yield and yield related traits

The yield and related traits recorded on 226 F₂ individual plants were presented in the Appendix I. Ten best transgressive segregants (Table 18) were identified in F₂ population for yield and yield related traits viz., JK-1-151, JK-1-164, JK-1-63, JK-1-195, JK-1-11, JK-1-83, JK-1-124, JK-1-160, JK-1-62 and JK-1-138 are promising and best performing over both the parental lines for yield and yield related traits.

Table 18. The top ten transgressive segregants identified in F₂ population for yield and yield related traits

SL. No.	F ₂ Progenies	Days to 50 % flowering	Days to maturity	Plant height (cm)	Total number of tillers	Productive tillers	Panicle length (cm)	Yield (g/pl)	Test weight (g)	Grain length (mm)	Grain breadth (mm)	L:B ratio	Husk colour
1	JK-1-151	107	143	127.00	26.00	25.00	23.50	63.00	28.35	7.80	2.09	3.73	Bl.
2	JK-1-164	125	161	106.00	36.00	35.00	22.60	61.00	23.63	6.80	1.60	4.25	Bl.
3	JK-1-63	105	141	115.00	35.00	33.00	18.56	60.00	22.98	6.82	1.67	4.08	Bl.
4	JK-1-195	133	157	90.00	33.00	32.00	21.50	60.00	29.27	8.74	2.99	2.92	Br.
5	JK-1-11	105	141	125.00	27.00	25.00	23.50	58.00	26.80	8.22	3.14	2.62	Bl.
6	JK-1-83	92	125	116.00	34.00	32.00	20.50	58.00	25.60	8.01	2.22	3.61	Bl.
7	JK-1-124	105	141	130.00	22.00	22.00	23.72	58.00	21.12	7.65	1.52	5.03	Bl.
8	JK-1-160	120	155	94.00	36.00	34.00	27.90	58.00	24.61	7.52	3.10	2.43	Bl.
9	JK-1-62	105	141	100.00	22.00	22.00	22.50	57.00	29.11	8.77	3.10	2.83	Br.
10	JK-1-138	105	141	105.00	35.00	34.00	28.52	57.00	18.58	7.90	1.60	4.94	Br.
	Mean	109.69	143.88	102.09	16.17	15.61	21.39	27.65	23.01	7.96	2.38	3.61	
	Jyothi	104.20	135.60	95.40	19.40	18.60	20.98	26.80	29.69	9.23	2.86	3.23	Br.
	Kiruwana	118.60	149.60	123.20	10.20	9.80	22.42	19.60	19.80	7.52	1.51	4.99	Bl.

Bl-Black

Br-Brown

Identification of leaf blast resistant lines in segregating population

The F₃ families derived from the cross, Jyothi (susceptible) and Kiruwana (resistant) were phenotyped for blast resistance under hot spot region during *Kharif* 2016 using Uniform Blast Nursery (UBN) technique at AHRS, Ponnampet, Karnataka. A total of 226 F₃ families and their parents were evaluated for blast reaction during early growth stage for rice blast. Each family evaluated for blast reaction by using 0 to 9 scale scoring of SES, IRRI (1996) (Plate 5). The parent Kiruwana shown resistance and whereas, the parent Jyothi was highly susceptible to leaf blast.

Among the 226 F₃ families (Table 19), none of the families recorded leaf blast disease score of 0 or immune; 26 families recorded score of 1; 51 families were of 2, 55 families were of 3; 46 families were of 4; 35 families were of 5; 17 families were of 6; 7 families were of 7 and only six families recorded score of 8. For genetic analysis the disease scores from 1- 4 were considered as resistant and those scores of ≥ 5 considered as susceptible.

Genetic analysis was conducted to test the goodness of fit of blast scores of F₃ families using a Chi-square test to the expected ratio for a single gene model. The expected and observed ratios of the F₃ families for leaf blast are shown in Table 20. The F₃families showed a goodness of fit to the expected segregation ratio (3:1) for a single gene model with Chi-square value of 1.705 (P =0.192). Zenbayashi *et al.* (2002) also reported the 3:1 ratio for partial resistance to susceptibility in F₃. The result confirmed the hypothesis that resistance reaction in Kiruwana to *Magnaporthe grisea* is controlled by a single dominant gene. The results obtained in this study are in accordance with the reports of Filippi and Prabhu (1996), Chen *et al.* (1999), Lang *et al.* (2001), Barman *et al.* (2004), Zhou *et al.* (2004), Padmavati *et al.* (2005), Sharma *et al.* (2007), Persaud *et al.* (2007), Lee *et al.* (2009), Ashkani *et al.* (2011) Hasan *et al.* (2017) and Zewdu *et al.* (2018) who were also reported that the rice blast is governed by single dominant gene.

4.3.1 Identification of superior F₃ families for yield and leaf blast resistance

Randomly selected ten plants of each F₃ family were transplanted in the main field after recording the leaf blast scores at the UBN nursery and general view was shown in plate 6. The yield and related traits recorded on these ten individual plants of each family of F₃ which are presented in the Appendix II. There were ten best performing F₃ families (Table 21) identified over Jyothi for earliness, leaf blast resistance, yield and yield related traits. The best F₃families were JK-1-137, JK-1-183, JK-1-195, JK-1-48, JK-1-83, JK-1-225, JK-1-110, JK-1-56, JK-1-99 and JK-1-69.



Plate 5. Evaluation of F₃ families of a cross Jyothi × Kiruwana for leaf blast under UBN by scoring with 0-9 scale of SES, IRRI (1996)

Table 19. Reaction of F₃ families for leaf blast under natural epiphytotic conditions

Disease scale	No. of F₃ Families	Grouping
0	-	Resistant (178 families)
1	26	
2	51	
3	55	
4	46	
5	18	Susceptible (48 families)
6	17	
7	7	
8	6	
9	-	

Table 20. Genetic analysis of blast resistance in F₃ families of cross Jyothi × Kiruwana

Sl. No.	Category	Observed phenotypes	Expected phenotypes (3:1)	χ^2	Table value	P-value
1	Resistant	178	169.50	1.705	3.841	0.192
2	Susceptible	48	56.50			
Total		226				



Plate 6. General view of F_3 families evaluated for yield and its related traits at AHRS, Ponnampet *Kharif*-2016

Table 21. The top ten F₃ families of the cross Jyothi × Kiruwana for yield and leaf blast resistance evaluated at AHRS, Ponnampet during *Kharif*-2016

Sl. No.	F ₂ Progenies	Days to 50 % flowering	Days to maturity	Plant height (cm)	Total number of tillers	Productive tillers	Panicle length (cm)	Grain Yield (g/pl)	Test weight (g)	Grain length (mm)	Grain breadth (mm)	L:B ratio	Leaf blast	Husk colour
1	JK-1-137	102	136	97.90	14.50	14.10	20.79	25.80	16.87	6.88	1.43	4.81	2	Bl.
2	JK-1-183	112	145	88.10	17.50	17.20	21.94	25.30	22.95	7.67	3.07	2.50	2	Br.
3	JK-1-195	109	144	83.40	18.33	17.22	21.76	24.96	26.78	8.65	2.86	3.02	3	Br.
4	JK-1-48	113	157	104.90	14.33	13.44	20.20	23.83	20.63	7.42	1.81	4.10	2	Seg.
5	JK-1-83	103	136	87.70	13.00	12.89	20.71	23.70	25.63	8.06	2.24	3.60	2	Bl.
6	JK-1-225	104	138	99.40	12.33	12.11	19.99	23.61	14.49	7.06	1.73	4.08	2	Bl.
7	JK-1-110	106	140	106.10	14.30	12.11	20.26	23.20	18.47	7.36	2.13	3.46	1	Seg.
8	JK-1-56	105	142	106.40	11.30	11.30	20.98	22.93	24.59	8.14	2.95	2.76	2	Br.
9	JK-1-99	101	133	80.50	12.00	10.71	16.06	22.93	24.79	7.53	3.16	2.38	1	Br.
10	JK-1-69	100	128	104.20	13.40	13.00	22.81	22.83	22.73	7.52	2.22	3.39	1	Seg.
	Mean	106.39	139.59	92.86	12.86	12.20	19.26	14.69	22.10	7.92	2.35	3.63		
	Jyothi	103	134	96.82	8.43	7.46	17.52	11.34	28.56	8.54	2.62	3.26	7	Br.
	Kiruwana	123	156	124.48	14.35	13.49	19.84	20.86	19.94	7.92	1.89	4.19	2	Bl.

Bl-Black

Br-Brown

Seg- Segregating for husk colour

Molecular analysis of leaf blast resistance in segregating population

During the last few years, the genetics of blast resistance in rice have been extensively studied and many dominant R genes conferring complete resistance to *Magnaporthe grisea* have been identified. The first *Pi* gene in rice was named by Kiyosawa (1966). To date, approximately 100 distinct blast resistance genes have been identified, of which at least 14 [*Pi-1* (Hua *et al.*, 2012), *Pi-2* and *Pi-9* (Liu *et al.*, 2002 and Deng *et al.*, 2006), *Pi-20(t)* (Li *et al.*, 2008), *Pi-33* (Berruyer *et al.*, 2003), *Pi-39* (Liu *et al.*, 2007), *Pi-40 (t)* (Jeung *et al.*, 2007), *Pi-47*, *Pi-48* (Haung *et al.*, 2011), *Pi-54rh* (Das *et al.*, 2012), *Pi-56* (Liu *et al.*, 2013), *Piz*, *Piz-t* (Zhou *et al.*, 2006) and *Pigm* (Deng *et al.*, 2006)] have been described as conferring broad spectrum resistance and most of them were mapped on rice chromosomes 2, 5, 6, 9, 11 and 12.

Molecular markers are useful for mapping genes of interest and for marker-assisted breeding against rice blast. Among various types of molecular markers PCR-based SSR markers are more preferable for this purpose (Swarup *et al.* 2006). Therefore, to fulfill the objective of molecular analysis of blast resistance in segregating population was to identify molecular marker(s) linked to blast resistance in rice, the mapping population by evaluating with SSR markers.

The molecular analysis of F₃ segregating families was carried out at the Department of Biotechnology, UAS, GKVK, Bengaluru. The polymorphic SSR markers found between parents were used for genotyping of the F₃ families.

4.4.1 Co-segregation of SSR marker with blast resistance

Two SSR markers, viz., RM 1337 [*Pi-20(t)*] and RM 5926 (*Pi-1*) showing polymorphism between parents were analyzed for their co-segregation in 226 F₃ families. Alleles at the SSR loci were detected on 3per cent agarose gel and were scored according to their parental bands. A ladder was added with the first load, used to confirm the allele sizes observed in the parental survey.

4.4.1.1 Co-segregation of SSR marker RM 1337

The molecular analysis of susceptible and resistant parents and 226 F₃ families with SSR marker RM1337 showed a fragment of ~200 bp amplified from the resistant plants that was absent in susceptible plants, whereas a fragment of ~250 bp was present in susceptible plants and absent in resistant plants. Both these fragments were present in heterozygous resistant plants. The data of the polymorphism was recorded as '0' for susceptible, '1' for resistant and '2' for heterozygote. About 51F₃ families had resistant fragment, 45 F₃ families had

susceptible fragment, whereas 130 F₃ families showed both the fragments (Table 22 and Plate 7).

Genetic analysis was conducted by measuring the goodness of fit to the expected ratio for a single model using a Chi-square test. The marker analysis showed a goodness of fit to the expected segregation ratio (1:2:1) for a single gene model with Chi-square value 5.43 (P=0.066). This confirmed that the resistance for blast in present investigation was governed by single dominant gene.

4.4.1.2 Co-segregation of SSR marker RM 5926

The molecular analysis of susceptible and resistant parents and 226 F₃ families with SSR marker RM 5926 showed a fragment of ~190 bp in the resistant parent, whereas a fragment of ~150 bp was present in susceptible plants, in addition to both these fragments were present in heterozygous resistant plants. The data for the polymorphism was recorded as '0' for susceptible and '1' for resistant and '2' for heterozygote. There were 39 F₃ families recorded resistant fragment, 64 recorded susceptible fragment and 123 families having both fragments. Genetic analysis was conducted by measuring the goodness of fit to the expected ratio for a single model using a Chi-square test. The marker analysis did not show a good fit to the expected segregation ratio (1:2:1) for a single gene model with Chi-square test (Table 23).

4.4.2 Simple linear regression analysis

Simple linear regression analysis was conducted to study the association between the molecular marker data with phenotypic data. The marker, RM1337 was found to be significantly linked with the phenotypic data for disease resistance (P < 0.001, Table 24), whereas, the marker RM 5926 on regression analysis was not found to be associated with leaf blast resistance (Table 25).

Li *et al.* (2008) reported that, the gene *Pi-20(t)* present in cultivar IR24 and it conferred a broad-spectrum resistance against diverse blast pathotypes (races) in China. This gene located near the centromere region of chromosome 12, was identified using 526 F₂ plants derived from a cross of Asominori, an extremely susceptible cultivar, with resistant cultivar IR24 and identified five cosegregating SSR markers (OSR32, RM28050, RM7102, RM1337 and RM5364) by linkage analysis, the marker RM1337 and RM5364 were found to be reliable markers of resistance conditioned by *Pi-20(t)*.

The SSR marker RM 247 is also found to be linked to the gene *Pi-20(t)* reported by Miah *et al.*, (2015). The gene *Pi-20(t)* located between two flanking RFLP markers by Imbe *et al.* (1997) at the genetic distance of 14.0 cM (XNpb402)

Table 22. Molecular evaluation of F₃ families with SSR marker RM 1337

Sl. No.	Category	Observed phenotypes	Expected phenotypes (1:2:1)	χ^2	Table value	p-value
1	Resistant	51	56.5	5.43	5.99	0.066
2	Heterozygote	130	113			
3	Susceptible	45	56.5			
	Total	226				

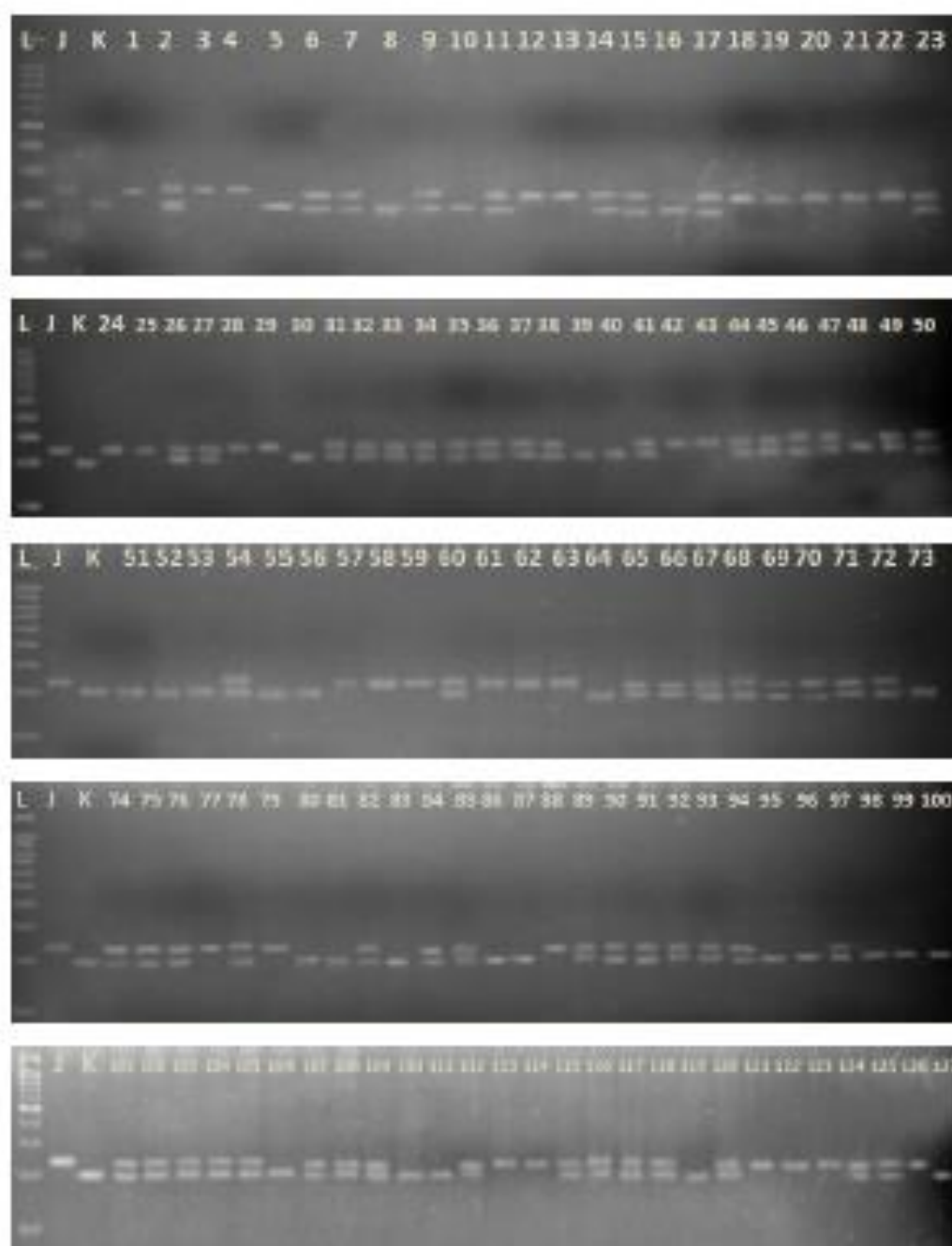


Plate 7. Genotyping of F₃ families using marker RM 1337 segregating for leaf blast resistance

L- Ladder (100bp), J-Jyothi (250bp), K-Kiruwana (200 bp)

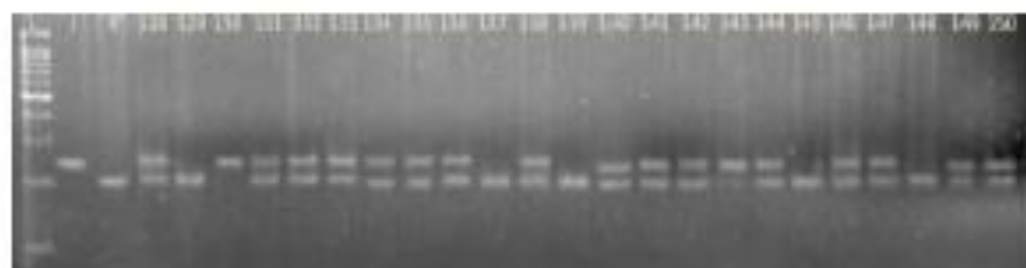


Plate 7 (continued). Genotyping of F_3 families using marker RM 1337 segregating for leaf blast resistance

L- Ladder (100bp), J-Jyothi (250 bp), K-Kiruwana (200 bp)

Table 23. Molecular evaluation of F₃ families with SSR marker RM 5926

Sl. No.	Category	Observed phenotype	Expected phenotype (1:2:1)	χ^2	Table value	p-value
1	Resistant	39	56.5	7.301	5.991	0.0260
2	Heterozygote	123	113			
3	Susceptible	64	56.5			
	Total	226				

Table 24. Trait association in F₃ families with marker RM 1337 for leaf blast resistance

Sl. No.	Source	Degrees of Freedom	Sum of Squares	Mean sum of Squares	F	P
1	Regression	1	200.80	200.80	99.26**	<0.001
2	Residual	224	453.15	2.02		
3	Total	225	653.95			

Table 25. Trait association in F₃ families with marker RM 5926 for leaf blast resistance

Sl. No.	Source	Degrees of Freedom	Sum of Squares	Mean sum of Squares	F	P
1	Regression	1	8.08	8.08	2.80 ^{NS}	0.096
2	Residual	224	645.87	2.88		
3	Total	225	653.95			

and 1.0 cM (XNpb88), respectively. The blast resistance genes, *Pi-57(t)*, *Pi-ta*, *Pi-ta2*, *Pi-6(t)*, *Pi-31(t)*, *Pi-21(t)*, *Pi-12(t)*, *Pi-tq6* and *Pi-32* were also reported on rice chromosome 12 (Lopez *et al.*, 2006).

In present study, the marker RM1337 identified to be tightly linked with disease resistance which has been identified by Li *et al.* (2008). In future, markers specific to chromosome 12 will be used for screening the parental lines and polymorphic markers to prepare framework map of the chromosome 12. The findings of this study could be directly useful in molecular analysis of segregating generations, breeding lines and varieties having Kiruwana as a donor parent. This approach will take less time and resources than field evaluation and useful in marker assisted selection in the absence of suitable testing environment.

Conclusions

Based on present study, following conclusions have been drawn

1. Wide range of variation was observed for leaf blast reaction and all agro-morphological characters indicates the genotypes showed substantial degree of variability for all agro morphological characters.
2. High heritability coupled with high genetic advance as percent mean recorded for plant height, total number of tillers per plant, number of productive tillers per plant, panicle length, grain yield per plant, grain breadth, L: B ratio, test weight, leaf blast and neck blast scores indicates that these traits were not much influenced by environmental factors, Hence, these traits expected to respond to the direct selection for trait improvement.
3. Diversity study indicated that the traits viz., reaction to leaf blast, grain length (mm), days to maturity and days to 50 per cent flowering contributed 82.35 per cent towards total divergence. Hence, for these characters more importance should be given during hybridization and selection in the segregating population.
4. The F₃ population derived from the cross Jyothi and Kiruwana segregated in 3:1 ratio for resistance and susceptibility indicating the resistance in Kiruwana is governed by single dominant gene.
5. Ten best performing F₃ families were identified over Jyothi for earliness, leaf blast resistance, yield and yield related traits viz., JK-1-137, JK-1-183, JK-1-195, JK-1-48, JK-1-83, JK-1-225, JK-1-110, JK-1-56, JK-1-99 and JK-1-69.
6. Genotyping of F₃ families revealed that, only RM1337 was found significantly associated with the leaf blast resistance after conducting chi-square test and simple linear regression.

Future line of research

Future research work directed towards the following areas

1. Rice germplasm lines Kiruwana, KPR-1, KPR-2 and IR-64 were identified as leaf blast resistant. These lines can be utilized in breeding programme for improvement of existing popular susceptible varieties
2. The identified leaf blast resistant lines (JK-1-137, JK-1-183, JK-1-195, JK-1-48, JK-1-83, JK-1-225, JK-1-110, JK-1-56, JK-1-99 and JK-1-69) can be advanced and stabilized for further utilization in breeding programme
3. Recombinant inbred lines can be developed by advancing the individual plant of each F₃ progeny line, this can also facilitate to test in multiple environments to identify the stable high yielding blast resistant genotypes
4. The marker found associated to the blast resistance can be validated in other mapping populations
5. Characterization and fine mapping of blast resistance loci in Kiruwana
6. Identify transgressive segregants similar to quality characteristics of Jyothi variety with blast resistance

Summary

V SUMMARY

The present investigation entitled “Genetic and molecular analysis of leaf blast resistance in rice (*Oryza sativa* L.)” was planned and executed to search the donor sources in the germplasm material for leaf blast resistance and utilizing resistant sources in crossing programme and to study the nature of blast inheritance and identifying the potential segregants for blast at field and molecular level using co-dominant SSR marker.

The basic experimental material consists of 35 rice germplasm lines, which were evaluated for leaf blast by screening them under “hot spot” location by adopting uniform blast nursery (UBN) procedure and to study genetic diversity present in rice germplasm lines for 12 different agro-morphological traits at Agricultural and Horticultural Research Station, Ponnampet, Kodagu District, Karnataka during *Kharif*-2014.

None of germplasm line recorded immune to the blast reaction, The resistant checks, Tadukan and Tetep shown highly resistant response, KPR-1, KPR-2, Kiruwana and IR-64 were recorded resistant response, whereas, Biliya recorded moderately resistant and on contrary Kesari, KHP-11, Hemavathi, Tunga, Jeerige sanna, Mysuru mallige, Gandasaali, Dodda abhilasha, Akkalu, MTU-1001, MO-4 and Kempu madras were shown moderate susceptibility. Puttabatta, Jyothi, JGL-1798, BPT-5204, CO-45, Amruth, Chamundi, and FR-43B were shown are susceptible reaction, whereas Jaya, Intan, Ambemori, Bheemasaali, Chittiga and FR-13A along with CO-39 and HR-12 recorded highly susceptible reaction to the leaf blast.

The wide range of variation was observed for all the studied characters. The analysis of variance exhibited statistically significant differences among genotypes for all the characters indicating the presence of substantial amount of variability. Among the studied characters, yield per plant was noticed highest GCV and PCV followed by leaf blast scores, whereas the character, days to maturity exhibited the lowest GCV and PCV.

Heritability (broad sense) of all the characters under study was categorized to very high, ranging from 64.30 to 97.60 per cent. The genetic advance was found highest for plant height (37.21) followed by days to maturity. However, when expressed in percentage of mean, it was highest for yield per plant followed by leaf blast. High heritability coupled with high genetic advance as percent mean were recorded for plant height, total number of tillers per plant, number of productive tillers per plant, panicle length, grain yield per plant, grain breadth, L: B ratio, test weight, leaf blast and neck blast scores indicates that these traits were not much

influenced by environmental factors. Hence, these traits expected to respond to the direct selection for trait improvement.

Diversity study grouped the total germplasm into six clusters based on D^2 values by following Tocher's method. Maximum number of germplasm (16) were grouped in cluster I followed by Cluster III (10). Cluster II had 6 genotypes and remaining Cluster IV, V and VI had solitary germplasm in each cluster. The genotypes within each cluster were closer to each other than the genotypes in different clusters. The maximum inter cluster distance was observed between cluster II and IV (990.00) and minimum between was found between cluster I and III (250.58). Among 12 characters studied, leaf blast has contributed major part of divergence followed by grain length. The contribution of other characters was least.

Based on disease screening, *per se* performance and diversity analysis, the landrace Kiruwana selected as donor parent to the Jyothi which is most popular, highly adoptable cultivar of hill zone and coastal zone of Karnataka. Parental polymorphism survey conducted at Department of Biotechnology, UAS, GKVK, Bengaluru by using 22 SSR markers, two were shown polymorphic between parents and these were revealed both the parental band types in true F_1 's developed cross between Jyothi $\times$ Kiruwana.

The F_2 population (226 individuals) raised by advancing true F_1 to study descriptive statistics and variability parameters. The positively skewed platykurtic distribution recorded for days to flowering, number of tillers per plant, productive tillers per plant, days to maturity, panicle length, grain yield per plant and L: B ratio indicating these were governed by large number of segregating genes and majority of them having decreasing effects displaying dominant and dominant based complementary epistasis. High heritability coupled with high GAM observed for days to flowering, plant height, number of tillers per plant, number of productive tillers per plant and days to maturity. Thus, these traits are most probably controlled by additive gene action and hence these traits can be fixed by selection.

Identification of the linked molecular marker(s) for blast resistance in rice was the major objective of present study. For this, 226 F_3 families were developed by selfing the individual F_2 plants of a cross, Jyothi and Kiruwana was evaluated for leaf blast. These 226 F_3 families were scored for leaf blast reaction. Among 226 F_3 families, 178 families showed resistant reaction and 48 families showed susceptible reaction. The observed frequencies were showed goodness of fit with chi-square (χ^2) test to the expected segregation ratio of 3:1 for single gene model. The results indicated the leaf blast resistance in Kiruwana is governed by single dominant gene.

Ten superior F₃ families were identified over Jyothi for earliness, leaf blast resistance, yield and yield related traits. The best F₃families viz., JK-1-137, JK-1-183, JK-1-195, JK-1-48, JK-1-83, JK-1-225, JK-1-110, JK-1-56, JK-1-99 and JK-1-69 were identified.

In molecular marker studies, genomic DNA was isolated from each of the parents and F₃ families using modified CTAB method. Segregation study with the marker RM 1337 showed a resistant parent fragment of 51 families and a fragment of susceptible parent in 45 plants, whereas 130 families amplified both the fragments. Genetic analysis with chi-square test indicated goodness of fit to the expected ratio of 1:2:1 for single gene model. The simple linear regression analysis indicated that the marker data with RM 1337 was significantly linked with phenotypic evaluation. This is only marker significantly associated with blast resistance among two polymorphic SSR markers studied between the parents.

References

VI REFERENCES

- AGRAWAL, K. B., 2003, Variability studies in segregating populations of rice. *Ann. Agril. Res. New series*, **24**: 707-709.
- AHN, S. N., KIM, Y. K., HONG, H. C., HAN, S. S., KWON, S. J., CHOI, H. C., MOON, H. P. AND MCCOUCH, S. R., 2000, Molecular mapping of a new gene for resistance to rice blast (*Pyricularia grisea* Sacc.). *Euphytica*, **116**: 17-22.
- ALI, A., HYUN, D. Y., CHOI, Y. M., LEE, S., OH, S., PARK, H. J. AND LEE, M. C., 2016a, Screening of rice germplasm for the distribution of rice blast resistance genes and identification of resistant sources. *Korean J. Plant Res.*, **29** (6): 658-669.
- ALI, E. B., ANIS, G., HEFEINA, A., BARUTÇULAR, C., ISLAM, M. S. AND EL SABAGH, A., 2016b, Genetic variability in F₂ generation for some physio-morphological characteristics in rice. *J. Agril. Biotech.*, **01**(02): 68-75.
- ANILKUMAR, VANNIARAJAN, C. AND RAMALINGAM, J., 2009, Association analysis of grain yield with quality traits and other yield components in segregating population of rice (*Oryza sativa* L.). *Indian J. Crop Sci.*, **4**(1-2): 71-75.
- ANJALI, D., 2009, Genetic variability for water use efficiency, grain yield and their related traits under aerobic condition in F₂ population of three crosses of rice (*Oryza sativa* L.). *M. Sc. (Agri.) Thesis*, Univ. Agril. Sci., Bangalore.
- ANONYMOUS, 2013, Vision 2050, Central Rice Research Institute Indian Council of Agricultural Research, Cuttack (Odisha) pp: 8-9.
- ANONYMOUS, 2016, Rice-Statistics and facts. <http://www.statista.com/topics/1443/rice/>.
- ASHKANI, S., RAFII, M. Y., SARIAH, M., AKMAR, A. S. N., RUSLI, I., RAHIM, H. A. AND LATIF, M. A., 2011, Analysis of simple sequence repeat markers linked with blast disease resistance genes in a segregating population of rice (*Oryza sativa* L.). *Genetics and Molecular Research*, **10**(3): 1345-1355.

- BANUMATHY, S., MANIMARAN, R., SHEEBA, A., MANIVANNAN, N., RAMYA, B., KUMAR, D. AND RAMASUBRAMANIAN, G.V., 2010, Genetic diversity analysis of rice germplasm lines for yield attributing traits. *Electronic J. Pl. Breed.*, **1**(4): 500-504.
- BARMAN, S. R., GOWDA, M., VENU, R. C. AND CHATTOO, B. B., 2004, Identification of a major blast resistance gene in the rice cultivar 'Tetep'. *Pl. Breed.*, **123** : 300 - 302
- BEKELE, B. D., RAKHI, S., NAVEEN, G. K., KUNDUR, P. J. AND SHASHIDHAR, H. E., 2013, Estimation of genetic variability and correlation studies for grain zinc concentrations and yield related traits in selected rice genotypes. *Asian J. Exp. Biol. Sci.*, **4**(3):345-351.
- BERRUYER, R., ADREIT, H., MILAZZO, J., GAILLARD, S., BERGER, A., DIOH, W., LEBRUN, M. H. AND THARREAU, D., 2003, Identification and fine mapping of *Pi-33*, the rice resistance gene corresponding to the *Magnaporthe grisea* virulence gene *ACE1*. *Theor. Appl. Genet.*, **107**:1139-1147.
- BHARADWAJ, RAJESH, M., TARA, S. C., RAO, S. K. AND KUMAR, K. S., 2007, Genetic variability, heritability and genetic advance in some new plant type based crosses of rice (*Oryza sativa* L.). *Indian J. Agril. Res.*, **41**: 189-194.
- BHINDA, M. S., KARNWAL, M. K. AND CHOUDHARY, M. K., 2017, Estimates of genetic variability, heritability and genetic advance for yield contributing and quality traits in advance breeding lines of rice (*Oryza sativa* L.). *Int. J. Adv. Biological Research*, **7**(2): 229-233.
- BHUVANESWARI, S., KUMAR, S., SINGH, M., TAKHELLAMBAM, S. AND SHASHIDHAR, K. S., 2015, Genetic variability and association studies on grain yield components in F₂ populations of black rice (*Oryza sativa* L.) of Manipur. *Indian J. Hill Farming*, **28**(2): 85-89.
- BURTON, G. W. AND DE VANE, E. H., 1953, Estimating heritability in tall Fescue (*Festuca aurundinacea*) from replicated clonal material. *Agron. J.*, **45**: 478-481.
- BURTON, G.W., 1952, Quantitative inheritance in grasses. Proceedings of the 6th International Grassland Congress, August 17-23, 1952, Pennsylvania State College, USA., pp: 277-283.

- CHANDRAMOHAN, Y., SRINIVAS, B., THIPPESWAMY, S. AND PADMAJA, D., 2016, Diversity and variability analysis for yield parameters in rice (*Oryza sativa* L.) genotypes *Indian J. Agril. Res.*, **50**(6): 609-613.
- CHANDRASHEKARA, M. V., SUNKAD, G., NAIK, M. K. AND NAGARAJU, P., 2007, Screening of rice genotypes against blast caused by *Pyricularia oryzae*, Cavara. *Karnataka J. Agril. Sci.*, **21**(2): 305-305.
- CHEN, C. H., VIÑA, M. D., INUKAI, T., MACKILL, D. J., RONALD, P. C. AND NELSON, R. J., 1999, Molecular mapping of the blast resistance gene, *Pi-44(t)*, in a line derived from a durably resistant rice cultivar. *Theor. Appl. Genet.*, **98**(6-7): 1046-1053.
- COLLARD, B. C. AND MACKILL, D. J., 2008, Marker-assisted selection: an approach for Precision plant breeding in the twenty-first century. *Philos. Trans. R. Soc. B.*, **363**: 557–572.
- CUONG, N. M., LANG, T. AND BUU, B. C. 2006, Applications of microsatellite and sequence tagged site marker to detect blast resistance in local rice (*Oryza sativa* L.). *Hanoi: Nong Nghiep*: 52–68.
- DAR, S. H., RATHER, A. G., NAJEEB, S. AND AHANGAR, M. A., 2015, Screening of rice germplasm against blast disease under temperate conditions. *Mol. Plant Breed.*, **6**(13): 1-4.
- DAS, A., SOUBAM, D., SINGH, P. K., THAKUR, S., SINGH, N. K. AND SHARMA, T. R., 2012, A novel blast resistance gene, *Pi-54rh* cloned from wild species of rice, *Oryza rhizomatis* confers broad spectrum resistance to *Magnaporthe oryzae*. *Funct. Integr. Genomics*, **12**:215-228.
- DEAN, R. A., TALBOT, N. J., EBBOLE, D. J., FARMAN, M. L., NICOL, R., PURCELL, S., NUSBAUM, C., GALAGAN, J. E. AND BIRREN, B. W., 2005, The genome sequence of the rice blast fungus *Magnaporthe grisea*. *Nature*, **434**: 980-986.
- DENG, Y., ZHU, X., SHEN, Y. AND HE, Z., 2006, Genetic characterization and fine mapping of the blast resistance locus *Pigm(t)* tightly linked to *Pi-2* and *Pi-9* in a broad-spectrum resistant Chinese variety. *Theor. Appl. Genet.*, **113**:705-713.
- DOYLE, J. J. AND DOYLE, J. L., 1990, A rapid total DNA preparation procedure for fresh plant tissue. *Focus*, **12**:13-15.

- DURAN, C., APPLEBY, N., EDWARDS, D. AND BATLEY, J., 2009, Molecular genetic markers: Discovery, applications, data storage and visualization. *Curr. Bioinform.*, **4**: 16-27.
- EIZENGA, G. C., AGRAMA, H. A., LEE, F. N., YAN, W. AND JIA, Y., 2006, Identifying novel resistance genes in newly introduced blast resistant rice germplasm. *Crop Sci.*, **46**:1870–1878.
- EL-BADRI, A., ANIS, G., HEFEINA, A., BARUTCULAR, C. AND EL-SABAGH, A., 2016, Genetic variability in F₂ generation for some physio-morphological characteristics in Rice. *J. Agr. Biotech.*, **01**(02):68-75.
- FENG, C., ROTICH, F. AND CORRELL, J. C., 2014, Screening for rice blast resistance of uniform rice regional nursery varieties. *B. R. Wells Arkansas Rice Research Studies*: 50-55.
- FILIPPI, M. C. AND PRABHU. A. S., 1996, Inheritance of blast resistance in rice to two *Pyricularia grisea* races, *IB-1* and *IB-9*. *Brazilian J. Genet.* **19**(4): 599 -604.
- FISHER, R. A., 1922, On the mathematical foundations of theoretical statistics. *Phil. Trans. R. Soc.*, **222**(A): 309 - 368.
- FJELLSTROM, R., MCCLUNG, A. M. AND SHANKAR, 2006, SSR markers closely linked to the *Pi-z* locus are useful for selection of blast resistance in a broad array of rice germplasm. *Mol. Breed.*, **17**:149–157.
- FJELLSTROM, R., MCCLUNG, A., GIBBONS, J. AND DEREN, C., 2004, Development of DNA markers suitable for marker assisted selection of three *Pi* genes conferring resistance to multiple *Pyricularia grisea* pathotypes. *Crop Sci.*, **44**:1790–1798.
- FUENTES, J. L., CORREA-VICTORIA, F. J., ESCOBAR, F., PRADO, G., ARICAPA, G., DUQUE, M. C. AND THOME, J., 2008, Identification of microsatellite markers linked to the blast resistance gene *Pi-1(t)* in rice. *Euphytica*, **160**:295–304.
- FUKUOKA, S., YAMAMOTO, S. I., MIZOBUCHI, R., YAMANOUCHI, R., ONO, K., KITAZAWA, N., YASUDA, N., FUJITA, Y., NGUYEN, T. T. T., KOIZUMI, S., SUGIMOTO, K., MATSUMOTO, T. AND YANO, M., 2014, Multiple functional polymorphisms in a single disease resistance gene in rice enhance durable resistance to blast. *Scientific Reports*, **4450**(4): 1-7.

- GALHANO, R. AND TALBOT, N. J., 2011, The biology of blast: understanding how *Magnaporthe oryzae* invades rice plants. *Fungal Biol. Rev.*, **25**: 61-67.
- GAO, L. Z., 2003, The conservation of Chinese rice biodiversity: genetic erosion, ethnobotany and prospects. *Genet. Resour. Crop Evol.*, **50**: 17-32.
- GARG, P., PANDEY, D. P. AND KAUSHIK, R. P., 2011, Genetic divergence for yield and quality traits in Rice (*Oryza sativa* L.). *J. Rice Research*, **4**(1-2): 1-5.
- GHAZANFAR, M. U., HABIB, A. AND SAHI, S. T., 2009, Screening of rice germplasm against *Pyricularia oryzae* the cause of rice blast disease. *Pakistan J. Phytopathology*, **21**(1): 41-44.
- GHOSH, S. C. AND SHARMA, D., 2012, Genetic parameters of agromorphophysiological traits in rice (*Oryza sativa* L.). *Electronic J. Pl. Breed.*, **3**(1): 711- 714.
- GOVINTHARAJ, P., TANNIDI, S., SWAMINATHAN, M. AND SABARIAPPAN, R., 2016, Estimates of genetic variability, heritability and genetic advance for blast resistance gene introgressed segregating population in rice. *Int. J. Curr. Microbiol. App. Sci.*, **5**(12): 672-677.
- HABIB, A. B., 2008, Genetic variation for grain quality, protein and micronutrients in F₂ generation of BPT – 5204 × HPR – 14 in rice (*Oryza sativa* L.) under aerobic condition. *M. Sc. (Agri.) Thesis*, Univ. Agril. Sci., Bangalore.
- HANSON, G. H., ROBINSON, H. F. AND COMSTOCK, R. E., 1956, Biometrical studies of yield in segregating population of Korean Lespedeza. *Agronomy J.*, **48**: 267-282.
- HASAN, N., RAFII, M.Y., RAHIM, H., NUSAIBAH, S.A., MAZLAN, N. AND ABDULLAH, S., 2017, Genetic analysis and identification of SSR markers associated with rice blast disease in a BC₂ F₁ backcross population. *Genet. Mol. Res.*, **16**(1):1-11.
- HASSAN, I. O., RAGAB, A. I., SOLIMAN, M. H., EL-SHAFFEY, R. A. AND EL-ASSAL, S. E. S., 2017, Genetic improvement of rice resistance to blast and bakanae diseases using mutation induction. *Biosci. Res.*, 2017 **14**(2): 246-256.
- HASIB, K. M. AND KOLE, P. C., 2008, Genetic variability for panicle characters in segregating populations of aromatic rice. *Madras Agril. J.*, **95**: 174-178.

- HAUSSMANN, B. I. G., PARZIES, H. K., PRESTERL, T., SUSIC, Z. AND MIEDANER, T., 2004, Plant genetic resources in crop improvement. *Pl. Genet. Resour.*, **2**: 3-21.
- HEFENA, A. G., SULTAN, M. S., ABDEL-MONEAM, M. A., HAMMOUD, S. A., CELALEDDIN, B. AND EL-SABAGH, A., 2016, Genetic variability, heritability and genetic advance for yield and associated traits in F₂ rice population. *J. Agril. Biotech.*, **1**(2): 49-58.
- HITTALMANI, S., PARCO, A., MEW, T., ZEIGLER, R. AND HUANG, N., 2000, Fine mapping and DNA marker-assisted pyramiding of the three major genes for blast resistance in rice. *Theor. Appl. Genet.*, **100**: 1121–1128.
- HOISINGTON, D., KHAIRALLAH, M., REEVES, T, RIBAUT, J. M., SKOVMAND, B., TABA, S. AND WARBURTON, M., 1999. Plant genetic resources: What can they contribute toward increased crop productivity? *Proc. Natl. Acad. Sci. USA.*, **96**: 5937-5943.
- HOSAGOUDAR, G. N., KOVI, B. S. AND SHEELA, H. K., 2017, Genetic variability, correlation and leaf blast resistance studies in early maturing rice genotypes under hilly conditions. *Int. J. Curr. Microbiol. App. Sci.*, **6**(12): 3451-3459.
- HOSSAIN, M. M. AND HEGDE, H. R., 2016, Screening of rice germplasm against *Pyricularia oryzae* the cause agent of rice blast fungus in upland areas. *Environment and Ecology*, **34**(1): 8-11.
- HUA, L., WU, J., CHEN, C., WU, W., HE, X., LIN, F., WANG, L., ASHIKAWA, I., MATSUMOTO, T., WANG, L. AND PAN, Q., 2012, The isolation of *Pi-1*, an allele at the *Pik* locus which confers broad spectrum resistance to rice blast. *Theor. Appl. Genet.*, **125**:1047-1055.
- HUANG, H., HUANG, L., FENG, G., WANG, S., WANG, Y., LIU, J., JIANG, N., YAN, W., XU, L., SUN, P., LI, Z., PAN, S., LIU, X., XIAO, Y., LIU, E., DAI, L. AND WANG, G. L., 2011, Molecular mapping of the new blast resistance genes *Pi-47* and *Pi-48* in the durably resistant local rice cultivar *Xiangzi 3150*. *Phytopathology*, **101**: 620-626.
- IDOWU, O. O., SALAMI, A. O., AJAYI, S. A., AKINWALE, R. O. AND SERE, Y., 2013, Varietal resistance of rice to blast fungus *Magnaporthe oryzae* at two sites in southwestern Nigeria. *African J. Biotech.*, **12**(33): 5173-5182.

- IMAM, J., ALAM, S., MANDAL, N. P., VARIAR, M. AND SHUKLA, P., 2014, Molecular screening for identification of blast resistance genes in North East and Eastern Indian rice germplasm (*Oryza sativa* L.) with PCR based makers. *Euphytica*.**196**:199–211.
- IMBE, T., ORA, S., YANORIA, M. J. T. AND TSUNEMATSU, H., 1997, A new gene for blast resistance in rice cultivar, IR24. *Rice Genet Newsl.*, **14**:60–62.
- International Rice Genome Sequencing Project (IRGSP), 2005, The map-based sequence of the rice genome. *Nature*, **436**:793–800.
- IRRI, 1996, Standard evaluation system for rice. 4th Edition, IRRI, The Philippines.
- JACKSON, S. A., 2016, Rice: The First Crop Genome, *Rice*, **9**: 14.
- JAYAWARDANA, W. A. D., JAYASEKERA, G. A. U., WIJESUNDERA, R. L. C., DISSANAYAKE, D. M. N., SOORIYAPATHIRANA, S. D. S. S., WEEBADDE, C. K., PERERA, K. L. N. S., GUNAPALA, K. R. D. AND HETTIGE, P., 2014, Evaluation of DNA markers linked to blast resistant genes, *Pikh*, *Pit* (*p*), and *Pita*, for parental selection in Sri Lankan rice breeding. *Tropical Agril. Res.*, **26**(1): 82 – 93.
- JEUNG, J. U., KIM, B. R., CHO, Y. C., HAN, S. S., MOON, H. P., LEE, Y. T. AND JENA, K. K., 2007, A novel gene, *Pi-40(t)*, linked to the DNA markers derived from NBS-LRR motifs confers broad spectrum of blast resistance on rice. *Theor. Appl. Genet.*, **115**: 1163–1177.
- JOHNSON, H. W., ROBINSON, H. F. AND COMSTOCK, R. E., 1955, Genotypic and phenotypic correlations in Soybean and their application in selection. *Agron. J.*, **47**: 477-483.
- JOSHI, B. K., BIMB, H. P., PARAJULI, G. AND CHAUDHARY, B., 2009, Molecular tagging, allele mining and marker aided breeding for blast resistance in rice. *BSN e-Bulletin*, **1**: 1-23.
- JOSHI, M. A., PRITPAL SINGH, SARAO, N. K., SHARMA, R. C. AND BHARAJ, T. S., 2008, Genetic diversity among the rice varieties cultivated in Punjab. *Oryza*, **45**(4):277-279.
- KAHANI, F. AND HITTALMANI, S., 2015, Genetic analysis and traits association in F₂ inter varietal populations in rice under aerobic condition. *Rice Res.*, **3**(4):1-5.

- KENENI, G., BEKELE, E., IMTIAZ, M. AND DAGNE, K., 2012, Genetic vulnerability of modern crop cultivars: causes, mechanism and remedies. *Int. J. Pl. Res.*, **2**:69–79.
- KHAN, M. A., 2015, Molecular breeding of rice for improved disease resistance, a review. *Australasian plant pathology*, **44**(3): 273-282.
- KHATUN, M. T., HANAFI, M. M., YUSOP, M. R., WONG, M. Y., SALLEH, F. M. AND FERDOUS, J., 2015, Genetic variation, heritability, and diversity analysis of upland rice (*Oryza sativa* L.) genotypes based on quantitative traits. *Bio Med. Res. Int.*:1-7.
- KHUSH, G. S., 2005, What it will take to feed 5.0 billion rice consumers in 2030. *Plant Mol. Biol.*, **59**: 1–6.
- KIRAN, K. K., 2012, Genetic variability for grain yield, its components and inheritance of resistance to BPH in two F₂ populations of rice (*Oryza sativa* L.). *M. Sc. (Agri.) Thesis*, Univ. Agril. Sci., Bangalore.
- KIYOSAWA, S., 1966, Studies on inheritance of resistance of rice varieties to blast, Inheritance of resistance of a rice variety *Pi* No. 1 to the blast fungus. *Japan J. Breed.* **16**: 243 - 250.
- KOTCH, G. P., ORTIZ, R. AND ROSS, W. M., 1992. Genetic analysis by use of potato haploid populations. *Genome*, **35**:103–8.
- KRISHNA, L., RAJU, C. D. AND RAJU, C. S., 2008, Genetic variability and correlation in yield and grain quality characters of rice germplasm. *The Andhra Agril. J.*, **55**: 276-279.
- KUMBHAR, S. D., KULWAL, P. L., PATIL, J. V., GAIKWAD, A. P. AND JADHAV, A. S., 2013, Inheritance of blast resistance and identification of SSR marker associated with it in rice cultivar RDN 98-2. *J. Genet.*, **92**(2):317-321.
- KUYEK, D., 2000, Implications of corporate strategies on rice research in Asia. *Grain*, 1-13.
- LAL, M. AND CHAUHAN, D. K., 2012, Studies of genetic diversity and cluster analysis in rice. *Int. J. Agril. and Stat. Sci.*, **8**(1):293-297.
- LANG, N. T., KHUSH, G. S., HUANG, N. AND BUU, B.C., 2001, Fine mapping for blast resistance gene in rice (*Oryza sativa* L.) using bulked segregant analysis. *Omon rice*, **9**: 1-8.

- LEE, S., WAMISHE, Y., JIA, Y. AND LIU, G., 2009, Identification of two major resistance genes against race *IE-1k* of *Magnaporthe oryzae* in the indica rice cultivar Zhe733. *Mol. Breed.*, **24**: 127-134.
- LI, J., LI, D., SUN, Y. AND XU, M., 2012, Rice Blast Resistance Gene *Pi-1* Identified by MRG 4766 Marker in 173 Yunnan Rice Landraces. *Rice Genomics and Genet.*, **3**(3): 13-18.
- LI, W., LEI, C., CHENG, Z., JIA, Y., HUANG, D., WANG, J., WANG, J., ZHANG, X., SU, N., GUO, X., ZHAI, H. AND WAN, Z., 2008, Identification of SSR markers for a broad-spectrum blast resistance gene *Pi-20(t)* for marker-assisted breeding. *Mol. Breed.*, **22**:141–149.
- LIANG, Z., WANG, L. AND PAN, Q., 2016, A new recessive gene conferring resistance against rice blast. *Rice*, **9**(47): 1-6.
- LIU, G., LU, G., ZENG, L. AND WANG, G. L., 2002, Two broad-spectrum blast resistance genes, *Pi-9(t)* and *Pi-2(t)*, are physically linked on rice chromosome 6. *Mol. Genet. Genomics*, **267**: 472-480.
- LIU, X., YANG, Q., LIN, F., HUA, L., WANG, C., WANG, L. AND PAN, Q., 2007, Identification and fine mapping of *Pi-39(t)*, a major gene conferring the broad-spectrum resistance to *Magnaporthe oryzae*. *Mol. Genet. Genomics*, **278**: 403-410.
- LIU, Y., LIU, B., ZHU, X., YANG, J., BORDEOS, A., WANG, G., LEACH, J. E. AND LEUNG, H., 2013, Fine-mapping and molecular marker development for *Pi-56(t)*, a NBS-LRR gene conferring broad spectrum resistance to *Magnaporthe oryzae* in rice. *Theor. Appl. Genet.*, **126**: 985-998.
- LOPEZ, J., TOHME, J., CORREA, F., MARTINEZ, C., HULBERT, S., ZEIGLER, R., GALLEGU, G., ESCOBAR, F., PRADO, G. AND ARICAPA, G., 2006, Mapping resistance genes associated with the durable blast resistance in the commercial rice cultivar Oryzica Llanos 5. Characterizing rice pests and genetics of resistance, *Annual report Rice*. CIAT, Pp.102-107.
- LUSH, J. L., 1949, Heritability of quantitative characters in farm animals. *Proceedings of 8th Congress of Genetics and Hereditas*. **35**(51): 356 -75.

- MADHUBABU, P., SUMAN, K., RAMYA, R., FIYAZ, A. R., RAO, S. D., SUDHAKAR, P., SATYA, K. A., RAVINDRA BABU, V. AND NEERAJA, C. N., 2017, Evaluation of grain yield, quality and nutrients content in four rice (*Oryza sativa* L.) genotypes. *Curr. J. App. Sci. and Tech.*, **22**(1): 1-12.
- MAHALANOBIS, P. C., 1928, A statistical study at chinese head measurement. *J. Asiatic Society of Bengal*.**25**:301-377.
- MAHALANOBIS, P. C., 1936, On the generalized distance in statistics. *Proc. Nat. Inst. Sci. of India***2**: 49-55.
- MALLIKARJUNA, N. M., 2013, Genetic analysis and breeding potential for grain yield and its stabilizing traits under aerobic condition in Rice (*Oryza sativa* L.). Ph.D. Thesis, Univ. Agril. Sci., Bangalore.
- MALLIMAR, M., SURENDRA, P., HANAMARATTI, N. G., JOGI, M., SATHISHA, T. N. AND HUNDEKAR, R., 2015, Genetic variability for yield and yield attributing traits in F₃ generation of rice (*Oryza sativa* L.). *Res. Environ. Life Sci.*, **9**(1): 24-28.
- MAXTED, N., GUARINO, L., MYER, L. AND CHIWONA, E. A., 2002, towards a methodology for on-farm conservation of plant genetic resources. *Genet. Resour. Crop Evol.*, **49**: 31-46.
- Mc COUCH, S. R., TEYTELMAN, L., XU, Y., LOBOS, K. B., CLARE, K., WALTON, M., FU, B., MAGHIRANG, R., LI, Z., XING, Y., ZHANG, Q., KONO, I., YANO, M., FJELLSTROM, R., DECLERCK, G., SCHNEIDER, D., CARTINHO, S., WARE, D. AND STEIN, L., 2002, Development and mapping of 2240 new SSR markers for rice (*Oryza sativa* L.). *DNA Res.*, **9**: 257–279.
- MIAH, G., RAFII, M. Y., ISMAIL, M. R., PUTEH, A. B., RAHIM, H. A., ASHKANI, S. AND LATIF, A., 2015, Inheritance patterns and identification of microsatellite markers linked to the rice blast resistance in BC₂F₁ population of rice breeding. *Bragantia, Campinas*, **74**(1): 33-41.
- MIZOBUCHI, R., SATO, H., FUKUOKA, S., YAMAMOTO, S., KAWASAKI-TANAKA, A. AND FUKUTA, Y., 2014, Mapping of a QTL for field resistance to blast (*Pyricularia oryzae* Cavara) in Inngoppor-tinawon, a Rice (*Oryza sativa* L.) landrace from the Philippines. *Japan Agril. Res. Quarterly*, **48**(4): 425 – 431.

- MOHANTA, B. K., ALAM, M. R., KABIR, M. E., ANAM, M. K., ALAM, M. K. AND HABIB M. A., 2003, Performance of different genotypes/cultivars to blast disease of rice in *Boro* and *T. Aman* crop in Bangladesh. *Asian J. Plant Sci.*, **2**(7): 575-577.
- MORRIS, M., DREHER, K., RIBAUT, J. M. AND KHAIRALLAH, M., 2003, Money matters (II): costs of maize inbred line conversion schemes at CIMMYT using conventional and marker-assisted selection. *Mol. Breed.*, **11**:235–247.
- NAIK, D., SAO, A., SARAWGI, A. K. AND SINGH, P., 2006, Genetic divergence studies in some indigenous scented rice (*Oryza sativa* L.) accessions of central India *Asian J. Pl. Sci.*, **5**: 197-200.
- NANDESHWAR, B. C., PAL, S., SENAPATI, B. K. AND DE, D. K., 2010, Genetic variability and character association among biometrical traits in F₂ generation of some rice crosses. *Electronic J. Pl. Breed.*, **1** (4): 758-763.
- NAVEENKUMAR, SINGH, D., GUPTA, S., SIROHI, A., RAMESH, B., SIROHI, P., SIROHI, P., SINGH, A., KUMAR, N., KUMAR, A., RAJENDRAKUMAR, KUMAR, R., SINGH, J., KUMAR, P., CHAUHAN, P., PURUSHOTTAM, AND CHAND, S., 2013, Determination and expression of genes for resistance to blast (*Magnaporthe oryza*) in Basmati and non-Basmati indica rice (*Oryza sativa* L.). *African J. Biotech.*, **12**(26): 4098-4104.
- NAYAK, A. R., CHAUDHURY, D. AND REDDY, J. N., 2004, Genetic divergence in scented rice. *Oryza*, **41**(3&4): 79-82.
- NGUYEN, T., KOIZUMI, S., LA, T., ZENBAYASHI, K., ASHIZAWA, T., YASUDA, N., IMAZAKI, I. AND MIYASAKA, A., 2006, *Pi 35(t)*, a new gene conferring partial resistance to leaf blast in the rice cultivar Hokkai 188. *Theor. Appl. Genet.*, **113**(4): 697–704.
- OU, S H., 1985, Blast- *Pyricularia oryzae*. In: Rice Diseases. 2nd ed. Slough U K: Commonwealth Mycological Institute, 109–201.
- OU, S. H., 1965, A proposal for an international program of research on the rice blast disease In: The rice blast disease. *Johns Hopkins Press*, Baltimore and Maryland, pp. 441-446.
- PADMAVATHI, G., RAM, T., SATYANARAYANA, K. AND MISHRA, B., 2005, Identification of blast (*Magnaporthe grisea*) resistance genes in rice. *Curr. Sci.*, **88**(4): 628-630.

- PAIKHOMBA, N., KUMAR, A., CHAURASIA, A. K., AND RAI, P. K., 2014, Assessment of genetic parameters for yield and yield components in hybrid rice and Parents. *J. Rice Res.*, **2**(1): 1-3.
- PAN, Q. H., WANG, L. AND TANISAKA, T., 1999, A new blast resistance gene identified in the Indian native rice cultivar Aus373 through allelism and linkage tests. *Plant Pathology*, **48**: 288–293.
- PANDEY, S., 2016, Screening of rice cultivars for quantification of apparent infection rate of leaf blast. *Middle East J. Agri. Res.*, **5**(4): 430-434.
- PANSE, V. G. AND SUKHATME, P. V., 1985, Statistical methods for agricultural workers. Indian Council of Agricultural Research Publication, 87-89.
- PANWAR, L. L. AND MATHUR, S. S., 2007, Variability studies in segregating populations of rice (*Oryza sativa* L.). *Ann. Agril. Res. New Series*, **28**(1):53-56.
- PARIHAR, A., PATHAK, A. R. AND PARIHAR, P., 2010, Identification of RAPD marker for the White Backed Plant Hopper (WBPH) resistant gene in rice. *African J. Biotech.*, **9**(10): 1423-1426.
- PATIL, P. V. AND SARAWGI, A. K., 2005, Studies on genetic variability, correlation and path analysis in traditional aromatic rice accessions. *Ann. Plant. Physiology*, **19**: 92-95.
- PATROTI, P., MADHAV, M. S., SURESH, J. AND ESWARI, K. B., 2015, Genetic variability, heritability and character association studies for grain yield and yield attributing traits in segregating population of rice (*Oryza sativa* L.). *J. Res. PJTSAU.*, **43**(1/2):33-39.
- PERERA, U. I. P., RATNASEKERA, D., SENANAYAKE, S. G. J. N. AND ABEYSIRIWARDENA, D. S. D. Z., 2014, Genetic parameters and correlations of yield attributing characteristics of weedy rice in Sri Lanka. *J. Natn. Sci. Foundation Sri Lanka*, **42**(4): 299-306.
- PERSAUD, M., KUMAR, A., SENGAR, R. B. S., SAO, A., DANTRE, R. K. AND SHRIVASTAVA, M. N., 2007, Genetic analysis of blast (*Pyricularia grisea* Sacc.) resistance in rice (*Oryza sativa* L.). *J. Bio. Sci.*, **7**(1): 215 – 217.
- PRABHU, S. M., GANESHAN, N. M., JAYAPRAKASH, P. AND SELVAKUMAR, R., 2017, Assessment of genetic variability and heritability in segregating populations. *Int. J. Agril. Sci. and Res.*, **7**(3): 267-270.

- PRASAD, M. S., KANTHI, B. A., BALACHANDRAN, S. M., SESHUMADHAV, M., MOHAN, K. M. AND VIRAKTAMATH, B. C., 2009a, Molecular mapping of rice blast resistance gene *Pi-1(t)* in the elite indica variety Samba mahsuri. *World J. Microbio. and Biotech.*, **25**(10): 1765–1769.
- PRASAD, R., PRASAD, L. C. AND AGRARWAL, R. K., 2009b, Genetic diversity in traditional aromatic rices of India. *Indian J. Plant Genet. Resour.*, **22**(2): 141-143.
- PRATAP, N., SINGH, P. K., SHEKHAR, R., SONI, S. K. AND MALL, A. K., 2012, Genetic variability, character association and diversity analyses for economic traits in rice (*Oryza sativa* L.), *SAARC J. Agril.*, **10**(2): 83-94.
- PURI, K. D., SHRESTHA, S. M., CHHETRI, G. B. K. AND JOSHI, K. D., 2009, Leaf and neck blast resistance reaction in tropical rice lines under green house condition, *Euphytica*, **165**: 523–532.
- QUDSIA, H., RIAZ, A. AND AKHTAR, M., 2017, Evaluation of rice germplasm for resistance against *Pyricularia oryzae* the cause of rice leaf blast. *Asian Res. J. Agril.*, **4**(3): 1-6.
- RAHIM, H. A., BHUIYAN, M. A. R., SAAD, A., AZHAR, M. AND WICKNESWARI, R., 2013, Identification of virulent pathotypes causing rice blast disease (*Magnaporthe oryzae*) and study on single nuclear gene inheritance of blast resistance in F₂ population derived from Pongsu Seribu 2 × Mahshuri. *Australian J. Crop Sci.*, **7**(11): 1597-1605.
- RAHMAN, A. U., SHAH, S. M. A., RAHMAN, H. U., SHAH, L., ALI, A. AND RAZA M. A., 2015, Genetic variability for morphological parameters in F₂ segregating populations of rice. *Academia J. Agril. Res.*, **3**(10): 296-302.
- RAHMAN, L., KHANAM, S., ROH, J. H. AND KOH, H. J., 2011, Mapping of QTLs involved in resistance to rice blast (*Magnaporthe grisea*) using *Oryza minuta* introgression lines. *Czech. J. Genet. Plant Breed.*, **47**(3): 85–94.
- RAJENDAR, R. M., SURENDAR, R. C., DAYAKAR, R. T. AND NARENDER, R. S., 2013, Study on genetic parameters in F₂ generation involving aromatic rice genotypes. *Intl. J. Appl. Bio. Pharm. Tech.*, **4**(4): 238-241.
- RAM, T., MAJUMDER N. D., MISHRA, B., ANSARI, M. M. AND PADMAVATHI, G., 2007, Introgression of broad spectrum blast resistance genes into cultivated rice (*Oryza sativa* sp. indica) from wild rice *Oryza rufipogon*. *Current Sci.*, **92**(2): 225-230.

- RAMANJANEYULU, A. V., GOURISHANKAR, V., NEELIMA, T. L. AND SHASHIBHUSAHN, D., 2014, Genetic analysis of rice (*Oryza sativa* L.) genotypes under aerobic conditions on alfisols. *SABRAO J. Breed. and Genet.*, **46**(1): 99-111.
- RANI, C. S., ANANDAKUMAR, C. R., RAVEENDRAN, M., SUBRAMANIAN, K. S. AND ROBIN, S., 2016, Genetic variability studies and multivariate analysis in F₂ segregating populations involving medicinal rice (*Oryza sativa* L.) cultivar Kavuni. *Int. J. Agril. Sci.*, **8** (15): 1733-1735.
- RAO, C. R. 1952, Advanced statistical methods in biometrical research. *Ed. 1 John Willey and Sons. Inc.*, New York.
- RAO, V. R. AND HODGKIN, T., 2002, Genetic diversity and conservation and utilization of plant genetic resources. *Plant Cell Tissue Org. Cult.*, **68**: 1-19.
- RAVINDRA BABU, V., SHREYA, K., DANGI, K. S., USHARANI, G. AND NAGESH, P., 2012, Genetic variability studies for qualitative and quantitative traits in popular rice (*Oryza sativa* L.) hybrids of India. *Int. J. Scie. And Res. Publications*, **2**(6):1-5.
- ROBINSON, H. F., COMSTOCK, R. E. AND HARNEY, P. H., 1949, Estimates of heritability and degree in corn. *Agron. J.*, **41**: 353-359.
- ROBSON, D. S., 1956, The application of K4 statistics to genetic variance component analysis. *Biometrics*, **12**: 433-444.
- ROHMAN, M. M., HAKIM, M. A., SULTANA, N. A., KABIR, M. E., HASANUZZAMAN, M. AND ALI, M., 2004, Genetic divergence analysis in sorghum (*Sorghum bicolor* L.). *Asian J. Plant Sci.*, **3**: 211-214.
- SABIN, K., BIJAY, S., AMRIT, B., RAMAN, G.D., BHUWAN, S., PRIYANKA, N., SUNDARMAN S. AND PRASAD, G. S., 2016, Screening of different rice genotypes against (*Pyricularia grisea*) Sacc. in natural epidemic condition at seedling stage in Chitwan, Nepal. *Advances in Crop Sci. and Tech.*, **4**(4): 2-6.
- SADIMANTARA, G. R., MUHIDIN, AND CAHYONO, E., 2014, Genetic analysis on some agro-morphological characters of hybrid progenies from cultivated paddy rice and local upland rice. *Adv. Stu. in Bio.*, **6**(1): 7-18.
- SALA, M. AND SHANTHI, P., 2016, Variability, heritability and genetic advance studies in F₂ population of rice (*Oryza sativa* L.). *Int. J. Fors. and Crop Imp.*, **7**(1): 57-60.

- SANGARE, J. R., KONATE, A. K., CISSE, F. AND SANNI, A., 2017, Assessment of genetic parameters for yield and yield related-traits in an intraspecific rice (*Oryza sativa* L.) population. *J. Plant Breed. Genet.*, **05**(02) :45-56.
- SANJEEV, K., SINGH, H. B. AND SHARMA, J. K., 2005, Genetic variability for morpho-physiological and some quality traits in rice (*Oryza sativa* L.). *Himachal J. Agril. Res.*, **31**: 163-165.
- SARAWGI, A. K., PACHAURI, A. K. AND NAIR, S. K., 2017, Correlation path analysis and assessment of genetic diversity for yield attributing traits in rice (*Oryza sativa* L.) genotypes. *Agril. Res. J.*, **54**(4): 449-454.
- SAVITHA, P. AND USHAKUMARI, R., 2015, Genetic variability studies in F₂ and F₃ segregating generations for yield and its components in rice (*Oryza sativa* L.). *Indian J. Sci. and Tech.*, **8**(17):1-7.
- SELVARAJ, C. I., NAGARAJAN, P., THIYAGARAJAN, K., BHARATHI, M. AND RABINDRAN, R., 2011a, Genetic parameters of variability, correlation and path coefficient studies for grain yield and other yield attributes among rice blast disease resistant genotypes of rice (*Oryza sativa* L.). *African J. Biotech.*, **10**(17): 3322-3334.
- SELVARAJ, C. I., NAGARAJAN, P., THIYAGARAJAN, K., BHARATHI, M. AND RABINDRAN, R., 2011b, Marker assisted selection for leaf blast disease resistance and other yield traits in rice (*Oryza sativa* L.) using RAPD Markers. *Electronic J. Pl. Breed.*, **2**(1):8-23.
- SENAPATHI, B. K. AND SARKAR, G., 2005, Genetic divergence in tall indica rice (*Oryza sativa* L.) under rainfed saline soil of Sundarban. *Oryza*, **42**(1): 70-72.
- SHAIKH, S. A., UMATE, S. M., SYED, A. J. AND DEOSARKAR, D. B., 2017, Study on genetic variability, heritability and genetic advance in rice (*Oryza sativa* L.) genotypes. *Int. J. Pure App. Biosci.*, **5**(4): 511-515.
- SHANTAVVA, G., MAHADEVU, P., VEERAGHANTI, S. S., SURESH, K. AND HITTALMANI, S., 2014, Variability studies for yield and its components in rice (*Oryza sativa* L.). *Trends in Biosci.*, **7**(10): 961-963.
- SHARMA, R. C., SHRESTHA, S. M. AND PANDEY, M. P., 2007, Inheritance of blast resistance and associated microsatellite markers in rice cultivar "Laxmi". *J. Phytopathol.* **155**: 749-753.

- SHET, R. M., RAJANNA, M. P., RAMESH, S., SHESHSHAYEE, M. S. AND MAHADEVU, P., 2012, Genetic variability, correlation and path coefficient studies in F₂ generation of aerobic rice (*Orzya sativa* L.). *Electronic J. Plant Breed.*, **3**(3): 925-931.
- SHILPA, H. B., SHIVAKUMAR, N., PATROTI, P., PRASAD, D. H., HITTALMANI, S., LOHITHASWA, H. C. AND RAMACHANDRA, C., 2014, Genetic variability, heritability and character association studies for grain yield and yield attributing traits in segregating population of rice (*Oryza sativa* L.). *Progressive Research (Conf. Spl.)*, **9**: 1125-1128.
- SHIVASUBRAMANIAN, S. AND MENON, N., 1973, Heterosis and inbreeding depression in rice. *Madras Agric. J.*, **60**: 1134-1144.
- SINGH, A. K., SINGH, P. K., ARYA, M., SINGH, N. K. AND SINGH, U. S., 2015, Molecular screening of blast resistance genes in rice using SSR markers. *Plant Pathol. J.*, **31**(1): 12-24.
- SINGH, P. K., MISHRA, M. N., HORE, D. K. AND VERMA, M. R., 2006, Genetic divergence in lowland rice of north eastern region of India. *Communications in Biometry and Crop Sci.*, **1**(1): 35-40.
- SINGH, R. K. AND CHOWDHARY, B. D., 1977, Biometrical Methods in Quantitative Genetic Analysis, Kalyani Publishers, New Delhi, pp. 110-115.
- SNEDECOR, G. W. AND COCHRAN, W. G., 1994, Statistical methods. Fifth edition. Iowa State University Press. Ames. Iowa, USA.
- SONG, F. AND GOODMAN, R. M., 2001, Molecular biology of disease resistance in rice. *Physiol. Mol. Pl. Pathol.*, **59**: 1-11.
- SOUROUSH, H. R., MESBAH, M., HOSSAINZADEH, A. AND BOZORGIPOUR, R., 2004, Genetic and phenotypic variability and cluster analysis for quantitative and qualitative traits of rice. *Seed and Plant Karaj, Iran*, **20**: 167-182.
- SREEWONGCHAI, T., TOOJINDA, T., THANINTORN, N., KOSAWANG, C., VANAICHIT, A., THARREAU, D. AND SIRITHUNYA, P., 2010, Development of elite indica rice lines with wide spectrum of resistance to Thai blast isolates by pyramiding multiple resistance *QTLs*. *Plant Breed.*, **129**:176-180.

- SRUJANA, G., SURESH, B. G., LAVANYA, G. R., RAM, B. J. AND SUMANTH, V., 2017, Studies on genetic variability, heritability and genetic advance for yield and quality components in rice (*Oryza sativa* L.). *J. Pharmacognosy and Phytochemistry*, **6**(4): 564-566.
- SUBUDHI, H. N., MEHER, J., BOSE, L. K. AND DAS, S., 2009, Genetic diversity studies of promising varieties of eastern India based on quality characters. *Oryza*, **46**(4):271-274.
- SURESH, A. V. AND REDDY, C. D. R., 2002, Studies on genetic variability parameters in a set of parental lines and their F₂ population in Rice. *The Andhra Agril. J.*, **49**: 307-312.
- SWARUP, V. AND CHAUGALE, D. S., 1962, Studies on genetic variation I (phenotypic variations and its heritable components in some important quantitative characters contributing towards yield). *Indian J. Genetics*, **22**: 31-36.
- TANDEKAR, K. AND KOSHTA, N., 2014, To study the agro morphological variation and genetic variability in rice germplasm. *Middle-East J. Sci. Res.*, **20**(2): 218-224.
- TEJASWINI, K. L. Y., MANUKONDA, S., RAMANA RAO, P. V., RAVI KUMAR, B. N. V. S. R., MOHAMMAD, L. A. AND RAJU, S. K., 2016, Cluster analysis studies in rice (*Oryza sativa* L.) using wards minimum variance method. *J. Agril.and Crop Res.*, **4**(9): 129-139.
- THIPPESWAMY, S., CHANDRAMOHAN, Y., SAMREEN, Z., SRINIVAS, B., PADMAJA D. AND PRAVALIKA, K., 2015, Identification of blast resistant rice (*Oryza sativa* L.) genotypes in indigenous and exotic germplasm and validation of *pi* gene linked molecular markers. *Electronic J. Plant Breed.*, 21-29.
- VAITHIYALINGAN, M. AND NANDARAJAN, 2006, Genetic variability, heritability and genetic advance in F₂ population of inter sub-specific crosses of rice. *Crop Res.*, **31**: 476-477.
- VANAJA, T. AND BABU, L. C., 2003, Associating between physic-chemical characters and cooking qualities in high yielding rice varieties of diverse origin. *Int. Rice Research News Letter*.**1**: 28-29.
- VANISHREE, S., SWAPNA, K., RAJU, C. D., RAJU, C. S. AND SREEDHAR, M., 2013, Genetic variability and selection criteria in rice. *J. Biol. Sci. opinion*, **1**(4): 341-346.

- VASUDEVAN, K., CRUZ, C. M. V., GRUISSEM, W. AND BHULLAR, N. K., 2014, Large scale germplasm screening for identification of novel rice blast resistance sources. *Front. Plant Sci.*, **5**:1-9.
- VENKANNA, V., LINGAIAH, N., RAJU, C. S. AND RAO, V. T., 2014, Genetic studies for quality traits of F₂ population in rice (*Oryza sativa* L.). *Int. J. App. Bio. and Pharmaceutical Tech.*, **5**(2): 125-127.
- VIJAYA, I. AND SHAILAJA, H., 2016, Assessment of genetic parameters for yield and its related traits in F₂ population of KRH-4 hybrid rice (*Oryza sativa* L.). *Int. J. Agril. Sci. and Res.*, **6**(3): 87–96.
- VIJAYKUMAR, NAVINKUMAR, AND SURESH, B. G., 2015, Systematic Evaluation of exotic rice germplasm for yield component characters and its grain yield. *Int. J. Res. Studies in Biosci.*, **3**(3): 53-56.
- VIRK, P. S., KHUSH, G. S. AND VIRMANI, S. S., 2003, Breeding Strategies to Enhance Heterosis in Rice. In: Hybrid Rice for Food Security, Poverty Alleviation and Environmental Protection, *Int. Rice Res. Inst.*, Los Banos, Philippines, pp: 21-29.
- VIVEKANANDA, P. AND SUBRAMANIAN, S., 1993, Genetic divergence in rainfed rice. *Oryza*, **30**: 60-62.
- WEBER, C. R. AND MOORTHY, B. R., 1952, Heritable and non-heritable relationships and variability of oil content and agronomic characters in the F₂ generation of soybean crosses. *Agron. J.*, **44**: 202-209.
- WOUW, V. D. M., HINTUM, V. T., KIK, C., VAN TREUREN, R. AND VISSER, B., 2010, Genetic diversity trends in twentieth century crop cultivars: a meta analysis. *Theor. Appl. Genet.*, **120**(6):1241-52.
- YADAV, M. K., ARAVINDAN, S., NGANGKHAM, U., SHUBUDHI, H. N., BAG, M. K., ADAK, T., MUNDA, S., SAMANTARAY, S. AND JENA, M., 2017, Use of molecular markers in identification and characterization of resistance to rice blast in India. *PLoS ONE*, **12**(4):1-12.
- YUGANDHAR, P. R., DAHAT, D. V., BARAHTA, K. K. AND SUNEETHA, K., 2017, Study on variability, heritability and genetic advance for agro-morphological and grain quality parameters in restorer lines of rice (*Oryza sativa* L.). *Int. J. Pure App. Biosci.*, **5**(4): 1202-1206.

- ZENBAYASHI, K., ASHIZAWA, T., TANI, T. AND KOIZUMI, S., 2002, Mapping of the QTL (Quantitative Trait Locus) conferring partial resistance to leaf blast in rice cultivar Chubu 32. *Theor. and App. Gen.*, **104**: 547-552.
- ZEWDU, Z., GIBSON, P., LAMO, J. AND EDEMA, R., 2017, Reaction of introduced Korean rice genotypes for resistance to rice blast in Uganda. *J. Plant Breed. and Crop Sci.*, **9**(7): 98-105.
- ZEWDU, Z., EDEMA, R. AND LAMO, J., 2018, Genetic study of resistance to rice blast in crosses between Korean and locally adapted rice genotypes. *Advances in Crop Sci. Tech.*, **6**(2): 1-5.
- ZHOU, B., QU, S., LIU, G., DOLAN, M., SAKAI, H., LU, G., BELLIZZI, M. AND WANG, G. L., 2006, The eight amino-acid differences within three leucine-rich repeats between *Pi-2* and *Piz-t* resistance proteins determine the resistance specificity to *Magnaporthe grisea*. *Mol. Plant Microbe. Interact.*, **19**: 1216-1228.
- ZHOU, J. H., WANG, J. L., XU, J. C., LEI, C. L. AND LING, Z. Z., 2004, Identification and mapping of rice blast resistance gene *Pi-g(t)* in the cultivar Guangchangzhan. *Plant Pathol.* **53**(2): 191- 196.

Appendices

VII APPENDICES

Appendix I. Individual plant data of F₂ segregating population of the cross Jyothi × Kiruwana for yield and its related traits during Summer 2016

Sl. No.	F ₂ lines	Days to 50% flowering	Days to maturity	Plant height (cm)	Total number of tillers	Productive tillers	Panicle length (cm)	Grain yield (g/pl.)	Test weight (g)	Grain length (mm)	Grain breadth (mm)	LB ratio	Husk colour
1	JK-1-1	95	128	110.00	11.00	11.00	16.42	23.00	21.61	8.16	2.13	3.83	Bl.
2	JK-1-2	99	130	111.00	15.00	15.00	21.10	39.00	22.86	7.63	1.88	4.06	Bl.
3	JK-1-3	101	133	118.00	6.00	6.00	22.56	8.00	20.56	8.12	2.03	4.00	Bl.
4	JK-1-4	103	135	115.00	10.00	10.00	18.20	16.00	24.81	8.43	2.40	3.51	Bl.
5	JK-1-5	108	140	120.00	14.00	14.00	21.00	35.00	25.87	7.69	3.26	2.36	Br.
6	JK-1-6	105	132	85.00	11.00	11.00	21.71	22.00	29.13	8.51	3.25	2.62	Bl.
7	JK-1-7	103	135	121.00	20.00	20.00	21.90	38.00	22.84	8.70	2.23	3.90	Bl.
8	JK-1-8	105	138	70.00	22.00	18.00	18.80	28.00	18.74	7.98	1.64	4.87	Bl.
9	JK-1-9	105	141	102.00	26.00	22.00	19.90	47.00	21.23	7.57	1.54	4.92	Bl.
10	JK-1-10	105	141	130.00	24.00	24.00	22.80	48.00	20.96	7.23	1.45	4.99	Bl.
11	JK-1-11	105	141	125.00	27.00	25.00	23.50	58.00	26.80	8.22	3.14	2.62	Bl.
12	JK-1-12	101	132	125.00	13.00	13.00	26.52	23.00	18.58	7.18	1.72	4.17	Bl.
13	JK-1-13	101	132	95.00	17.00	16.00	19.90	26.00	19.98	7.78	1.89	4.12	Bl.
14	JK-1-14	103	133	110.00	12.00	12.00	22.10	25.00	18.38	7.18	1.68	4.27	Bl.
15	JK-1-15	100	132	106.00	15.00	15.00	20.90	31.00	17.60	7.05	1.59	4.43	Bl.
16	JK-1-16	102	134	105.00	12.00	12.00	19.56	21.00	26.66	8.76	3.16	2.77	Br.
17	JK-1-17	100	134	95.00	15.00	14.00	18.18	30.00	24.74	7.61	3.21	2.37	Br.
18	JK-1-18	101	137	95.00	16.00	15.00	18.70	18.00	29.06	8.84	3.12	2.83	Bl.
19	JK-1-19	103	140	127.00	9.00	9.00	21.40	22.00	22.40	8.19	2.53	3.24	Bl.
20	JK-1-20	107	143	103.00	11.00	11.00	21.80	20.00	31.40	9.05	3.23	2.80	Bl.
21	JK-1-21	112	148	127.00	9.00	9.00	22.40	19.00	32.97	8.42	3.42	2.46	Br.
22	JK-1-22	99	130	104.00	16.00	16.00	19.96	28.00	18.31	7.41	1.62	4.57	Bl.
23	JK-1-23	105	140	116.00	16.00	15.00	19.06	38.00	18.36	7.36	1.75	4.21	Bl.
24	JK-1-24	105	141	127.00	6.00	6.00	20.08	14.00	24.61	7.47	3.24	2.31	Bl.
25	JK-1-25	88	123	105.00	14.00	14.00	19.44	25.00	20.67	7.35	2.21	3.33	Bl.
26	JK-1-26	103	137	118.00	13.00	13.00	20.20	28.00	23.53	8.13	2.16	3.76	Bl.
27	JK-1-27	101	136	128.00	5.00	5.00	21.68	14.00	19.32	7.28	2.14	3.40	Bl.

Contd...

28	JK-1-28	103	137	102.00	4.00	4.00	17.80	8.00	17.96	7.54	1.86	4.05	Bl.
29	JK-1-29	89	124	115.00	13.00	13.00	24.50	32.00	22.61	8.22	2.22	3.70	Bl.
30	JK-1-30	92	124	90.00	13.00	13.00	18.08	17.00	19.82	7.59	1.70	4.46	Bl.
31	JK-1-31	105	141	114.00	22.00	22.00	22.16	51.00	23.92	7.50	1.50	5.00	Bl.
32	JK-1-32	107	143	115.00	10.00	10.00	23.37	34.00	18.74	7.22	1.85	3.90	Bl.
33	JK-1-33	103	139	110.00	8.00	8.00	21.92	21.00	27.37	8.26	3.33	2.48	Br.
34	JK-1-34	103	134	95.00	19.00	18.00	18.80	17.00	21.00	7.50	1.97	3.81	Bl.
35	JK-1-35	107	140	128.00	13.00	13.00	21.50	33.00	18.21	6.95	1.76	3.95	Bl.
36	JK-1-36	99	132	75.00	17.00	16.00	20.78	21.00	24.24	8.55	2.30	3.72	Bl.
37	JK-1-37	90	124	85.00	18.00	17.00	23.20	25.00	28.58	8.34	3.26	2.56	Br.
38	JK-1-38	101	138	130.00	14.00	14.00	18.25	38.00	20.57	6.87	1.58	4.35	Bl.
39	JK-1-39	107	142	96.00	14.00	14.00	20.80	35.00	19.44	7.54	1.51	4.99	Bl.
40	JK-1-40	107	142	130.00	11.00	11.00	22.20	19.00	22.25	8.35	1.83	4.56	Bl.
41	JK-1-41	94	128	110.00	14.00	14.00	22.00	32.00	20.93	7.42	2.29	3.24	Bl.
42	JK-1-42	105	141	75.00	13.00	12.00	16.68	17.00	18.64	7.26	1.61	4.51	Bl.
43	JK-1-43	105	141	130.00	10.00	10.00	21.02	24.00	18.34	7.07	1.88	3.76	Bl.
44	JK-1-44	108	142	83.00	8.00	8.00	17.44	10.00	17.95	7.07	1.84	3.84	Bl.
45	JK-1-45	99	134	110.00	14.00	13.00	19.20	25.00	14.30	6.80	1.45	4.69	Bl.
46	JK-1-46	105	141	120.00	6.00	6.00	19.67	10.00	22.50	7.26	3.19	2.28	Br.
47	JK-1-47	105	141	90.00	11.00	11.00	21.80	25.00	29.13	8.68	3.29	2.64	Br.
48	JK-1-48	95	130	95.00	4.00	4.00	17.84	6.00	19.46	7.34	1.73	4.24	Bl.
49	JK-1-49	105	141	117.00	15.00	15.00	24.00	38.00	26.12	7.79	3.27	2.38	Br.
50	JK-1-50	105	141	128.00	10.00	10.00	22.80	30.00	26.17	7.66	3.33	2.30	Br.
51	JK-1-51	97	133	70.00	13.00	12.00	17.10	19.00	20.43	8.23	1.71	4.81	Bl.
52	JK-1-52	107	143	126.00	12.00	12.00	23.00	37.00	23.86	8.41	2.10	4.00	Bl.
53	JK-1-53	101	135	90.00	6.00	6.00	17.33	3.00	16.04	8.51	2.05	4.15	Bl.
54	JK-1-54	105	141	113.00	17.00	17.00	21.50	39.00	21.70	7.26	1.54	4.71	Bl.
55	JK-1-55	97	132	112.00	13.00	13.00	20.40	27.00	29.81	8.76	3.27	2.68	Br.
56	JK-1-56	107	143	130.00	9.00	9.00	22.48	15.00	25.55	8.09	3.15	2.57	Br.
57	JK-1-57	89	123	115.00	19.00	19.00	20.60	39.00	19.01	7.31	1.72	4.25	Bl.
58	JK-1-58	105	141	115.00	11.00	11.00	21.26	17.00	25.59	8.10	3.22	2.52	Bl.
59	JK-1-59	105	141	120.00	12.00	12.00	22.60	32.00	16.68	6.86	1.61	4.26	Bl.
60	JK-1-60	107	133	148.00	12.00	12.00	22.10	26.00	26.78	8.46	3.04	2.78	Br.
61	JK-1-61	105	141	140.00	18.00	17.00	25.50	56.00	28.60	8.29	3.29	2.52	Bl.
62	JK-1-62	105	141	100.00	22.00	22.00	22.50	57.00	29.11	8.77	3.10	2.83	Br.

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63	JK-1-63	105	141	115.00	35.00	33.00	18.56	60.00	22.98	6.82	1.67	4.08	Bl.
64	JK-1-64	93	124	65.00	22.00	22.00	17.10	30.00	17.06	7.68	1.45	5.30	Bl.
65	JK-1-65	105	141	110.00	7.00	7.00	18.38	13.00	16.98	7.34	2.10	3.50	Bl.
66	JK-1-66	99	135	115.00	13.00	13.00	22.30	29.00	18.37	7.35	1.91	3.85	Bl.
67	JK-1-67	105	141	80.00	14.00	14.00	19.30	26.00	26.32	7.75	3.39	2.29	Br.
68	JK-1-68	99	137	95.00	8.00	8.00	19.90	23.00	26.66	8.41	3.13	2.69	Br.
69	JK-1-69	93	125	97.00	10.00	10.00	19.68	19.00	20.47	7.43	2.19	3.39	Bl.
70	JK-1-70	101	137	103.00	10.00	10.00	19.26	20.00	22.77	8.06	2.22	3.63	Bl.
71	JK-1-71	90	124	110.00	8.00	8.00	20.80	20.00	19.77	7.68	1.68	4.57	Bl.
72	JK-1-72	105	141	117.00	13.00	13.00	24.40	24.00	18.19	6.93	1.96	3.54	Bl.
73	JK-1-73	101	136	115.00	16.00	16.00	20.40	36.00	24.56	7.57	3.18	2.38	Br.
74	JK-1-74	105	141	135.00	6.00	6.00	21.60	15.00	21.78	7.53	2.09	3.60	Bl.
75	JK-1-75	101	136	75.00	18.00	18.00	18.00	21.00	25.86	7.93	3.17	2.50	Br.
76	JK-1-76	90	126	75.00	11.00	11.00	15.38	14.00	27.92	8.63	3.01	2.87	Br.
77	JK-1-77	88	123	93.00	7.00	7.00	18.80	9.00	21.53	7.65	2.48	3.08	Bl.
78	JK-1-78	103	140	130.00	9.00	9.00	22.10	23.00	25.53	8.65	3.05	2.84	Br.
79	JK-1-79	97	128	73.00	14.00	14.00	18.16	18.00	17.77	7.13	1.80	3.96	Bl.
80	JK-1-80	101	136	110.00	14.00	14.00	18.10	25.00	13.52	6.90	1.36	5.07	Bl.
81	JK-1-81	97	128	100.00	18.00	18.00	19.67	32.00	23.11	8.63	1.76	4.90	Bl.
82	JK-1-82	99	135	110.00	7.00	7.00	20.40	21.00	24.26	7.51	3.18	2.36	Br.
83	JK-1-83	92	125	116.00	34.00	32.00	20.50	58.00	25.60	8.01	2.22	3.61	Bl.
84	JK-1-84	86	120	118.00	35.00	31.00	19.80	50.00	24.15	7.73	3.01	2.57	Bl.
85	JK-1-85	112	148	78.00	14.00	14.00	20.20	31.00	27.94	8.50	3.08	2.76	Br.
86	JK-1-86	99	134	72.00	24.00	24.00	18.30	45.00	25.34	7.84	3.06	2.56	Br.
87	JK-1-87	89	124	100.00	26.00	25.00	18.20	27.00	13.34	8.02	1.83	4.38	Bl.
88	JK-1-88	97	131	100.00	7.00	7.00	18.90	5.00	17.74	7.87	1.65	4.77	Bl.
89	JK-1-89	109	143	80.00	22.00	22.00	21.50	37.00	16.47	7.18	1.53	4.69	Bl.
90	JK-1-90	105	141	122.00	8.00	8.00	21.40	20.00	22.13	8.11	1.91	4.25	Bl.
91	JK-1-91	103	131	75.00	19.00	19.00	17.40	21.00	25.51	8.00	3.11	2.57	Br.
92	JK-1-92	95	129	60.00	18.00	18.00	17.54	19.00	18.97	7.31	1.83	3.99	Bl.
93	JK-1-93	97	130	130.00	13.00	13.00	24.20	43.00	20.91	7.61	1.97	3.86	Bl.
94	JK-1-94	95	128	120.00	8.00	8.00	21.08	20.00	19.04	8.29	1.90	4.36	Bl.
95	JK-1-95	109	145	125.00	7.00	7.00	24.22	12.00	30.98	9.23	3.14	2.94	Bl.
96	JK-1-96	90	123	65.00	8.00	8.00	15.06	11.00	15.46	7.11	2.06	3.45	Bl.
97	JK-1-97	107	141	105.00	8.00	8.00	17.20	16.00	20.42	7.47	2.29	3.26	Bl.

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98	JK-1-98	109	143	116.00	6.00	6.00	19.80	15.00	24.27	8.26	2.56	3.23	Bl.
99	JK-1-99	109	143	120.00	10.00	10.00	21.00	27.00	24.16	7.48	3.14	2.38	Br.
100	JK-1-100	99	135	96.00	9.00	9.00	16.00	15.00	18.76	8.69	3.36	2.59	Br.
101	JK-1-101	103	139	109.00	9.00	9.00	21.90	32.00	28.84	7.55	1.57	4.81	Bl.
102	JK-1-102	105	141	100.00	12.00	12.00	18.60	12.00	22.90	8.27	2.37	3.49	Bl.
103	JK-1-103	101	138	72.00	6.00	6.00	17.50	15.00	20.56	7.42	2.14	3.47	Bl.
104	JK-1-104	108	143	116.00	11.00	11.00	20.40	28.00	25.16	7.89	3.16	2.50	Br.
105	JK-1-105	99	136	70.00	10.00	10.00	19.20	11.00	22.50	9.02	3.15	2.86	Br.
106	JK-1-106	97	133	100.00	6.00	6.00	21.18	36.00	17.06	6.86	1.58	4.34	Bl.
107	JK-1-107	90	125	87.00	14.00	14.00	20.00	32.00	28.01	8.66	3.12	2.78	Br.
108	JK-1-108	99	135	65.00	13.00	12.00	15.40	20.00	18.33	7.23	1.92	3.77	Bl.
109	JK-1-109	105	141	105.00	18.00	17.00	20.10	34.00	18.22	6.84	1.44	4.75	Bl.
110	JK-1-110	106	143	120.00	15.00	15.00	20.94	41.00	20.43	7.50	2.00	3.75	Bl.
111	JK-1-111	113	149	105.00	21.00	17.00	18.60	16.00	24.03	7.99	2.96	2.70	Bl.
112	JK-1-112	104	140	100.00	4.00	4.00	23.04	32.00	19.22	7.74	1.88	4.12	Bl.
113	JK-1-113	111	147	115.00	21.00	19.00	22.68	23.00	28.18	8.45	3.30	2.56	Bl.
114	JK-1-114	101	137	80.00	11.00	11.00	21.70	23.00	19.55	7.40	2.00	3.70	Bl.
115	JK-1-115	108	143	125.00	14.00	13.00	21.66	17.00	21.36	8.14	2.17	3.75	Bl.
116	JK-1-116	105	141	119.00	8.00	8.00	20.60	32.00	22.07	7.53	2.51	3.00	Bl.
117	JK-1-117	113	149	119.00	12.00	11.00	20.00	13.00	22.40	8.36	2.22	3.77	Bl.
118	JK-1-118	103	137	90.00	7.00	7.00	19.40	28.00	21.04	7.77	1.54	5.05	Bl.
119	JK-1-119	105	141	104.00	12.00	12.00	17.76	22.00	24.62	8.62	2.58	3.34	Bl.
120	JK-1-120	105	138	124.00	12.00	11.00	17.10	13.00	20.28	8.12	1.87	4.34	Bl.
121	JK-1-121	113	149	97.00	9.00	9.00	19.86	12.00	20.60	7.64	2.16	3.54	Bl.
122	JK-1-122	97	129	94.00	8.00	8.00	24.02	26.00	22.64	8.22	2.40	3.43	Bl.
123	JK-1-123	109	144	125.00	12.00	12.00	26.50	48.00	19.08	7.50	1.30	5.77	Bl.
124	JK-1-124	105	141	130.00	22.00	22.00	23.72	58.00	21.12	7.65	1.52	5.03	Bl.
125	JK-1-125	104	141	113.00	30.00	29.00	18.63	17.00	24.49	6.76	1.38	4.90	Bl.
126	JK-1-126	105	141	78.00	8.00	8.00	20.00	30.00	24.42	7.57	3.09	2.45	Bl.
127	JK-1-127	104	140	97.00	15.00	15.00	18.20	32.00	25.40	7.69	3.07	2.50	Br.
128	JK-1-128	104	139	110.00	23.00	23.00	18.60	41.00	15.95	7.19	1.50	4.79	Bl.
129	JK-1-129	105	141	120.00	26.00	26.00	21.80	37.00	21.41	8.00	2.10	3.81	Bl.
130	JK-1-130	97	130	70.00	16.00	16.00	19.80	46.00	20.43	8.26	1.64	5.04	Bl.
131	JK-1-131	105	141	100.00	19.00	19.00	20.20	43.00	25.53	8.40	3.26	2.58	Bl.
132	JK-1-132	105	141	100.00	17.00	17.00	19.34	23.00	16.38	7.19	1.23	5.85	Bl.

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133	JK-1-133	99	135	120.00	23.00	23.00	20.48	44.00	16.89	7.09	1.40	5.06	Bl.
134	JK-1-134	105	141	130.00	9.00	9.00	22.74	25.00	24.55	7.47	3.29	2.27	Br.
135	JK-1-135	99	133	77.00	20.00	20.00	23.06	35.00	26.06	8.06	3.10	2.60	Bl.
136	JK-1-136	105	141	60.00	6.00	6.00	23.72	13.00	21.09	7.93	1.90	4.17	Bl.
137	JK-1-137	105	138	105.00	35.00	33.00	23.42	51.00	18.23	6.92	1.47	4.71	Bl.
138	JK-1-138	105	141	105.00	35.00	34.00	28.52	57.00	18.58	7.90	1.60	4.94	Bl.
139	JK-1-139	105	138	110.00	35.00	34.00	22.56	55.00	19.70	6.88	1.20	5.73	Bl.
140	JK-1-140	105	141	125.00	18.00	18.00	22.18	38.00	20.24	7.71	1.89	4.08	Bl.
141	JK-1-141	105	137	105.00	30.00	30.00	19.90	45.00	17.16	7.38	1.47	5.02	Bl.
142	JK-1-142	105	141	126.00	28.00	28.00	27.10	56.00	22.02	7.81	1.31	5.96	Bl.
143	JK-1-143	105	141	110.00	32.00	31.00	21.70	39.00	18.13	7.30	1.82	4.01	Bl.
144	JK-1-144	105	138	105.00	8.00	8.00	25.30	24.00	16.44	7.28	1.35	5.39	Bl.
145	JK-1-145	99	134	65.00	19.00	19.00	19.16	20.00	28.20	8.68	3.28	2.65	Br.
146	JK-1-146	105	141	77.00	35.00	33.00	18.20	45.00	24.07	7.76	3.03	2.56	Br.
147	JK-1-147	104	141	140.00	17.00	17.00	25.40	43.00	24.85	7.55	3.24	2.33	Br.
148	JK-1-148	104	137	60.00	28.00	27.00	18.40	30.00	18.26	7.54	1.66	4.54	Bl.
149	JK-1-149	105	139	110.00	8.00	8.00	19.70	12.00	24.04	8.39	2.93	2.86	Br.
150	JK-1-150	105	139	110.00	12.00	12.00	20.10	30.00	22.71	7.93	2.18	3.64	Br.
151	JK-1-151	107	143	127.00	26.00	25.00	23.50	63.00	28.35	7.80	2.09	3.73	Bl.
152	JK-1-152	114	149	130.00	25.00	24.00	21.20	50.00	21.57	8.09	1.85	4.37	Bl.
153	JK-1-153	105	141	116.00	25.00	25.00	20.98	40.00	20.15	7.15	1.78	4.02	Bl.
154	JK-1-154	105	139	60.00	35.00	33.00	19.00	50.00	22.75	7.99	1.61	4.96	Bl.
155	JK-1-155	123	158	67.00	35.00	32.00	21.66	43.00	21.00	8.06	1.56	5.17	Bl.
156	JK-1-156	123	158	100.00	23.00	23.00	22.20	34.00	17.10	7.52	1.63	4.61	Bl.
157	JK-1-157	125	160	98.00	28.00	26.00	25.04	28.00	29.67	9.01	3.29	2.74	Br.
158	JK-1-158	124	158	89.00	28.00	27.00	24.50	30.00	27.48	8.55	2.99	2.86	Br.
159	JK-1-159	120	155	60.00	16.00	14.00	19.90	8.00	17.98	7.99	1.64	4.87	Bl.
160	JK-1-160	120	155	94.00	36.00	34.00	27.90	58.00	24.61	7.52	3.10	2.43	Bl.
161	JK-1-161	127	161	86.00	22.00	22.00	17.20	27.00	16.83	7.20	1.59	4.53	Bl.
162	JK-1-162	121	155	92.00	35.00	32.00	20.60	50.00	29.45	8.63	3.12	2.77	Bl.
163	JK-1-163	126	159	108.00	34.00	33.00	25.28	57.00	26.71	8.18	3.17	2.58	Br.
164	JK-1-164	125	161	106.00	36.00	35.00	22.60	61.00	23.63	6.80	1.60	4.25	Bl.
165	JK-1-165	125	161	103.00	32.00	30.00	24.70	50.00	19.38	7.39	1.84	4.02	Bl.
166	JK-1-166	126	159	93.00	20.00	18.00	24.30	9.00	29.36	8.69	3.11	2.79	Br.
167	JK-1-167	125	157	100.00	35.00	33.00	23.80	44.00	30.27	8.83	3.21	2.75	Br.

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168	JK-1-168	134	166	100.00	4.00	4.00	21.66	8.00	13.23	7.13	1.35	5.28	Bl.
169	JK-1-169	134	166	68.00	9.00	9.00	19.60	18.00	21.96	8.81	2.12	4.16	Bl.
170	JK-1-170	115	150	103.00	8.00	8.00	18.36	17.00	22.40	7.79	2.24	3.48	Bl.
171	JK-1-171	130	158	91.00	10.00	10.00	17.20	12.00	16.60	7.34	1.40	5.24	Bl.
172	JK-1-172	119	154	108.00	22.00	22.00	22.80	43.00	18.84	8.09	1.50	5.39	Bl.
173	JK-1-173	134	167	112.00	10.00	10.00	28.30	18.00	13.41	6.97	1.24	5.62	Bl.
174	JK-1-174	117	153	102.00	35.00	33.00	24.80	46.00	29.54	8.65	3.19	2.71	Br.
175	JK-1-175	124	160	91.00	13.00	13.00	23.86	23.00	29.47	8.71	3.04	2.87	Br.
176	JK-1-176	124	160	98.00	12.00	12.00	24.98	29.00	28.66	8.69	3.14	2.77	Br.
177	JK-1-177	130	162	103.00	10.00	10.00	25.30	26.00	28.20	8.63	3.00	2.88	Br.
178	JK-1-178	130	162	83.00	4.00	4.00	24.54	11.00	26.80	8.74	3.05	2.87	Bl.
179	JK-1-179	130	162	86.00	10.00	10.00	22.50	8.00	28.83	8.64	3.04	2.84	Br.
180	JK-1-180	133	163	100.00	20.00	19.00	23.70	25.00	30.31	9.01	3.19	2.82	Br.
181	JK-1-181	127	160	110.00	6.00	6.00	27.50	3.00	23.00	8.62	2.57	3.35	Bl.
182	JK-1-182	115	150	98.00	19.00	19.00	25.20	23.00	28.16	8.59	3.07	2.80	Br.
183	JK-1-183	115	150	94.00	19.00	19.00	23.50	13.00	25.89	7.74	3.11	2.49	Br.
184	JK-1-184	119	155	100.00	21.00	21.00	24.00	45.00	20.90	8.93	1.87	4.78	Bl.
185	JK-1-185	123	157	100.00	33.00	33.00	23.40	50.00	28.50	8.89	2.91	3.05	Br.
186	JK-1-186	124	158	100.00	36.00	35.00	20.64	52.00	20.61	8.23	1.57	5.24	Bl.
187	JK-1-187	124	162	87.00	7.00	4.00	24.30	7.00	24.66	8.54	2.50	3.42	Bl.
188	JK-1-188	123	160	93.00	16.00	16.00	23.50	30.00	26.59	8.86	2.82	3.14	Br.
189	JK-1-189	127	159	105.00	10.00	10.00	24.00	22.00	28.15	8.93	2.96	3.02	Bl.
190	JK-1-190	125	161	73.00	12.00	12.00	26.80	15.00	17.59	8.04	1.47	5.47	Bl.
191	JK-1-191	123	160	82.00	19.00	16.00	23.20	13.00	27.56	8.67	2.98	2.91	Bl.
192	JK-1-192	125	158	84.00	10.00	10.00	22.40	18.00	29.56	8.54	3.05	2.80	Br.
193	JK-1-193	136	165	89.00	23.00	21.00	22.70	39.00	29.21	8.90	3.12	2.85	Br.
194	JK-1-194	125	159	105.00	28.00	25.00	22.44	30.00	14.06	7.06	1.30	5.43	Bl.
195	JK-1-195	133	157	90.00	33.00	32.00	21.50	60.00	29.27	8.74	2.99	2.92	Br.
196	JK-1-196	125	158	106.00	14.00	12.00	20.60	23.00	21.87	8.55	2.16	3.96	Bl.
197	JK-1-197	125	155	118.00	10.00	8.00	23.70	18.00	24.92	8.37	2.31	3.62	Bl.
198	JK-1-198	127	163	114.00	10.00	8.00	21.50	22.00	19.50	8.16	2.41	3.39	Bl.
199	JK-1-199	125	158	100.00	19.00	19.00	25.50	32.00	30.22	8.82	3.07	2.87	Br.
200	JK-1-200	127	160	90.00	25.00	22.00	23.20	27.00	27.55	8.92	3.04	2.93	Bl.
201	JK-1-201	125	157	81.00	6.00	4.00	17.00	8.00	18.54	9.08	2.40	3.78	Bl.

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202	JK-1-202	124	158	96.00	10.00	10.00	22.10	8.00	27.27	8.71	2.88	3.02	Br.
203	JK-1-203	125	161	96.00	12.00	12.00	24.00	7.00	26.03	8.76	2.62	3.34	Br.
204	JK-1-204	122	155	98.00	34.00	34.00	23.80	45.00	28.05	8.55	2.99	2.86	Br.
205	JK-1-205	126	159	103.00	29.00	29.00	24.25	43.00	29.66	8.98	3.27	2.75	Br.
206	JK-1-206	127	159	89.00	12.00	12.00	24.54	27.00	27.88	8.55	2.99	2.86	Br.
207	JK-1-207	128	160	94.00	20.00	20.00	22.70	5.00	28.63	8.78	3.00	2.93	Bl.
208	JK-1-208	128	163	118.00	10.00	10.00	26.60	9.00	21.68	7.26	2.83	2.57	Bl.
209	JK-1-209	125	158	100.00	18.00	18.00	21.30	25.00	29.85	8.96	2.99	3.00	Br.
210	JK-1-210	125	158	104.00	15.00	15.00	23.70	38.00	30.36	9.02	3.26	2.77	Bl.
211	JK-1-211	115	147	96.00	10.00	10.00	22.40	18.00	28.19	8.79	3.05	2.88	Br.
212	JK-1-212	114	147	91.00	16.00	16.00	16.80	7.00	12.64	6.83	1.36	5.02	Bl.
213	JK-1-213	125	158	91.00	10.00	10.00	22.30	5.00	27.67	8.74	2.93	2.98	Bl.
214	JK-1-214	126	158	90.00	17.00	17.00	24.50	17.00	27.97	8.01	3.29	2.43	Bl.
215	JK-1-215	128	159	96.00	18.00	18.00	23.80	24.00	28.56	8.91	2.74	3.25	Bl.
216	JK-1-216	128	159	90.00	11.00	11.00	22.60	10.00	28.77	8.93	2.93	3.05	Bl.
217	JK-1-217	126	158	88.00	24.00	24.00	22.90	27.00	27.94	8.56	3.06	2.80	Br.
218	JK-1-218	130	163	108.00	14.00	14.00	23.85	16.00	28.33	7.97	3.39	2.35	Br.
219	JK-1-219	131	163	78.00	6.00	6.00	19.70	9.00	16.17	7.48	1.66	4.51	Bl.
220	JK-1-220	132	165	96.00	17.00	17.00	23.25	26.00	29.47	8.92	3.07	2.91	Br.
221	JK-1-221	129	161	98.00	21.00	21.00	25.74	27.00	29.90	8.85	3.04	2.91	Bl.
222	JK-1-222	129	161	100.00	22.00	22.00	24.10	47.00	29.91	8.93	3.17	2.82	Br.
223	JK-1-223	130	162	86.00	23.00	23.00	25.50	26.00	24.15	7.96	3.19	2.50	Bl.
224	JK-1-224	130	162	94.00	35.00	35.00	24.50	40.00	27.65	8.56	3.04	2.82	Br.
225	JK-1-225	128	159	110.00	6.00	6.00	24.70	10.00	13.84	6.98	1.63	4.28	Bl.
226	JK-1-226	128	159	134.00	5.00	5.00	18.80	12.00	24.31	7.81	2.93	2.67	Br.
	Mean	109.69	143.88	102.09	16.17	15.61	21.39	27.65	23.01	7.96	2.38	3.61	
	Jyothi	104.20	135.60	95.40	19.40	18.60	20.98	26.80	29.69	9.23	2.86	3.23	Br.
	Kiruwana	118.60	149.60	123.20	10.20	9.80	22.42	19.60	19.80	7.52	1.51	4.99	Bl.

Bl-Black

Br-Brown

Appendix II. Mean of F₃ families of cross Jyothi × Kiruwana for yield and its related traits conducted at AHRS, Ponnampet during Kharif 2016

Sl. No.	F ₃ Families	Days to 50 % flowering	Days to maturity	Plant height (cm)	Total number of tillers	Productive tillers	Panicle length (cm)	Grain yield (g/pl)	Test weight (g)	Grain length (mm)	Grain Breadth (mm)	LB ratio	Leaf Blast	Husk colour
1	JK-1-1	99	128	88.00	8.44	6.54	12.34	6.44	18.32	7.80	2.08	3.75	5	Seg.
2	JK-1-2	114	136	105.70	12.80	12.25	22.02	19.93	19.43	7.51	1.81	4.15	4	Seg.
3	JK-1-3	108	130	110.00	8.96	7.44	14.36	7.46	17.56	8.15	2.13	3.83	5	Seg.
4	JK-1-4	108	132	84.00	7.48	6.76	14.23	4.48	21.34	8.35	2.26	3.69	7	Bl.
5	JK-1-5	116	140	96.20	11.63	11.50	19.74	10.50	23.37	7.52	3.04	2.47	4	Seg.
6	JK-1-6	105	132	86.00	6.54	5.66	12.12	3.96	25.33	8.52	3.19	2.67	6	Bl.
7	JK-1-7	98	124	79.00	6.48	5.32	11.98	3.88	20.22	8.55	2.20	3.89	7	Bl.
8	JK-1-8	100	136	72.60	12.67	12.43	18.42	18.93	19.48	7.77	1.54	5.05	3	Seg.
9	JK-1-9	103	136	84.50	13.70	13.30	18.68	17.60	17.42	7.41	1.67	4.44	3	Seg.
10	JK-1-10	100	126	101.50	11.10	10.67	18.90	12.70	19.26	7.26	1.62	4.48	4	Seg.
11	JK-1-11	110	142	120.00	9.96	8.98	16.87	10.14	24.82	8.16	3.09	2.64	5	Seg.
12	JK-1-12	104	134	104.00	10.32	9.56	17.44	12.92	16.34	7.11	1.68	4.23	6	Bl.
13	JK-1-13	108	140	117.00	9.58	8.42	15.64	9.08	16.46	7.67	1.79	4.28	5	Bl.
14	JK-1-14	104	136	109.80	11.90	11.00	20.64	14.61	17.38	7.04	1.57	4.48	4	Seg.
15	JK-1-15	106	140	97.00	13.28	13.25	21.10	14.06	18.23	7.21	1.48	4.87	2	Seg.
16	JK-1-16	101	137	102.60	12.13	12.00	19.29	13.00	23.66	8.64	3.08	2.81	1	Br.
17	JK-1-17	102	137	95.20	12.67	12.67	18.81	11.75	23.43	7.54	3.11	2.42	4	Br.
18	JK-1-18	104	132	97.44	10.58	8.74	16.46	10.44	24.06	8.54	3.03	2.82	5	Seg.
19	JK-1-19	98	127	92.54	9.84	8.44	14.32	8.16	23.40	8.04	2.44	3.30	6	Seg.
20	JK-1-20	100	130	94.54	11.32	10.86	16.98	9.08	28.81	8.75	3.01	2.91	6	Br.
21	JK-1-21	101	132	89.65	10.48	9.56	15.68	11.64	30.72	8.45	3.37	2.51	6	Seg.
22	JK-1-22	101	130	86.65	8.78	7.44	16.84	12.86	16.84	7.35	1.63	4.51	5	Bl.
23	JK-1-23	107	142	93.50	12.11	12.00	19.97	14.83	18.23	7.26	1.59	4.57	4	Seg.
24	JK-1-24	99	130	83.54	8.66	8.26	15.74	7.26	22.56	7.41	3.15	2.35	6	Seg.
25	JK-1-25	98	128	72.86	10.72	8.44	14.56	4.98	16.54	7.01	2.08	3.37	8	Bl.
26	JK-1-26	105	130	93.10	11.80	11.80	19.06	17.74	22.58	8.17	2.12	3.85	3	Br.
27	JK-1-27	105	134	102.90	12.20	11.60	19.34	15.80	18.24	7.14	2.08	3.43	4	Seg.
28	JK-1-28	98	129	87.16	10.38	9.24	13.48	9.44	15.67	7.44	1.81	4.11	6	Seg.
29	JK-1-29	94	126	79.36	9.44	8.36	13.12	5.24	17.98	8.07	2.01	4.01	8	Bl.

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30	JK-1-30	103	136	86.90	12.00	11.89	19.02	21.17	19.67	7.33	1.73	4.24	4	Seg.
31	JK-1-31	99	130	84.50	12.00	11.50	17.76	17.20	22.72	7.52	1.30	5.78	3	Seg.
32	JK-1-32	103	135	86.90	11.50	11.33	19.33	15.20	18.69	7.36	1.86	3.96	3	Seg.
33	JK-1-33	107	142	96.40	12.00	11.00	18.62	13.94	25.73	8.09	3.28	2.47	4	Br.
34	JK-1-34	121	154	87.60	12.67	12.67	19.78	10.13	20.43	7.51	1.79	4.20	4	Seg.
35	JK-1-35	103	138	95.10	10.67	10.56	19.83	16.17	16.21	7.05	1.61	4.38	3	Bl.
36	JK-1-36	106	143	77.80	13.50	13.40	19.21	15.20	22.24	8.43	2.32	3.63	2	Seg.
37	JK-1-37	110	145	87.00	12.40	12.40	19.71	17.88	25.43	8.28	3.22	2.57	3	Br.
38	JK-1-38	102	136	100.00	11.40	11.10	20.02	14.00	19.84	6.84	1.54	4.44	4	Seg.
39	JK-1-39	102	134	74.82	9.56	9.22	17.21	9.12	19.48	7.51	1.49	5.04	5	Seg.
40	JK-1-40	104	138	105.60	14.13	14.00	21.47	12.72	22.85	8.41	1.79	4.70	3	Seg.
41	JK-1-41	112	149	102.10	13.00	12.89	20.53	21.90	20.43	7.44	2.21	3.37	4	Seg.
42	JK-1-42	108	140	87.44	11.42	10.82	18.22	10.68	16.44	7.16	1.63	4.39	6	Bl.
43	JK-1-43	96	129	72.86	8.24	7.66	12.86	7.12	15.02	6.92	1.81	3.82	8	Seg.
44	JK-1-44	102	134	85.50	14.22	14.14	19.28	16.00	18.47	7.21	1.88	3.84	3	Bl.
45	JK-1-45	104	138	93.30	14.00	14.25	18.79	18.07	16.33	6.89	1.49	4.62	2	Bl.
46	JK-1-46	102	136	119.00	13.30	12.90	20.91	18.14	22.58	7.34	3.21	2.29	3	Seg.
47	JK-1-47	111	154	85.90	14.90	14.00	21.60	20.94	26.45	8.56	3.18	2.69	1	Seg.
48	JK-1-48	113	157	104.90	14.33	13.44	20.20	23.83	20.63	7.42	1.81	4.10	4	Seg.
49	JK-1-49	100	132	97.00	14.00	13.33	21.14	16.39	27.52	7.62	3.28	2.32	2	Br.
50	JK-1-50	103	138	105.00	12.22	11.56	19.88	15.19	26.70	7.69	3.32	2.32	2	Br.
51	JK-1-51	102	136	79.30	15.40	15.33	19.72	20.70	19.98	8.17	1.67	4.89	2	Seg.
52	JK-1-52	106	137	91.60	12.30	11.89	19.20	16.30	21.94	8.32	2.04	4.08	3	Seg.
53	JK-1-53	112	146	103.00	13.50	12.80	20.51	22.30	15.14	8.47	1.98	4.28	2	Seg.
54	JK-1-54	102	136	92.80	13.60	13.40	20.19	12.70	22.37	7.29	1.59	4.58	4	Bl.
55	JK-1-55	107	139	91.20	12.89	12.11	20.77	18.06	27.94	8.65	3.24	2.67	3	Br.
56	JK-1-56	105	142	106.40	11.30	11.30	20.98	22.93	24.59	8.14	2.95	2.76	2	Br.
57	JK-1-57	98	126	75.82	11.74	10.62	18.22	11.66	17.65	7.24	1.65	4.39	5	Bl.
58	JK-1-58	108	130	87.46	10.62	9.34	17.81	10.14	22.99	7.95	3.14	2.53	5	Bl.
59	JK-1-59	94	127	70.66	8.64	7.14	15.62	5.38	15.02	6.66	1.48	4.50	7	Seg.
60	JK-1-60	107	138	115.80	12.60	11.90	19.95	17.84	27.85	8.43	2.97	2.84	2	Br.
61	JK-1-61	106	141	114.10	11.40	11.38	22.52	14.28	29.63	8.34	3.24	2.57	1	Bl.
62	JK-1-62	109	145	85.30	13.30	13.22	22.15	17.80	31.08	8.79	3.15	2.79	2	Br.
63	JK-1-63	107	146	92.50	12.10	11.60	19.35	16.39	26.56	6.69	1.91	3.50	1	Bl.
64	JK-1-64	105	139	76.00	14.20	13.78	19.08	22.61	18.69	7.66	1.65	4.64	2	Bl.

65	JK-1-65	104	136	112.60	13.30	12.70	22.05	19.88	16.67	7.24	2.07	3.50	3	Seg.
66	JK-1-66	102	134	103.80	13.20	12.70	20.40	15.00	18.42	7.37	1.94	3.80	3	Seg.
67	JK-1-67	93	127	85.80	13.30	13.11	20.04	19.30	28.53	7.69	3.37	2.28	1	Br.
68	JK-1-68	104	137	104.20	14.90	13.67	20.04	20.10	24.54	8.32	3.09	2.69	2	Br.
69	JK-1-69	100	128	104.20	13.40	13.00	22.81	22.83	22.73	7.52	2.22	3.39	1	Seg.
70	JK-1-70	102	137	99.40	17.60	16.60	21.79	18.00	20.79	8.56	2.16	3.96	1	Bl.
71	JK-1-71	104	136	99.10	13.40	13.00	19.81	16.36	20.54	7.69	1.75	4.39	2	Seg.
72	JK-1-72	103	133	96.30	13.80	13.20	18.35	12.30	20.76	7.01	1.94	3.61	2	Bl.
73	JK-1-73	103	137	88.90	11.70	10.78	17.18	19.28	23.52	7.47	3.16	2.36	2	Br.
74	JK-1-74	107	141	110.10	12.40	12.10	19.73	17.70	19.89	7.48	2.11	3.55	3	Seg.
75	JK-1-75	109	140	73.60	12.80	12.20	18.84	19.60	22.56	7.87	3.12	2.52	2	Br.
76	JK-1-76	102	136	81.70	13.30	13.00	20.43	14.10	25.99	8.56	2.94	2.91	4	Br.
77	JK-1-77	99	128	77.54	10.82	9.54	16.82	10.72	18.88	7.59	2.34	3.24	5	Bl.
78	JK-1-78	102	134	115.60	12.00	11.70	21.04	14.61	24.87	8.62	3.06	2.82	3	Br.
79	JK-1-79	95	126	81.68	7.76	6.52	14.54	9.38	16.72	7.08	1.74	4.07	6	Bl.
80	JK-1-80	102	136	87.40	14.90	14.20	18.40	22.00	15.92	6.96	1.34	5.19	1	Seg.
81	JK-1-81	108	142	88.60	13.00	12.80	16.35	22.75	23.54	8.64	1.79	4.83	3	Seg.
82	JK-1-82	101	138	89.50	11.22	11.22	18.69	16.72	22.62	7.54	3.14	2.40	2	Br.
83	JK-1-83	103	136	87.70	13.00	12.89	20.71	23.70	25.63	8.06	2.24	3.60	2	Bl.
84	JK-1-84	103	136	86.40	11.50	11.30	18.81	16.72	24.59	7.76	3.08	2.52	2	Bl.
85	JK-1-85	105	138	78.20	12.10	11.22	20.42	15.60	26.99	8.46	3.08	2.75	2	Br.
86	JK-1-86	105	136	74.60	11.50	11.00	17.12	17.70	26.47	7.91	3.09	2.56	1	Br.
87	JK-1-87	103	132	78.00	11.60	11.30	17.70	14.60	15.44	8.22	1.86	4.42	2	Bl.
88	JK-1-88	102	134	91.40	11.10	10.70	17.95	10.60	15.46	7.77	1.61	4.83	6	Seg.
89	JK-1-89	104	134	78.50	11.10	11.11	18.53	17.84	17.99	7.24	1.61	4.50	2	Seg.
90	JK-1-90	101	135	91.20	11.90	11.80	18.10	12.40	20.23	8.16	1.96	4.16	2	Seg.
91	JK-1-91	101	134	73.10	11.20	10.80	17.38	14.30	24.54	8.07	3.04	2.65	2	Br.
92	JK-1-92	100	132	64.20	11.90	11.50	17.59	16.20	17.70	7.26	1.80	4.03	2	Seg.
93	JK-1-93	101	136	80.40	10.57	10.40	17.64	17.50	22.87	7.69	1.98	3.88	1	Seg.
94	JK-1-94	101	137	93.60	10.33	10.33	16.83	14.83	19.52	8.14	1.88	4.33	2	Seg.
95	JK-1-95	100	131	78.10	11.50	11.22	18.07	17.61	27.65	9.09	3.15	2.89	3	Seg.
96	JK-1-96	106	140	78.00	12.33	11.22	19.11	21.83	15.93	7.17	2.06	3.48	2	Seg.
97	JK-1-97	101	134	86.30	11.70	11.38	17.69	12.13	17.84	7.41	2.23	3.32	4	Seg.
98	JK-1-98	102	132	92.90	11.50	11.30	18.53	17.50	24.22	8.23	2.54	3.24	1	Seg.
99	JK-1-99	101	133	80.50	12.00	10.71	16.06	22.93	24.79	7.53	3.16	2.38	1	Br.

100	JK-1-100	101	134	83.40	12.40	12.00	17.31	12.90	17.65	8.62	3.33	2.59	3	Br.
101	JK-1-101	98	128	83.70	11.40	11.00	16.86	16.30	27.89	7.62	1.58	4.82	1	Seg.
102	JK-1-102	106	138	95.70	12.10	11.00	19.07	14.83	21.99	8.18	2.31	3.54	1	Seg.
103	JK-1-103	104	138	75.20	12.10	11.70	17.20	17.50	21.54	7.38	2.15	3.43	1	Seg.
104	JK-1-104	102	135	92.90	12.60	11.44	20.05	15.60	23.21	7.85	3.12	2.52	3	Br.
105	JK-1-105	102	135	78.40	13.00	12.10	19.68	13.10	23.20	9.12	3.11	2.93	3	Br.
106	JK-1-106	102	134	89.30	13.10	12.80	18.60	19.20	19.56	6.76	1.53	4.42	1	Bl.
107	JK-1-107	106	139	77.60	14.70	11.70	20.74	12.70	27.09	8.62	3.07	2.81	2	Br.
108	JK-1-108	110	145	68.60	13.80	13.60	18.97	11.60	20.39	7.39	1.94	3.81	1	Bl.
109	JK-1-109	103	136	90.80	13.00	12.30	13.39	19.30	17.29	6.80	1.41	4.82	2	Bl.
110	JK-1-110	106	140	106.10	14.30	12.11	20.26	23.20	18.47	7.36	2.13	3.46	1	Seg.
111	JK-1-111	111	146	98.78	15.76	14.98	19.54	14.93	20.42	7.67	2.83	2.71	3	Seg.
112	JK-1-112	106	141	100.60	13.40	13.20	19.87	14.20	17.43	7.72	1.81	4.27	4	Seg.
113	JK-1-113	113	145	84.52	11.74	10.22	15.68	10.82	23.44	8.41	3.24	2.60	5	Seg.
114	JK-1-114	94	125	76.58	10.86	8.52	12.64	6.84	16.59	7.32	1.92	3.81	8	Seg.
115	JK-1-115	104	139	112.50	11.10	11.00	19.18	11.90	20.64	8.09	2.14	3.78	4	Seg.
116	JK-1-116	104	136	87.40	11.40	11.44	17.85	15.06	20.82	7.48	2.44	3.07	3	Seg.
117	JK-1-117	104	141	103.20	12.30	11.50	19.54	13.70	20.98	8.29	2.17	3.82	3	Seg.
118	JK-1-118	103	136	82.70	13.30	12.90	20.47	14.00	20.29	7.67	1.51	5.08	1	Seg.
119	JK-1-119	107	140	102.90	12.70	12.20	19.84	12.80	25.69	8.67	2.61	3.32	3	Seg.
120	JK-1-120	102	136	94.30	14.90	14.44	18.48	15.90	18.87	8.02	1.84	4.36	2	Seg.
121	JK-1-121	109	141	111.42	12.32	11.72	17.64	13.74	17.68	7.56	2.11	3.58	5	Bl.
122	JK-1-122	103	130	100.42	11.54	9.92	15.86	8.82	19.86	8.14	2.29	3.55	6	Seg.
123	JK-1-123	113	148	84.36	8.94	7.12	12.42	7.86	17.54	7.46	1.27	5.87	6	Seg.
124	JK-1-124	108	142	95.80	13.30	13.00	21.48	16.70	22.18	7.63	1.55	4.92	4	Bl.
125	JK-1-125	106	140	101.50	12.33	11.78	19.35	16.78	22.43	6.73	1.27	5.30	3	Seg.
126	JK-1-126	113	145	98.76	13.42	11.76	16.74	10.84	20.49	7.49	3.04	2.46	6	Bl.
127	JK-1-127	104	139	92.10	14.40	13.80	18.70	18.50	23.94	7.58	3.03	2.50	4	Br.
128	JK-1-128	102	134	109.30	12.50	11.80	20.32	11.80	16.84	7.12	1.47	4.84	3	Seg.
129	JK-1-129	104	137	70.10	15.40	14.60	18.74	17.20	22.42	7.13	2.07	3.44	2	Seg.
130	JK-1-130	105	140	93.48	8.66	7.14	13.54	6.46	16.39	8.14	1.60	5.09	7	Bl.
131	JK-1-131	110	143	104.10	11.60	11.10	19.79	14.30	26.86	8.44	3.26	2.59	2	Seg.
132	JK-1-132	101	134	105.50	13.40	13.20	19.05	16.60	15.35	7.15	1.24	5.77	3	Bl.
133	JK-1-133	103	138	106.10	13.80	13.70	21.60	18.30	14.83	7.03	1.33	5.29	4	Seg.
134	JK-1-134	104	138	117.60	11.70	11.20	20.91	11.40	23.65	7.43	3.18	2.34	4	Br.

135	JK-1-135	106	143	89.10	13.70	13.60	21.34	19.00	24.04	8.03	3.04	2.64	2	Seg.
136	JK-1-136	106	140	75.10	13.90	13.60	19.19	14.70	22.44	7.98	1.92	4.16	1	Bl.
137	JK-1-137	102	136	97.90	14.50	14.10	20.79	25.80	16.87	6.88	1.43	4.81	4	Bl.
138	JK-1-138	104	138	111.50	13.50	13.00	22.96	20.06	18.52	7.94	1.61	4.93	2	Seg.
139	JK-1-139	104	138	101.90	15.10	14.33	22.39	17.06	18.34	6.81	1.23	5.54	4	Bl.
140	JK-1-140	102	134	92.40	12.00	11.20	18.06	14.90	18.54	7.66	1.83	4.19	3	Seg.
141	JK-1-141	104	135	84.40	12.50	11.50	18.60	12.10	18.67	7.35	1.51	4.87	2	Seg.
142	JK-1-142	111	149	99.40	13.50	12.60	21.01	11.40	20.08	7.73	1.27	6.09	3	Seg.
143	JK-1-143	97	127	68.76	8.16	7.42	12.66	8.08	15.36	7.28	1.76	4.14	7	Bl.
144	JK-1-144	105	137	87.70	12.70	12.50	18.93	12.94	17.45	7.15	1.30	5.50	3	Seg.
145	JK-1-145	104	138	76.00	15.50	14.60	20.55	16.10	25.27	8.54	3.23	2.64	2	Br.
146	JK-1-146	104	136	81.20	13.60	13.20	19.13	10.90	23.05	7.68	3.01	2.55	2	Br.
147	JK-1-147	110	153	125.10	13.10	12.90	22.10	17.90	25.96	7.60	3.22	2.36	2	Br.
148	JK-1-148	111	152	76.20	19.00	18.80	19.86	10.90	19.69	7.58	1.71	4.43	1	Bl.
149	JK-1-149	115	158	109.00	13.30	12.40	22.26	15.44	22.95	8.23	2.83	2.91	2	Br.
150	JK-1-150	113	157	95.70	15.80	14.80	20.65	12.20	23.98	7.94	2.22	3.58	2	Br.
151	JK-1-151	109	145	115.90	14.30	13.40	21.91	9.90	26.56	7.73	2.04	3.79	3	Seg.
152	JK-1-152	107	142	104.10	15.80	14.78	20.83	13.20	19.74	8.02	1.80	4.46	3	Seg.
153	JK-1-153	94	126	82.42	10.54	7.74	14.36	6.26	15.61	6.95	1.67	4.16	8	Seg.
154	JK-1-154	105	141	120.50	16.80	16.70	19.99	12.93	20.53	7.89	1.57	5.03	1	Seg.
155	JK-1-155	108	143	78.50	16.90	16.80	21.21	16.30	22.34	8.13	1.54	5.28	4	Seg.
156	JK-1-156	106	140	97.90	15.30	14.50	21.83	14.10	18.68	7.56	1.62	4.67	2	Bl.
157	JK-1-157	114	156	88.80	15.30	15.10	21.63	12.60	26.98	8.96	3.26	2.75	3	Br.
158	JK-1-158	113	154	89.90	15.60	15.30	22.45	14.20	25.86	8.52	2.93	2.91	3	Br.
159	JK-1-159	103	135	105.70	14.60	14.20	21.56	19.30	18.89	7.93	1.67	4.75	3	Seg.
160	JK-1-160	113	156	87.00	15.40	14.70	23.36	11.70	21.19	7.43	3.04	2.44	2	Seg.
161	JK-1-161	107	142	105.10	16.10	15.70	22.18	10.93	14.88	7.13	1.53	4.66	4	Seg.
162	JK-1-162	125	154	98.54	13.44	11.86	18.58	12.18	26.55	8.58	3.06	2.80	5	Seg.
163	JK-1-163	116	158	78.90	13.90	13.70	20.60	19.50	27.59	8.24	3.14	2.62	4	Br.
164	JK-1-164	104	130	97.10	14.60	14.40	20.81	11.00	23.85	6.76	1.58	4.28	4	Seg.
165	JK-1-165	123	153	119.52	15.64	14.64	19.68	18.14	16.86	7.25	1.81	4.01	6	Bl.
166	JK-1-166	111	149	85.30	12.60	12.30	22.77	13.30	28.75	8.56	3.04	2.82	4	Br.
167	JK-1-167	111	152	86.10	13.90	13.40	22.38	11.70	28.69	8.79	3.12	2.82	3	Br.
168	JK-1-168	106	140	102.60	12.40	12.10	20.79	10.90	14.44	7.17	1.38	5.20	4	Seg.
169	JK-1-169	108	143	83.50	15.60	15.60	21.07	16.20	22.63	8.85	2.17	4.08	4	Seg.

170	JK-1-170	102	135	110.10	15.30	14.50	21.41	10.83	23.67	7.84	2.27	3.45	4	Seg.
171	JK-1-171	97	126	68.58	10.34	8.12	13.58	6.74	14.72	7.21	1.32	5.46	8	Bl.
172	JK-1-172	107	142	95.90	13.70	13.70	20.02	14.30	19.89	8.13	1.53	5.31	3	Seg.
173	JK-1-173	110	146	95.80	14.30	14.30	20.19	20.40	15.47	6.99	1.31	5.34	2	Seg.
174	JK-1-174	111	148	88.80	15.10	14.56	22.29	12.00	27.49	8.58	3.14	2.73	3	Br.
175	JK-1-175	109	142	86.50	15.50	15.30	21.89	20.82	27.97	8.45	3.00	2.82	4	Br.
176	JK-1-176	109	143	87.70	14.80	14.70	21.66	12.70	26.81	8.63	3.12	2.77	4	Br.
177	JK-1-177	110	145	88.60	14.50	14.40	22.12	14.90	29.25	8.67	3.20	2.71	4	Br.
178	JK-1-178	124	150	97.64	8.66	8.22	18.54	10.72	24.57	8.61	2.89	2.98	5	Seg.
179	JK-1-179	107	143	86.10	15.70	14.67	21.23	15.10	25.84	8.43	3.02	2.79	4	Br.
180	JK-1-180	112	149	88.30	14.60	14.30	21.30	15.80	31.33	9.09	3.24	2.81	3	Br.
181	JK-1-181	105	138	94.50	16.90	16.40	23.98	17.20	22.76	8.54	2.53	3.38	4	Seg.
182	JK-1-182	112	143	90.00	15.00	14.80	22.77	14.90	29.43	8.64	3.14	2.75	4	Br.
183	JK-1-183	112	145	88.10	17.50	17.20	21.94	25.30	22.95	7.67	3.07	2.50	3	Br.
184	JK-1-184	110	148	95.50	15.90	15.70	20.81	11.30	18.88	8.86	1.82	4.87	2	Bl.
185	JK-1-185	111	148	92.20	16.70	15.20	23.84	15.60	29.52	8.91	2.94	3.03	4	Br.
186	JK-1-186	105	139	102.40	15.60	14.70	21.21	14.20	18.64	8.21	1.52	5.40	4	Seg.
187	JK-1-187	126	152	116.76	8.94	7.46	15.42	11.92	23.69	8.52	2.46	3.46	5	Bl.
188	JK-1-188	130	159	112.34	12.16	11.86	16.58	13.98	23.96	8.73	2.76	3.16	5	Br.
189	JK-1-189	129	160	105.74	13.26	12.24	17.32	13.16	24.34	8.82	2.83	3.12	5	Seg.
190	JK-1-190	107	130	85.68	9.48	7.56	14.52	7.84	15.21	7.93	1.44	5.51	7	Seg.
191	JK-1-191	126	154	94.68	7.78	6.65	15.64	10.36	24.33	8.53	2.84	3.00	5	Bl.
192	JK-1-192	106	142	86.60	16.70	15.40	22.39	15.00	31.23	8.59	3.12	2.75	4	Br.
193	JK-1-193	108	140	89.50	13.70	13.60	22.94	16.90	26.43	8.78	3.04	2.89	3	Br.
194	JK-1-194	126	160	112.64	12.12	10.64	16.42	7.74	13.11	6.67	1.32	5.05	6	Seg.
195	JK-1-195	109	144	83.40	18.33	17.22	21.76	24.96	26.78	8.65	2.86	3.02	3	Br.
196	JK-1-196	126	154	98.36	12.56	11.62	18.42	15.18	17.79	8.35	2.12	3.94	6	Bl.
197	JK-1-197	108	142	111.50	12.50	11.90	19.89	17.92	26.95	8.42	2.36	3.57	1	Seg.
198	JK-1-198	132	163	121.42	18.34	17.46	20.64	22.24	18.95	8.32	2.44	3.41	1	Bl.
199	JK-1-199	109	145	87.90	16.40	14.90	22.23	14.50	31.87	8.86	3.15	2.81	1	Br.
200	JK-1-200	112	150	85.00	15.50	15.10	21.06	9.60	25.43	8.83	3.01	2.93	1	Seg.
201	JK-1-201	104	138	90.20	14.90	14.70	21.00	12.60	19.89	9.13	2.44	3.74	2	Bl.
202	JK-1-202	108	142	90.20	15.10	15.10	22.22	18.40	25.74	8.65	2.83	3.06	3	Br.

203	JK-1-203	107	145	87.70	15.11	14.63	23.10	21.95	21.44	8.66	2.54	3.41	3	Br.
204	JK-1-204	108	140	87.30	13.90	13.80	21.88	17.00	27.54	8.53	2.87	2.97	3	Br.
205	JK-1-205	110	143	85.50	13.70	13.10	21.48	14.90	31.33	9.05	3.31	2.73	3	Br.
206	JK-1-206	110	144	84.80	15.10	15.10	22.13	16.83	26.48	8.45	2.94	2.87	2	Br.
207	JK-1-207	108	140	87.50	15.40	14.44	22.15	17.20	25.38	8.71	2.89	3.01	3	Seg.
208	JK-1-208	116	148	86.32	10.74	8.82	16.42	8.82	18.21	7.14	2.71	2.63	7	Seg.
209	JK-1-209	108	143	88.70	15.80	15.80	21.70	18.84	31.43	9.08	2.98	3.05	2	Br.
210	JK-1-210	110	145	90.70	14.70	13.67	22.00	15.00	28.62	8.89	3.17	2.80	2	Seg.
211	JK-1-211	108	143	87.30	13.60	13.10	22.46	15.06	29.58	8.84	3.13	2.82	4	Br.
212	JK-1-212	102	134	103.60	14.00	12.44	20.65	13.70	14.11	6.69	1.41	4.74	4	Bl.
213	JK-1-213	109	142	147.90	13.60	12.60	21.22	17.40	26.64	8.69	2.87	3.03	3	Seg.
214	JK-1-214	120	154	66.76	8.12	7.42	15.32	9.36	25.78	7.96	3.24	2.46	6	Seg.
215	JK-1-215	132	164	124.56	12.34	11.48	17.96	15.78	26.66	8.85	2.64	3.35	3	Seg.
216	JK-1-216	109	143	86.20	14.50	13.60	21.92	15.10	29.74	9.05	2.96	3.06	3	Seg.
217	JK-1-217	107	140	84.10	14.50	13.90	21.79	16.00	25.94	8.49	3.01	2.82	3	Br.
218	JK-1-218	109	144	83.20	13.40	12.20	20.00	12.40	29.98	8.07	3.40	2.37	4	Br.
219	JK-1-219	103	137	84.50	13.90	13.00	20.20	11.18	18.99	7.67	1.73	4.43	2	Seg.
220	JK-1-220	109	145	84.00	13.80	12.70	21.81	13.00	27.65	8.86	3.02	2.93	4	Br.
221	JK-1-221	106	139	88.40	13.70	13.60	22.59	15.30	31.23	8.94	3.08	2.90	4	Seg.
222	JK-1-222	109	145	133.30	13.20	12.30	20.55	12.90	26.98	8.86	3.13	2.83	4	Br.
223	JK-1-223	106	140	84.60	13.00	12.89	21.26	15.50	26.58	8.07	3.24	2.49	2	Seg.
224	JK-1-224	111	145	84.50	13.30	12.25	20.71	13.06	25.59	8.46	3.00	2.82	2	Br.
225	JK-1-225	104	138	99.40	12.33	12.11	19.99	23.61	14.49	7.06	1.73	4.08	3	Bl.
226	JK-1-226	104	138	106.50	15.20	13.10	22.35	21.90	26.16	7.89	2.96	2.67	3	Br.
Mean		106.39	139.59	92.86	12.86	12.20	19.26	14.69	22.10	7.92	2.35	3.63		
Jyothi		103	134	96.82	8.43	7.46	17.52	11.34	28.56	8.54	2.62	3.26	7	Br.
Kiruwana		123	156	124.48	14.35	13.49	19.84	20.86	19.94	7.92	1.89	4.19	2	Bl.

Bl-Black
Br-Brown
Seg- Segregating for husk colour