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Genetic variability studies of short duration fine grain paddy varieties having resistance to blast diseases

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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 17 different varietal lines including existing variety as check. Mean performance of individual rice genotypes revealed that the days to 50% flowering found to vary from 72.50 days to 112.00. Plant height was found to vary from 65.35 cm to 104.66 cm with average height of 87.68 cm. Number of panicles per m² area ranged from 333.96 (Tunga) to 493.68 (Sambamasuri) with mean of 439.87 panicles/m² area. The genotype Tunga produced maximum grain yield (5527.78 kg/ha) followed by IVT-L-RSL-524 (3972.22 kg/ha), whereas AVT-L-1723 was found to be inferior in grain yield (2652.78 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 days to 50% flowering 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 plant height and panicles number/m² could be used as indirect selection criteria for their simultaneous improvement.

Keywords: heritability, genetic advance, correlation, leaf blast

Introduction

Rice (*Oryza sativa* L.) is one of the most important cereal of the world belonging to family, *Poaceae* and is staple food of about 65% of the world's population. It is cultivated over a wide range of climatic conditions; considered as a promising option for diversifying agriculture in various agro-climatic zones and ranks as second most important food crops in India. The production of rice to be achieved by 2020 is 128 million tonnes to feed the growing population of India Kumar *et al.* (2010) [14]. Rice is the most valuable and primary food crop for more than 50 % of the world's population Khush (2005) [13] and Latif *et al.* (2011) [15]. About 161.40 million hectares area is been cultivated by rice, globally and production is about 506.30 million tonnes with the productivity of 3.14 tonnes per hectare (Anon, 2015) [3].

In most of the Asian countries, agriculture and rice play an important role in the economic development. In most of the parts of Asia, rice plays a vital role in society, culture and politics, employing more people directly and indirectly more than any other industry. Particularly in the poorer countries in Asia, a healthy rice industry is critical to the employment of the consumer and rice producers. Proper yields should be achieved by the farmers without causing any harm to the environment in order to make happy living by supplying high quality rice to the rice-eating people at affordable price. Supporting this, a strong research on rice sector helps to decrease the cost, improving the production and to take care of the environmental sustainability. Certainly, for livelihood and productivity, rice research has been a key.

Rice itself contributes 17 percent of annual Gross Domestic Product (GDP) and has occupied a prerequisite place in Indian agriculture. The major rice growing states in India are Karnataka, Andhra Pradesh, Bihar, Uttar Pradesh, Madhya Pradesh, West Bengal and Punjab. In Karnataka, rice is being cultivated in an area of 1.32 million hectare with the annual production of 3.54 million tonnes and productivity of 3.09 t/ha (Anon, 2014) [2].

Although India has maximum acreage under cultivation among the rice growing countries, it lags behind with respect to productivity level. Low rice productivity is attributed to the lack of high yielding varieties, various biotic and abiotic stresses and several other constraints. Among various biotic stresses, leaf blast caused by *Pyricularia grisea* is one of the major diseases of rice causing substantial yield losses. Therefore, evaluation of advanced varietal rice genotypes for disease reaction helps in subsequent release of blast resistant varieties for commercial cultivation.

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The major objective of plant breeder is to create maximum extent of genetic variability in the existing genetic stock. Variation is the basis of plant breeding. Thus the success of any improvement programme will largely depend on the magnitude and range of variability in the available genetic stocks (Basavaraja *et al.*, 2013) [4]. An in-depth understanding of genetic resources might also serve in detecting desirable genotypes for forthcoming hybridization program.

In a rice improvement programme, it is the germplasm, which virtually determines the success and nature of end product. The development of superior rice population involves the perspicacious use of available genetic variability to cater the need of various farming situations of rice. The grain yield is the primary trait targeted for improvement of rice productivity in both favourable and unfavourable environments from its present level. 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. Heritability and genetic advance are other important selection parameters. The estimates of heritability help the plant breeder in determining the character for which selection would be rewarding. The breeders are interested in selection of superior genotypes based on their phenotypic expression. The major function of heritability estimates is to provide information on transmission of characters from the parents to the progeny. Heritability estimates can anticipate improvement by selection of useful characters. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone. Therefore, estimates of GCV, PCV, heritability and genetic advance will play an important role in exploiting future research projections of rice improvement. The present investigation was carried out to estimate the variability parameters among 17 rice genotypes.

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 seventeen rice genotypes comprising of breeding lines from the AICRP trial and existing varieties. The seedlings were raised nursery and later 30 days 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 whereas, panicles number/m² was taken on area 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) [19], phenotypic and genotypic coefficient of variation were estimated by the

formula as suggested by Burton (1952) [5], 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) [7].

Result and Discussion

Results on field screening of genotypes for leaf blast reaction revealed that out of seventeen entries, none of the genotypes was found to be highly resistant and 7 (AVT-L-1723, IVT-L-RSL-524, IVT-L-RSL-501, AICRIP-4, Co-43, AVT-L-1904 and Tunga (LC)) genotypes found moderately susceptible 6 (AVT-01-L-1902, IVT-L-1805, IVT-L-1806, IVT-L-2048, IVT-L-RSL-342 and Narmadha) genotypes found susceptible while remaining 4 (AVT-01-L-1916, IVT-L-2045, IVT-L-RSL-308 and Sambamasuri) genotypes found highly susceptible reaction (The information on SES scores of individual entries is given in Table 1).

The mean performance of individual rice genotypes revealed that the genotype IVT-L-2045 (65.33 cm) was found shortest while Narmadha (104.66 cm) found to be the tallest. The maximum number of panicles/plant was observed in Sambamasuri (11.33) while Tunga (7.66) showed minimum number of panicles/plant. The same genotypes recorded maximum (493.68) and minimum (333.96) number of panicles/m² area respectively. The rice genotypes in present study differed significantly for grain yield. Tunga gave maximum grain yield (5527.78 kg/ha) followed by IVT-L-RSL-524 (3972.20 kg/ha) whereas AVT-01-L-1916 recorded lowest grain yield (2211.11 kg/ha). Similar findings on mean performance of rice genotypes for various traits were also reported by Hammound (2005) [8], Sedeek *et al.*, (2009) [24], Anis *et al.*, (2016) [1], Hosagoudar and Basavaraj (2018) [9].

The analysis of variance (Table 2) revealed that sum of squares due to genotypes were highly significant for all the characters under study which indicated enough variability existed among the genotypes. The observed differences among the genotypes may be attributed to their different geographical origin. Similar reports on phenotypic variation among rice genotypes were observed by Elayaraja *et al.*, (2005) [6], Pandey *et al.*, (2009) [18], Hosagoudar and Basavaraj.

The estimation of genetic parameters indicated that phenotypic variance was higher than genotypic variance for all the traits which revealed considerable effect of environment on the expression of these traits. Consequently phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the characters. The estimates of PCV was high for grain yield (22.83 %) and while moderate PCV values were observed for followed by days to 50% flowering (14.77 %), panicles/m² area (11.87 %), plant height (11.83 %) and number of panicles/plant (11.80 %). Similarly, GCV were moderate for grain yield (19.96 %) and for days to 50% flowering (14.39 %). While low GCV values were observed for plant height (10.48 %), followed by number of panicles/plant (8.72 %) and number of panicles/m² area (8.85 %) percent variability is represented graphically in Figure 1. Similar findings were reported by Jayasudha and Sharma (2010) [12], Hosagoudar and Basavaraj (2018) [9].

The large difference between PCV and GCV values observed for panicles per plant followed by panicles per plant and grain yield/ha area indicated large effect of environment on the

expression of these traits. On the contrary, 100 seed weight and straw yield were least affected by environment as indicated by less difference between PCV and GCV values. Ramanjaneyulu *et al.*, (2014) [21] also reported less difference between PCV and GCV for plant height.

The estimates of PCV and GCV clearly indicate the presence of degree of genetic variation; however, it is the estimates of heritability and genetic advance which determine the amount of heritable portion of variation. According to Lush (1949), heritability (broad sense) is the ratio of genotypic variance to phenotypic variance, expressed in percentage. Heritability is classified as high (above 60%), medium (30% - 60%) and low (below 30%). The estimates of heritability are more advantageous when expressed in terms of genetic advance. High estimates of heritability were exhibited for most of the character under study (Table 3) and (Fig. 1).

The estimates of heritability (broad sense) ranged from 54.70 percent to 95.00 percent. Days to 50% flowering (95.00%) showed highest heritability followed by Plant height (78.40%) and grain yield/ha (76.40%), whereas number of panicles/m² as well as number of panicles per plant showed (55.60%) and

(54.70%) heritability respectively. Similar findings of high heritability for Days to 50% flowering were reported by Nishanth *et al.*, (2017) [17].

High heritability values of a trait indicate less effect of environment on their expression. The plant breeder, therefore adopt simple selection method on the basis of the phenotype of the characters which ultimately improves the genetic background of these traits. The estimates of genetic advance as per cent of mean provide more reliable information regarding the effectiveness of selection in improving the traits.

Genetic advance denotes the improvement in the mean performance of the selected individuals over the base population. Perusal of Table 3 revealed high estimates of genetic advance for the traits under study.

The genetic advance as per cent of mean was found to be highest for grain yield/ha (35.95%) followed by days to 50% flowering (28.91%), plant height (19.12%), number of panicles/m² (13.59%) and number of panicles per plant (13.28%). Percent heritability and genetic advance is graphically represented in Figure 1.

Table 1: Mean performance of 17 early maturing rice genotypes

Sl. No.	Genotype	Leaf Blast (SES Score 0-9 scale)	Days to 50% flowering	Plant Height (cm)	Panicle number/plant	Panicle number/m ² area	Grain yield/ha (Kg)
1	AVT-L-1723	5	101.00	71.83	8.83	384.78	2652.78
2	AVT-L-1904	5	107.50	99.50	10.33	450.12	3208.33
3	AVT-01-L-1902	7	75.00	90.83	9.16	399.30	3786.11
4	AVT-01-L-1916	9	100.00	93.50	10.66	464.64	2211.11
5	Co-43	5	98.50	88.33	10.16	442.86	3291.66
6	AICRIP-4	5	91.50	88.83	10.00	435.60	3544.44
7	IVT-L-1805	7	83.00	92.33	9.00	392.04	3805.56
8	IVT-L-1806	7	73.50	81.33	10.00	435.60	2744.44
9	IVT-L-2045	9	97.00	65.33	8.83	384.78	3036.11
10	IVT-L-2048	7	85.50	89.83	11.00	479.16	3066.67
11	IVT-L-RSL-308	9	98.00	81.83	11.16	486.42	3266.66
12	IVT-L-RSL-342	7	72.50	82.83	11.00	479.16	3969.44
13	IVT-L-RSL-501	5	112.00	81.66	11.00	479.16	3777.78
14	IVT-L-RSL-524	5	74.50	90.83	10.66	464.64	3972.22
15	Tunga (LC)	4	82.50	99.67	7.66	333.96	5527.78
16	Narmadha	7	102.00	104.66	10.83	471.90	3711.11
17	Sambamasuri	9	74.50	87.50	11.33	493.68	2886.11
	Mean		89.91	87.68	10.09	439.87	3438.72
	CV		3.30	13.10	14.20	14.22	13.60
	CD (0.05)		8.67	24.36		132.56	991.62

LC- Local check.

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

Source of variation	D.F.	Mean sum of squares				
		Days to 50% flowering	Plant Height (cm)	Panicle number/plant	Panicle number/m ² area	Grain yield/ha (Kg)
Replication	1	1.441	587.390	1.588	366.179	627175.90
Genotypes	16	344.014**	192.284**	2.195**	4235.32**	1087873.69**
Error	16	8.816	23.260	0.643	1209.94	145301.16

** 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 genotypes

Sl. No.	character	Variances		Coefficient of variation%		h ² bs (%)	GAM (%)
		Vg	Vp	GCV	PCV		
1	Days to 50% flowering	167.59	176.41	14.39	14.77	95	28.91
2	Plant Height (cm)	84.50	107.77	10.48	11.83	78.40	19.12
3	Panicle number/plant	0.77	1.42	08.72	11.80	54.70	13.28
4	Panicle number/m ² area	1512	2722	8.85	11.87	55.60	13.59
5	Grain yield/ha (Kg)	471286	616587	19.96	22.83	76.40	35.95

Vg: Genotypic variance, Vp: Phenotypic variance, GCV: Genotypic coefficient of variation, PCV: Phenotypic coefficient of variation, h²bs: Broad sense heritability, GAM: Genetic advance as percent of mean.

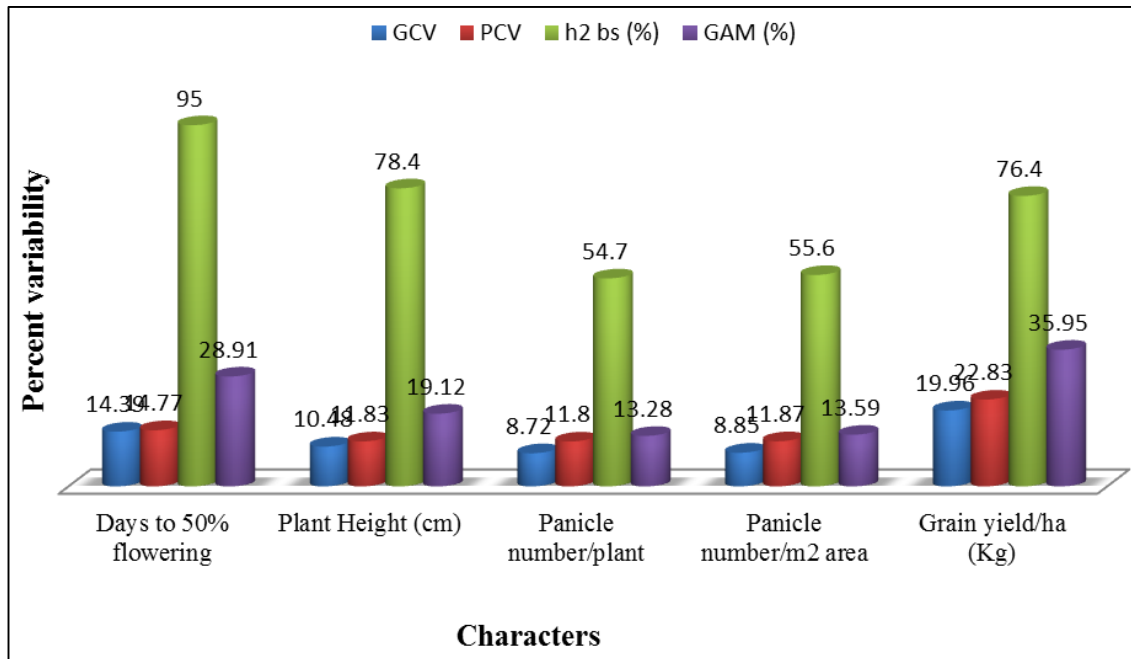


Fig 1: Genotypic (GCV), Phenotypic (PCV) coefficient of variation, heritability and genetic advance as percent of mean for yield and yield attributed traits in 17 rice genotypes

Since the broad sense heritability includes both additive and non-additive components of genetic variance, heritability alone will not be of much practical value hence the concurrent use of genetic advance along with heritability would be more useful in predicting the resultant effect of selection on phenotypic expression (Johnson *et al.*, 1955) [11]. In the present study, grain yield/ha, and days 50% flowering showed high genotypic variance, high heritability and high genetic advance. These findings were in accordance with the results of Selvaraj *et al.*, (2011) [25] and Rita *et al.*, (2009) [22]. The additive gene action is involved in the expression of those characters which show high genotypic variance coupled with high heritability and genetic advance (Panse, 1957) [20] thus can be improved through simple or progeny selection methods while the characters with high heritability coupled with moderate or low genetic advance can be improved by inter-mating superior individuals from segregating population of a cross (Samadhia, 2005) [23].

Conclusion

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 IVT-L-2045 followed by AVT-L-1723 can be selected for the dwarfness trait, while the genotype Narmadha can be selected for tallness trait. The genotypes Sambamasuri and IVT-L-RSL-308 recorded higher number of panicles/plant as well as number of panicles/m². 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. The estimates of PCV were higher than the GCV which indicated high influence of environment on the expression of the traits. The traits like grain yield/ha, and days 50% flowering exhibited high genotypic variance, high heritability coupled with high genetic advance as percent of mean can be considered as relative measures of selection for the higher yield.

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