Journal of Pharmacognosy and Phytochemistry

Available online at www.phytojournal.com

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Genetic variability and blast resistance studies in rice genotypes under rainfed shallow low land conditions

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Abstract

The present study was carried out at Agricultural and Horticultural Research Station, Ponnampet, University of Agricultural and Horticultural Sciences, Shivamogga during 2015. The experimental material comprised of 58 different varietal lines including existing varieties as checks. Mean performance of individual rice genotypes revealed that the days to 50% flowering found to vary from 97.50 days to 126.50. Plant height was found to vary from 58.00 cm to 105.34 cm with average height of 83.06 cm. The genotype IET-25041 produced maximum grain yield (5068.15 kg/ha) followed by IET-25038 (4674.08 kg/ha), whereas IET-25010 was found to be inferior in grain yield (182.22 kg/ha). Analysis of variance revealed highly significant sum of squares due to genotypes for all the characters indicating existence of ample variability among the genotypes. The traits such as plant height and grain yield which showed high heritability coupled with high genetic advance could be used as selection criteria for their improvement since these are governed by additive gene action. The traits like days to 50% flowering and number of panicles per plant could be used as indirect selection criteria for their simultaneous improvement.

Keywords: Heritability, genetic advance, correlation, leaf blast

Introduction

Rice (*Oryza sativa* L.) belonging to the family of grasses Gramineae (Poaceae), is one of the important food crops among three major food crops in the world and forms the main diet of about more than half of the world's population. The area under rice cultivation is estimated to be 160.07 million hectares with global production 483.81 Million tons (USDA, 2017). Asia shares 90 percent production of rice alone and ranked first in production. Rice accounts for about 42 per cent of total food grain production and >55 per cent of diet in India. The production is very low in India due to non-availability of high yielding varieties.

A better understanding of the relationship between grain yield and its component traits becomes necessary for making an efficient selection for the development of new varieties with improved economically important traits (Kumar *et al.,* 2013) [12]. Development of high yielding varieties requires the knowledge of existing genetic variability. Variation is the basis of plant breeding. As success of any crop improvement programme largely depends on the magnitude and range of variability on the available genetic stock. A critical estimate of genetic variability is a prerequisite for initiating appropriate breeding procedures in crop improvement programmes. Hence, it becomes necessary to spilt over-all variability into its heritable and nonheritable components with the help of certain genetic parameters, which may enable the breeders to plan a proper breeding programme. Therefore, the progress of a population mainly depends upon the amount and magnitude to genotypic variability present in the population. Information of genetic variability among growth as well as yield components in rice has been reported by many workers (Sivasubramanian and Madhava Menon, 1973; Latif and Zamin 1965) [20, 13].

Plant breeders mostly evaluate their germplasm to generate breeding materials of which the superior lines will be selected for further crop improvement. The success of increasing the productivity of any crop through breeding largely depends on the presence of variability among the breeding materials (Adeyemo and Ojo, 1991; Padulosi, 1993) [2, 14]. Genetic variability studies are important in selection of parents for hybridization (Chaudhary and Singh, 1982) because crop improvement depends upon magnitude of genetic variability in base population (Adebisi *et al.*, 2001) [1]. Once genetic variability has been ascertained, crop improvement is possible through the use of appropriate selection method, and increasing total yield would be made easier by selecting for yield components because they are more often easily inherited than total yield itself (Ukaoma *et al.*, 2013) [21]

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Material and Methods

The present studies were carried out at farm of Agricultural and Horticultural Research Station, Ponnampet, University of Agricultural and Horticultural Sciences, Shivamogga. During *Kharif* season, 2015, in a randomized complete block design with three replications. The experimental materials comprised of fifty eight rice genotypes comprising of initial variety trials from the AICRP and existing varieties. The seedlings were raised nursery and later 30 days old seedlings were transplanted in a plot of 6.75 m² size for each genotype by maintaining 15 × 15cm spacing. Agronomic practices were followed based on the zonal recommendations to raise a good and healthy crop. The observations were recorded on five randomly selected plants from each plot for quantitative traits namely plant height and panicles number per plant. Days to 50% flowering and yield were taken on plot basis, Further the grain yield values recorded from the net plot (kg/plot) were converted into hectare (kg/ha). The AHRS, Ponnampet is considered as one of the hot spot for leaf blast disease hence genotypes were also evaluated for disease reaction under field condition and the genotypes were scored based on leaf blast severity following SES scale of IRRI (1996).

The mean data after computing for each character was subjected to standard method of analysis of variance following Panse and Sukhatme (1967) [16], phenotypic and genotypic coefficient of variation were estimated by the formula as suggested by Burton (1952) [4], heritability (broad sense) and genetic advance as per cent of mean were calculated by the formula given by Johanson *et al.,* (1955) [11]. The simple correlation coefficients were calculated to determine the direction and magnitude of associations among different characters and tested against Table 't' values (Fisher and Yates, 1963) [6].

Result and Discussion

Results on field screening of genotypes for leaf blast reaction revealed that out of fifty eight entries, none of the genotypes was found to be highly resistant. 17 (IET-24998, 25001, 25003, 25007, 25008, 25012, 25020, Tunga (LC), 25023, 25024, 25025, 25028, 25029, Dhanrasi (NC), 25039, 25041, 25048) genotypes found resistant, 25 (IET-24999, 25004, 25005, 25016, 25021, 25033, 25034, 25035, 24521, 25038, 25040, 25045, 24488, 25002, 25010, 25014, 25015, 25022, 25026, 25032, Savitri (ZC), 25044, 24491, 25046, 25031) genotypes were found to be moderately resistant, 14 (IET-24997, 25000, 25006, 25009, 25011, 25013, 25017, 25018, 25030, 25036, 25037, 25042, 25043, 25047) genotypes were found to be moderately susceptible, 1 (IET-25019) genotype was found to be susceptible and 1 (IET-25027) genotype found highly susceptible. (The information on SES scores of individual entries is given in (Table 1) similar findings were also reported by Hosagoudar *et al.,* (2017 & 2018) [8].

Table 1: Mean performance of 58 rice genotypes under rainfed shallow low land

S. No.	Genotypes	Leaf Blast (SES Score 0-9 scale)	Days to 50% flowering	Plant height (cm)	Number of panicles per plant	Grain yield/ha (kg)
1	IET -24997	5	113.50	81.67	4.50	2527.41
2	24488	3	122.50	86.67	8.83	3162.96
3	24998	1	110.50	74.83	10.33	3262.22
4	24999	2	110.50	73.00	8.17	2640.00
5	25000	4	108.50	63.67	10.33	918.52
6	25001	1	112.50	100.33	9.17	3082.96
7	25002	3	112.50	78.17	9.00	2688.89
8	25003	1	119.50	87.33	9.50	1552.59
9	25004	2	110.50	58.00	10.33	3182.22
10	25005	2	121.50	79.83	9.83	680.00
11	25006	5	108.50	59.33	12.50	3034.07
12	25007	1	99.50	77.67	9.17	3155.56
13	25008	1	102.50	78.83	10.50	3871.11
14	25009	6	109.50	61.50	11.83	1275.56
15	25010	3	126.50	81.50	7.33	182.22
16	25011	4	114.50	82.33	9.50	1927.41
17	25012	1	114.50	105.33	6.17	2440.00
18	25013	4	110.50	72.33	13.33	3848.89
19	25014	3	112.50	72.83	12.83	4487.41
20	25015	3	102.50	73.67	10.33	3982.22
21	25016	2	117.50	75.50	9.50	2274.07
22	25017	4	114.50	69.17	9.67	1234.07
23	25018	5	118.50	81.67	8.33	3287.41
24	25019	7	121.50	101.83	9.67	922.96
25	25020	1	117.50	84.00	9.33	2149.63
26	Tunga (LC)	1	114.00	91.83	9.67	3312.59
27	25021	2	115.50	89.00	12.17	1445.93
28	25022	3	113.50	83.83	9.67	1908.15
29	25023	1	111.50	104.17	8.83	4305.19
30	25024	1	114.00	90.17	8.00	3554.07
31	25025	1	114.50	100.17	6.50	2920.00

32	25026	3	111.00	85.00	9.67	3194.07
33	25027	8	107.00	101.67	10.00	1985.19
34	25028	1	115.50	82.00	10.00	682.96
35	25029	1	102.50	81.67	10.50	4306.67
36	25030	4	97.50	80.67	11.83	4400.00
37	25031	3	107.00	67.50	8.00	3392.59
38	25032	3	119.00	85.00	10.50	826.67
39	25033	2	107.50	82.83	11.00	3602.96
40	25034	2	118.00	99.00	10.17	1625.19
41	25035	2	113.50	102.00	10.50	2573.33
42	25036	5	113.00	87.50	10.67	3059.26
43	24521	2	115.00	95.17	8.00	2922.96
44	Dhanrasi (NC)	1	114.50	89.17	9.17	2045.93
45	25037	4	111.00	70.67	11.00	2435.56
46	25038	2	119.50	80.67	9.83	4674.07
47	25039	1	113.00	83.00	7.50	2349.63
48	25040	2	109.50	87.17	8.83	3850.37
49	25041	1	114.50	87.67	8.50	5068.15
50	Savitri (ZC)	3	118.50	83.50	13.17	3585.19
51	25042	4	113.00	76.83	9.00	3111.11
52	25043	5	120.50	87.33	10.17	487.41
53	25044	3	120.50	85.00	8.17	2906.67
54	25045	2	111.50	104.67	5.67	1413.33
55	24491	3	107.00	74.00	10.00	4842.96
56	25046	3	108.50	79.83	10.00	2890.37
57	25047	5	117.00	72.67	9.00	1982.22
58	25048	1	107.00	85.17	9.17	3826.67
		Mean	112.69	83.06	9.73	2711.34
		CV	0.728	4.044	17.473	14.046
		CD (0.05)	1.644	6.727	3.407	762.610

NC- National check; ZC- Zonal check; LC- Local check.

Table 2: ANOVA for different yield related traits in rice genotypes

Source of variation		Mean sum of squares			
	d. f.	Days to 50% flowering	Plant height (cm)	Number of panicles per plant	Grain yield/ha (kg)
Replication	1	01.04	20.723	69.31	2285645.00
Genotypes	57	65.80**	255.40**	07.65**	2817963.44**
Error	57	0.674	011.28	02.89	145035.33

** indicates significance at 1% level of significance

Table 3: Estimates of mean and other genetic parameters for different yield and yield attributing traits in rice genotype

Character	Variances		Coefficient of variation%		h^2 bs (%)	GAM (%)
	Vg	Vp	GCV	PCV		
Days to 50% flowering	32.56	33.24	05.06	05.12	98.00	10.32
Plant Height (cm)	122.06	133.34	13.30	13.90	91.50	26.21
Number of Panicle /plant	02.38	05.28	15.84	12.58	45.10	21.91
Grain yield/ha (Kg)	1336464	1481499	42.70	44.89	90.20	83.42

Vg: Genotypic variance, Vp: Phenotypic variance, GCV: Genotypic coefficient of variation, PCV: Phenotypic coefficient of variation, h^2 bs: Broad sense heritability, GAM: Genetic advance as percent of mean.

The mean performance of individual rice genotypes revealed that the genotype IET-25004 (58.00 cm) was found shortest while IET-25045 (104.67 cm) found to be the tallest. The maximum number of panicles/plant was observed in Savitri (13.17) while IET-24997 (4.50) showed minimum number of panicles/plant. The rice genotypes in present study differed significantly for grain yield. IET-25041 gave maximum grain yield (5068.15 kg/ha) followed by IET-24491 (4842.96 kg/ha) whereas IET-25010 recorded lowest grain yield (182.22 kg/ha). Similar findings on mean performance of rice genotypes for various traits were also reported by Sedeek *et al.,* (2009) [18], Anis *et al.,* (2016) [3] and Hosagoudar *et al.,* (2017 & 2018) [8].
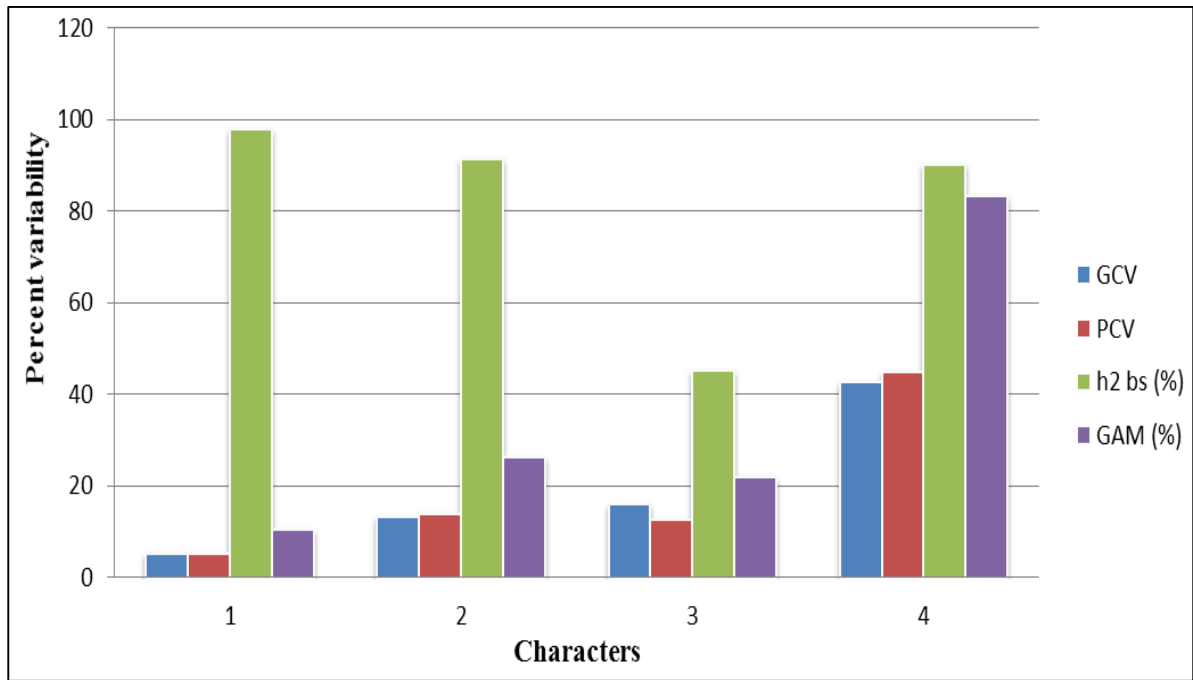
Fig 1: Genotypic (GCV) Phenotypic (PCV) coefficient of variation, Heritability & Genetic advance percent of mean for yield and yield attributed traits in 58 rice genotypes

The analysis of variance revealed that all the genotypes showed a significant difference for all the characters studied, which indicated enough variability existed among the genotypes. Similar reports on phenotypic variation among rice genotypes were observed by Elayaraja *et al.,* (2005) [5], Pandey *et al.,* (2009) [15] and Hosagoudar *et al.,* (2017 & 2018) [8]. The source of any kind of selection depends on the existence of the genetic variability. The presence of significant amount of variability in the initial breeding material assures the production of suitable recombinants for crop improvement. The estimate of the phenotypic coefficient of variation (PCV), the genotypic coefficient of variation (GCV), heritability and genetic advance (as a percent of mean) were presented in Table 2 and Fig 1. Phenotypic coefficients of variation were higher than the corresponding genotypic coefficients of variation, indicating the considerable influence of the environment on the expression of the traits. The estimates of PCV was high for grain yield (44.89%) and while moderate PCV values were observed for number of plant height (13.90%) followed by panicles/plant (12.58%) and while low PCV values were observed for days to 50% flowering (5.12%). Similarly, GCV was high for grain yield (42.70%) and while moderate GCV values were observed for number of panicles/plant (15.84%) followed by plant height (13.30%) and while low PCV values were observed for days to 50% flowering (5.06%) percent variability is represented graphically in Figure 1. Similar findings were reported by Jayasudha and Sharma (2010) [10], Harsha *et al.,* (2017) [7] and Hosagoudar *et al.,* (2017 & 2018) [8]. The close association found between the phenotypic and genotypic coefficient of variation which is further supported by high values of heritability of the characters studied.

The estimates of heritability help the plant breeder in selection of elite genotypes from diverse genetic population, hence prior knowledge about the heritability of the traits is a prerequisite for the selection programme (Singh *et al.,* 2011). The broad sense heritability estimates for the traits observed were days to 50% flowering (98.00%), plant height (91.50%), number of panicles per plant (45.10%), grain yield (90.20%). These results are in collaboration with the results obtained by Harsha *et al.,* (2017) [7] and Hosagoudar *et al.,* (2018) [8, 9] heading, for days to 50% flowering days, plant height and grain yield. Ravindra *et al.,* (2012) [17] for number of panicles per plant. The presence of high heritability with high genetic advance showed additive effects of the gene on the character and they response to selection effectively as they are least affected by the environmental condition.

Conclusion

The mean performance of individual rice genotypes revealed that the genotype IET-25004 (58.00 cm) was found shortest while IET-25045 (104.67 cm) found to be the tallest. The maximum number of panicles/plant was observed in Savitri (13.17) while IET-24997 (4.50) showed minimum number of panicles/plant. The rice genotypes in present study differed significantly for grain yield. IET-25041 gave maximum grain yield (5068.15 kg/ha) followed by IET-24491 (4842.96 kg/ha) whereas IET-25010 recorded lowest grain yield (182.22 kg/ha).

The present investigation was carried out in order to study the nature and amount of variability, heritability and genetic advance and association between traits under study. Based on mean performance of individual rice genotypes the genotype IET-25004 followed by IET-25006 can be selected for the dwarfness trait, while the genotype IET-25045 can be selected for tallness trait. The genotypes IET-25013 and Savitri recorded higher number of panicles/plant. Analysis of variance revealed highly significant sum of squares due to genotypes for all the characters indicated the existence of ample variability among the genotypes. Selection for the traits having high heritability coupled with high genetic advance is likely to accumulate more additive genes leading to further improvement of their performance. In the present study, high heritability along with high genetic advance was noticed for the traits, plant height and yield. Other characters showed high heritability along with moderate or low genetic advance which can be improved by intermating superior genotypes of segregating population developed from certain breeding methods.

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