

Original Research Article

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Special Genetic Stocks against Paddy Blast (*Pyricularia oryzae*)

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ABSTRACT

The trireplicated field experiment was conducted at Rice Research Block of S. G. College of Agriculture and Research Station, Jagdalpur, Chhattisgarh, India with 6 test entries, 2 recurrent parents and 2 donor parents. BPT 5204 (Samba Mahsuri) the recurrent parent 1 (RP 1) for the four test genotype recorded average plot yield of 4.00 kg/ha placing second in the experiment. None of the entry recorded on par with recurrent parent 01 statically however, all the genotypes no significant difference was observed with respect to grain yield. When the recurrent parent 02 (Improved Sambha Mahsuri) was taken into account, genotype RP-Patho-1-2-15 recorded higher plot yield (4.23 kg) and was at par. Flowering duration wise, RP-Patho-1-2-15 and RP-Patho-3-56-11 were similar to the recurrent parent with flowering of 78 and 79 DAS accordingly while RP-Patho-3-73-6 was six days in advance (70 days) to the recurrent parent (76 days). All the test isogenic lines with a plant height of 79-85 cm were similar to the recurrent parent (82 cm). Blast and bacterial leaf blight resistance gene carrying genotypes RP-Patho-2-18-5 and RP-Patho-2-16-4 gave plot grain yield 3.77kg, which out yielded recurrent parent 02 but lesser than recurrent parent 01. However flowering was delayed (96 DAS and 99 DAS) and plant height was increased in both the isogenic lines (83cms and 81 cms). Summarily, all the genotypes were similar to recurrent parent, indicating the recovery of crossed material to desired genetic background.

Keywords

NILs, Recurrent parent, Doner Parent, Blast

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Introduction

Rice production is constrained by substantial number of fungal, bacterial and viral origin diseases. Rice blast (caused by *Magnaporthe grisea*) and bacterial leaf blight (BLB, caused by *Xanthomonas oryzae* pv. *Oryzae*, *Xoo*) are two most destructive diseases leading to severe yield losses in rice production worldwide (Zhan *et al.*, 2012). Rice blast, caused by the filamentous ascomycete fungus

Magnaporthe oryzae (anamorph *Pyricularia oryzae*), is major threats for rice production and leads to significant yield loss, as high as 70–80% during an epidemic (Khush, 2009). Host plant resistance is emerging as most effective, economical and environmentally safe measure for controlling paddy blast in combination with pathological management. So far, 73 blast resistance genes have been identified (Sujatha *et al.*, 2011) and some of them have been incorporated into modern rice

varieties (Sundaram *et al.*, 2008; 2009) through marker assisted selection (MAS). Among these, few genes like *Pi-1*, *Pi-2*, *Pi-9*, *Pi-54* etc. (for blast resistance) are being extensively used in rice breeding programmes globally as are highly effective and having tightly linked molecular markers. With these background, some of the ICAR-IIRR (Formerly DRR) Hyderabad developed MAS breeding lines, obtained under AICRIP programme, possessing high level of resistance against blast (conferred by *Pi1* or *Pi54*) and bacterial blight (conferred by *Xa21*) was evaluated for blast resistance in Bastar plateau of Chhattisgarh.

Materials and Methods

The test genotypes were obtained from Indian Institute of Rice Research, (ICAR-IIRR, formerly DRR), Hyderabad under AICRIP programme. The trial was constituted with 6 test entries, 2 recurrent parents and 2 donor parents.

The trireplicated field experiment was conducted at Rice Research Block of S. G. College of Agriculture and Research Station, Jagdalpur, Chhattisgarh, India in *Kharif* 2013-14 with 5x3m (gross plot) plot size, Randomized Complete Block Design. Standard agronomic package was followed to raise the crop.

Restriction selection indice was constructed based on previous research review and four quantitative parameters were selected for genetic evaluation.

The observation was recorded on net plot basis (heading date and plot yield), unit plot basis (panicles/sq M) and arithmetic mean basis among random selections. Days to 50 percent flowering was recorded when half of plant flowered among the plot. Panicle count was made with one square meter square at

maturity. The disease scoring was made visually giving the score 1-9. Statistical analysis was done with SPARK 2.

Results and Discussion

The experimental yield ranged from 2.67kg/plot (Improved sambha Mahsuri) to 4.23/plot (RP-Patho-1-2-15). The Recurrent parent 01 (BPT 5204) was the earliest to flower with 50% flowering in 91 DAS followed by donor parent 01 (92 DAS) while RP-Patho-1-2-15 and RP-Patho-3-73-6 recorded to be late flowering genotypes with 113 DAS days to 50 percent flowering. The experimental mean for blooming period was 101 DAS. RP-Patho-3-73-6, BPT 5204 and RP-Patho-1-2-15 were short in plant height (70, 76 and 78cms respectively) while Tetep was recorded to be tallest (115 cms) (Table 1) whereas, the mean plant height was reported to be 84.5 cms. Panicles count was significantly higher for BPT 5204, RP-Patho-3-73-11 and RP-Patho-1-6-5 (348, 324 and 312 correspondingly) while RP-Patho-1-2-15 and Tetep exhibited comparative lower count. The grain yield was in perfect direction with panicles number. BPT 5204 (Samba Mahsuri) the recurrent parent 1 (RP 1) for the four test genotype recorded average plot yield of 4.00 kg/ha placing second in the experiment. None of the entry recorded on par with recurrent parent 01 statically however, all the genotypes no significant difference was observed with respect to grain yield. When the recurrent parent 02 (Improved Sambha Mahsuri) was taken into account, genotype RP-Patho-1-2-15 recorded higher plot yield (4.23 kg) and was at par. Flowering duration wise, RP-Patho-1-2-15 and RP-Patho-3-56-11 were similar to the recurrent parent with flowering of 78 and 79 DAS accordingly while RP-Patho-3-73-6 was six days in advance (70 days) to the recurrent parent (76 days). All the test isogenic lines with a plant height of 79-85 cm were similar to the recurrent parent (82 cm).

Table.1 Ancillary traits data following restriction selection indices

	Plant height (cm)		Days to 50 percent flowering		Panicles/sqm		Grain yield/Plot	
	Mean	SE	Mean	SE (±)	Mean	SE (±)	Mean	SE (±)
RP- Patho-1-2-15	78	4.98	113	0.88	257	12.42	4.23	0.15
RP- Patho-1-6-5	90	3.84	108	0.33	312	24.12	3.87	0.41
RP- Patho-3-56-11	79	4.33	113	0.83	324	12.2	3.7	0.3
RP- Patho-3-73-6	70	4.97	107	1.16	331	12.44	3.03	0.35
RP- Patho-2-18-5	83	4.33	99	0.88	286	7.26	3.87	0.26
RP- Patho-2-16-4	81	3.18	96	0.81	272	5.81	3.87	0.23
BPT 5204 (RP 1)	76	4.63	91	0.67	348	10.1	4	0.17
Improved Samba Mahsuri (RP 2)	82	2.72	94	0.58	276	8.95	2.67	0.09
Tetep (DP 1)	115	4.53	92	0.57	264	6.96	3.17	0.34
C 101 LAC (DP 2)	91	3.53	98	0.33	300	10.44	3.43	0.2

Blast and bacterial leaf blight resistance gene carrying genotypes RP-Patho-2-18-5 and RP-Patho-2-16-4 gave plot grain yield 3.77kg, which out yielded recurrent parent 02 but lesser than recurrent parent 01. However flowering was delayed (96 DAS and 99 DAS) and plant height was increased in both the isogenic lines (83cms and 81 cms). The same trend was continued with panicle count. The donor lines Tetep (DP 1) and C 101 LAC (DP 2) showed optimal adaption to Southern Chhattisgarh rice growing ecology. Average plant height of Tetep was 91 cms and attained 50 percent flowering by 98 DAS. Since vegetative span was lengthened, panicle count (300) and plot yield also increased accordingly (3.43). Taking into account another donor parent (Tetep), it exhibited faster growth rate and attained 115cms plant height by 92 DAS of preflowering period. Compare to DP 2 produced lesser panicle population (264) and plot grain yield (3.15kg) (ICAR-DRR, 2014).

Visual observation showed that all the near isogenic lines were parallel to the respective recurrent parent; blast prevalence was modest in both Recurrent Parents. Incidence of blast reported in Tetep (1-2%), C 101 LAC (8-10%), all isogenic lines (5-8%). Blast resistance genes *Pi 1* carrying genotypes RP-Patho-1-2-15 and RP-Patho-1-6-5, the infestation the comparatively higher (Score 6) however those with *Pi 54* (RP-Patho-3-56-11 and RP-Patho-3-73-6). Similarly RP-Patho-3-56-11 and RP-Patho-3-73-6, having the blast resistance gene, (*Pi 54*) showed average disease incidence (Score 4). However, dual genetic resistance background i.e. both blast and bacterial blight resistance genes *Xa 21+ Pi-54*; provided excellent resistance even in hot spot centre for the disease. In previous studies multiple resistance gene pyramiding has been reported by Chen *et al.*, 2009 and Zhan *et al.*, (2012). In genotype RP-Patho-2-16-4 the disease was scaled to be 01, which

was quite similar to recurrent parent 02 (Improved Sambha Mahsuri). Visual evaluation of donor parents revealed average disease incidence (score 4). Reproductive behaviour was similar to BPT 5205 and Improved Sambha Mahsuri for all genotypes except RP-Patho-1-2-15 and RP-Patho-2-16-4 but it may attribute to G x E interactions rather than genetic segregation. Similarly, for above ground plant canopy length all test genotypes were relatively more closure to both the recurrent parents which shows comparative expression of photosynthates source sink balance in Near Isogenic Lines (NILs). However, donor parent i.e. Tetep; plant height was significantly higher might be due to regional quantitative adaptability (Kumar *et al.*, 2015). Looking for sink strength, BPT 5205 recorded significantly higher potential of dry matter accumulation than remaining population due to genetic establishment in given environment. Parallel observation was recorded for RP-Patho-3-56-11, RP-Patho-3-73-6 and RP-Patho-2-18-5 showing potent leaf blast and bacterial leaf blight resistance for Southern province of Chhattisgarh. Ultimately, when crop yield was taken into account, the normal distribution curve shifted towards the recurrent parent 01 and the entire test entries lied between 1750 kg/ha to 3075 kg/ha. Summarily, sustainable yield potential was realized despite of target disease incidence all genotypes may be considered as resistance genotypes.

With advances in molecular biology, breeding for resistance genes has become wise and efficient strategy in crop improvement. In present investigation evaluation was made of DRR bred materials for hot spot of paddy blast. All the genotypes were similar to recurrent parent with respect to flowering duration, canopy length, and plot grain yield and disease reaction indicating the recovery of crossed material to desired genetic

background after introgression of dual resistance gene and equally and effectively even in hot spot centre for the disease.

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