VALIDATION OF MOLECULAR MARKERS FOR BLAST RESISTANCE AND ASSESSMENT OF PRODUCTIVITY IN LANDRACES AND PROMISING BREEDING LINES OF RICE (*Oryza sativa* L.)

VAIBHAV V. PATIL

DEPARTMENT OF GENETICS AND PLANT BREEDING
COLLEGE OF AGRICULTURE, DHARWAD
UNIVERSITY OF AGRICULTURAL SCIENCES,
DHARWAD – 580 005

JUNE, 2015

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Thesis submitted to the
University of Agricultural Sciences, Dharwad
In partial fulfillment of the requirements for the
Degree of

Master of Science (Agriculture)

in

Genetics and Plant Breeding

By
VAIBHAV V. PATIL

DEPARTMENT OF GENETICS AND PLANT BREEDING
COLLEGE OF AGRICULTURE, DHARWAD
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DEPARTMENT OF GENETICS AND PLANT BREEDING
COLLEGE OF AGRICULTURE, DHARWAD
UNIVERSITY OF AGRICULTURAL SCIENCES, DHARWAD

CERTIFICATE

This is to certify that the thesis entitled "VALIDATION OF MOLECULAR MARKERS FOR BLAST RESISTANCE AND ASSESSMENT OF PRODUCTIVITY IN LANDRACES AND PROMISING BREEDING LINES OF RICE (*Oryza sativa* L.)*"* submitted by Mr. VAIBHAV V. PATIL for the degree of MASTER OF SCIENCE (Agriculture) in GENETICS AND PLANT BREEDING to the University of Agricultural Sciences, Dharwad, is record of research work done by him during the period of his study in this University, under my guidance and supervision and the thesis has not previously formed the basis for the award of any degree, diploma, associateship, fellowship or other similar titles.

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Acknowledgement

In every one's life, the day arises when one has to shape the feelings in words. Sometimes, the words become unable to express the feelings of the mind, because, the feelings of heart are beyond the reach of the words. When, I came to complete this manuscript, so many memories have rushed through my mind, which are full of gratitude to those who encouraged and helped me at various stages of this research. It gives me immense pleasure to record my feelings at this place

I consider myself very much fortunate and it is indeed true that I have had a chance to work under the noble guidance of Dr. N. G. HANAMARATTI, Professor (GPB), Agricultural Research Station (Paddy) Malagi, UAS, Dharwad. I wish to express my deep sense of gratitude and heartfelt thanks for his inspiring guidance, meritorious support, sustained interest in planning and execution of research, meticulous and critical evaluation of the manuscript, personal interest, genuine counseling, continuous and unitary words of encouragement.

The moral zeal and constant assurance at every count bestowed by members of my advisory committee Dr. SUMA BIRADAR, Scientist, AICRP on Wheat, Main Agricultural Research Station, Dharwad, Dr. PRASHANTHI S. K., Professor of Biotechnology and Dr. V. K. DESHPANDE, Professor of Seed Science and Technology, College of Agriculture, Dharwad, University of Agricultural Sciences, Dharwad, for their timely suggestions from the beginning of this investigation, valuable counsel and keen interest have helped me to shape this manuscript in the present form.

I express my sense of respect and sincere thanks to Dr S. A. Desai Professor, Dr. S. K. Deshpande, Professor and Head Dr. B. R. Patil, Professor, Dept. of Genetics and Plant Breeding, College of Agriculture, UAS, Dharwad, for their constant help and encouragement through out my study period.

I have no words to express my heartfelt to my parents Vijay and Nirmala, my elder sister Varsha and brother Varun, whose abundant love,

affection, selfless sacrifice and blessings in all my endeavours motivated me to work towards the cherished goal and academic excellence.

I would like to thank my friends Shivakumar, Ramesh, Deepak, Ravi, Manjunath and my other unmentioned dear friends for their kind co-operation and timely help throughout the study.

I am very thankful to non-teaching faculty Mr. F. Lobo, Mr. Salim, Mr. Mallikarjun, Department of Genetics and Plant Breeding, for their kind co-operation and help during the period of my research work.

I convey my whole hearted thanks to Mr. Arjun and Mr. Kalmesh (Arjun Computers), for their meticulous typing of the manuscript neatly, timely and more vitally their co-operation and affection towards me.

…Any omission in this brief acknowledgement does not mean lack of gratitude.

DHARWAD

JUNE, 2015 (VAIBHAV V. PATIL)

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1. INTRODUCTION

Rice (*Oryza sativa* L.) is the staple food crop of nearly three-fourths of the population in India. Its cultivation dates back to the ancient periods earlier to 3000 B.C. The traditional use of rice in the Hindu religious ceremonials associated with birth, marriage and funeral indicates its intimate association with the life of our people. Even, a number of festivals such as Bihu in Assam, Pongal in Tamil Nadu, Nuakhai in Orissa and Onam in kerala are associated with rice harvest.

Rice is a member of the family *Poaceae*. Archeological evidence indicates a sophisticated rice cultivation system existed in china over 7,000 years ago. There are 42 rice producing countries in the world, ranging from the mountainous Himalayan to low land delta areas in Kerala. Rice is the staple food in Asia, Latin America, parts of Africa and the Middle East. The rice cultivation area stretches from 53^0N latitude to 35^0S latitude. In India, the rice cultivation area extends from 8^0S to 34^0S latitude *i.e.*, extending almost throughout the country.

During the period from 1967 to 2004, the rice area has increased from 115.50 million ha to 153.26 million ha production from 215.66 million tonnes to 449.05 million tonnes and productivity from 1.54 tonnes/ha to 2.93 tonnes/ha. Presently world-wide the area under rice cultivation is 160.6 million ha, with production of 476 million tonnes and productivity of 2.96 tonnes/ha (Anon., 2015). China is the leading country in rice production with production of 141.6 million tonnes followed by India and Indonesia. India is the largest exporter of rice in the world followed by Thailand and Vietnam. In India the area under rice cultivation is around 43.95 million ha, with the production of 106.54 million tonnes and productivity of 2.424 tonnes/ ha (Anon., 2014).

Among all the states, Uttar Pradesh has got highest area of 5.98 million ha and West Bengal has the highest production of 15.31 million tonnes whereas Punjab has got highest productivity of 3.952 tonnes per ha. In Karnataka rice is cultivated in an area of 1.33 million ha with the production of 3.76 million tonnes and productivity of 2.828 tonnes per ha (Anon., 2015). Rice crop is grown under different ecosystems in India based on the prevailing environment of the region as upland rice, lowland rice, irrigated lowlands and aerobic ecosystems.

Upland rice is grown in around 5.50 million ha as direct seeded in flat lands of western Ghats region of Karnataka, Coastal Orissa, Assam and Eastern Uttar Pradesh; gently rolling lands of Chhattisgarh and Madhya Pradesh; slopy lands in Jharkhand, Western Orissa, Meghalaya and Uttaranchal. With different rice growing ecosystems across India the goal to produce 140 million tonnes by 2025 is challenging to feed the large growing population. This is due to the constraint that lies with genetics of the crop, bio-physical and the environmental factors.

Environment plays a very crucial role in deciding the total architecture of the crop. Rice as such gets affected by several biotic and abiotic stresses during its entire growth period. The biotic stresses are very much important as these render heavy losses in the yield of the crop. The biotic stresses include diseases like Blast, Bacterial blight, Sheath blight, Brown spot, Rice tungro and major pests like Brown plant hopper, Stem borer, Leaf hopper, Leaf roller etc,.

Blast of rice caused by the fungus *Magnaporthe oryzae* (anamorph, *Pyricularia grisea)* is the most destructive disease. The fungus can infect the rice plant at any growth stage. Large lesions are formed on leaf with gray centers. The lesions collapse and leaves of the susceptible varieties may be killed. The fungus may also attack the stem at the nodes (node blast) in which the stem bends and breaks at the nodes causing complete spikelet sterility. Even neck blast causes partial to complete sterility in the panicle.

Blast being the major disease causes a yield loss upto 65 per cent in susceptible cultivars of rice (Bhatt 1988). Both leaf blast and neck blast are severe at different stages of growth but yield reduction by neck blast infection is twice as that of the leaf blast (Hawang *et al.,* 1987). Use of host resistance provides efficient and environmentally safe alternatives against chemical control in blast management.

Resistance to *M. oryzae* is known to follow a classical gene-for-gene system where a major resistance gene (R gene) prevents infection by race of *M. oryzae* harboring the avirulance gene (Flor, 1971). Several genes have been located in the germplasm of rice crop inferring resistance to the blast disease. But when blast resistance of a cultivar is based on a single resistance gene, it can be rapidly overcome by the emergence of virulent races of the pathogen (Hittalamani *et al.,* 2000). Two genes *Pita and Pita*^{2} being dominant governing major resistance occupy near-

centromeric region on chromosome 12 and linked closely (0.4 cM) confers broader resistance (Shikari *et al.,* 2013). To date, over 100 blast resistance genes to *M. oryzae* from *japonica* (45%), *indica* (51%) and other (4%) genotypes have been identified and documented (McCouch *et al.,* 1994; Ballini *et al.,* 2008; Huang *et al.,* 2010; Xiao *et al.,* 2010; Sharma *et al.,* 2012). Further with fine mapping and cloning of many blast resistance genes, many PCR-based markers have been developed to screen and identify different blast resistance genes, the markers increase the precision of identification and incorporation of resistance genes in a breeding programme (Jia *et al.,* 2003; Wang *et al.,* 2007; Liu *et al.,* 2013).

Molecular markers are widely used in characterizing germplasm collections which contain untapped alleles for resistant genes. Abundance of linked and gene based markers like SSRs, STS and SNPs which can be detected easily making them allele specific PCR primers and thus a handy tool for allele mining and MAS. Most of the resistant genes are race specific (Mackill and Bonman, 1992: Deng *et al.,* 2006). Highly adaptive and virulent races of *M. oryzae* challenge the effectiveness of resistant genes. Thus, blast resistance conferred by resistant genes is often short lived due to the emergence of virulent races of the pathogen which negate the effect of introduced resistance genes (Zeigler *et al.,* 1995). Hence, it is important to identify broad-spectrum blast resistant genes for effective protection against dynamic blast races.

Therefore, there is need for screening and identification of different effective and broad-spectrum blast resistance genes in diverse germplasm for deployment in high yielding varieties. The promising breeding lines with blast resistance genes can be identified with linked or gene specific markers and could be deployed in target environment. With these points in view, the present investigation was proposed with the following objectives.

1. Phenotyping of landraces and promising breeding lines for blast resistance under epiphytotic condition.
2. Validation of molecular markers for blast resistant genes in land races and promising breeding lines.
3. Assessment of blast resistant genotypes for productivity under rainfed condition.

2. REVIEW OF LITERATURE

Rice is central to the lives of billions of people around the world. It is the world's most important food crop and a primary source of energy for more than half the world's population. Rice crop is grown under different eco-systems like upland, lowland, irrigated and rainfed ecosystems. Upland rice is grown in around 5.50 m. hectares as direct seeded in flat lands of Western Ghats region of Karnataka, coastal Orissa, Assam and Eastern Uttar Pradesh along with other states like Madhya Pradesh, Jharkhand.

The main target of rice crop breeder as such is to enhance the productivity of the crop to meet the food requirement of the growing population. But the improvement in yielding ability has been restricted because of bio-physical parameters, environmental factors and genetic factors affecting the crop growth. Environmental factors include both biotic and abiotic stresses affecting the yield of the crop at different magnitude. Biotic stresses include diseases like Blast, Bacterial blight, Sheath blight, Rice tungro and pests like Brown Plant Hopper, Stem Borer and Green Leaf Hopper.

Rice is affected by blast as a major disease causing a yield loss upto 65% in susceptible cultivars (Bhatt, 1988). Use of host resistance provides efficient and environmentally safe alternatives against chemical control in disease management. With the same objectives of involving resistant genes for crop improvement a brief review is presented on the following headings:

2.1 Phenotyping of landraces and promising breeding lines for blast resistance under epiphytotic condition

2.2 Validation of molecular markers for blast resistant genes in land races and promising breeding lines

2.3 Assessment of blast resistant genotypes for productivity under rainfed condition

2.1 Phenotyping of landraces and promising breeding lines for blast resistance under epiphytotic condition

Rice is grown under different ecosystems while Northern Karnataka follows upland cultivation of rice under rainfed situation. Blast disease appears to be a major disease in rice cultivation in all ecosystems, more severe in rainfed uplands reducing the yield to a greater extent world-wide. A genotype with resistance to both leaf and neck blast offer scope in breeding programme to evolve multiple disease resistant genotype with high yield potential. Several germplasm lines and promising varieties have been screened under epiphytotic conditions at multiple locations (Chandrashekara *et al.,* 2008). Scoring has been done on a scale of 0-9, the procedure given by Mayee and Datar (1986).

Screening germplasm for resistance against blast disease provides good source of resistant genotypes and helps in designing the future breeding programmes. Samples of 311 genetically diverse varieties were obtained and screened against 29 diverse blast isolates in Thailand (Salih *et al.,* 2013). Thirty five accessions were found resistant to all the tested blast isolates. Moreover four accessions were highly resistant without any symptom expression. Such lines could be further used in future breeding works targeting disease resistance or could be used as new variety.

Evaluation of infection type, numbers of sporulated lesions, percentage of infected leaf area and lesion size traits were considered for evaluating the genotypes for resistance and susceptibility in a study by Pasha *et al.* (2013). The rice genotypes were classified based on the characters exhibited by highly resistant genotype considered in the evaluation set as a check (Iran-47). The genotypes were classified based on the resistant characters exhibited by the variety.

Involvement of resistant genotypes in crop improvement programmes has been the most economical and effective way of controlling the disease. However, the useful life span of many cultivars is only for few years, due to the breakdown of the resistance in the face of high pathogenic variability of the fungus (Kiyosawa *et al.,* 1986). Mahadevappa *et al.* (1991) identified IR-64 with a score of 2 as against 7 for the susceptible check S-317 for leaf blast, it had no neck infection. Even a cold tolerant variety CTH-1 was identified resistant to blast besides being non-lodging.

Large scale germplasm screening for identification of novel rice blast resistance sources is a routine practice carried out at International Rice Research Institute, IRRI (Philippines). Seed bank represent a rich stock of genetic diversity and however, they are still under explored for identifying novel genes and/or their functional alleles. So the study was conducted having a large scale screen for new rice blast resistance sources in 4246 geographically diverse rice accessions originating from13 major rice growing countries (Vasudevan *et al.,* 2014). A two-step resistance screening protocol was used involving natural infection in a rice uniform blast nursery and subsequent artificial infections with five single rice blast isolates. The nursery-resistant accessions showed varied disease responses when infected with single isolates, suggesting the presence of diverse resistance genes/alleles in this accession collection.

Evaluation of resistant genotypes under epiphytotic conditions is the only viable and economical method to screen the genotype for the resistance or susceptibility. Saifulla *et al.* (1996) evaluated promising rice genotypes under natural epiphytotic conditions at ARS Ponnampet. Of the 14 entries tested IET 10337, IET 10336, IET 9926, Jeerigesanna were found to possess moderate level of resistance against blast disease in all the seasons.

With the same objectives different germplasm accessions and landraces were screened in order to obtain diverse genotypes varying in their mode of resistance. The genotypes were screened for total leaf area per cent infection to blast (Pasha *et al.,* 2013). Different lines were screened at different eco-systems of rice growing regions like low-, mid-, and up-land conditions by involving resistant as well as susceptible genotypes (Puri *et al.,* 2006).

Like the screening of rice genotypes across different eco-systems the screening at multi-locations has been done for favoring cultivation of suitable genotypes in respective regions. The role of genotype, environment and their interaction was studied for their impact on disease development and related severity scores (Idowu *et al.,* 2013). Varieties were screened for resistance to the fungus at Ibadan and Ikenne under natural infection for two years. Moroberekan was resistant to blast fungus across years and sites. Even by considering the locations, Ibadan was identified as a better site for screening rice genotypes for blast resistance.

The screening experiments have been conducted even under drought conditions to obtain blast resistant genotypes which can be further used in breeding programmes targeting a drought prone area with blast resistance and better yield levels (Kumar *et al.,* 2012).

Among the leaf and neck blast stages of the disease, neck blast causes most severe damage. In the early neck infection grain filling does not occur and panicles remain erect like a dead heart caused by a stem borer. In the late infection partial grain filling occurs. Due to the weight of such partially filled grains the base of the rachis may break down (Vidyachandra and Kumar Anil, 1995).

Chaudhary *et al.* (2005) evaluated 36 rice breeding lines including checks for resistance to blast both under field and greenhouse conditions. They assessed the qualitative resistance based on lesion type and quantitative resistance based on lesion area under disease progress curve. The results revealed that, the varieties NR 1558, NR 601-1-1-9, BW306-2 and CN 836-3-10 were promising for quantitative resistance to both leaf and neck blast. The varieties Radha-12, Savitri, and Janaki possessed higher level of quantitative resistance.

Incidence of the blast disease in fine grains has been observed more than that of course grains. Study has been conducted on the same objective by taking rice germplasm consisting course and fine varieties to determine the source of resistance in rice germplasm at Rice Research Institute Kala Shah Kaku by artificial inoculation of the pathogen (Ghazanfar *et al.,* 2009). The screening revealed that none of the test lines was immune or highly resistant. One variety in course type was found resistant but none of the fine type lines were found resistant and all were susceptible. Thus prevalence of the resistance against rice blast pathogen is more common in the course as compared to the fine germplasm lines of rice.

Resistance to the blast disease contributes to increase in different ways. It reduces yield loss and increases the adaptability of rice genotypes to different production areas wherein previously the production or cultivation was limited because of the severity of the disease. For example, in India modern cultivars with built in disease resistance likely to contribute 7 to 10% extra yield in rice production (Evensone *et al.,* 2003).

2.2 Validation of molecular markers for blast resistant genes in land races and promising breeding lines

Blast of rice being caused by *Magnaporthe oryzae* causes moderate to huge production losses world over. With the availability of resistant genes the investigation by several workers has been done with the objectives of screening several germplasm accessions, land races and promising genotypes across different environments. The presence of PCR based and gene based markers being closely linked to these resistance governing genes make it easy to validate best land races, germplasm accessions as donors in further breeding programmes. Pita-Pita2 are such two genes which are dominant governing blast resistance (Shikari *et al.,* 2013).

Phenotypic and molecular assessment of genotype is very important in order to identify a resistant genotype. Phenotypic assessment was done based on the traits like infection type (IT), per cent diseased leaf area (DLA) and lesion number, lesion size. Molecular assessment was done using three STS and four microsatellite markers which are linked to resistant genes on rice chromosome (Fatemeh *et al.,* 2012). Genotypes were classified into three groups with high, intermediate resistance and susceptible resistance. Molecular assessment showed that at least one race-specific resistance gene in the genetic sources was available in the resistant genotypes.

Germplasm accessions from North East and Eastern India were validated for the presence of diverse blast resistant genes. Markers like SNPs, STS, Candidate gene markers were used (Imam *et al.,* 2014). Pita 3, YL155/187, YL183/YL 87, Pb 28, 195R-1 primers were linked to major genes of resistance. Molecular markers along with screening under artificial condition increase the precision of breeder in obtaining resistant genotypes. Polymorphic markers as RAPD, SSRs even help in characterizing the given land races and germplasm accessions for presence of diverse resistance genes (Selvaraj *et al.,* 2011a). Three SSR markers RM5757, RM451 and RM492 on chromosome four and two are linked to leaf blast.

Even panicle blast causing complete loss has got resistance genes in different land races and varieties. For such investigation markers like RFLP, SNPs, SSRs, InDel are being deployed in order to identify the best donors for resistance genes in prevailing environments (Fujii *et al.,* 2000; Tacconi *et al.,* 2010).

Analysis of different kind of markers help in developing marker rich maps that are further useful in gene based breeding programmes. SSRs and SNPs are the modern class of markers which are gaining great importance in the field of molecular breeding. Analysis of SSRs linked with blast disease resistance genes in segregating population can help in effective selection of resistant genotypes (Ahskani *et al.,* 2011). SSR markers linked to resistance genes were identified in the respective resistant genotypes. RM168 (116 bp), RM8225 (221 bp), RM1233 (175 bp), RM6836 (240 bp), RM5961 (129 bp), and RM413 (79 bp). These diagnostic markers could be used in marker assisted selection programs to develop a durable blast resistant variety.

Evaluation of segregating populations will help keeping track of the resistance genes along with studying their inheritance pattern (Kumbhar *et al.,* 2013). Bulk segregant analysis was conducted using 25 SSR markers which yielded two markers as being polymorphic between the parents and the bulks. One of these markers RM 204 has been reported on chromosome 6. Along with identification of resistance genes even the QTLs associated with it were identified. Further the information can be used in developing recombinant inbred lines (RILs).

In addition to a large amount of information accumulated during the long history of genetic studies on resistance to rice blast, recent progress in rice genomics has enabled us to use DNA markers for breeding the resistant varieties by marker assisted selection (Koide *et al.,* 2009). In this regard they have summarized the reported rice blast resistance genes and their selection markers to encourage further utilization for breeding. Assembled list of the reported DNA markers for blast resistance genes, including the sequences of the primer pairs, genetic distances from the resistance genes have been published to help the rice breeders to enhance the resistance to the disease. The updated list of important rice blast resistance genes is given in Table 1.

Resistance genes for blast disease of rice are polymorphic in nature and different kind of genes present on different chromosome across the genome. Allele mining for individual gene is gaining more importance in the era of molecular breeding (Ramkumar *et al.,* 2011). *Pi* 54 (which was earlier known as *Pik*^{h}) is one of the major resistant gene and has been observed to show resistance against many isolates of the blast pathogen in India. The gene is found polymorphic and has been validated across different genotypes for screening them as either resistant or susceptible.

Table 1: Summary of reported important rice blast resistant genes with linked molecular markers

Sl. No.	Chr. Number	Target Gene	Type of Marker	Marker Name	Distance (cM)	Reference
1	Chromosome 1	*Pit*	SNP	t311	0.44	Hayashi *et al.*,2006
			SNP	t256	0	Hayashi *et al.*,2006
			SNP	t8042	0.28	Hayashi *et al.*,2006
		Pi27 (t)	SSR	RM151	11.9	Zhu *et al.,* 2004
			SSR	RN259	9.7	Zhu *et al.,* 2004
		Pitp (t)	SSR	RM246	0	Barman *et al.,* 2004
		Pi35 (t)	SSR	RM1216	<3.5	Nguyen *et al.,* 2006
			SSR	RM1003	<3.5	Nguyen *et al.,* 2006
		Pi37	SSR	RM302	0	Chen *et al.,* 2005
			SSR	RM212	0	Chen *et al.,* 2005
			SSR	FPSM1	0.07	Chen *et al.,* 2005
			STS	FSTS2	0.14	Chen *et al.,* 2005
2	Chromosome 2	*Pid l (t)*	SSR	RM262	14.5	Chen *et al.,* 2004
		Pig (t)	SSR	RM166	2.4-4.0	Zhou *et al.*,2004
		Piy1	SSR	RM3248	1.3	Lei *et al.,* 2005
			SSR	RM20	1.7	Lei *et al.,* 2005
		Piy2	SSR	RM3248	1.3	Lei *et al.,* 2005
			SSR	RM20	1.7	Lei *et al.,* 2005
		Pib	SNP	b213	-	Hayashi *et al.*,2006
			SSR	RM138	3.1	Fjellstorm *et al.*,2004
			SSR	RM166	2.3	Fjellstorm *et al.*,2004
			SSR	RM208	0	Fjellstorm *et al.*,2004
			SSR	RM266	2.2	Fjellstorm *et al.*,2004
3	Chromosome 4	*Pi 21*	STS	P702D03_#79	0	Fukuoka *et al.*,2007
		Pi39	SSR	RM3843	0	Terashima *et al.*,2007
			SSR	RM5473	0	Terashima *et al.*,2007
4	Chromosome 5	*Pi10*	InDel	OPF62700	<7	Naqvi and Chattoo 1996
5	Chromosome 6	*Pi40 (t)*	SSR	RM3330	2.4	Jeung *et al.,* 2007
			SSR	RM527	1.1	Jeung *et al.,* 2007
			CAPS	S2539	3.8	Jeung *et al.,* 2007
		Piz	InDel	z4794	0.32	Hayashi *et al.*,2006
			SNP	z60510	0.11	Hayashi *et al.*,2006
			SNP	z5765	0.13	Hayashi *et al.*,2006
		Piz-t	InDel	z4794	0.41	Hayashi *et al.*,2006
			SNP	z60510	0.17	Hayashi *et al.*,2006

Contd……

Sl. No.	Chr. Number	Target Gene	Type of Marker	Marker Name	Distance (cM)	Reference
6	Chromosome 8	*Pi36*	SSR	RM5647	0.4	Liu *et al.,*2005
			CAPS	CRG2	0	Liu *et al.,*2005
			CAPS	CRG4	0	Liu *et al.,*2005
		Pi33	SSR	RM72	<11.5	Berruyer *et al.,*2003
			SSR	RM44	<11.5	Berruyer *et al.,*2003
7	Chromosome 9	*Pi5 (t)*	CAPS	94A20r	5.2	Jeon *et al.,*2003
8	Chromosome 11	*Pia*	CAPS	yca72	-	Kwon *et al.*, 2008
		PiCO39 (t)	CAPS	RGA8	0	Chauhan *et al.,* 2002
		Pi38	SSR	RM206	4	Gowda *et al.,*2006
			SSR	RM21	16	Gowda *et al.,*2006
		Pik	InDel	k6816	1.4	Hayashi *et al.,*2006
			SNP	k6438	1.4	Hayashi *et al.,*2006
			SNP	k6415	-	Hayashi *et al.,*2006
			SNP	k3951	0	Hayashi *et al.,*2006
		Pik-m	InDel	k6816	1.3	Hayashi *et al.,*2006
			SNP	k641	1.3	Hayashi *et al.,*2006
			SNP	k6441	0	Hayashi *et al.,*2006
		Pik-p	SNP	k641	1.9	Hayashi *et al.,*2006
		Pik-h (*Pi 54*)	SSR	RM206	0.7	Sharma *et al.,*2002
			SSR	TRS26	0.7	Sharma *et al.,*2002
			SSR	RM224	0	Sharma *et al.,*2002
			SSR	RM224	0	Sharma *et al.,*2002
9	Chromosome 12	*Pita*	SNP	ta642	1.2	Hayashi *et al.,*2006
			SNP	ta801	0	Hayashi *et al.*
			SNP	ta577	0	Hayashi *et al.*
			SNP	Pi-ta 1042	-	Hayashi *et al.*
		Pita-2	SNP	ta62	0	Hayashi *et al.,*2006
			SNP	ta801	0	Hayashi *et al.,*2006
			SSR	RM155	3.5	Fjellstrom *et al.,*2004
			SSR	RM702	1.1	Fjellstrom *et al.,*2004
		Pi39 (t)	CAPS	39M6	0	Liu *et al.,*2007
			CAPS	39M7	0.09	Liu *et al.,*2007

Rice is the most important cereal crop in the world and hence demands the identification of resistant gene with help of markers to overcome the disease incidence. 48 elite Indian and Exotic rice lines were evaluated under epiphytotic condition and AUDPC was calculated for both resistant and susceptible genotypes. Later, 10 RAPD and 2 SCAR markers were used to identify the resistant genes (Kumar *et al.,* 2010). Amplification with RAPD and SCAR primers revealed a non-allelic relationship among resistant genotypes and thus, there is a good possibility of obtaining enhanced resistance through gene pyramiding.

Across globe rice genotypes have been validated along with markers tightly linked to the resistant genes. The information is used in generating successful crossing programmes involving resistant and susceptible genotypes (Matsushita *et al.,* 2011). Rice cultivar Chumroo has shown durable blast resistant in the area of its cultivation. It was crossed with susceptible cultivar, Koshihikari. The F_1 were showing resistance and further generation a normal segregation was seen. *Pi46* (t) was mapped using SSR markers in the resistant genotype Chumroo.

Effective control of blast, a devastating fungal disease of rice, would increase and stabilize worldwide food production. Resistance mediated by quantitative trait loci (QTLs) confers broad-spectrum resistance compared to individual R gene. Pyramiding the QTLs hence is a good approach in building up the resistance (Fukuoka *et al.,* 2015). Near Isogenic Lines were developed by involving four major QTLs conferring resistance to blast fungus.

Compared to low land cultivars upland rice cultivars show higher levels of blast resistance. Cross involving upland and low land cultivars were used for mapping the QTLs responsible for resistance (Miyamoto *et al.,* 2001). Two putative QTLs have been mapped on chromosome 4. Further the QTL can be used in breeding programme involving building up the resistance.

QTLs have been found to have major role in conferring the resistance to diverse and varied isolates of the pathogen *Magnaporthe grisea* Barr. QTLs can be developed by different approaches like NILs, SSSLs *etc.* The SSSLs (Single Segment Substitution Lines) are found more useful as these lines cover majority of the genome of the donor

parent (Zhang *et al.,* 2011). Several SSSLs were found conferring 100% resistance with many QTLs being mapped on different chromosomes.

With the increasing demand for rice production across the globe targeting multiple trait improvement is the need of the breeder. With the molecular breeding approach involving marker-assisted selection and genetic transformation resistance for both blast and bacterial blight disease of rice has been achieved in rice genotypes (Narayanan *et al.,* 2002). IR 50 an elite Indica rice line was improved by this method along with back crossing using C101A51 as a donor parent for blast resistant gene. For further incorporation of bacterial blight resistance *Xa* 21 was transferred to blast resistant line. Bioassay data showed that transgenic IR 50 was resistant to both pathogens.

Allele mining is the field of biotechnology that offers greater scope for utilization of important alleles in crop improvement. Extensive collection of the genotypes leads to development of set of resistant genotypes which can be further used for allele mining (Sharma *et al.,* 2014). Out of 52 lines screened across different blast epidemic areas lead to development of set of 48 blast resistant genotypes. Mining of three blast resistance genes *Pi54, Pita* and *Piz (t)* was done along with allele specific DNA markers.

2.3 Assessment of blast resistant genotypes for productivity under rainfed condition

Resistant genotypes are known to give higher yield than the susceptible genotypes. In order to obtain the resistant genotypes the lines were being evaluated for resistant genes across multi-locations (Muralidharan *et al.,* 2004). Several cultivars showed durable kind of resistance Tadukan being a notable one for its nature of blast resistance. A 57 another cultivar is identified as a best line for blast resistance across the country.

Even different workers studied with the same objective of obtaining a blast resistant genotype among different land races and germplasm accessions which are better in yield across locations. Such few lines even showed good general combining ability and few crosses with specific combining ability a phenomenon which can be tapped in obtaining good hybrids involving such blast resistant gene donors (Selvaraj *et al.,* 2011b; El-Namaky *et al.,* 2010).

Yield of any crop is decided by the kind of its growth and development. As far as the blast resistance is considered it provides the crop better chances of expressing itself at its best as for the yielding ability is considered. Several measures like GCV, PCV and Heritability of yield attributing traits gives direct measure of yield. Several traits like plant height, tillers per plant, number of productive tillers per plant, panicle length etc were studied showing positive response of blast resistance and yielding ability in rice (Selvaraj *et al.,* 2011c).

Different statistical analyses are done for evaluating resistant genotype for yield estimation. The objective of such experiments aim at selecting stable, high yielding, early maturing disease-resistant genotypes (Lakew *et al.,* 2014). Combined analysis of variance revealed significant variations in genotypes for most of the parameters except fertile tillers per plant. Mean squares due to the genotype X location X year interaction was significant for days to maturity, 1000 seed weight and grain yield. G 15 had relatively stable in grain yield across environments and also showed relatively better resistance (AMMI, GXE bi plot). G15 could be recommended for cultivation by the farmers and hence can be popularized in large scale cultivation.

Study of interaction between the resistant gene yield attributes is more important for successful selection of a better resistant genotype (Divya *et al.,* 2014). The epistatic interaction model was found adequate to explain the gene action in most of the traits. The interaction was complementary for number of productive tillers, economic yield, lesion number, infected leaf area and potential disease incidence but duplicate epistasis was observed for the remaining traits.

Rice has low productivity due to low genetic potential of the varieties and prevailing diseases. So the nuclear core collections are evaluated for availability of resistant and better performing genotypes (Santos *et al.,* 2013). The agronomic traits like average flowering, height and productivity of the genotypes along with the resistance for diseases were evaluated. Scott-Knott test showed high variability in variability in productivity and in resistance to the disease.

Blast of rice being a major disease, across the globe different investigations have been carried out in identifying blast resistant and superior genotypes having good yielding ability. The disease being season specific, performance of different genotypes

to blast disease in Boro and T. aman crop has been assessed in Bangladesh (Mohanta *et al.,* 2003). On the basis of disease intensity, three genotypes were highly resistant, 12 resistant and one was susceptible at T. aman season. At boro season three lines were highly resistant, 8 resistant and four were susceptible. Considering both the seasons, the accession numbers 56, 57,64,66,71 and 73 showed comparatively better performance.

The core collection of any crop gives the plant breeder an opportunity to select the target genotype that he/she desires. Genetic assessment of the core set along with screening the selected genotypes for blast resistance helps in selecting a superior genotype (Saini *et al.,* 2013). Variability for yield and yield attributing traits was assessed. High variability with respect to plant height, culm length, stem thickness, days to heading, leaf blade length, total tillers per plant, productive tillers per plant, panicle length, spikelets per panicle, grains per panicle, test weight of grain, grain length, grain width, straw yield per plant and grain yield per plant indicated good scope for improvement.

Cultivation of blast resistant genotype is the main aim of the plant breeder across the globe. Internationally research has been under progress and is continuous in developing resistant genotype across European and other continents which have significant area under rice cultivation (Rampant *et al.,* 2011). International accessions have been screened in Italy for blast resistant and better yielding ability. Phylogenic tree was formed and different groups were formed in the *japonica* germplasm accessions. The integrated genotype-phenotype analysis revealed that specific sub-groups are characterized by uniform classes of grain type, or by similar plant size.

The performance of a genotype is assessed by the variability for yield and its component characters of the crop. Similarly 81 genotypes were evaluated during *Kharif* 2010 for different quantitative traits (Sangam *et al.,* 2011). Among the all traits number of spikelets per panicle exhibited high estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) followed by harvest index, grain yield per hill and number of panicles per hill. Broad sense heritability was highest for biological yield per hill, which suggested that this trait would respond to selection owing their high genetic variability and transmissibility. Maximum genetic advance as per cent of mean was recorded for number of spikelets per panicle with high value of heritability.

Even slow blasting genotypes are of great importance in highly endemic area. Cultivation of such genotypes will reduce the disease incidence and will have good yielding ability. Slow blasting resistance is characterized by longer incubation period and latent period, shorter infectious period, lower infection efficiency, number of lesions per leaf, necrotic zone area, chlorotic zone area, mean lesion area, lesion cover, sporulation capacity and finally lower area under disease progress curve (Mukharjee *et al.,* 2013). Multivariate analysis was conducted to cluster the genotypes into a array of spectrum ranging from slow-blasting resistance to those possessing fast-blasting attributes.

Soma clones are found to offer slow blasting mechanism against blast resistance and have been found on par with existing cultivars. For selection of good genotypes both green house and field selection procedures were followed (Araujo *et al.,* 2000). Somaclones with both vertical resistance and slow blasting resistance were obtained. Green house selection with specific physiological races yielded 44 genotypes with slow blasting resistance and similar plant type and yield potential as that of cultivated variety.

2.3.1 Assessment of genetic parameters in rice genotypes under rainfed and upland ecosystem

Assessment of genetic variability through different parameters like PCV, GCV, Heritability *etc.*, leads to effective selection by the breeder. Analysis of variance reveals the relationship among the characters for the genetic parameters and indicates the level of genetic variability (Fukrei *et al.,* 2011). Core set of germplasm was analyzed for yield and other nineteen component traits. Heritability (h^2_{bs}) estimates were generally high except for flag leaf. GCV was high for flag leaf area, plant height, no. of tillers per plant, no. of filled grains per panicle. Broad sense heritability and genetic advance as percentage of mean indicated that panicle weight and gain yield per plant are important yield components.

Genetic analysis for quantitative traits offers better options to the plant breeders to carry out effective selection of superior genotypes. Along with the genetic parameters, direct and indirect effects of yield components on yield among the genotypes gives out good information on the genetic variability among the genotypes (Aditya and Bharatiya 2013). The estimate of GCV and PCV was highest for grain yield per plot. Heritability in broad sense was highest for plant height and fertile grains per panicle. Estimates of direct and indirect effect revealed that L/B ratio had the highest positive effect on grain yield followed by kernel width, grains per panicle and tillers per plant.

Rice accessions in Nagaland were evaluated for quantitative traits using different genetic parameters (Toshimenla and Changkija, 2013). Maximum genotypic and phenotypic variances were observed for days to 80% flowering, days to maturity, plant height, leaf length and yield per plant. High estimates of heritability coupled with moderate or high value of genetic advance as percentage of means was observed for yield per plant, 100 seed weight, leaf length, days to 80% flowering, leaf width, number of unfilled grains, days to maturity and panicle weight.

Clustering of accessions with diversity analysis and PCA is an important yardstick in assessing the genotypes genetically along with other genetic parameters (Khare *et al.,* 2014). High heritability coupled with high to moderate phenotypic and genotypic coefficient of variation and genetic advance as per cent of mean was recorded for grain yield per plant, plant height, test weight, fertile spikelet per panicle. Positive and significant associations were observed for days to 50 per cent flowering, days to maturity, plant height, panicle length, fertile spikelet per panicle. Clustering into seven groups was done based on the quantitative traits and cluster III had highest number of genotypes.

In vitro characterization of the accessions in multiple locations using morphometric markers is found to be more effective method in analyzing the genetic diversity (Lasalita-Zapico *et al.,* 2010). Cluster analysis revealed four groups, each group representing a distinct set of morpho-agronomic values. Principal Component Analysis sorted the cultivars into four clusters with two PCA accounting for 82.7 per cent variation. Pearson's correlation analysis of the morphological traits suggests that

these traits are significantly and positively correlated with each other except for the flag leaf angle.

Heritability value for a trait indicates the effect of environment on that trait and estimates the total genetic variation present for that trait (Seyoum *et al.,* 2012). In the experiment involving fourteen genotypes, high heritability was obtained for plant height; followed by 50% flowering, test weight, panicle length and spikelet per panicle. High to medium estimates of heritability and genetic advance were obtained for plant height, days to 50% flowering, panicles per plant, grains per panicle and test weight. Thus, selection for more number of grains per panicle, tillers per plant and panicle per plant along with large panicle size helps in improving the yield of the variety.

The association among the traits is of prime importance in order to have effective selection for the traits that attribute to other important quantitative traits like yield. Exotic lines were used to study the genetic variation and interrelationship of grain yield and its component traits (Sravan *et al.,* 2012). Grain yield per plant had significant positive correlation with biological yield per plant, harvest index, panicles per plant, plant height, spikelets per panicle, panicle length, test weight, spikelet fertility and flag leaf length.

Correlation studies are very much important in hybrid breeding programme as such studies provide a yardstick for efficient selection of parental lines followed by development of superior hybrids (Ravindra Babu *et al.,* 2012). Significant positive association of grain yield per plant with number of productive tillers per plant was observed. Hence, selection for these traits can improve yield. Path coefficient analysis revealed that panicle length and number of productive tillers per plant exhibited positive direct effect on yield. Among these characters, number of productive tillers per plant possessed both positive association and high direct effects.

Association studies on different traits are quite useful for quantitative assessment of the variation in yield and yield components, their interrelationship, and direct and indirect effects of different characters on grain yield (Karim *et al.,* 2014). Analysis of phenotypic and genotypic correlation co-efficient of quantitative characters and partitioning of genotypic correlation to grain revealed that the correlation coefficients of grain yield per hill with 1000-grain weight and harvest index were

positive and highly significant. Spikelet sterility showed highly significant negative correlation with grain yield at genotypic level only. Such information can be effectively utilized further for directed selection for the traits that indirectly help in improvement of yield.

3. MATERIAL AND METHODS

The investigation was carried out during *kharif* 2014 at Agricultural Research Station, Mugad, the centre working exclusively on rainfed drill sown rice in north Karnataka. The Research station is located at an altitude of 697 meters above mean sea level (MSL), $15^0 15^{'}$ north latitude and $70^0 40^{'}$ east longitude, which falls in Northern Transitional Agro-climatic zone of Karnataka. The soils of this tract vary widely in their productivity/fertility. Most of these soils are laterite, characterized by low water and nutrient holding capacities and thus are low in productivity. The soil fertility gradually rises from upper terraces to lower terraces. In general, the soil texture is grouped under silty-clay-loam to clayey with pH around 6.5.

The average rainfall of the research Station was 1016.20 mm in 75 rainy days distributed mainly during *kharif* (June to October) season. The rainfall pattern of five critical months (June to October) is provided in the Appendix 1.

3.1 Experiment-I: Phenotyping of landraces and promising breeding lines of rice for blast resistance under field condition

3.1.1 Experimental material

The landraces (52 in number) maintained in ARS, Mugad, which were collected from western ghat region and different parts of Karnataka were included in this investigation. These landraces are important reservoirs of valuable traits including disease resistance (Hanamaratti *et al.,* 2008). The promising breeding lines (95 in number) from different programmes are also important genetic material utilized in this investigation. The list of genotypes along with their pedigree have been mentioned in Table 2.

The 160 genotypes were grown in *kharif* 2014, at Agricultural Research Station, Mugad. The seeds of these genotypes were directly sown under Uniform Blast Nursery (UBN) for evaluating their performance for resistance against blast of rice.

Table 2: List of genotypes used in the present investigation along with pedigree

Sl. No.	Name	Pedigree	Sl. No.	Name	Pedigree
1	BA-60-6-2	BPT-5204 x Antarsali	22	BD-RSS-17-1	BPI-5204 x Dodiga
2	RF-53-102-3	(IR 64 x Binam) // IR-64	23	BA-35-1-1	BPT-5204 x Antarsali
3	MGD-V-14-1	Mutant CRMS-32 B	24	YSM-42-1-7	Mutant of Yalakkisali
4	MGD-V-14-2	Mutant of SIRI-1253	25	MGD-V-14-10	BPT-5204 x Chittimutyalu
5	SMW-11-09-30-L-1	BPT-5204 x WAB-11	26	MSB-48-1-4	Mutant of Medinisanna bhatta
6	MGD-V-14-3	BPT 5204 x SUREKHA	27	KRGL-64-1-4-2	Mutant of Karigajaville
7	RSS-17-1	Mutant of Ratansagar	28	YSM-31-1-1	Mutant of Yalakkisali
8	MGD-V-14-4	Mutant of BPT-5204	29	YSM-7-1	Mutant of Yalakkisali
9	MGD-V-14-5	IR-78875 x Amrut	30	KRGL-7-1-1	Mutant of Karigajaville
10	IR 78875	Promising breeding line from IRRI	31	MSB-50-1-3	Mutant of Medinisanna bhatta
11	ARB-6	Promising genotype from UASB	32	YSM-66-1-1	Mutant of Yalakkisali
12	MGD-V-14-6	BPT-5204 x Kavya	33	MSB-50-1-3-1	Mutant of Medinisanna bhatta
13	BA60-6	BPT-5204 x Antarsali	34	MGD-V-14-11	BPT-5204 x Kavya
14	IET-22552	Promising breeding line from AICRIP	35	SMW-XV-101	BPT-5204 x WAB-10
15	MGD-1202	Promising breeding line from Mugad	36	BA-35-1-1-2	BPT-5204 x Antarasali
16	VARALU	Promising genotype from ANGRAU, Hyderabad	37	SMW-11-01-45-4	BPT-5204 x WAB-11
17	MGD-V-14-7	Selection from IET-22554	38	SMW-101-103-1	BPT-5204 x WAB-10
18	MGD-V-14-8	BPT-5204 x Kavya	39	SMW-XV-103	BPT-5204 x WAB-10
19	MGD-V-14-9	BPT-5204 x Kavya	40	SMW-XV-105	BPT-5204 x WAB-10
20	BD-17-2-1	BPI-5204 x Dodiga	41	MGD-1201-2	Promising breeding line from Mugad
21	BD-17-2-2	BPI-5204 x Dodiga	42	SMW-11-09-50-1	BPT-5204 x WAB-11

Contd…..

Sl. No.	Name	Pedigree	Sl. No.	Name	Pedigree
43	SMW-11-09-45-11	BPT-5204 x WAB-11	66	KRGL-7-1-9	Mutant of Karigajaville
44	MGD-V-14-12	SIRI-1253 x MGD-1201	67	KRGL-12-13	Mutant of Karigajaville
45	SMW-11-09-5-1-3-1	BPT-5204 x WAB-11	68	YSM-82-1-2	Mutant of Yalakkisali
46	SMW-11-09-45-5	BPT-5204 x WAB-11	69	MGD-V-14-16	Promising breeding line
47	SRIRAM SONA	Promising genotype from UASR	70	MGD-V-14-17	Promising breeding line
48	SMW-11-09-45-1	BPT-5204 x WAB-11	71	YSM-15-1-13	Mutant of Yalakkisali
49	RSS-17	Mutant from Ratansagar	72	KRGL-20-1-3	Mutant of Karigajaville
50	RSS-17-2	Mutant from Ratansagar	73	KRGL-29-1-3	Mutant of Karigajaville
51	IET-22801-2	Mutant from IET-22801	74	MGD-1202-1	Mutant of MGD-1202
52	SMW-10-2	BPT-5204 x WAB-10	75	GSM-45-1-7	Mutant of Jeerigesanna
53	27-P-11-3-2-1	BPT-5204 x MGD-1201	76	KRGL-7-1-5-A	Mutant of Karigajaville
54	SMW-11-09-45-102	BPT-5204 x WAB-11	77	YSM-7-1-20-A	Mutant of Yalakkisali
55	MGD-V-14-13	BPT-5204 x MGD-1201	78	MSB-43-1-6-B	Mutant of Medinisanna bhatta
56	SMW-11-09-5-1-3	BPT-5204 x WAB-11	79	KRGL-1-7-5	Mutant of Karigajaville
57	SMW-11-09-50-1-103	BPT-5204 x WAB-11	80	KRGL-20-1-5-A	Mutant of Karigajaville
58	SMW-11-09-60-1-2	BPT-5204 x WAB-11	81	MSB-48-1-12	Mutant of Medinisanna bhatta
59	MGD-V-14-14	BPT-5204 x MGD-1201	82	MGD-V-14-18	Promising breeding line
60	MGD-V-14-15	Promising breeding line from Mugad	83	MSB-50-1-4	Mutant of Medinisanna bhatta
61	BA-60-3-2	BPT-5204 x Antarsali	84	MGD-V-14-19	BPT-5204 x Chittimutyalu
62	SMW-10-09-11	BPT-5204 x WAB-10	85	GUDDENELLU	Traditional Landrace
63	BA-60-6-1	BPT-5204 x Antarsali	86	ADNENKELTI	Traditional Landrace
64	BA-60-6-3	BPT-5204 x Antarsali	87	KARE KALVI	Traditional Landrace
65	BA-15-31-1-1	BPT-5204 x Antarsali	88	MADRAS BHATTA	Traditional Landrace

Contd…..

Sl. No.	Name	Pedigree	Sl. No.	Name	Pedigree
89	NEERGULLI	Traditional Landrace	112	KONNUR BHATTA	Traditional Landrace
90	GHEERSALI	Traditional Landrace	113	DODIGA	Traditional Landrace
91	BETIGA	Traditional Landrace	114	HUGGI BHATTA	Traditional Landrace
92	MUTALGA	Traditional Landrace	115	BOLA SALI	Traditional Landrace
93	KARIGAJIVILE	Traditional Landrace	116	GOPAL DODIGA	Traditional Landrace
94	PARIMALASANNA	Traditional Landrace	117	KUNKUM SALI-1	Traditional Landrace
95	NYARE MINDA	Traditional Landrace	118	KOTAMBARI SALI-1	Traditional Landrace
96	BILIDADI GORATIGA	Traditional Landrace	119	MALABANGAR KADDI	Traditional Landrace
97	JADDU BHATTA	Traditional Landrace	120	KYASAKKI	Traditional Landrace
98	CHITIGA	Traditional Landrace	121	VARESANNA	Traditional Landrace
99	BANGAR KOVI	Traditional Landrace	122	BUDDA	Traditional Landrace
100	NAVALI SALI	Traditional Landrace	123	BIDAR LOCAL	Traditional Landrace
101	KARE SALI PURPLE	Traditional Landrace	124	PONNAMPET LOCAL	Traditional Landrace
102	MALE BANGAR KADDI	Traditional Landrace	125	GEERASALI	Traditional Landrace
103	GUMKADLI	Traditional Landrace	126	UDAR SALI	Traditional Landrace
104	MUGAD SUGANDHA	Traditional Landrace	127	KOTAMBARISALI-2	Traditional Landrace
105	KARE BHATTA	Traditional Landrace	128	KARKALA DODIGA	Traditional Landrace
106	FARM VALLYA	Traditional Landrace	129	JEERIGE SANNA	Traditional Landrace
107	KALASAL	Traditional Landrace	130	KARE KANTIGA	Traditional Landrace
108	CHAKKOVA	Traditional Landrace	131	OLLE FARM BHATTA	Traditional Landrace
109	BILI NELLU	Traditional Landrace	132	ALUR SANNA	Traditional Landrace
110	MEESE BHATTA	Traditional Landrace	133	KUMUDA-1	Traditional Landrace
111	GOURI SALI	Traditional Landrace	134	WARI	Traditional Landrace

Contd…..

Sl. No.	Name	Pedigree	Sl. No.	Name	Pedigree
135	KUNKUMSALI-2	Traditional Landrace	148	GGV-05-01	Check
136	KEMPASALE	Traditional Landrace	149	PSB-68	Check
137	BIL-118	Swarna x WAB-460	150	INTAN	Check
138	RF-55-9	(Teqing x Binam) // Teqing	151	MTU1001	Check
139	RF-55-254	(Teqing x Binam) // Teqing	152	SIRI 1253	Check
140	RF 55-198	(Teqing x Binam) // Teqing	153	BPT 5204	Check
141	BIL-3	(Swarna x WAB-460) / Swarna	154	MGD-101	Check
142	BIL-149	(Swarna x WAB-460) / Swarna	155	ABHILASHA	Check
143	BIL-57	(Swarna x WAB-460) / Swarna	156	MAS-26	Check
144	RF 55-218	(Teqing x Binam) // Teqing	157	IR-64	Check
145	BIL-48	(Swarna x WAB-460) / Swarna	158	MAS-946-1	Check
146	BIL-77	(Swarna x WAB-460) / Swarna	159	RASI	Check
147	BIL-174	(Swarna x WAB-460) / Swarna	160	HR-12	Check (Susceptible)

3.1.2 Nursery preparation

Dry method of nursery raising was followed to screen for leaf blast resistance. A single row of rice accession was sown in nursery bed per replication as per the recommendations of uniform blast nursery trials of IRRI. All around the nursery and after every ten test entries a spreader row with susceptible check (HR-12) was also sown in order to entice the fungal spores and to aggravate the disease development.

3.1.3 Observations recorded

The observation was recorded on leaf blast disease severity. The scale used for ranking the genotypes was given by International Rice Research Institute (IRRI) in Standard Evaluation System (Table 3) (SES, 1996).

The genotypes are grown in UBN to provide Epiphytotic condition for disease development. Leaves of individual lines are observed for lesion formation and total leaf area affected by the disease. Based on the SES system the scoring was done.

3.2 Experiment-II: Validation of molecular markers for blast resistance genes in land races and promising breeding lines

3.2.1 Experimental site

The investigation was conducted in the Laboratory of the Department of Genetics and Plant Breeding, University of Agricultural Sciences Dharwad.

3.2.2 Experimental material

The experimental material involved the genomic DNA of the selected genotypes which have shown resistance to blast disease. For validation of resistant genes, SSR markers being reported to be linked to the resistant genes which are found to be effective and broad-spectrum have been used.

3.2.3 Procedure for extraction of genomic DNA

i. Fresh leaf sample weighing around 1 to 2 gram was taken.

ii. With the help of liquid nitrogen the leaves were ground to fine powder.

Table 3: Standard Evaluation System as per IRRI for scoring the genotypes against blast of rice

Scale	Characters observed on plant
0	No lesions on leaf
1	Small brown specks of pinhead size without sporulating centre
	Small roundish to slightly elongated grey spot about 1-2 mm in diameter with distinct brown margin and lesions are found on lower leaves
3	Lesion type same as that of scale 2 but significant number of lesions are seen on upper leaves
4	Typical sporulating blast lesions 3mm or longer infecting less than 2% of leaf area
5	Typical blast lesion infecting 2-10% of leaf area
6	Blast lesion infecting 11-25% leaf area
7	Blast lesion infecting 26-50% leaf area
8	Blast lesion infecting 51-75% leaf area
9	More than 75% leaf area affected

Plate 1. General view of the Uniform Blast Nursery

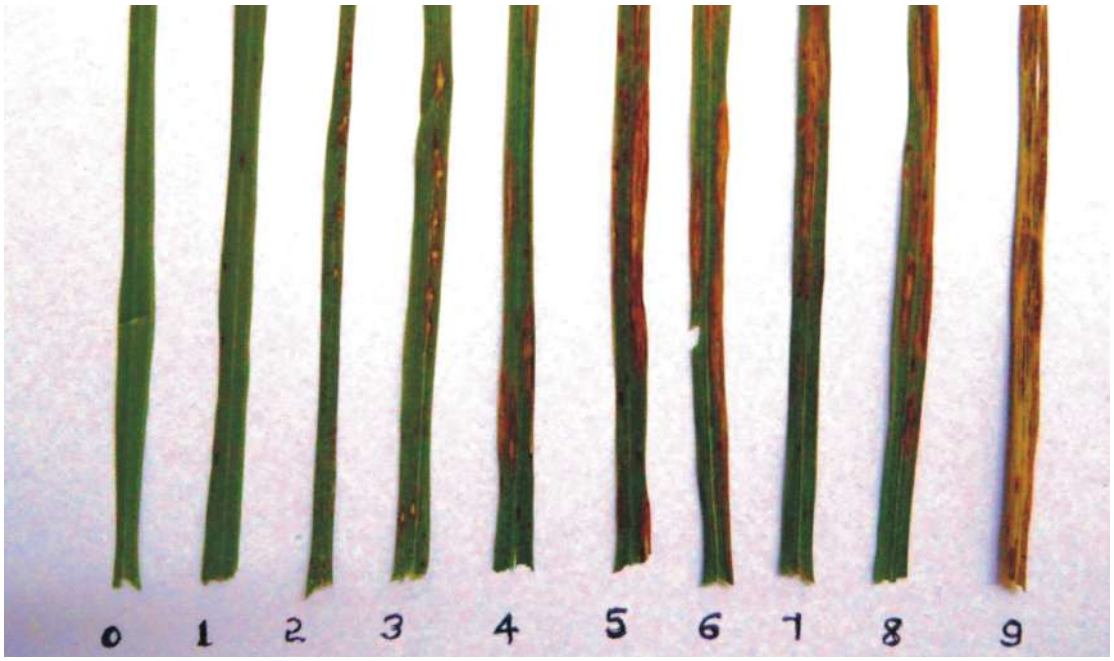

Plate 2. Characteristic symptom observed on leaves with different scale of scoring

iii. To this fine powder of leaf sample pre-warmed cTAB extraction buffer was added in 2 ml micro tube at the quantity of 1 ml per tube.

iv. The tubes were kept in water bath at 65^{0} c for 10-15 min with intermittent mixing.

v. Sample was cooled to room temperature.

vi. Equal volume of chloroform and isoamylalcohol (24:1) was added and mixed by inverting.

vii. The mixture was spun at 8000 RPM for 30 min.

viii. Supernatant was taken to fresh tube carefully.

ix. Equal volume of pre chilled isopropanol was added and mixed gently.

x. The suspension was allowed to settle over night at -20^{0} c.

xi. DNA or pellet was spooled out by spinning at 8500 RPM for 15 min.

xii. Supernatant was discarded and was drained out completely.

xiii. Pellet was washed with 70 per cent alcohol.

xiv. Pellet was dried completely after removing the alcohol.

xv. Pellet containing DNA was dissolved in suitable quantity of $T_{10}E_1$ solution.

xvi. DNA was stored at -20^{0} c.

Later, the DNA being extracted is used for PCR reaction using proper SSR primers which are specific to the resistant genes. Positive bands are considered for the presence of resistant genes in the respective genotypes.

3.2.4 Amplification conditions for SSR primers

PCR amplification of the markers was performed into the 10 µl reaction volume consisting of 20 ng. of genomic DNA. 20ng primers, 0.1 mM of dNTP's, 1X assay buffer (10 mM Tris pH-8, 50 mM KCl, 1.8mM MgCl2 and 0.01 mg/ml gelatin) and 1U of *Taq* polymerase enzyme (Genei). DNA amplification was performed with Eppendorf thermo cyclers under the following PCR conditions: 95°C for 1 minute for denaturation followed by 30 cycles of denaturation at 94°C. One minute of annealing at 58°C and final extension at 72°C for one minute. The amplified

products were run on 3.5% agarose gel containing ethidium bromide for studying polymorphism.

The primers linked with specific genes and which are broad-spectrum and resistant to prevailing races of the pathogen in major rice growing eco-system have been utilized for validating the resistant gene and their product size is mentioned in the Table 4.

3.3 Experiment III: Assessment of blast resistant genotypes for productivity under rainfed condition

3.3.1 Experimental site

The investigation was carried out during *kharif* 2014 at Agricultural research Station, Mugad centre in North Karnataka working on upland drill sown rice crop. Each genotype was sown in 2 rows of 1.5 m length with spacing of 20 cm between rows.

3.3.2 Genetic material and layout

All the 160 genotypes including landraces and promising breeding lines were evaluated for productivity and productivity related traits. Genotypes showing disease resistance along with good productivity traits were selected.

The experiment was laid out in Randomized Complete Block design with two replications and all the entries allotted randomly using lottery method. Genotypes were raised by direct hand sowing with a spacing of 20 cm between rows. Recommended cultural operations and plant protection measures as per agronomic package of practice were taken up to ensure a healthy stand of the crop. The list of genotypes used for the investigation is mentioned in the Table 2.

3.3.3 Observations recorded

Five plants in each replication of a genotype were selected at random for recording the observations. The average of the observations recorded were taken for further analysis. The characters observed for evaluating the lines are described below.

Table 4: List of markers used for validation of blast resistant genes along with product size and primer sequence

Sl. No.	R Gene	Chromosome number	Marker name	Product size (bp)	Primer sequence 5'-3'	Genetic distance (cM)	Reference
1	*Piz*	6	RM6858	120	F ATTAATACCGCTACCACGCG R TCCTCCTCCACCTCAATCAC	0.2	Hayashi *et al.* (2006)
2	*Pia*	11	RM4862	164	F CAACTTTCTGGCATAAACTA R TGGTGAAAGATATTTCAGACTGGTGAAAGATATTTCAGAC	0.8	Kwan *et al.* (2008)
3	*Pi54*	11	RM224	157	F ATCGATCGATCTTCACGAGG R TGCTATAAAAGGCATTCGGG	0.0	Sharma *et al.* (2002)
4	*Pit*	1	RM5552	112	F ATCAGCCCAGAGGGAGTAAC R AGATTCTGGGATCACGTTG	0.5	Hayashi *et al.* (2006)
5	*Pi38*	11	RM206	147	F CCCATGCGTTTAACTATTTCTCGTTCCATCGATCCGTATGG R CGTTCCATCGATCCGTATGG	4.0	Gowda *et al.* (2006)

Growth characters

1. Days to 50% flowering
2. Plant height (cm)

Yield characters

1. Number of tillers per meter row
2. Number of panicles per meter row
3. Panicle length (cm)
4. Panicle weight (g)
5. Number of grains per panicle
6. 1000 grain weight (g)
7. Grain yield (g per plot)
8. Grain yield (q ha^{-1})

3.3.3.1 Days to Fifty per cent flowering

The number of days taken by each genotype, from the day of sowing to opening of first flower in 50 per cent of the plants was recorded.

3.3.3.2 Plant height (cm)

The height of the plant was measured from the base of main tiller to the tip of the panicle excluding awns if any and expressed in centimeters (cm).

3.3.3.3 Panicle length (cm)

The height of the plant was measured from ciliate ring to the tip of the panicle at the time of harvest and expressed in centimeter (cm).

3.3.3.4 Tiller number per meter row

Number of tillers was counted for the plants in meter row at the time of harvest.

3.3.3.5 Number of panicles per meter row

Numbers of panicles were counted per meter row to estimate the total productive tillers in order to access the yielding ability of the genotype.

3.3.3.6 Panicle weight (g)

The average weight of the panicle (g) was recorded from randomly picked panicles from individual genotypes.

3.3.3.7 Number of grains per panicle

The grains from randomly picked panicles are counted individually.

3.3.3.8 Test weight (g)

Weight of 1000 randomly selected grains was recorded and expressed in grams as test weight.

3.3.3.9 Grain yield per plot (g)

The grain yield of all the plants in the plot is estimated after the harvest. The plot indicates the area given for individual genotype under the study.

3.3.3.10 Grain yield (q ha^{-1})

Based on the plot yield along with the plot area the possible yield of all the genotypes under the hectare is calculated as below

$$\text{Yield (q ha}^{-1}\text{)} = \text{Net plot yield (g)} \times \frac{10000}{\text{Net plot size}} \times 10^5$$

3.3.4 Statistical analysis

The average values of five plants used for recording observation were computed for each of the characters for each genotype in each replication and were subjected to statistical analysis.

3.3.4.1 Analysis of variance

The analysis of variance for all the characters under the study was carried out using mean data in order to assess the genetic variability among genotypes as given by Cochran and Cox (1957). The level of significance was tested at 5 per cent and 1 per cent using F test. The model of ANOVA is presented as below.

Sl. No.	Source of variation	d.f.	M.S.S.	Expected M.S.S.
1	Replication	r-1	M_r	$\sigma^2_g r + \sigma^2_e$
2	Genotypes	g-1	M_t	$\sigma^2_e + \sigma^2_g$
3	Error	(r-1) (g-1)	M_e	σ^2_e
	Total	rg-1	$M_r + M_t + M_e$	

Where,

r = number of replications

g = number of treatments (genotypes)

3.3.4.2 Estimation of genetic variability parameters

3.3.4.2.1 Phenotypic and genotypic variance

Phenotypic and genotypic components of variance were estimated by using the formula given by Cochran and Cox (1957).

$$\text{Genotypic variance } (\sigma^2_g) = \frac{\text{MSS due to genotypes} - \text{MSS due to error } (\sigma^2_e)}{r}$$

Phenotypic variance (σ^2_p) = Genotypic variance (σ^2_g) + Environmental variance (σ^2_e)

3.3.4.2.2 Co-efficient of variability

Both phenotypic and genotypic co-efficient of variability for all the characters were estimated using the formulae of Burton and De Vane (1953).

Genotypic Co-efficient of Variability

$$\text{GCV per cent} = \frac{\sqrt{\text{Genotypic variance}}}{\text{Grand mean}} \times 100$$

Phenotypic Co-efficient of Variability (PCV) :

$$\text{PCV per cent} = \frac{\sqrt{\text{Phenotypic variance}}}{\text{Grand mean}} \times 100$$

PCV and GCV were classified as per Sivasubramanian and Menon (1973) and as shown below:

0-10 per cent- Low; 10-20 per cent- Moderate; >20 per cent- High

3.3.4.2.3 Heritability in broad sense (h^2)

Heritability (broad sense) was estimated for all the characters as the ratio of genotypic variance to the total variance as suggested by Lush (1949) and Hanson *et al.* (1956).

$$h^2 = \frac{\sigma^2_g}{\sigma^2_p}$$

According to Robinson *et al.* (1966) heritability estimates in cultivated plants can be placed in following categories.

5-10%- Low, 10-30%- Moderate, 30% and above- High

3.3.4.2.4 Genetic Advance (GA)

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

$$GA = h^2 K \sigma_p$$

Where,

h^2 = Heritability estimate

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

σ_p = Phenotypic standard deviation

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

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

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

0-10% - Low

10- 20%- Moderate

>20% - High

3.3.4.2.5 Correlation studies

To determine the degree of association of characters with yield and also among the yield components, the correlation co-efficients were calculated.

Phenotypic co-efficients of correlation between two characters were determined by using variance and covariance components as suggested by Al-Jibourie *et al.* (1958).

$$r_p(xy) = \frac{Cov_p(xy)}{\sigma^2_p(x).\ \sigma^2_p(y)}$$

Where,

r_p (xy) is the phenotypic correlation co-efficient

Cov_p is phenotypic co-variances of xy

σ^2_p phenotypic variance of x and y

The calculated value of 'r' was compared with Table 'r' value with n-2 degree of freedom at 5 per cent and 1 per cent level of significance, where n refers to number of pairs of observations.

4. EXPERIMENTAL RESULTS

The results obtained from the present investigation are presented under the following headings.

4.1 Phenotyping of landraces and promising breeding lines for blast resistance under epiphytotic condition

4.2 Validation of molecular markers for blast resistance genes in land races and promising breeding lines

4.3 Assessment of blast resistant genotypes for productivity and related genetic parameters

4.1 Phenotyping of landraces and promising breeding lines for blast resistance under field condition

Screening of advanced breeding lines and local landraces was carried out for field resistance to leaf blast disease at ARS Mugad during *kharif* 2014. The result on disease incidence in the genotypes was analyzed through square root transformation. The maximum score recorded for respective genotype is mentioned in Table 5.

Further classification of genotypes was made into immune, highly resistant, resistant, moderately resistant, moderately susceptible and susceptible genotypes. The details are furnished in the Table 6. None of the genotypes considered in the present study did show immune or resistant reaction to the disease. Six genotypes among the set of one hundred sixty genotypes recorded resistant reaction. Seventy six genotypes were found to be moderately resistant whereas, sixty four genotypes were moderately susceptible and fourteen genotypes were susceptible to disease reaction.

Overall, the set of genotypes including both traditional landraces and promising breeding lines involved in the study have got more number of lines lying in the moderately resistant category.

Table 5: Response of rice genotypes to leaf blast described as Disease Score (0 to 9 scale)

Sl. No.	Genotypes Screened	Disease Score	Sl. No.	Genotypes Screened	Disease Score
1	BA-60-6-2	2	81	MSB-48-1-12	5
2	RF-53-102-3	4	82	MGD-V-14-18	5
3	MGD-V-14-1	3	83	MSB-50-1-4	4
4	MGD-V-14-2	5	84	MGD-V-14-19	3
5	SMW-11-09-30-L-1	3	85	GUDDENELLU	3
6	MGD-V-14-3	6	86	ADNENKELTI	5
7	RSS-17-1	4	87	KARE KALVI	5
8	MGD-V-14-4	3	88	MADRAS BHATTA	6
9	MGD-V-14-5	3	89	NEERGULLI	6
10	IR 78875	3	90	GHEERSALI	4
11	ARB-6	3	91	BETIGA	4
12	MGD-V-14-6	4	92	MUTALGA	5
13	BA60-6	6	93	KARIGAJIVILE	4
14	IET-22552	3	94	PARIMALASANNA	4
15	MGD-1202	4	95	NYARE MINDA	6
16	VARALU	4	96	BILIDADI GORATIGA	7
17	MGD-V-14-7	2	97	JADDU BHATTA	7
18	MGD-V-14-8	5	98	CHITIGA	7
19	MGD-V-14-9	2	99	BANGAR KOVI	7
20	BD-17-2-1	2	100	NAVALI SALI	4
21	BD-17-2-2	2	101	KARE SALI PURPLE	6
22	BD-RSS-17-1	3	102	MALE BANGAR KADDI	5
23	BA-35-1-1	4	103	GUMKADLI	4
24	YSM-42-1-7	4	104	MUGAD SUGANDHA	4
25	MGD-V-14-10	3	105	KARE BHATTA	5
26	MSB-48-1-4	5	106	FARM VALLYA	5
27	KRGL-64-1-4-2	4	107	KALASAL	5
28	YSM-31-1-1	5	108	CHAKKOVA	4
29	YSM-7-1	4	109	BILI NELLU	5
30	KRGL-7-1-1	5	110	MEESE BHATTA	5
31	MSB-50-1-3	4	111	GOURI SALI	5
32	YSM-66-1-1	5	112	KONNUR BHATTA	3

Contd….

Sl. No.	Genotypes Screened	Disease Score	Sl. No.	Genotypes Screened	Disease Score
33	MSB-50-1-3-1	4	113	DODIGA	3
34	MGD-V-14-11	5	114	HUGGI BHATTA	3
35	SMW-XV-101	4	115	BOLA SALI	4
36	BA-35-1-1-2	3	116	GOPAL DODIGA	5
37	SMW-11-01-45-4	6	117	KUNKUM SALI-1	6
38	SMW-101-103-1	6	118	KOTAMBARI SALI-1	3
39	SMW-XV-103	6	119	MALABANGAR KADDI	3
40	SMW-XV-105	7	120	KYASAKKI	3
41	MGD-1201-2	7	121	VARESANNA	2
42	SMW-11-09-50-1	6	122	BUDDA	3
43	SMW-11-09-45-11	7	123	BIDAR LOCAL	3
44	MGD-V-14-12	6	124	PONNAMPET LOCAL	4
45	SMW-11-09-5-1-3-1	7	125	GEERASALI	3
46	SMW-11-09-45-5	6	126	UDAR SALI	4
47	SRIRAM SONA	5	127	KOTAMBARISALI-2	3
48	SMW-11-09-45-1	6	128	KARKALA DODIGA	3
49	RSS-17	6	129	JEERIGE SANNA	4
50	RSS-7-1	3	130	KARE KANTIGA	5
51	IET-22801-2	3	131	OLLE FARM BHATTA	3
52	SMW-10-2	4	132	ALUR SANNA	4
53	27-P-11-3-2-1	4	133	KUMUDA-1	5
54	SMW-11-09-45-102	4	134	WARI	5
55	MGD-V-14-13	4	135	KUNKUMSALI-2	4
56	SMW-11-09-5-1-3	4	136	KEMPASALE	4
57	SMW-11-09-50-1-103	5	137	BIL-118	6
58	SMW-11-09-60-1-2	4	138	RF-55-9	5
59	MGD-V-14-14	4	139	RF-55-254	5
60	MGD-V-14-15	5	140	RF 55-198	6
61	BA-60-3-2	4	141	BIL-3	5
62	SMW-10-09-11	5	142	BIL-149	4
63	BA-60-6-1	5	143	BIL-57	4
64	BA-60-6-3	4	144	RF 55-198	5
65	BA-15-31-1-1	6	145	BIL-48	4
66	KRGL-7-1-9	6	146	BIL-77	4

Contd….

Sl. No.	Genotypes Screened	Disease Score	Sl. No.	Genotypes Screened	Disease Score
67	KRGL-12-13	5	147	BIL-174	3
68	YSM-82-1-2	6	148	GGV-05-01	4
69	MGD-V-14-16	7	149	PSB-68	5
70	MGD-V-14-17	7	150	INTAN	5
71	YSM-15-1-13	6	151	MTU1001	5
72	KRGL-20-1-3	6	152	SIRI 1253	4
73	KRGL-29-1-3	6	153	BPT 5204	4
74	MGD-1202-1	6	154	MGD-101	5
75	GSM-45-1-7	8	155	ABHILASHA	4
76	KRGL-7-1-5-A	8	156	MAS-26	4
77	YSM-7-1-20-A	4	157	IR-64	4
78	MSB-43-1-6-B	6	158	MAS-946-1	3
79	KRGL-1-7-5	7	159	RASI	3
80	KRGL-20-1-5-A	6	160	HR-12	7

Table 6: Classification of genotypes based on reaction to disease

Sl. No.	Disease score	Kind of reaction	Number of genotypes
1	0	Immune	NIL
2	1	Highly Resistant (HR)	NIL
3	2	Resistant (R)	6
4	3 and 4	Moderately resistant (MR)	76
5	5 and 6	Moderately Susceptible (MS)	64
6	7, 8 and 9	Susceptible (S)	14

4.2 Validation of molecular markers for blast resistance genes in land races and promising breeding lines

Molecular markers increase the precision of identification and incorporation of resistant genes in breeding programme. Many PCR-based markers have been developed to screen and identify different resistant genes.

In the present investigation, validation of blast resistant genes was carried out by using reported molecular markers which were linked to these resistant genes and even utilized by different workers with different set of genotypes at different locations. The genotypes which harboring different resistant genes are listed in Table 7.

Genotypes MGD-V-14-5 carries resistant gene like *Piz* and *Pi54* and is found resistant to blast under epiphytotic conditions with score of three. Genotype MGD-V-14-7 harbors genes like *Piz, Pia, Pit* and *Pi38* and is resistant to blast disease with the score of 2. It is the single genotype which is found to harbor four different resistant genes. *Pi54* is the important broad-spectrum gene found to confer resistance to different isolates of blast pathogen, and the genotypes like, IET-22801-2, SMW-11-09-5-1-3 and Jeerige sanna have shown positive results for the presence of this resistant gene.

The genotype Rasi, have been found to be harboring resistant genes like *Piz*, *Pit* and *Pi38*. Among all the genes screened, *Piz* have been found to be present in more number of resistant genotypes namely, MGD-V-14-5, MGD-V-14-7, BA-60-6-2,BA-60-3-2, SMW-11-09-30-L-1 and in landraces like Huggi Bhatta and Jeerigesanna.

4.3 Assessment of blast resistant genotypes for productivity and related genetic parameters

4.3.1 Analysis of variance

The mean sum of squares for plant height, yield component traits and blast index in 160 genotypes of rice are presented in Table 8. Highly significant differences among the genotypes were observed for all the characters indicating presence of sufficient amount of variability for all the characters among the genotypes studied.

Table 7: Blast resistant genotypes with different resistant genes

Sl. No.	Genotype	Resistant gene	Blast score
1	BA-60-6-2	*Piz*	2 (R)
2	SMW-11-09-30-L-1	*Piz*	3 (MR)
3	MGD-V-14-5	*Piz*	3 (MR)
4	MGD-V-14-7	*Piz*	2 (R)
5	BA-60-3-2	*Piz*	4 (MR)
6	Huggi Bhatta	*Piz*	3 (MR)
7	Budda	*Piz*	3 (MR)
8	MGD-V-14-7	*Pia*	2 (R)
9	MGD-V-14-5	*Pi54*	3 (MR)
10	IET-22801-2	*Pi54*	3 (MR)
11	SMW-11-09-5-1-3	*Pi54*	4 (MR)
12	Budda	*Pi54*	3 (MR)
13	Jeerige sanna	*Pi54*	4 (MR)
14	MGD-V-14-7	*Pit*	2 (R)
15	Rasi	*Pit*	3 (MR)
16	MGD-V-14-7	*Pi38*	2 (R)
17	Rasi	*Pi38*	3 (MR)
18	HR-12 (Susceptible check)	-	7 (S)

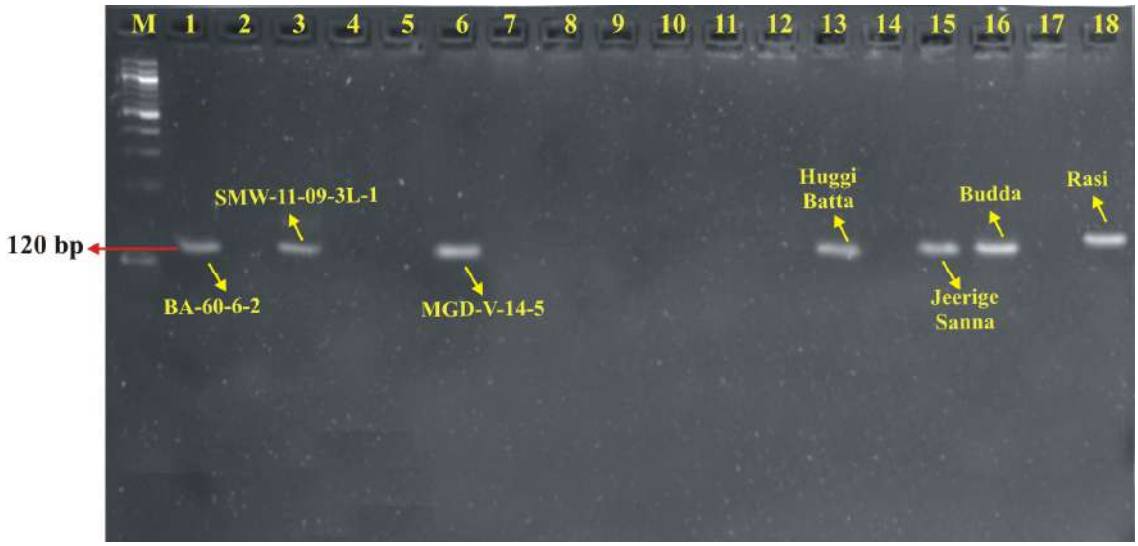

Plate 3. Resistant genotypes for Piz

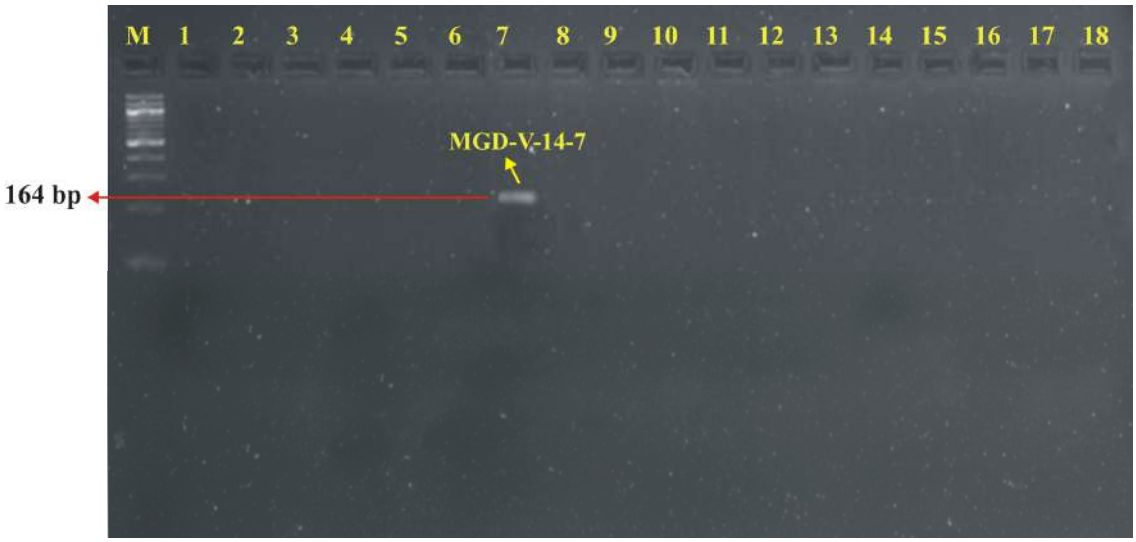

Plate 4: Resistant genotypes for Pia

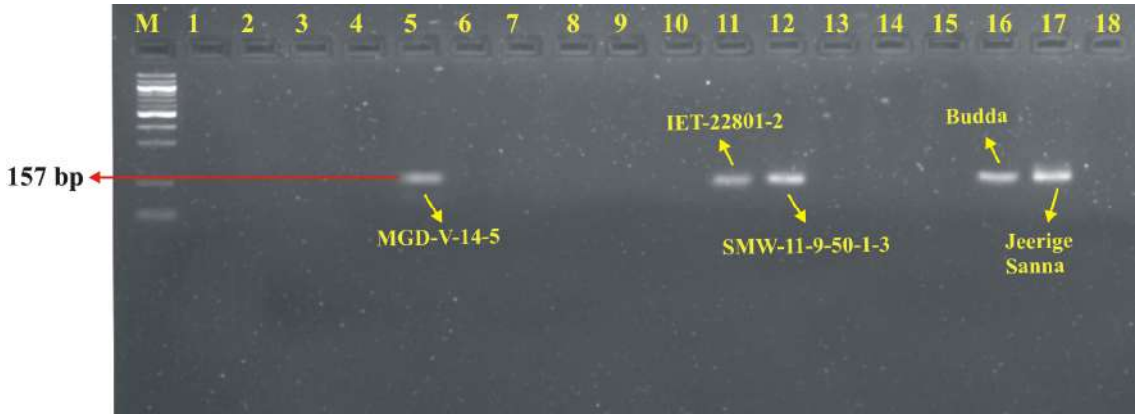

Plate 5. Resistant genotypes for Pi54

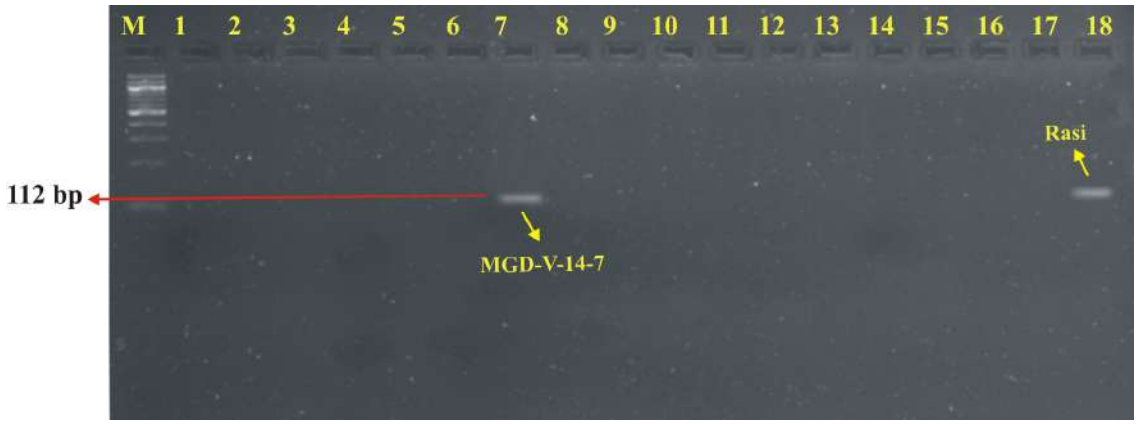

Plate 6. Resistant genotypes for Pit

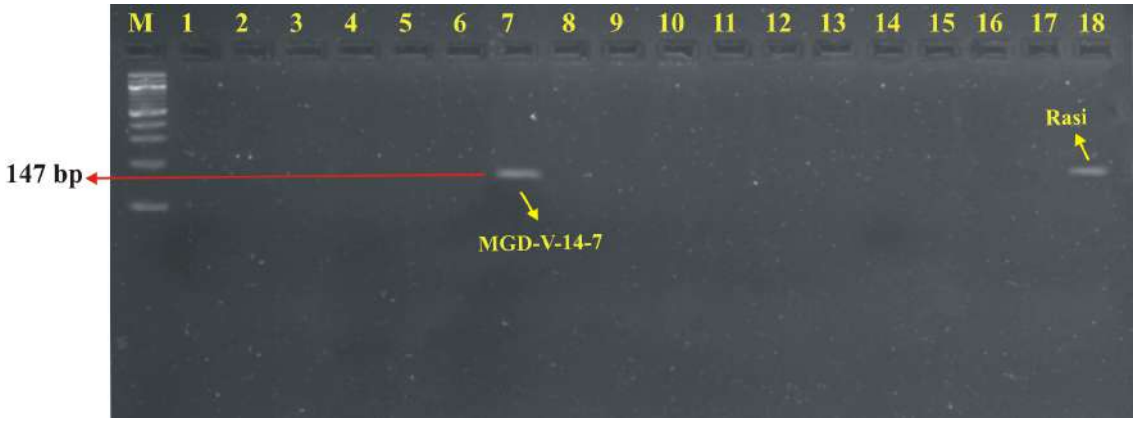

Plate 7. Resistant genotypes for Pi38

Table 8: Analysis of variance for yield, yield attributing traits along with disease susceptibility Index

Sources of variation	d.f.	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}
Replication	1	36.90*	0.46	0.01	0.01	0.59	1.96**	59.15	0.54	160.33	4.45	0.10*
Genotype	160	249.21**	770.66***	2.86**	2.61**	18.61***	0.63*	1113.45**	34.82**	5621.80*	156.16**	0.22*
Error	160	6.25	0.65	0.09	0.10	0.20	0.06	27.42	0.63	210.31	5.84	0.03

X_1 Days to 50 per cent flowering
X_2 Plant height (cm)
X_3 Tiller number
X_4 Panicle number
X_5 Panicle length (cm)
X_6 Panicle weight (g)
X_7 Number of grains per panicle
X_8 Test weight (g)
X_9 Grain yield per plot (gram)
X_{10} Yield (q ha^{-1})
X_{11} Disease susceptibility index (transformed)

4.3.2 Mean performance of all the genotypes

The mean performance of all 160 rice genotypes in respect of grain yield and its component traits along with reaction to blast disease are presented in Table 9 and briefly explained below.

1. Days to 50 per cent flowering

Among the genotypes evaluated, ARB-6 took minimum number of days for 50 per cent flowering (84 days) followed by IR-78875 (84.5 days), IET 22552 (84.5 days) and MGD-V-14-5 (86 days). Whereas, Vare sanna had maximum number of days (125.5 days) followed, by Intan (110.5 days).

2. Plant height (cm)

The genotype, IR 64 (53.00 cm) was most dwarf among the genotypes followed by MAS-946-1 (56.50 cm) and BPT-5204 (56.60 cm). The Chitiga (134.00 cm) recorded tallest plant height followed by Neergulli (131.8 cm) and Kunkumsali-2 (131.20 cm) and Malabangar kaddi (131.00 cm).

3. Tiller number per meter row

Maximum number of tillers per meter row were observed in the genotype, HR-12 (100) followed by SMW-XV-105 (90) and BA-35-1-1-2. Lowest numbers of tillers were observed in the genotype, Olle farm bhatta (40) followed by Jeerige sanna (40) and BIL-47 (50).

4. Number of panicles per meter row

The genotype HR-12 (90), SMW-XV-105 (80), MGD-1201-2 (80) and YSM-15-1-13 (80), had higher number of panicles per plant. Whereas, Karekantiga (40) had the lowest number of panicles per plant followed by Kotambari Sali (40), Dodiga (40) and BIL-77 (40).

5. Panicle length (cm)

Maximum panicle length of 26.20 cm was recorded for the genotype, Karigajavile followed by Gheersali (25.70 cm) and Bili nellu (25.50 cm), the genotype

Table 9: Mean performance of one hundred sixty genotypes in respect of productivity traits and blast resistance

Genotypes	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}
BA-60-6-2	89.5	96.2	78.0	69.0	22.1	3.89	148.00	23.924	221.0	36.8	1.732
RF-53-102-3	87.0	92.5	71.0	63.0	21.6	3.43	146.15	24.910	207.5	34.6	2.118
MGD-V-14-1	90.0	102.5	75.0	66.0	24.1	3.30	139.75	24.683	209.5	34.9	1.866
MGD-V-14-2	96.5	99.7	77.0	67.0	21.5	3.68	121.50	18.381	258.0	43.0	2.091
SMW-11-09-30-L-1	109.0	109.2	69.0	60.0	22.6	4.12	167.35	22.874	237.0	39.5	2.000
MGD-V-14-3	96.5	88.7	73.0	63.0	21.9	3.55	128.25	18.623	214.0	35.7	2.646
RSS-17-1	86.5	102.6	73.0	63.0	22.1	2.70	121.65	25.029	121.0	20.2	2.236
MGD-V-14-4	94.5	88.3	73.0	60.0	22.5	4.35	116.61	21.602	269.0	44.8	1.866
MGD-V-14-5	86.0	103.2	66.0	56.0	21.5	3.56	151.90	25.032	234.7	39.1	1.866
IR 78875	84.5	109.5	74.0	66.0	21.2	3.50	120.45	18.105	219.7	36.6	1.984
ARB-6	84.0	91.2	58.0	53.0	20.8	4.12	197.10	23.689	157.5	26.3	1.984
MGD-V-14-6	95.0	100.8	71.0	62.0	21.8	4.25	103.25	19.515	238.5	39.8	2.118
BA60-6	96.5	122.5	61.0	52.0	21.6	3.76	142.45	18.191	187.2	31.2	2.441
IET-22552	84.5	84.6	66.0	57.0	18.6	3.74	130.80	17.356	162.5	27.1	2.000
MGD-1202	95.5	87.7	56.0	53.0	19.7	4.21	141.10	17.596	263.5	43.9	2.236
VARALU	88.0	86.3	78.0	73.0	19	3.39	130.15	19.457	166.0	27.7	2.118
MGD-V-14-7	101.5	118.9	82.0	75.0	24.9	4.29	151.00	19.743	227.6	37.9	1.732
MGD-V-14-8	94.0	93.7	60.0	56.0	20.6	3.52	131.15	17.061	159.0	26.5	2.225
MGD-V-14-9	88.0	82.8	66.0	63.0	21.2	3.58	138.25	18.001	206.5	34.4	1.732

Contd……

Genotypes	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}
BD-17-2-1	95.0	112.3	79.0	75.0	23.9	4.11	137.95	19.790	236.4	39.4	1.732
BD-17-2-2	94.5	107.7	82.0	74.0	22.7	4.11	117.25	19.904	153.5	25.6	1.732
BD-RSS-17-1	92.0	109.3	66.0	59.0	20.7	3.02	113.60	18.351	184.0	30.7	1.866
BA-35-1-1	109.5	107.8	70.0	61.0	20.7	2.39	98.05	22.451	200.1	33.4	2.118
YSM-42-1-7	106.5	123.0	69.0	63.0	20.4	2.70	132.75	18.461	221.0	36.8	2.118
MGD-V-14-10	109.5	103.3	52.0	45.0	19.6	2.78	108.75	16.497	227.5	37.9	1.866
MSB-48-1-4	95.5	79.5	53.0	45.0	21.4	3.00	122.50	23.391	270.5	45.1	2.343
KRGL-64-1-4-2	107.5	61.5	49.0	44.0	17.9	3.10	96.85	16.902	173.0	28.8	2.118
YSM-31-1-1	104.5	81.5	48.0	42.0	20.4	3.21	117.05	20.496	220.1	36.7	2.343
YSM-7-1	101.0	90.8	55.0	46.0	22.4	3.24	113.75	17.400	224.1	37.3	2.118
KRGL-7-1-1	108.5	73.9	51.0	44.0	18.5	3.22	111.05	20.258	191.5	31.9	2.343
MSB-50-1-3	106.5	72.5	50.0	44.0	19.7	3.55	121.60	16.112	206.0	34.3	2.118
YSM-66-1-1	105.5	93.7	57.0	54.0	4.8	3.15	117.90	16.218	228.0	38.0	2.343
MSB-50-1-3-1	96.0	73.2	73.0	68.0	5.8	3.69	123.55	16.324	161.5	26.9	2.118
MGD-V-14-11	94.0	105.8	85.0	76.0	20.3	3.15	126.15	18.989	198.0	33.0	2.343
SMW-XV-101	105.5	111.2	85.0	76.0	20.7	3.45	101.65	17.953	219.4	36.6	2.118
BA-35-1-1-2	91.5	107.8	86.0	75.0	19.6	3.88	109.50	17.651	248.0	41.3	2.000
SMW-11-01-45-4	93.0	84.4	83.0	75.0	18.5	3.23	111.95	18.767	215.5	35.9	2.646
SMW-101-103-1	108.0	93.6	81.0	76.0	20.9	3.10	139.50	18.946	213.1	35.5	2.646
SMW-XV-103	107.5	90.7	79.0	73.0	19.9	3.82	129.40	19.071	229.0	38.2	2.646
SMW-XV-105	101.0	83.8	90.0	83.0	20.8	2.83	109.85	20.603	264.0	44.0	2.737

Contd……

Genotypes	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}
MGD-1201-2	98.5	93.9	86.0	81.0	20.7	2.85	110.15	23.120	256.0	42.7	2.737
SMW-11-09-50-1	107.0	89.5	78.0	73.0	20.1	2.77	99.50	25.768	204.0	34.0	2.548
SMW-11-09-45-11	102.0	88.3	65.0	61.0	20.9	2.97	114.30	24.133	236.0	39.3	2.828
MGD-V-14-12	101.5	94.5	76.0	72.0	21.8	2.65	119.45	26.507	219.0	36.5	2.548
SMW-11-09-5-1-3-1	94.0	93.9	75.0	69.0	20.2	2.70	136.90	13.515	188.5	31.4	2.737
SMW-11-09-45-5	91.5	90.4	64.0	60.0	21.2	2.70	100.35	14.827	239.5	39.9	2.646
SRIRAM SONA	106.5	94.8	69.0	61.0	20.4	2.37	101.20	17.111	220.0	36.7	2.449
SMW-11-09-45-1	91.0	86.2	74.0	66.0	20.7	2.87	106.80	18.744	213.0	35.5	2.646
RSS-17	109.0	106.6	66.0	61.0	20.7	3.03	122.55	17.626	262.5	43.8	2.548
RSS-7-1	90.0	104.3	66.0	60.0	21.3	2.95	122.70	19.314	182.8	30.5	2.000
IET-22801-2	87.0	86.4	66.0	60.0	21.6	2.68	110.85	23.785	235.0	39.2	1.866
SMW-10-2	92.0	83.1	84.0	77.0	19.5	2.64	129.65	18.400	193.0	32.2	2.118
27-P-11-3-2-1	92.5	81.8	70.0	64.0	19.6	2.64	129.10	19.523	223.0	37.2	2.118
SMW-11-09-45-102	109.0	101.2	70.0	63.0	19.5	2.36	125.45	18.842	136.5	22.8	2.236
MGD-V-14-13	110.5	107.5	63.0	55.0	19.7	2.44	103.15	22.941	178.5	29.8	1.984
SMW-11-09-5-1-3	93.5	86.1	62.0	56.0	20.7	2.34	109.80	24.022	275.0	45.8	2.118
SMW-11-09-50-1-103	86.5	84.4	71.0	65.0	20.2	3.09	109.45	20.983	232.5	38.8	2.225
SMW-11-09-60-1-2	91.0	81.9	65.0	58.0	20.3	2.67	119.10	19.944	187.0	31.2	2.118
MGD-V-14-14	89.5	112.7	61.0	55.0	20.4	2.36	119.95	20.136	198.5	33.1	2.118
MGD-V-14-15	86.5	88.2	67.0	59.0	20.6	2.88	150.45	17.912	208.5	34.8	2.225
BA-60-3-2	88.5	103.0	67.0	57.0	18.9	2.33	128.00	17.912	223.5	37.3	2.118

Contd……

Genotypes	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}
SMW-10-09-11	86.5	93.6	68.0	60.0	21.7	3.23	152.70	19.116	272.5	45.4	2.343
BA-60-6-1	91.0	94.2	74.0	67.0	21.9	2.96	139.50	19.050	248.5	41.4	2.225
BA-60-6-3	109.5	92.7	69.0	63.0	21.1	2.98	123.60	23.331	267.5	44.6	2.236
BA-15-31-1-1	110.0	97.1	63.0	58.0	21.7	3.46	137.95	19.841	313.5	52.3	2.548
KRGL-7-1-9	92.0	88.9	80.0	75.0	19.4	2.95	120.90	19.584	139.5	23.3	2.646
KRGL-12-13	92.0	108.4	85.0	77.0	20.2	3.29	129.00	15.926	263.1	43.8	2.449
YSM-82-1-2	88.5	116.8	67.0	63.0	20.7	3.46	128.90	20.661	187.0	31.2	2.548
MGD-V-14-16	105.5	99.2	79.0	70.0	20	3.97	136.40	23.427	269.5	44.9	2.828
MGD-V-14-17	93.0	94.6	72.0	66.0	21.9	3.86	147.75	20.535	199.5	33.3	2.737
YSM-15-1-13	91.0	82.6	86.0	79.0	21.4	3.07	134.60	23.914	251.1	41.8	2.548
KRGL-20-1-3	106.0	80.7	70.0	63.0	20.4	2.83	125.35	22.355	217.5	36.3	2.548
KRGL-29-1-3	88.0	104.2	71.0	62.0	20.1	2.44	121.90	19.538	155.3	25.9	2.548
MGD-1202-1	89.0	85.5	69.0	62.0	20.8	2.45	141.30	18.482	154.0	25.7	2.646
GSM-45-1-7	100.5	108.7	64.0	61.0	20	3.03	143.35	19.458	143.5	23.9	2.914
KRGL-7-1-5-A	94.0	103.7	63.0	60.0	20	2.95	126.30	19.117	182.6	30.4	2.914
YSM-7-1-20-A	90.0	86.6	66.0	57.0	21.4	2.73	144.85	15.947	160.6	26.8	2.236
MSB-43-1-6-B	93.0	106.4	70.0	64.0	20.1	3.42	144.65	14.745	229.5	38.3	2.548
KRGL-1-7-5	87.5	114.9	72.0	66.0	21.4	2.78	128.05	15.988	257.7	42.9	2.737
KRGL-20-1-5-A	94.0	111.6	67.0	60.0	21.4	3.15	121.50	20.151	195.4	32.6	2.548
MSB-48-1-12	94.0	113.3	71.0	63.0	22.9	3.84	144.10	26.888	252.5	42.1	2.343
MGD-V-14-18	102.0	89.0	78.0	73.0	25.4	3.20	175.80	19.494	242.0	40.3	2.343

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Genotypes	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}
MSB-50-1-4	94.5	91.7	61.0	58.0	21.7	2.95	107.15	22.486	176.8	29.5	2.118
MGD-V-14-19	91.5	120.7	56.0	55.0	21.7	2.46	92.30	20.708	138.2	23.0	1.866
GUDDENELLU	97.0	115.2	52.0	51.0	25	2.73	98.70	25.560	143.5	23.9	1.866
ADNENKELTI	93.5	113.6	68.0	60.0	25.2	3.71	108.45	24.125	231.8	38.6	2.343
KARE KALVI	93.5	105.3	64.0	58.0	24	2.59	117.30	23.620	154.1	25.7	2.449
MADRAS BHATTA	90.5	124.2	56.0	48.0	25.2	2.86	138.95	26.643	141.3	23.6	2.548
NEERGULLI	107.0	131.8	62.0	56.0	25.2	3.00	88.95	22.060	173.4	28.9	2.548
GHEERSALI	107.5	116.8	59.0	54.0	25.7	3.11	101.60	20.998	174.0	29.0	2.236
BETIGA	91.0	126.1	68.0	61.0	25.2	3.31	100.55	25.901	209.5	34.9	2.118
MUTALGA	92.5	123.4	67.0	64.0	22.8	2.93	111.95	24.120	193.6	32.3	2.225
KARIGAJIVILE	106.5	125.6	79.0	71.0	26.2	2.97	119.95	20.362	217.7	36.3	2.343
PARIMALASANNA	107.5	123.4	68.0	61.0	23.8	2.27	129.20	14.065	140.8	23.5	2.343
NYARE MINDA	104.5	119.2	62.0	50.0	21.6	2.94	141.40	19.897	151.3	25.2	2.548
BILIDADI GORATIGA	108.0	121.9	74.0	67.0	20.7	2.90	100.35	25.064	200.2	33.4	2.737
JADDU BHATTA	107.0	110.7	74.0	64.0	19.8	3.14	96.70	24.987	184.0	30.7	2.737
CHITIGA	91.5	134.0	70.0	61.0	24.5	2.79	101.15	25.212	176.6	29.4	2.737
BANGAR KOVI	109.0	99.1	65.0	58.0	20.2	3.39	135.20	19.908	225.5	37.6	2.737
NAVALI SALI	91.0	111.4	80.0	70.0	19.8	3.21	108.00	30.472	233.0	38.8	2.548
KARE SALI PURPLE	101.0	94.9	63.0	55.0	17.8	2.57	102.50	21.262	105.2	17.5	2.548
MALE BANGAR KADDI	106.0	128.6	85.0	73.0	24.1	2.49	98.75	19.636	138.0	23.0	2.225
GUMKADLI	97.5	119.5	83.0	73.0	21.5	2.42	100.00	26.196	180.7	30.1	2.343

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Genotypes	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}
MUGAD SUGANDHA	95.0	127.8	74.0	65.0	20.3	3.39	100.70	28.566	229.4	38.2	2.236
KARE BHATTA	100.0	124.4	70.0	62.0	21.2	2.91	102.45	27.358	186.1	31.0	2.449
FARM VALLYA	107.5	108.1	65.0	56.0	23.3	2.58	145.20	20.443	230.0	38.3	2.548
KALASAL	90.5	122.3	73.0	64.0	24.7	2.38	110.15	18.251	155.6	25.9	2.343
CHAKKOVA	107.5	124.9	54.0	43.0	21.4	2.38	128.00	26.621	104.5	17.4	2.118
BILI NELLU	109.5	87.2	73.0	62.0	20.8	2.38	159.15	23.962	238.5	39.8	2.343
MEESE BHATTA	86.5	104.2	60.0	52.0	25.5	3.12	117.35	26.990	167.7	27.9	2.225
GOURI SALI	88.5	103.7	61.0	53.0	23	2.36	103.90	21.633	126.5	21.1	2.343
KONNUR BHATTA	90.5	114.3	63.0	55.0	21.3	2.19	98.50	23.523	122.0	20.3	1.866
DODIGA	89.5	103.4	54.0	46.0	21.4	3.25	108.05	28.056	155.0	25.8	1.866
HUGGI BHATTA	107.5	122.1	46.0	37.0	21.1	3.24	93.55	18.855	124.3	20.7	1.984
BOLA SALI	91.5	124.5	65.0	50.0	20.6	3.46	104.65	29.733	179.6	29.9	2.236
GOPAL DODIGA	86.5	124.3	65.0	53.0	24.4	2.38	99.85	31.699	128.9	21.5	2.449
KUNKUM SALI-1	106.0	104.1	62.0	53.0	19.9	2.35	118.55	25.217	127.1	21.2	2.548
KOTAMBARI SALI-1	87.5	110.0	46.0	37.0	20.6	2.14	101.65	15.836	80.5	13.4	1.866
MALABANGAR KADDI	91.5	131.0	67.0	55.0	24.1	2.25	112.05	27.572	126.0	21.0	2.000
KYASAKKI	107.5	119.9	46.0	41.0	21.2	2.49	110.80	26.122	109.7	18.3	2.000
VARESANNA	125.5	104.0	55.0	47.0	21.6	2.45	115.60	25.148	184.1	30.7	1.732
BUDDA	92.0	97.8	46.0	39.0	21.5	3.53	96.70	26.069	163.4	27.2	2.118
BIDAR LOCAL	106.5	127.3	55.0	46.0	22.2	2.85	96.10	21.532	135.3	22.5	1.866
PONNAMPET LOCAL	106.5	129.8	58.0	50.0	21.8	2.43	103.50	27.284	124.1	20.7	2.236

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Genotypes	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}
GEERASALI	91.0	126.6	54.0	48.0	21	2.68	104.45	26.065	132.0	22.0	2.000
UDAR SALI	91.0	112.0	54.0	49.0	20	2.59	108.25	18.012	130.4	21.7	2.236
KOTAMBARISALI-2	92.5	127.3	54.0	47.0	21.5	3.19	98.35	25.344	155.6	25.9	2.000
KARKALA DODIGA	88.5	128.3	55.0	46.0	21.6	3.96	102.20	24.895	190.4	31.7	2.000
JEERIGE SANNA	107.0	130.4	44.0	39.0	24.5	2.80	97.45	24.225	111.6	18.6	2.118
KARE KANTIGA	107.5	120.4	54.0	47.0	21.3	3.05	130.50	28.060	148.6	24.8	2.343
OLLE FARM BHATTA	96.0	123.1	44.0	36.0	23.3	2.62	123.45	22.010	184.0	30.7	2.000
ALUR SANNA	106.0	107.2	55.0	49.0	20.4	3.32	115.70	19.378	168.2	28.0	2.236
KUMUDA-1	93.0	113.0	55.0	46.0	19.8	2.24	73.95	14.403	172.5	28.8	2.343
WARI	93.5	125.0	55.0	49.0	23.2	3.56	93.25	23.830	157.4	26.2	2.225
KUNKUMSALI-2	90.5	131.2	53.0	47.0	21.1	2.56	106.60	14.401	189.4	31.6	2.118
KEMPASALE	90.0	126.1	45.0	40.0	20.8	3.35	119.50	30.567	124.6	20.8	2.236
BIL-118	107.5	120.8	54.0	46.0	21.3	2.93	176.90	20.617	129.5	21.6	2.548
RF-55-9	87.5	95.8	56.0	49.0	20.9	2.89	143.95	23.692	229.5	38.3	2.449
RF-55-254	87.5	104.0	64.0	55.0	20.8	3.61	198.75	24.626	311.5	51.9	2.343
RF 55-198	88.5	108.1	66.0	58.0	21.1	3.79	183.15	24.061	277.0	46.2	2.548
BIL-3	106.0	82.0	48.0	43.0	19.1	2.45	96.40	20.137	89.5	14.9	2.343
BIL-149	96.0	85.4	62.0	53.0	18.2	2.91	102.10	24.084	137.5	22.9	2.118
BIL-57	107.5	91.2	61.0	54.0	19.9	2.93	123.40	24.207	221.5	36.9	2.236
RF 55-198	91.5	77.4	54.0	47.0	16.6	2.68	79.15	26.660	173.7	29.0	2.343
BIL-48	104.5	87.6	62.0	52.0	21.9	2.94	101.15	18.056	157.0	26.2	2.236

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Genotypes	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}
BIL-77	101.0	77.0	45.0	38.0	19.8	2.96	106.90	20.604	150.5	25.1	2.118
BIL-174	92.0	71.5	55.0	48.0	17.4	2.76	106.50	20.181	135.4	22.6	2.000
GGV-05-01	93.0	83.9	57.0	47.0	20.2	2.84	104.75	17.557	215.0	35.8	2.236
PSB-68	98.5	91.2	57.0	50.0	23.3	2.56	168.40	29.885	329.5	54.9	2.225
INTAN	110.5	94.3	68.0	58.0	22.7	2.70	103.15	24.662	216.0	36.0	2.449
MTU1001	94.5	76.7	70.0	62.0	23.1	2.32	115.00	19.100	247.2	41.2	2.343
SIRI 1253	105.5	66.7	54.0	49.0	23.1	3.18	165.50	17.262	273.7	45.6	2.236
BPT 5204	107.5	56.6	63.0	56.0	19.2	2.81	160.50	16.733	274.2	45.7	2.118
MGD-101	93.0	92.2	80.0	71.0	19.7	2.77	125.00	24.713	304.9	50.8	2.225
ABHILASHA	109.0	89.5	60.0	52.0	25	3.62	146.00	26.783	327.9	54.7	2.343
MAS-26	93.0	53.0	73.0	64.0	17	3.44	148.50	22.221	270.2	45.0	2.118
IR-64	92.0	62.4	75.0	69.0	19	3.17	134.00	20.631	266.2	44.4	2.118
MAS-946-1	91.0	56.5	70.0	56.0	18.6	2.57	128.50	18.996	244.0	40.7	1.866
RASI	86.5	58.0	71.0	62.0	17.9	2.89	140.50	20.930	240.9	40.2	2.548
HR-12	92.0	110.1	100.0	86.0	22.6	3.22	132.00	23.276	202.2	33.7	2.646
S.Em$\pm$	2.508	0.804	0.294	0.322	0.444	0.249	0.249	0.794	11.201	1.866	0.159
C.D.	4.919	1.585	0.064	0.634	0.875	0.489	10.302	1.561	22.037	3.672	0.313

X_1 Days to 50 per cent flowering
X_2 Plant height (cm)
X_3 Tiller number
X_4 Panicle number
X_5 Panicle length (cm)
X_6 Panicle weight (g)
X_7 Number of grains per panicle
X_8 Test weight (g)
X_9 Grain yield per plot (gram)
X_{10} Yield (q ha^{-1})
X_{11} Disease Susceptibility Index (transformed)

RF-55-198 and MAS-26 recorded lower panicle length of 16.60 cm and 17.00 cm respectively.

6. Panicle weight (g)

Among the genotypes evaluated, MGD-V-14-4 had highest panicle weight of 4.354 g followed by MGD-V-14-7 (4.289 g), MGD-V-14-6 (4.245 g) and MGD-1202 (4.211 g) while, lower panicle weight was recorded for Kotamabrisali-1 (2.143g), Konnur Bhatta (2.185 g), Kumuda-1 (2.235 g) and Malabangar kadi (2.248 g).

7. Number of grains per panicle

Maximum grains per panicle of 199 was recorded for the genotype RF-55-9 followed by ARB-6 (197), RF-55-198 (183) and BIL-118 (176), while genotype Kumuda-1 recorded minimum number of grains per panicle (74) followed by RF-55-(79), Neergulli (89) and MGD-V-14-19 (92).

8. Test weight (g)

Among all the genotypes studied the genotype SMW-11-09-2-1-3-1 had minimum test weight (13.515 g) followed by Parimalasanna (14.025 g) and Kunkumsali-2 (14.401 g). On the other hand Gopal dodiga recorded maximum test weight of 31.699 g followed by Kempasale (30.567g) and Navalisali (30.472 g).

9. Grain yield per plot (g)

Highest grain yield per plot was recorded for the genotype PSB-68 (329.5 g) followed by Abhilasha (327.9), BA-15-31-1-1 (313.5) and RF-5-254 (311.5). Whereas, lowest grain yield was observed for Chakkova (104.5) followed by BIL-3 (89.5) and Kotambarisali (80.5).

10. Yield (q ha^{-1})

Among all the genotypes under the investigation, PSB-68 had highest yield of 54.917 q ha^{-1} followed by Abhilasha (54.653 q ha^{-1}), BA-15-31-1-1 (52.250 q ha^{-1}) and RF-55-254 (51.917 q ha^{-1}). The lowest yield was observed for Chakkova (17.419 q ha^{-1}), BIL-3 (14.917 q ha^{-1}) and Kotambarisali (13.414 q ha^{-1}).

11. Disease Susceptability Index

Among the genotypes studied, BA-60-6-2 had the lowest disease score index of 1.732 followed by MGD-V-14-7 (1.732), MGD-V-14-9 (1.732) and BD-17-2-1 (1.732). On the other side, KRGL-7-1-5-A had the highest disease score index of 2.914 followed by GSM-45-1-7 (2.794) and MGD-V-14-16 (2.828).

4.3.3 Genetic variability parameters

To know the extent of genetic variability present in the diverse genotypes, the data on mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2) and genetic advance as per cent mean (GAM) are presented in Table 10 and briefed character wise.

1. Days to 50 per cent flowering (days)

Days to 50 per cent flowering ranged between 84.00 to 126.00 days with a mean value of 97.00 days, indicating presence of high variability for this trait. The phenotypic (8.41%) and genotypic (8.51%) co-efficients of variations were low accompanied with high heritability of 98.20 per cent and moderate genetic advance of 17.23 as per cent of mean.

2. Plant height (cm)

The overall mean plant height of the genotypes was 100.585 cm with a range of 53 to 134.00 cm. Low phenotypic (6.976%) and genotypic (6.993%) coefficients of variation with high heritability of 99.50 per cent and moderate genetic advance of 14.158 as per cent of mean was observed for this trait.

3. Tiller number per meter row

The overall tiller number of the genotype per meter row was 7 with a range of 4 to 10. The phenotypic (5.22%) and genotypic (3.21%) coefficients of variation were low accompanied with high heritability of 37.80 per cent and low genetic advance of 4.07 as per cent of mean was observed for the trait.

Table 10: Mean, range and genetic parameters for yield, yield traits and blast susceptibility index of one hundred sixty rice genotypes

Sl. No.	Characters	Mean	Range		GCV (%)	PCV (%)	h^2_{bs} (%)	GA	GA as per cent of mean
			Minimum	Maximum					
1	Days to 50 per cent flowering	96.50	84.00	126.00	08.41	08.51	98.20	16.12	17.23
2	Plant height (cm)	100.60	53.00	134.00	06.97	06.99	99.50	14.15	14.33
3	Number of tillers	06.55	04.00	010.00	03.21	05.22	37.80	00.30	04.07
4	Number of panicles	05.82	04.00	009.00	03.53	06.65	28.20	00.25	43.86
5	Panicle length (cm)	20.94	16.60	26.20	03.93	04.00	96.80	01.77	07.98
6	Panicle weight (g)	03.01	02.14	04.35	11.76	13.90	71.60	00.75	20.51
7	Number of grains per panicle	121.20	74.00	199.00	11.82	12.11	95.20	33.01	23.76
8	Test weight (g)	21.33	13.51	31.69	12.66	13.08	93.71	05.71	25.24
9	Grain yield per plot (g)	197.11	80.50	329.50	20.43	20.58	98.60	87.63	41.78
10	Yield (q ha^{-1})	32.85	13.41	54.91	20.45	20.60	98.60	14.61	41.82
11	Disease susceptibility Index	02.26	01.73	02.91	12.45	15.31	65.71	00.43	25.16

4. Number of panicles per meter row

Number of productive tillers ranged from 4 to 9 per plant with a mean value of 5.825 panicles per plant. Low PCV (6.65%) with GCV (3.53%) were recorded for this trait with moderate heritability and high genetic advance as per cent of mean of 28.20 per cent and 43.869 respectively.

5. Panicle length (cm)

Panicle length varied from 16.60 to 26.20 cm with a mean value of 20.945 cm. The genotype showed low PCV (4.004%) and GCV (3.939%) values accompanied with high heritability (96.80%) and low genetic advance as per cent of mean (7.982).

6. Panicle weight (g)

Panicle weight ranged from 2.143 to 4.34 g with a mean value of 3.018 g. The genotypes showed moderate GCV (11.766%) with high PCV (13.90%) values accompanied with high heritability (71.60%) and high genetic advance as per cent of mean (20.51).

7. Number of grains per panicle

The genotypes varied from a range of 74 to 199 with regard to number of grains per panicle and the overall mean for this trait was 121.206. PCV (12.11%) and GCV (11.82%) values were moderate with high heritability (95.20%) and genetic advance as per cent of mean (23.76).

8. Test weight (g)

Test weight ranged from 13.515 to 31.699g with a mean value of 21.338 g, the PCV (13.08%) and GCV (12.66%) values were moderate. This trait also recorded high heritability (93.70%) and genetic advance as per cent of mean (25.24).

9. Grain yield per plot (g)

Grain yield per plot ranged from 80.50 to 329.50 with a mean value of 197.112 g, the PCV (20.58%) and GCV (20.43%) values were high. This trait also recorded high heritability of 98.60 per cent and high genetic advance as per cent of mean (41.78).

10. Yield (q ha^{-1})

Grain yield varied among genotypes from 13.414 to 54.917 q ha^{-1} with an overall mean value of 32.851 q ha^{-1} indicating presence of sufficient amount of variability for the trait. The PCV (20.60%) and GCV (20.45%) were high and coupled with high heritability (98.60%) and genetic advance as per cent of mean (41.82).

11. Disease Susceptability Index

Average disease score of 2.260 was observed with a range of 1.732 to 2.914. Phenotypic (15.31) and genotypic (12.45) co-efficient of variances was observed as a moderate value. High heritability and high genetic advance as mean of per cent of 65.70 per cent and 25.163 was observed respectively.

4.3.4 Correlation studies among the genotypes for yield and yield attributing traits

Selection for specific character is known to result in correlated response in certain other characters. Generally, plant breeders make selection for one or two attributes at a time. Then it becomes important to know the effect on other characters. Improvement on grain yield per plant, the most important target character in many cereal crops, it can be achieved by direct selection through other easily observable characters. But, this needs a good understanding of association of different traits with grain yield per plant and their possible associations among themselves. The phenotypic and genotypic correlations of grain yield per plant with other quantitative characters in 160 genotypes studied are presented in Table 11 and 12.

4.3.4.1 Association between grain yield per plant and its component characters

Highly significant and positive genotypic and phenotypic correlations were observed for grain yield qt per ha with days to 50% flowering (0.5730 G, 0.5704P), number of panicles per plant (0.4279G, 0.2014P), panicle length (0.2751G, 0.2627P), panicle weight (0.946G, 0.8097P), number of grains per panicle (0.365G, 0.343P), test weight (0.575G, 0.535P).

Table 11: Genotypic correlation coefficients among yield, yield traits and blast susceptibility in the rice genotypes

	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}
X_1	1.00	0.44	-0.62**	-0.71*	0.02	0.75**	0.50	-0.47	0.57*	0.57*	0.12
X_2		1.00	-0.31*	-0.34*	0.47*	0.06	0.37*	0.31	0.03	0.03	-0.56**
X_3			1.00	0.96***	0.05	0.07	0.62*	0.19	0.25	0.25	-0.33
X_4				1.0000	0.08	0.34	0.45*	0.03	0.42	0.42	-0.56**
X_5					1.00	0.11	0.29	0.41	0.07	0.27	-0.45*
X_6						1.00	0.73**	0.45*	0.94***	0.94***	-0.40
X_7							1.00	0.41	0.36	0.36	-0.59**
X_8								1.00	0.57*	0.57*	-0.60**
X_9									1.00	0.99***	-0.23
X_{10}										1.00	-0.23
X_{11}											1.00

X_1 Days to 50 per cent flowering
X_2 Plant height (cm)
X_3 Tiller number
X_4 Panicle number
X_5 Panicle length (cm)
X_6 Panicle weight (g)
X_7 Number of grains per panicle
X_8 Test weight (g)
X_9 Grain yield per plot (gram)
X_{10} Yield (q ha^{-1})
X_{11} Disease Susceptibility Index (transformed)

Table 12: Phenotypic correlation coefficients among yield, yield traits and disease susceptibility index in the rice genotypes

	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}
X_1	1.00	0.44	-0.31*	-0.30	0.04	0.64*	0.49	-0.46	0.57*	0.57*	0.06
X_2		1.00	-0.19	-0.19	0.46*	0.08	0.37*	0.31	0.03	0.03	-0.45*
X_3			1.00	0.97***	0.003	0.05	0.40	0.23	0.13	0.13	-0.36
X_4				1.00	0.03	0.01	0.25	0.15	0.20	0.20	-0.47*
X_5					1.00	0.29	0.27	0.40	0.36	0.26	-0.36
X_6						1.00	0.56*	0.27	0.80***	0.80***	-0.23
X_7							1.00	0.36	0.34	0.34	-0.40
X_8								1.00	0.53*	0.53*	-0.48*
X_9									1.00	0.99***	-0.21
X_{10}										1.00	-0.21
X_{11}											1.00

X_1 Days to 50 per cent flowering
X_2 Plant height (cm)
X_3 Tiller number
X_4 Panicle number
X_5 Panicle length (cm)
X_6 Panicle weight (g)
X_7 Number of grains per panicle
X_8 Test weight (g)
X_9 Grain yield per plot (gram)
X_{10} Yield (q ha^{-1})
X_{11} Disease Susceptibility Index (transformed)

4.3.4.2 Association among grain yield attributing characters

1. Days to 50 per cent flowering

Days to 50 per cent flowering had negative significant correlation with tiller number (-0.623 G,-0.318P) and positive significant correlation with plant height (0.444G, 0.441P) and panicle weight (0.759G, 0.647P) at both genotypic and phenotypic level.

2. Plant height (cm)

Two out of eleven characters studied had significant and positive correlation with plant height at both genotypic and phenotypic levels *viz.*, panicle length (0.476G, 0.466P) and grains per panicle (0.375G, 0.368P). On contrary, it had significant and negative association with tiller number (-0.310G, -0.195P), number of panicles per plant (-0.343 G, -0.192P) and Disease Score Index (-0.5651 G, -0.4512P).

3. Tiller number per meter row

The correlation of this trait was highly significant with number of panicles per plant (0.965G, 0.977 P). Correlation with number of grains per panicle (0.629 G, 0.397P) was significant genotypically. Negative correlation was observed with Disease Score Index (-0.331 G, -0.364 P)

4. Number of panicles per meter row

Number of grains per panicle exhibited positive correlation with panicle weight (0.343G, 0.012P) and significant correlation with grains per panicle (0.457G, 0.253P) at genotypic level, test weight (0.039G, 0.156P) not significant at both genotypic and phenotypic level. DSI (-0.566G,-0.4771P) had negative correlation at both genotypic and phenotypic level.

5. Panicle length (cm)

Out of eleven characters studied, panicle length had positive and significant correlation with plant height (0.476G, 0.466P) and positive correlation with panicle weight (0.116G, 0.285P), number of grains per panicle (0.291G, 0.271P) and negative correlation with DSI (-0.459G,-0.362P) significant at genotypic level.

6. Panicle weight (g)

Panicle weight had significant and positive correlation at both genotypic and phenotypic levels with number of grains per panicle (0.739G, 0.598P), test weight (0.453G, 0.276P) grain yield per plot (0.945G, 0.809P) and yield per ha (0.946G, 0.809P). DSI had negative correlation with panicle weight (-0.407G, -0.235P).

7. Number of grains per panicle

Number of grains per panicle had positive correlation with test weight (0.411G, 0.360P), grain yield per plot (0.361G, 0.342P), yield (0.3605G, 0.347P) and negative correlation with DSI (-0.598G, -0.401P) significant at genotypic level.

8. Test weight (g)

Two traits *viz*., grain yield per plot (0.574G, 0.535P), yield per ha (0.575G, 0.535P) recorded positive and significant correlation with test weight at both genotypic and phenotypic levels, whereas, disease score index had a negative and significant correlation at both phenotypic and genotypic levels.

9. Grain weight (gram per plot)

Grain weight had positive significant correlation with days to fifty per cent flowering (0.573G, 0.571P), panicle weight (0.945G, 0.809P), test weight (0.574G, 0.538P) and yield per ha (0.998G, 0.998P). Negative correlation at genotypic level with DSI (-0.237G, -0.217P) was observed.

10. Yield (q ha^{-1})

Out of all the traits studied, days to fifty per cent flowering (0.573G, 0.570P), panicle weight (0.946G, 0.809P), test weight (0.575G, 0.535P) and grain yield per plot (0.998G, 0.998P) had positive and significant correlation with yield per ha. DSI was negatively (-0.2394G, -0.217P) correlated at both genotypic and phenotypic levels.

11. Disease Susceptibility Index

The transformed value of disease reaction over all the genotypes under study was negatively correlated with all the traits and was significant with plant height (-0.565G, -0.451P), panicle number (-0.566G, -0.477P), test weight (-0.608G, -0.485P) at both genotypic and phenotypic levels, genotypically it significant negative correlation was observed with number of grains per panicle (-0.5987G). Days to fifty per cent flowering alone showed positive correlation (0.122G, 0.0678P) with very low magnitude.

5. DISCUSSION

Rice is the most important cereal crop grown worldwide as a staple food for more than a billion people. As the rice area is decreasing it is challenging task to increase the productivity of rice to achieve a target rice production of 140 million tonnes by 2025 to meet increasing demand of growing population. There are many constraints in increasing the productivity which includes biotic and abiotic stresses. Among biotic stresses blast disease is a most important disease which causes yield loss upto 65% in susceptible cultivars (Bhatt 1988). The crop is cultivated across different countries under different environmental conditions and thus the crop has got very diverse genetic base. Many of the important alleles are yet untapped and are reserved in the genome of uncultivated weedy forms and traditional landraces. In India western ghat is the important reservoir for all such important, untapped genes conferring different qualitative traits including blast resistance.

One of the important objectives of rice breeding is to incorporate disease resistant genes, in particular blast resistant genes in development of High Yielding Varieties which is cheapest and eco-friendly strategy of blast management. Invent of many molecular markers which are linked to blast resistant genes could be very handy in development of blast resistant genotypes. These molecular markers increase the precision and efficiency of identification and incorporation of the resistant genes.

Among the reported blast resistant genes, in the present investigation we have considered the broad-spectrum and effective blast resistant genes such as *Pi* 54 (Ramkumar *et al.,* 2011), *Piz* (Hayashi *et al.,* 2006), *Pia* (Kwan *et al.,* 2008), *Pit* (Hayashi *et al.,* 2006) and *Pi38* (Gowda *et al.,* 2006). These resistant genes have been validated among traditional landraces from western ghat regions and superior breeding lines derived from different breeding programme which includes traditional landraces in their pedigree.

Further these genotypes were also assessed for their productivity under rainfed condition with the objective of developing high yielding and blast resistant varieties suitable for rainfed upland eco-system. The results obtained from this investigation are discussed in brief under the following sub-headings.

5.1 Phenotyping of landraces and promising breeding lines for blast resistance under epiphytotic condition

The selected traditional landraces and promising breeding lines that are derived from different breeding programme were evaluated under UBN for evaluating them for resistance reaction to leaf blast.

The genotypes like BA-60-6-2, MGD-V-14-7, MGD-V-14-9 and BD-17-2-1 exhibited resistance reaction to blast at field level and the lines like MGD-V-14-1, MGD-V-14-5, MGD-V-14-2 and RF-53-102-3 exhibited moderate resistance to blast. The genotypes, MGD-V-14-3, MGD-V-14-8, MGD-V-14-18 were found to be moderately susceptible and the genotypes, SMW-XV-105, MGD-1201-2 and HR-12 were observed to be susceptible to blast under field condition.

Among the traditional landraces Varesanna alone was found resistant to the disease, whereas, the lines like Budda, Jeerigasanna, Guddenellu and Konnur Bhatta were found to be moderately resistant. The landraces like Kare kalvi, Adnenkelti and Madras Bhatta were recoreded to be moderately susceptible and the landraces, Bilidadai Goratiga, Jaddu Bhatta, Chitiga were found to be susceptible to blast.

Similar results were observed for screening of different genotypes in UBN by Saifulla *et al.* (1996), Pasha *et al.* (2013) and Vasudevan *et al.* (2014). There were no genotypes in the set of collection that exhibited highly resistant characters to the disease.

Knowledge on screening of genotypes phenotypically under epiphytotic condition give a fair idea about the quantum of resistance that can be offered by the genotypes to blast fungus and the information can be utilized in large scale screening of different set of genotypes.

5.2 Validation of molecular markers for blast resistance genes in land races and promising breeding lines

Different primers have been used in the present investigation in order to validate the resistant genotypes for the presence of different resistance genes. There was no any single genotype containing all the five resistant genes studied. The genotype MGD-V-14-7 has been validated for the presence of four major genes (*Piz, Pia, Pit* and

Pi38). The resistant gene *Piz* was found in the genotypes like BA-60-6-2, SMW-11-09-30-L-1, BA-60-3-2, MGD-V-14-5, MGD-V-14-7, Huggi bhatta, Jeerige Sanna, Rasi, Budda had shown presence of the resistant gene *Piz*. The broad-spectrum gene, *Pi54* was found to be present in the genotypes, MGD-V-14-5, IET-22801-2, SMW-11-09-5-1-3, Budda and Jeerige sanna. The variety Rasi has been found to harbor three resistant genes (*Piz, Pit* and *Pi38*).

The results obtained are in line with the reports given by Selvaraj *et al.* (2011a), Ahskani *et al.* (2011), Kumbhar *et al.* (2013) and Matsushita *et al.* (2011). Different molecular markers have been used in mapping these resistant genes on different chromosome.

Ramkumar *et al.* (2011), worked extensively on allele mining for individual genes and identified a major gene, *Pi* 54 (earlier known as Pik^h) which has been observed to show resistance against many isolates of the blast pathogen in India.

This knowledge of availability of different genes and associated markers help in screening diverse sources of resistance for the presence of different genes which can be further effectively utilized in crop improvement through Marker Assisted Selection.

5.3 Assessment of blast resistant genotypes for productivity and genetic parameters

The analysis of variance among 160 genotypes indicated highly significant differences among the genotypes with respect to all the characters studied including the Disease Susceptibility Index a transformed value to the actual blast score. All the genotypes displayed considerable amount of differences in their mean performance with respect to all the characters studied. This had been exemplified by highly significant mean sum of squares for these traits, which indicated that, the genotypes under study were genetically diverse.

Mean performance of genotypes for productivity and blast resistance

The mean performance of 160 genotypes used in the present study indicated that no single genotype was superior in respect of all the traits studied. However, the genotype ARB-6 was superior for three characters *viz.*, days to 50 per cent flowering, days to maturity, number of grains per panicle. The genotype HR-12 was superior to

both tiller number and panicle number per meter row. PSB-68 was superior to the characters like grain yield per plot. For blast resistance the promising breeding line BA-60-6-2 was found superior.

Genetic variability parameters

The range in mean values does not reflect the total variance in the material studied. Hence, actual variance has to be estimated for the characters to know the extent of existing variability. So, the co-efficient of variation (PCV and GCV) which is calculated by considering the respective means have been used for the comparisons. High values of these parameters indicate wider variability and vice versa. In the same context, narrow differences between the phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) implies lesser influence of environment on these traits.

High GCV and PCV were recorded for the character grain yield q ha^{-1}. Similar results were also reported by Fukrei *et al.* (2011), Aditya and Bharatiya (2013), Toshimenla and Changkija (2013). Higher magnitude of PCV and GCV for these characters indicates presence of high degree of variability and better scope for improvement.

The moderate phenotypic co-efficient of variation and genotypic co-efficient of variation was observed for characters like panicle weight, number of grains per panicle, test weight and disease susceptibility index (DSI). This indicates the existence of comparatively moderate variability for these traits, which could be exploited for improvement of these traits through selection in advanced generations. On the other hand, low GCV and PCV were observed for the traits like days to fifty per cent flowering, plant height, number of tillers per meter row, number of panicles per meter row and panicle length.

The results are in accordance with the earlier reports where in, moderate PCV and GCV were observed for the traits like grain yield per plant, plant height, test weight and fertile spikelet per panicle were reported (Khare *et al.,* 2014).

On the whole, co-efficient of variation indicated moderate amount of variability for most of the traits with exception for few traits. The close correspondence between the estimates of GCV and PCV for most of the traits indicated lesser environmental influence on the expression of these traits, which is also reflected by their high heritability values.

Broad sense heritability gives an idea about portion of observed variability attributable to genetic differences. The difference between PCV and GCV estimates indicates the relative influence of environment on the character, which in turn decides the extent of their heritability. If the difference is low for a character then the influence of environment is less coupled with high heritability. Wide differences indicate considerable influence of the environment, thus resulting in low heritability estimates.

Heritability estimates accompanied with genetic gain would be more useful and efficient in practicing the effectiveness of selecting the best individual. Hence, it is essential to consider the predicted genetic advance with heritability estimate as a tool in selection programme for better efficiency in selection.

In the present investigation, high heritability coupled with high genetic advance as per cent of mean was recorded for characters like, panicle weight, number of grains per panicle, test weight, grain yield and disease susceptibility index. Moderate genetic advance as per cent of mean was observed for traits like days to fifty per cent flowering and plant height. This indicates that there was low environmental influence on the expression of these characters and hence breeder can practice selection.

High heritability and genetic advance as per cent of mean was earlier reported by Seyoum *et al.* (2012), Toshimenla and Changkija (2013) and Aditya and Bharatiya (2013) for traits like plant height, days to 50% flowering, test weight, panicle length and yield per plant.

The present study revealed high heritability coupled with high genetic advance as per cent of mean for most of the characters indicating the presence of considerable genetic variation. Therefore, improvement of these characters could be effective through phenotypic selection.

Association of grain yield with yield traits and blast resistance

Grain yield being a complex polygenic character, direct selection based on these traits would not yield fruitful results without giving due importance to their genetic background. The association of yield and its component traits reflects the nature and degree of relationship between them. The correlation analysis helps in examining the possibility of improving yield through indirect selection of its component traits which are highly correlated. In present investigation, correlation analysis was carried out in 160 rice genotypes including both promising breeding lines and local landraces.

Highly significant and positive correlation was observed for grain yield with the traits like days to 50% flowering, panicle weight and test weight. Other traits like, plant height, number of tillers per meter row, number of panicles per meter row, panicle length and number of grains per panicle were also positively associated although not significant.

Among yield attributing traits, positive and significant association was observed for the trait like plant height with panicle length, number of grains per panicle and panicle length had positive and significant association with traits like plant height, panicle weight and number of grains per panicle. This suggests that inter relation among the traits should be considered while breeding genotypes for different purposes.

The results are in line with the reports made by Sravan *et al.* (2012) and Ravindra Babu *et al.* (2012), as significant positive correlation was being observed for grain yield with number of productive tillers per plant, test weight, panicle weight and biological yield per plant.

There was significant and negative correlation observed for disease susceptibility index with traits like plant height, tiller number per meter row, panicle number per meter row, panicle length, number of grains per panicle, test weight and grain yield. This indicates that disease incidence has got negative impact on yield and yield attributing traits. Such significant negative correlation was reported by Karim *et al.* (2014), for spikelet sterility with grain yield at genotypic level. This emphasis need for development of blast resistant genotypes for attaining better productivity in rice.

Identification of superior genotypes for productivity and blast resistance:

Genotypes like, SMW-11-09-5-1-3, MGD-V-14-4, MGD-V-14-2, MGD-V-14-6 and MGD-V-14-7 were found to be superior for grain yield (more than 43 q ha^{-1}) and fine grained which is on par with recently released fine grain genotype Mugad Siri-1253. These superior genotypes are early maturing (around 10-15 days) compared to Mugad Siri-1253 (Table 13). These genotypes were observed to be grouped in resistant or moderately resistant category for blast disease. The genotype MGD-V-14-5, harbors *Piz* and *Pi54* blast resistant genes and is also superior for productivity (39.10 q ha^{-1}) and early maturing (119 days) with LS grain type.

The superior genotypes which did not report for any of the selected genes can further be screened for other different resistant genes and can be utilized as better donors for these genes.

Genotypes like MGD-V-14-5, MGD-V-14-7 can be utilized as donors in different breeding programmes targeting resistance breeding to rice blast or even can be released as superior genotypes for cultivation after multi-location testing (MLT) and farm trials.

Table 13: Superior genotypes for productivity and blast resistance

Genotypes	Grain yield (q ha^{-1})	Days to 50% flowering	Grain type	Kind of reaction	Resistant gene
SMW-11-09-5-1-3	45.80	93.50	MS	MR	*Pi54*
MGD-V-14-4	44.80	94.50	MS	MR	-
MGD-V-14-2	43.00	96.50	MS	MR	-
BA-35-1-1-2	41.30	91.50	SB	MR	-
MGD-V-14-6	39.80	95.00	MS	MR	-
SMW-11-09-30-L-1	39.50	109.00	MS	MR	*Piz*
BD-17-2-1	39.40	95.00	SB	R	-
IET-22801-2	39.20	87.00	MS	MR	*Pi54*
MGD-V-14-5	39.10	86.00	LS	MR	*Piz,Pi54*
MGD-V-14-7	37.90	101.50	MS	R	*Piz,Pia,Pit* and *Pi38*
MGD-V-14-10	37.90	109.50	MS	MR	-
YSM-7-1	37.30	101.00	MS	MR	-
BA-60-3-2	37.30	88.50	LS	MR	*Piz*
27-P-11-3-2-1	37.20	92.50	MS	MR	-
BA-60-6-2	36.80	89.50	LS	R	*Piz*
YSM-42-1-7	36.80	106.50	MS	MR	-
IR 78875	36.60	84.50	LS	MR	-
SMW-XV-101	36.60	105.50	MS	MR	-
MGD-V-14-1	34.90	90.00	MS	MR	-
Checks					
MGD-101	50.80	93.00	SB	MR	-
SIRI 1253	45.60	105.50	MS	MR	-
MAS-26	45.00	93.00	LS	MR	-
IR-64	44.40	92.00	LS	MR	-
MTU1001	41.20	94.50	SB	MR	-
BPT 5204	41.00	107.50	MS	MR	-
MAS-946-1	40.70	91.00	LS	MR	-
RASI	40.20	86.50	SB	MR	*Piz,Pit* and *Pi38*
HR-12	33.70	92.00	LB	S	-
S.Em$\pm$	1.866	2.508			
C.D.	3.672	4.919			

Where,

MS - Medium Slender
SB - Short Bold
LS - Long Slender
LB - Long Bold

R - Resistant
MR - Moderately Susceptible
MS - Moderately Susceptible
S - Susceptible

Future line of work

- The information generated on resistant genotypes can be further utilized in different breeding programmes targeting disease resistance as parental material.

- The genotypes like, MGD-V-14-5, MGD-V-14-7 along with the variety Rasi have shown resistant reaction to the disease and are even good yielding. So these lines can further be released for commercial cultivation after multi-location and farm trails.

- Traditional landraces with score of 2 and 3 which did not confirm the presence of resistant genes studied in this investigation can be screened for other reported markers and further new source of resistance can be tapped from these landraces.

- The broad-spectrum gene like *Pi54* which confers resistance to diverse isolates of the pathogen can be deployed in advanced breeding activities like gene stacking.

- Traditional landraces that did not confirm the presence of any of the genes can be mined for different diverse resistant genes.

6. SUMMARY AND CONCLUSIONS

The present investigation was undertaken on selected 160 promising breeding lines and traditional landraces of rice at the Agricultural Research Station, Mugad during *kharif* 2014, with the important objectives like screening these genotypes for blast resistance and validating the resistant genotypes using molecular markers for different resistant genes along with assessing the productivity and related traits using suitable statistical tools.

Salient findings of the investigation

- Among 160 genotypes studied for blast resistance under epiphytotic condition, different sub- groups were made into immune, resistant, moderately resistant, moderately susceptible and susceptible. Further the genotypes were classified based in the symptoms exhibited.

- Genotypes like BA-60-6-2, MGD-V-14-7, MGD-V-14-9, BD-17-2-1 along with traditional landrace Varesanna were found to be resistant. Genotypes RF-53-102-3, MGD-V-14-1, MGD-V-14-2, MGD-V-14-5 and landraces like Budda, Jeerige sanna, Guddenellu and Konnur Bhatta exhibited moderate resistance reaction. MGD-V-14-3, MGD-V-14-8, MGD-V-14-18, Kare kalvi, Adnenkelti and Madras Bhatta were found to be moderately susceptible.

- Genotypes, SMW-XV-105, MGD-1201-2, HR-12, Bilidadi goratiga, Jaddu Bhatta and Chitiga were susceptible to blast. No single genotype was found to be immune or highly resistant to the disease.

- Validation of resistant genes using molecular markers was carried out and MGD-V-14-7 was found to be carrying the genes like *Piz, Pia, Pit* and *Pi3. Pi54*, the broad-spectrum gene was found to confer resistance to several genotypes like SMW-11-09-5-1-3, IET-22801-2, MGD-V-14-5, Budda and Jeerige sanna.

- The genotypes, MGD-V-14-5, MGD-V-14-7, Huggi bhatta, Jeerige Sanna, Rasi, Budda had shown presence of the resistant gene *Piz*. The variety Rasi has been found to harbor resistant genes like *Piz, Pit* and *Pi38*. None of the genotype was found to harbor all the resistant genes used for validation.

- No single genotype was superior in respect of all the traits studied. However, the genotype ARB-6 was superior for three characters *viz*., days to 50 per cent flowering, days to maturity, number of grains per panicle. The genotype HR-12 was superior to both tiller number and panicle number. PSB-68 was superior to the characters like grain weight per plot and total yield per ha.

- High GCV and PCV was recorded for the character yield (q ha^{-1}). Higher magnitude of PCV and GCV for these characters indicates presence of high degree of variability and better scope for improvement.

- The moderate phenotypic co-efficient of variation and genotypic co-efficient of variation was observed for characters like panicle weight, number of grains per panicle, test weight and disease susceptibility index (DSI). This indicates the existence of comparatively moderate variability for these traits, which could be exploited for improvement of these traits through selection in advanced generations.

- Low GCV and PCV were observed for days to fifty per cent flowering, plant height, number of tillers per meter row, number of panicles per meter row and panicle length.

- High heritability coupled with high genetic advance as per cent of mean were recorded for characters like, panicle weight, number of grains per panicle, test weight, grain yield and disease susceptibility index. This indicates that there was low environmental influence on the expression of these characters and hence breeder can practice selection.

- Moderate genetic advance as per cent of mean was observed for traits like days to fifty per cent flowering and plant height.

- Correlation studies indicated that, highly significant and positive correlation was observed for grain yield with the traits like days to fifty per cent flowering, panicle weight, test weight. Other traits like, plant height, number of tillers per plant, number of panicles per plant, panicle length and number of grains per panicle were positively associated but were not significant.

- Among yield related traits, positive and significant association was observed for the trait like plant height with panicle length, number of grains per panicle and the trait panicle length had positive and significant association with traits like plant height, panicle weight and number of grains per panicle.

- For disease incidence, disease susceptibility index was found to be negatively correlated with all the traits considered in the investigation. This indicates that disease incidence has got negative impact on yield and yield attributing traits.

- With the investigation on assessment of productivity and blast resistance using molecular markers for blast resistance, superior genotypes with respect to blast resistance along with high productivity have been obtained for further breeding activities.

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Appendix I: Monthly rainfall data for the experimental year (2014) and previous year, mean rainfall of past 20 years (1992-2011) and number of rainy days during experimental year of the A.R.S., Mugad, UAS, Dharwad (Karnataka)

Months	Rainfall (mm)			
	Normal (1992-2011)	2012	2013	2014
January	1.80	0.00	10.20	0.00 (0)
February	1.40	0.00	0.00	0.00 (0)
March	12.60	0.00	8.80	0.80 (0)
April	50.40	69.40	6.60	43.20 (2)
May	74.40	21.00	128.00	178.60 (7)
June	175.70	75.80	110.50	48.00 (6)
July	238.30	162.20	280.20	318.20 (17)
August	189.30	139.80	141.00	198.40 (17)
September	132.00	115.20	26.40	87.60 (11)
October	127.60	44.60	92.60	105.20 (7)
November	35.40	88.60	88.60	44.80 (2)
December	4.30	20.60	3.80	49.20 (1)

*- value in the parenthesis indicates the number of rainy days during the experimental year

VALIDATION OF MOLECULAR MARKERS FOR BLAST RESISTANCE AND ASSESSMENT OF PRODUCTIVITY IN LANDRACES AND PROMISING BREEDING LINES OF RICE (*Oryza sativa* L.)

VAIBHAV V. PATIL 2015 Dr. N. G. HANAMARATTI
Major Advisor

ABSTRACT

A field experiment was conducted at Agricultural Research Station, Mugad, University of Agricultural Sciences, Dharwad, to screen 160 rice genotypes which includes both traditional landraces and promising breeding lines for blast resistance along with validation of reported resistant genes. Under epiphytotic condition, the genotypes BA-60-6-2, MGD-V-14-7, MGD-V-14-9, BD-17-2-1 and waresanna exhibited resistance reaction and the lines like MGD-V-14-1, MGD-V-14-5, MGD-V-14-2, RF-53-102-3, Budda, Jeerigasanna, Guddenellu and Konnur Bhatta exhibited moderate resistance to blast. The genotypes, MGD-V-14-3, MGD-V-14-8, MGD-V-14-18, Kare kalvi, Adnenkelti and Madras Bhatta were found to be moderately susceptible and SMW-XV-105, MGD-1201-2, HR-12, Bilidadai Goratiga, Jaddu Bhatta, Chitiga were observed to be susceptible to blast under field condition.

Validation for resistant genes using tightly linked molecular markers was carried out and the genotype MGD-V-14-7 was found to harbor four resistant genes, (*Piz, Pia, Pit* and *Pi38*). The genotypes, BA-60-6-2, SMW-11-09-30-L-1, BA-60-3-2, MGD-V-14-5, MGD-V-14-7, Huggi bhatta, Jeerige Sanna, Rasi, Budda showed the presence of the gene *Piz*. The broad-spectrum gene *Pi54* was validated in the genotypes like MGD-V-14-5, IET-22801-2, SMW-11-09-5-1-3, Budda and Jeerige sanna. Such genotypes can be utilized in disease resistance breeding programme targeting diverse races of blast pathogen.

Assessment of resistant genotypes for yield and yield attributing traits along with genetic variability parameters revealed the presence of wide genetic variability among the genotypes for productivity traits. The genotypes SMW-11-09-5-1-3, MGD-V-14-4, MGD-V-14-2, MGD-V-14-6 and MGD-V-14-7 were found to be superior for productivity with blast resistance, fine grains and early maturing compared to recently released fine grain genotype Mugad Siri-1253.