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Genetic variability, blast reaction studies and identification of blast tolerant lines in elite genotypes of rice (*Oryza sativa* L.)

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Abstract

The present study was conducted at Agricultural and Horticultural Research station, Ponnampet, Karnataka. Experiment was composed of seventy two rice genotypes those were evaluated to study the genetic variability, heritability and genetic advance for grain yield with four yield associated traits. The experiment was conducted by using simple lattice design with two replications with local checks during the 2016 *kharif* main cropping season. The analysis of variance revealed statistically significant differences ($p < 0.05$) indicating the existence of genetic variability among the seventy two genotypes for all the traits studied. Significant differences were observed for grain yield that ranged from 9100.00 to 7496.00 kg/ha with overall mean value of 4455.00 kg/ha. Higher PCV and GCV values were exhibited by yield kg/ha which suggests the possibility of improving this trait through selection. The highest heritability was recorded for plant height and yield kg/ha followed by days to fifty per cent flowering and panicles per meter square. High to medium heritability coupled with high GCV and high genetic advance as per cent of means were exhibited for plant height, grain yield kg/ha. High genetic advances as per cent of means were recorded by yield kg per hectare, panicles per square metre, Plant height (cm) and days to fifty per cent flowering. Conducted a large-scale screening for rice blast resistance genotypes in seventy two diverse rice accessions originating from major rice-growing regions of Karnataka and the few genotypes among them were shown tolerant.

Keywords: Variability, heritability, genetic advance, blast

Introduction

Rice is a self-pollinated cereal crop belonging to the family Gramineae (synonym-Poaceae) under the order Cyperales and class Monocotyledon having chromosome number $2n=24$ (Hooker, 1979) [6]. The genus *Oryza* includes a total of 25 recognized species out of which 23 are wild species and two, *Oryza sativa* and *Oryza glaberrima* are cultivated (Brar 2003) [1]. It can survive as a perennial crop and can produce a ratoon crop for up to 30 years but cultivated as annual crop and grown in tropical and temperate countries over a wide range of soil and climatic condition. Rice and agriculture are still fundamental to the economic development of most of the Asian countries. In much of Asia, rice plays a central role in politics, society and culture, directly or indirectly employs more people than any other sector. A healthy rice industry, especially in Asia's poorer countries, is crucial to the livelihoods of rice producers and consumers alike. Farmers need to achieve good yields without harming the environment so that they can make a good living while providing the rice-eating people with a high-quality, affordable staple. Underpinning this, a strong rice research sector can help to reduce costs, improve production and ensure environmental sustainability. Indeed, rice research has been a key to productivity and livelihood.

Yield enhancement is the major breeding objective in rice breeding programmes and knowledge on the nature and magnitude of the genetic variation governing the inheritance of quantitative characters like yield and its components is essential for effective genetic improvement. A critical analysis of the genetic variability parameters, namely, Genotypic Coefficient of Variability (GCV), Phenotypic Coefficient of Variability (PCV), heritability and genetic advance for different traits of economic importance is a major pre-requisite for any plant breeder to work with crop improvement programs. The present investigation was undertaken in this context to elucidate information on variability, heritability, genetic advance in promising rice genotypes. A good knowledge of genetic resources might also help in identifying desirable high yielding genotypes for future hybridization program.

Crop plant diseases caused by various pathogens such as viruses, bacteria, oomycetes and fungi pose major challenges to global crop production and food security. Global climate change is predicted to further increase the negative impact of biotic stresses.

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Higher temperatures and erratic weather pattern are likely to change the geographical pathogen distribution. This in turn might decrease the effectiveness of existing resistance genes in crop varieties (Garrett *et al.*, 2006; Milus *et al.*, 2009) [2, 9] by promoting more aggressive races of pathogens.

Ponnampet is place in Karnataka state is one of the hot spots for rice blast disease therefore conducted blast screening experiment on all seventy two rice genotypes and followed by select the tolerant genotypes.

Material and Methods

The experiment was carried out during *kharif*, 2016 at Agricultural and Horticultural Research Station, Ponnampet. The material comprised of 72 elite rice genotypes (Table 1) sown in a simple lattice design with two replications with spacing of 20 x 15 cm. Data were recorded on five randomly selected plants in each entry in each replications for the traits days to 50% flowering, Plant height (cm), number of panicles per square metre, except yield which recorded in kg/plot converted into kg/ha. The data subjected to INDOSTAT software to estimate Genetic coefficient of variation (%), phenotypic coefficient of variation (%), Heritability (%) (Broad sense), Genetic Advance and Genetic Advance as per cent of mean. The estimates for variability treated as per the categorization proposed by Siva Subramanian and Madhavamenon (4), heritability and genetic advance as percent of mean estimates according to criteria proposed by Johnson *et al.* (2). Along with the yield parameters blast scoring also done by using standard blast scale 0-9 (Table 2).

Results and discussion

In the present study analysis of variance revealed the existence of significant differences among genotypes for all traits studied. The mean, variability estimates *i.e.*, Genetic coefficient of variation (%), phenotypic coefficient of variation (%), Heritability (%) (Broad sense), Genetic Advance as percent of mean are presented in Table 3. All traits under studied have higher phenotypic coefficient of variation than genotypic coefficient of variation. The magnitude of phenotypic coefficient of variation and genotypic coefficient of variation was moderate to high for the traits panicles per square metre and yield (Roy *et al.* 2001) [11]. The high PCV observed for yield per hectare (Roy, 2001) [11]. The high GCV obtained for number of panicles per square metre indicating the improvement is possible through selection (Manjunatha *et al.* 2018) [18]. Genotypic coefficient

of variation measures the extent of genetic variability percent for a trait but does not assess the amount of genetic variation which is heritable. Heritability estimates were high for all the characters. The heritability estimates along with genetic advance can be useful to predict effect of selection in selection programmes. The traits like days to fifty percent flowering, yield (Thirumala rao *et al.* 2014) [15] and plant height exhibited high magnitude of genetic advance as percent of mean. The traits plant height, days to fifty percent flowering, panicles per square metre and yield have high heritability along with genetic advance as percent of mean indicate that these characters attributable to additive gene effects which are fixable revealing that improvement in these characters would be possible through direct selection.

Domestication and modern breeding has reduced genetic diversity of crop plants (Tanksley and McCouch, 1997) [14] by replacing landraces and traditional farmer cultivars with modern, high yielding varieties. Although this has allowed filtering out genes that cause detrimental traits, the reduction in genetic variation now limits the options of plant breeders to develop new varieties with the existing germplasm. New varieties are constantly needed to meet consumer demands and for protection of crops against highly unpredictable biotic and abiotic stresses that are encountered in agricultural systems. Breeding of improved varieties requires the identification of novel functional genes or alleles, and this calls for making effective use of our global crop genetic resources available in seed bank collections. These seed collections represent a wide range of genetic diversity that is critical for maintaining and enhancing the yield potential and other quality traits, because they can provide new sources of resistance and tolerance to various stresses. Many of the genes for highly relevant traits in modern crop cultivars have been transferred from their wild relatives and landraces, for example the *Rht* and *sd-1* genes that confer dwarf stature in rice and wheat, respectively (Hedden, 2003; Hoisington *et al.*, 1999) [4, 5]. In the case of rice, the six wild species *O. rufipogon*, *O. longistaminata*, *O. nivara*, *O. breviligulata*, *O. glumaepatula*, and *O. meridionalis* together with the two cultivated species *O. sativa* and *O. glaberrima* have been identified as the primary gene pool for rice cultivars because genes can be easily transferred between these species (Khush, 1997) [8]. The wild species have been used as a source of many relevant genes for rice breeding, and *O. rufipogon* has been suggested as source of broad-spectrum rice blast resistance genes (Ram *et al.*, 2007) [10].

Table 1: Rice genotypes, Grain type and blast disease reaction during the experiment in research station.

Sl. No.	Genotypes	Grain type	Blast score
1	24367	SB	7
2	23930	SB	6
3	24451	LB	5
4	24474	SB	8
5	24471	LB	9
6	25033	MS	8
7	25038	SB	7
8	25044	SB	5
9	24367	SB	7
10	24241	SS	5
11	24395	MS	4
12	24284	LB	7
13	24297	MS	4
14	24236	MS	4
15	23725	MS	3
16	23610	MS	4
17	25241	SB	5

18	25260	LS	6
19	25272	MS	9
20	25273	MS	4
21	25286	MS	6
22	25287	SB	3
23	25264	SB	6
24	25269	MS	7
25	25261	SB	4
26	25231	LS	6
27	25255	MS	4
28	25249	LS	6
29	25268	MS	4
30	25281	MS	3
31	25248	MS	4
32	25251	MS	6
33	25252	SB	7
34	25263	LS	8
35	25246	MS	5
36	25228	SB	4
37	PA6444	SB	5
38	25259	LS	5
39	25271	MS	4
40	25266	SB	9
41	Tunga	SB	3
42	25278	LS	5
43	25236	MS	4
44	25340	SB	5
45	25244	LS	4
46	MTU1010	SB	5
47	Swarna sub-1	MS	9
48	Pushyami	SB	5
49	Dhanurasi	SB	4
50	Savitri	MS	5
51	Swarna	SB	5
52	IET Sanna	MS	3
53	KPR-1	SB	1
54	JGL-1798	MS	6
55	KPR-2	MS	3
56	IR-64	SB	5
57	Jaya	SB	5
58	Jyothi	B	7
59	MTU-1001	B	5
60	Thanu	SB	7
61	CTH-03	B	3
62	Narmada	LB	7
63	Intan	SB	7
64	KHP-09	MS	5
65	Abhilash Tall	SB	7
66	Bhagya jyothi	SB	7
67	IET-7191	MS	5
68	MO-04	B	5
69	CTH-01	MS	5
70	CO-43	SB	3
71	TG-(S)-14	SB	3
72	FC-01	SB	5

*SB: Short Bold MS: Medium Slender, B: Bold, LB: Long Bold

Table 2: Standard screening scale (0-9 grade for disease rating) was used for blast disease of rice (Source-IRRI, 1996; Ghazanfar *et al.*, 2009)

Grade	Disease severity	Host response
0	Lesion are not present	Highly resistant (HR)
1	Small brown specks of pin point size on lower leaves	Resistant (R)
2	Small roundish to slightly elongated, necrotic gray spots, about 1-2 mm in diameter, with a distinct brown margin. Lesions are mostly found on the lower leaves	Moderately resistant (MR)
3	Lesion type same as in 2, but significant number of lesions on the upper leaves	Moderately resistant (MR)
4	Typical susceptible blast lesions, 3 mm or longer infecting less than 4% of leaf area	Moderately susceptible (MS)
5	Typical susceptible blast lesions of 3 mm or longer infecting 4-10% of the leaf area	Moderately susceptible (MS)
6	Typical susceptible blast lesions of 3 mm or longer infecting 11-25% of the leaf area	Susceptible (S)

7	Typical susceptible blast lesions of 3 mm or longer infecting 26-50% of the leaf area	Susceptible (S)
8	Typical susceptible blast lesions of 3 mm or longer infecting 51-75% of the leaf area many leaves are dead	Highly susceptible (HS)
9	Typical susceptible blast lesions of 3 mm or longer infecting more than 75% leaf area affected	Highly Susceptible (HS)

Table 3: Various genetic variability parameters estimated among the seventy two genotypes of rice.

Parameters	Traits	Days to fifty per cent flowering	Plant height (cm)	Panicles per m ²	Yield (kg/ha)
	Mean	107.00	82.00	343.00	4455.00
	Range	64.00-143.00	58-110	228.00-480.00	9100-7496.00
	Genotypic variability	306.00	136.00	935.76	2149257.00
	Phenotypic variability	321.62	150.00	3782.20	2266315.00
	GCV	16.12	14.37	18.94	32.90
	PCV	16.62	15.10	17.00	33.75
	Heritability	0.95	0.90	0.89	0.95
	Genetic advance	35.15	22.83	31.14	2941.00
	Genetic advance as per cent mean	32.59	28.92	24.65	66.00

Conclusion

Seventy two rice genotypes including standard checks were evaluated for four yield and yield attributing traits. Results of the present investigation on variability, heritability and genetic advance indicated a scope for improvement of grain yield through selection as well as the eight genotypes were shown tolerant to rice blast disease during severe screening in hot spot therefore those are act as source of resistance for rice blast disease and can be used in future breeding programme.

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