



E-ISSN: 2278-4136

P-ISSN: 2349-8234

JPP 2018; 7(5): 2139-2142

Received: 07-07-2018

Accepted: 09-08-2018

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Assessment of genetic variability and blast resistance studies in advanced rice (*Oryza sativa* (L.)) 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 13 different advanced varietal lines including existing varieties as checks. Mean performance of individual rice genotypes revealed that the days to 50% flowering found to vary from 106.33 days to 120.33. Plant height was found to vary from 56.50 cm to 97.00 cm with average height of 78.09 cm. IET-24451 gave maximum grain yield (3797.49 kg/ha) followed by IET-24471 (3729.39 kg/ha). The genotype IET-24451 produced maximum grain yield (3797.49 kg/ha) followed by IET-24471 (3729.39 kg/ha), whereas IET-23930 was found to be inferior in grain yield (1573.48 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, number of panicles per plant, number of panicles per m² 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 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), one of the three most important food crops in the world, forms the staple diet of 2.7 billion people. Around 32-59% of the dietary energy and 25-44% of the dietary protein in 39 countries was obtained from rice. In India it's being the staple food for more than 64% of the people, India's national food security relies on its growth and stability of its production. India is the largest producer of rice grain among worldwide. The global human population continues to grow and it is estimated that rice production will need to increase 40% by 2030 to meet the food. For further improvement in the yield of rice, it is essential to have a thorough knowledge on the variability present in the genotypes. It has been realized that heritability estimates in broad sense along with the genetic advance is more useful in producing the resultant effect for selection of the best individuals as reported by Johnson *et al* (1995) ^[10]. Genetic advance for any quantitative character can predicted with the help of heritability and aids in exercising the necessary selection pressure. Knowledge on nature and magnitude of genotypic and phenotypic variability present in any crop species plays an important role in formulating successful breeding programmes by Allard (1960) ^[1].

It is very difficult to evaluate whether observed variability is highly heritable or not. For any crop improvement it depends on magnitude of genetic variability present in base population. Environmental effects influence the total observable variations of quantitative traits. Therefore, partitioning of overall variance due to genetic and non-genetic causes becomes necessary for effective breeding programme. The genotypic coefficient of variation estimates the heritable variability, whereas phenotypic component measures the role of environment on the genotype. High PCV and low GCV for a character indicated high influence of environment in its expression. The phenomenon of transmission of characters from parents to offspring is usually measured in terms of heritability. Therefore the estimates of heritability and genetic advance would help to formulate a sound breeding programme.

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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 thirteen rice genotypes comprising of advanced 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) [13], phenotypic and genotypic coefficient of variation were estimated by the formula as suggested by Burton (1952) [3], heritability (broad sense) and genetic advance as per cent of mean were calculated by the formula given by Johanson *et al.*, (1955) [10]. 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) [5].

Result and Discussion

Results on field screening of genotypes for leaf blast reaction revealed that out of thirteen entries, none of the genotypes was found to be highly resistant. 3 genotypes found resistant (IET-24471, Tunga (LC), Savitri (ZC)), 8 genotypes were found to be moderately resistant (IET-24443, Dhanrasi (NC), 24480, 24474, 23565, 23930, 24450, 24367), 2 genotypes were found to be moderately susceptible (IET-24451, 23561), none of the genotype was found to be susceptible and 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) [7,8].

Table 1: Mean performance of 13 advanced 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	Number of panicle per m ²	Grain yield/ha (kg)
1	24443	2	106.33	76.50	9.67	421.08	2774.19
2	Dhanrasi (NC)	2	114.00	84.67	8.00	348.48	1659.50
3	24480	3	112.33	73.33	8.00	348.48	3514.34
4	24451	4	110.00	84.17	9.83	428.34	3797.49
5	24474	3	114.33	67.67	8.83	384.78	3082.44
6	23565	2	120.33	80.83	8.67	377.52	1866.19
7	23930	3	109.67	56.50	8.17	355.74	1573.48
8	Savitri (ZC)	1	115.00	75.00	9.17	399.30	3155.91
9	24471	1	110.00	97.00	6.17	268.62	3729.39
10	23561	5	108.33	82.50	7.50	326.70	2666.67
11	Tunga (LC)	1	116.00	90.00	10.33	450.19	3302.87
12	24367	2	116.33	82.67	7.83	341.22	2093.19
13	24450	3	107.00	64.33	9.33	406.56	2136.20
		Mean	112.28	78.09	8.58	373.61	2719.37
		CV	1.08	8.37	9.50	9.50	13.29
		CD (0.05)	2.58	12.94	2.12	92.65	748.76

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

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

Source of variation	d.f	Mean sum of squares				
		Days to 50% flowering	Plant height (cm)	Number of panicles per plant	Number of panicles/m ²	Grain yield/ha (kg)
Replication	1	0.90	13.32	5.71	10872.83	530.35
Genotypes	12	61.17**	106.20**	2.91**	5527.92**	705909.42**
Error	12	01.43	35.88	0.96	1839.55	120127.53

** 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 (%)
	V _g	V _p	GCV	PCV		
Days to 50% flowering	16.92	17.59	03.66	03.74	96.20	09.49
Plant Height (cm)	117.48	121.62	13.80	14.12	96.60	36.01
Panicle number/plant	01.04	01.72	11.87	15.31	60.20	24.31
Panicle per m ²	1969.94	3272.83	11.88	15.31	60.20	24.33
Grain yield/ha (Kg)	597073.30	650754.80	28.41	29.67	91.80	71.85

V_g: Genotypic variance, V_p: Phenotypic variance, GCV: Genotypic coefficient of variation, PCV: Phenotypic coefficient of variation, h² bs: Broad sense heritability, GAM: Genetic advance as percent of mean.

The mean performance of individual rice genotypes revealed that the genotype IET-23930 (56.50 cm) was found shortest while IET-24471 (97.00 cm) found to be the tallest. The maximum number of panicles/plant was observed in Tunga (10.33) while IET-24471 (6.17) showed minimum number of panicles/plant. The maximum number of panicles/m² was observed in Tunga (450.19) while IET-24471 (268.62) showed minimum number of panicles/ m². The rice genotypes

in present study differed significantly for grain yield. IET-24451 gave maximum grain yield (3797.49 kg/ha) followed by IET-24471 (3729.39 kg/ha) whereas IET-23930 recorded lowest grain yield (1573.48 kg/ha). Similar findings on mean performance of rice genotypes for various traits were also reported by Sedeeq *et al.*, (2009) [16], Anis *et al.*, (2016) [2] and Hosagoudar *et al.*, (2017 & 2018) [7, 8].

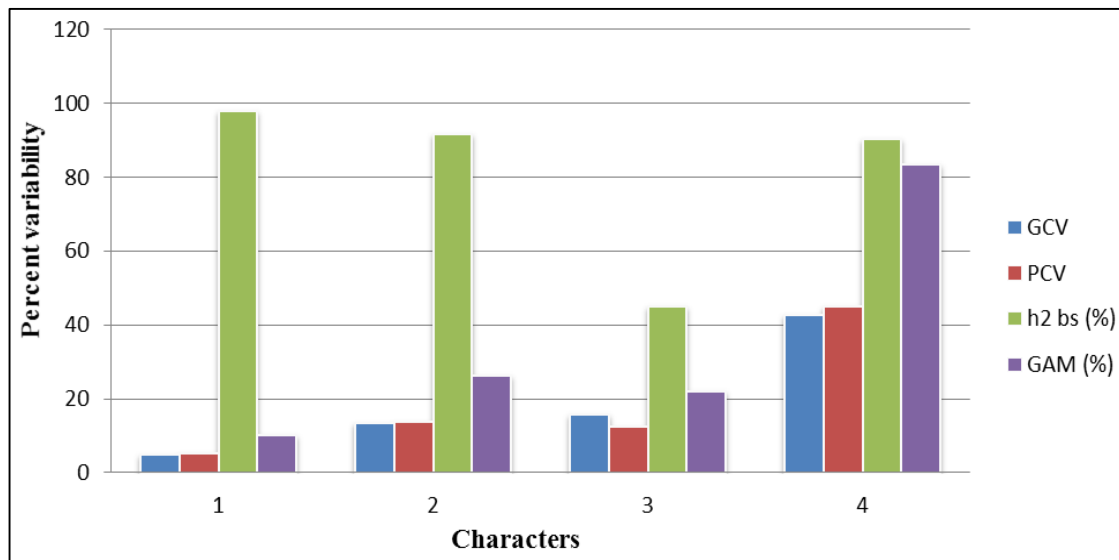


Fig 1: Genotypic (GCV) Phenotypic (PCV) coefficient of variation, Heritability & Genetic advance percent of mean for yield and yield attributed traits in 58 rice genotypes

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) [4], Pandey *et al.*, (2009) [12] and Hosagoudar *et al.*, (2017 & 2018) [7, 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 (29.67%) and while moderate PCV values were observed for number of panicles/plant (15.31%) followed by number of panicles/m² (15.31%) followed by plant height (14.12%) and while low PCV values were observed for days to 50% flowering (03.74%). Similarly, GCV for grain yield (28.41%) and while moderate GCV values were observed for plant height (13.80%), followed by number of panicles/m² (11.88%) followed by number of panicles/plant (11.87%) and while low GCV values were observed for days to 50% flowering (03.66%) percent variability is represented graphically in Figure 1. Similar findings were reported by Jayasudha and Sharma (2010) [9], Harsha *et al.*, (2017) [6], Prabhu (2017) [14], Lingaiah *et al.*, (2014) [11] and Hosagoudar *et al.*, (2017 & 2018) [7, 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) [17]. The broad sense heritability estimates for the traits observed were days to 50% flowering (96.20%), plant height (96.60%), number of panicles per plant (60.20%) number of panicles per m² (60.20%), grain yield (91.80%). These results are in collaboration with the results obtained by Ravindra *et al.*, (2012) [15], Lingaiah *et al.*, (2014) [11], Harsha *et al.*, (2017) [6], Prabhu (2017) [14] and Hosagoudar *et al.*, (2018) [7, 8]. 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-23930 (56.50 cm) was found shortest while IET-24471 (97.00 cm) found to be the tallest. The maximum number of panicles/plant was observed in Tunga (10.33) while IET-24471 (6.17) showed minimum number of panicles/plant. The rice genotypes in present study differed significantly for grain yield. I0ET-24451 gave maximum grain yield (3797.49 kg/ha) followed by IET-24471 (3729.39 kg/ha) whereas IET-23930 recorded lowest grain yield (1573.48 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-23930 followed by IET-24474 can be selected for the

dwarfness trait, while the genotype IET-Tunga can be selected for tallness trait. 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.

Reference

- Allard RW. Principles of plant breeding. John Wiley and Sons. Inc. U.S.A, 1960, 485.
- Anis G, Sabagh AL, Ghareb A, EL-Rewainy I. Evaluation of promising lines in rice (*Oryza sativa* L.) to agronomic and genetic performance under Egyptian conditions. Intern. J Agron. and Agri. Res. 2016; 8(3):52-57.
- Burton GW. Quantitative inheritance in grasses. Proc. VI. Institute Grass land Congr. 1952; 1:155-157.
- Elayaraja K, Prakash M, Saravana K, Kuma BS, Ganesan J. Studies on variability, heritability and genetic advance for quantitative characters in rice (*Oryza sativa* L.). Crop Res. 2005; 29:134-137.
- Fisher RA, Yates F. Statistical Tables for Biol. Agric and Medic Res., Oliver and Boyd, London, 1963, 46-63.
- Harsha, Indra D, Sudhir K, Mohammed T. Assessment of genetic variability and inter-character association studies in rice genotypes (*Oryza sativa* L.). Int. J Curr. Microbiol. App. Sci. 2017; 6(9): 2041-2046
- Hosagoudar GN, Basavaraj SK. Evaluation of advanced varietal rice genotypes for leaf blast reaction, genotypic performance and correlation studies. Int. J Curr. Microbiol. App. Sci. 2018; 7(4):75-81
- Hosagoudar GN, Umeshbabu BS, Basavaraj SK. Genetic variability studies of short duration fine grain paddy varieties having resistance to blast diseases. Journal of Pharmacognosy and Phytochemistry. 2018; 7(4):935-939
- Jayasudha S, Sharma D. Genetic parameters of variability, correlation and path-coefficient for grain yield and physiological traits in rice (*Oryza sativa* L.) under shallow low land situation. Electronic J of Pl. Breeding. 2010; 1(5):33-38.
- Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in Soybean. Agron J. 1955; 47:314-318.
- Lingaiah N, Venkanna V, Cheralu C. Genetic variability analysis in rice (*Oryza sativa* L.) Int. J pure app. Biosci. 2014; 2(5):203-204.
- Pandey P, John P, Anurag, Tiwari DK, Yadav SK, Kumar B. Genetic variability, diversity and association of quantitative traits with grain yield in rice (*Oryza sativa* L.). J of Bio-Sci. 2009; 17(1):77-82.
- Panse VG, Shukhatme PV. Statistical Methods for agricultural workers. 2nd edition, ICAR, New Delhi, 1967; 152-157.
- Prabhu SM, Meenakshi GN, Jeyaprakash P, Selvakumar R, Prabhakaran NK. Assessment of genetic variability studies among the backcross populations in rice [*Oryza sativa* (L.)]. Int. J Pure App. Biosci. 2017; 5(4):368-372
- Ravindra BV, Shreya K, Kuldeep SD, Usharani G, Siva SA. India International Journal of Scientific and Research Publications. 2012; 2(3):36.39.
- Sedeek SM, Hammoud SA, Ammar MH, Metwally TF. Genetic variability, heritability, genetic advance and cluster analysis for some physiological traits and grain yield and its components in rice (*Oryza sativa* L.). J of Agri. Res. 2009; 35(3):858-878.
- Singh SK, Singh CM, Lal GM. Assessment of genetic variability for yield and its component characters in rice. *Oryza*. 2011; 1(4):73-76.