



Research Article

ASSESSMENT OF PARENTAL GENETIC VARIABILITY IN RICE

AMEENAL M., SHALINI T., GOVINTHARAJ P.*, MANONMANI S. AND ROBIN S.

Department of Rice, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore, 641003, Tamil Nadu, India

*Corresponding Author: Email-govinth.tnau@gmail.com

Received: October 17, 2016; Revised: October 22, 2016; Accepted: October 24, 2016; Published: November 06, 2016

Abstract- The present investigation was carried out to estimate variability parameters for seven characters in ten rice genotypes (two maintainer lines viz., TNAU CMS 2B and COMS 23B, two restorer lines viz., CB 87 R and CB 174 R and C101 PKT, C101 LAC, BL-245, RIL10, Zenith, IRBB 60). The parental lines viz., TNAUCMS 2B, COMS 23B, CB 87 R, C101 PKT and C101 LAC were early and short stature. Variability studies revealed the higher magnitude of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for plant height, number of productive tillers per plant and number of grains per panicle. Higher heritability estimates in broad sense with high genetic advance as percent of mean (except single plant yield) was found for all the traits studied.

Keywords- Genetic variability, Heritability, Genetic advance as per cent of mean, Rice

Citation: Ameen M., et al., (2016) Assessment of Parental Genetic Variability in Rice. International Journal of Agriculture Sciences, ISSN: 0975-3710 & E-ISSN: 0975-9107, Volume 8, Issue 54, pp.-2917-2919.

Copyright: Copyright©2016 Ameen M., et al., This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution and reproduction in any medium, provided the original author and source are credited.

Academic Editor / Reviewer: Gunasekaran Karthika

Introduction

Rice, (*Oryza sativa* L.) is the world's second most important cereal food crop, it is the major caloric source, with nearly 2.7 billion people depending on it as their main food [1]. Rice production is affected by various biotic and abiotic factors [2]. Rice diseases are among the most significant limiting factors threatening food productivity [3]. Annually plant diseases cause huge economic losses and millions are spent in combating diseases on economically important crops [4, 5]. Losses caused by plant diseases affect commercial farmers, subsistence farmers growing food for survival, food markets, wholesalers and the final consumers [6]. Significant yield losses from diseases still occur in rice in spite of continuous improvements in rice breeding. Among the diseases in rice, blast caused by the fungus *Magnaporthe grisea* (anamorph: *Piricularia grisea*) ranks first because of its severity under conducive conditions. Bacterial Blight caused by *Xanthomonas oryzae* pv. *oryzae* (Xoo) is another important disease of rice and is an endemic constraint to rice production worldwide [7].

A number of rice-growing countries in the tropics have explored hybrid rice technology as an approach to build the yield capability in rice to ensure self-sufficiency. However the released hybrid cultivars are seriously damaged by diseases. The susceptibility period for the disease is no longer than that of varieties. During grain filling, hybrid rice management practices such as leaf cutting and rope pulling cause wounds increasing susceptibility to pests and diseases. In order to realize the potentiality of hybrids, there is a need to enhance the disease resistance in parents. Furthermore, a more prominent measure of hereditary assorted qualities is needed in hybrid rice breeding program to reduce the vulnerability to diseases [8].

Genetic variability present in the base population is essential for successful crop improvement programme. Variability expressed in a crop is a result of interaction of heritable and non heritable factors and heritable factors should be given due consideration in the development of high yielding varieties. The degree of heritable variability present in a crop is of awesome significance, since greater the variation wider the scope for selection. The extent of variability is measured by

different variability parameters like PCV, GCV, heritability, genetic advance as percent of mean

The present studies is aimed to assessing genetic variability parameters of yield and yield components in ten parents and to pyramid the blast and bacterial blight resistant genes into the parental lines of released hybrids CORH 3 and CO 4 from Tamil Nadu Agricultural University.

Materials and Methods

Two maintainer lines viz., TNAU CMS 2B and COMS 23B, two restorer lines viz., CB 87 R and CB 174 R and the donor parents for both the diseases (Blast and Bacterial blight) were used for this study. The seed materials were obtained from Department of Rice, Tamil Nadu Agricultural University, Coimbatore. The details about the parental materials used in study [Table-1 & 2]. Seven biometrical traits were recorded on parents under study

Table-1 Details of Recurrent parents used for the study

S. No	Parents	Salient features
1.	TNAU CMS 2B	Matures in 118 days, medium slender grain type
2.	CB 87 R	Matures in 120-125 days, semi dwarf, long slender grain type
3.	COMS 23B	Matures in 128 days, long slender grain type
4.	CB 174 R	Matures in 135 days, medium slender grain type

Table-2 Details of Donor parents used for the study

S.No	Parents	Resistant gene	Chromosome number
BLAST			
1.	C101 PKT	Pi-4(t)	12
2.	C101 LAC	Pi-1(t)	11
3.	BL-245	Pi-2(t), Pi-4(t)	6
4.	RIL10	Pi12(t)	12
5.	Zenith	Piz	6
BACTERIAL LEAF BLIGHT			
6.	IRBB60	Xa21, xa5, xa13	11,5,8

Estimation of genetic parameters in parents

Genetic parameters like variability, GCV, PCV, heritability and genetic advance as percent of mean were calculated by adopting following formula.

Genotypic and phenotypic variance

Genotypic variance (GV) and phenotypic variance (PV) were computed according to the method suggested by Johnson [9]. These components were obtained from the following expectations

Source of variation	Mean square	Expected mean square
Genotype	μ_1	$2e + r(2g)$
Error	μ_2	$2e$

where,

$$\text{Genotypic variance} = \mu_1 - \mu_2 / r$$

$$\text{Phenotypic variance} = (2g + 2e)$$

r = number of replications.

Genotypic and phenotypic coefficient of variation

Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated using the formula suggested by Johnson [9].

$$\text{GCV} = \sqrt{\frac{\text{Genotypic variance}}{\text{Mean}}} \times 100$$

$$\text{PCV} = \sqrt{\frac{\text{Phenotypic variance}}{\text{Mean}}} \times 100$$

Categorization of the range of variation was effected as proposed by Sivasubramanian and Madhavamenon [10].

Percentage of variability	Category
0 – 10	Low
11-20	Moderate
More than 20	High

Heritability

Heritability in broad sense was calculated following the method advocated by Lush [11] and expressed in percentage.

$$\text{Heritability (broad sense)} = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100$$

As suggested by Robinson [12] heritability values were categorized as follows.

Low	–	0 to 30 per cent
Medium	–	31 to 60 per cent
High	–	> 60 per cent

Genetic advance

Genetic advance was estimated by the method given by Johnson [9].

$$\text{Genetic advance} = \frac{\text{Genotypic variance}}{\text{Standard deviation}} \times K$$

Where,

K = Selection differential 2.06 at 5 per cent selection intensity.

$$\text{Genetic advance as per cent of mean} = \frac{\text{Genetic advance}}{\text{General mean}} \times 100$$

The range of genetic advance was classified as suggested by Johnson [9].

Low	–	less than 10 per cent
Moderate	–	10 to 20 per cent
High	–	more than 20 per cent.

Results

Analysis of variance

The analysis of variance for seven traits recorded in ten rice parental lines is presented in [Table-3]. The analysis of variance revealed that significant differences among the parental lines were found for all characters.

Table-3 Analysis of variance for various biometrical traits

Source of variation	Degrees of Freedom	Mean sum of Square						
		DF	PH	NPT	PL	NG	1000 GWT	SPY
Replication	2	13.48	33.10	0.633	2.800	447.218	5.655	0.21
Treatment	9	347.83**	1559.40**	44.22**	30.32**	5979.88**	19.40**	9.90**
Error	18	10.25	25.17	1.744	1.09	543.198	2.96	1.37
Total	29	115.24	501.86	14.85	10.28	2222.584	8.25	3.93

PH: Plant height, NPT: Number of productive tillers, PL: Panicle length, NG: Number of grains per panicle, 1000GW: Thousand grain weight, SPY: Single plant yield

Variability studies

Phenotypic variance

The values of range, mean, genotypic and phenotypic variance, phenotypic and genotypic coefficient of variance, heritability and genetic advance as per cent of mean for seven different characters [Table-4]. Number of filled grains per panicle had the highest phenotypic variance (2354.09) followed by plant height (536.58) and days to fifty percent flowering (122.77) respectively.

Moderate phenotypic variance was recorded by the character, number of productive tillers per plant (15.90) followed by panicle length (10.84). Lowest phenotypic variance was recorded by the character thousand grain weight (8.44) followed by single plant yield (4.21).

Genotypic variance

Number of grains per panicle had the highest genotypic variance (1810.89) followed by, plant height (511.41) and days to fifty percent flowering (112.52) respectively. Moderate genotypic variance was recorded by the character number of productive tillers per plant (14.15).

Lowest genotypic variance was recorded by the character panicle length (9.74), followed by, thousand grain weight (5.47) and single plant yield (2.84).

Genotypic and phenotypic coefficient of variation

The GCV was found to be less than PCV for all studied traits. High genotypic coefficient of variation was recorded by the characters, number of grains per panicle (27.63%), number of productive tillers per plant (24.54%), plant height (21.54%).

Medium genotypic coefficient of variation was recorded by the characters panicle length (12.85%), thousand grain weight (12.64%), days to fifty percent flowering (11.59%). Low PCV was expressed in single plant yield (6.82%)

Phenotypic coefficient of variation was high for number of grains per panicle (31.50%), number of productive tillers per plant (26.01%), plant height (22.06%), and medium phenotypic coefficient of variation was recorded in thousand grain weight (15.70%), panicle length (13.55%), days to fifty percent flowering (12.11%). PCV was low for panicle length (13.55%), single plant yield (8.30%).

Heritability and genetic advance

Estimates of heritability were high for all the characters studied viz., plant height (95.31%), days to fifty percent flowering (91.65%), panicle length (89.89%), number of productive tillers per plant (89.03%), number of grains per panicle (76.93%), single plant yield (67.46%) and thousand grain weight (64.85%).

Genetic advance as percent of mean was highest for the characters number of grains per panicle (49.92) followed by number of productive tillers per plant (47.70%), plant height (43.31%), panicle length (25.09%), days to fifty percent flowering (22.87%). Thousand grain weight (20.97%). Genetic advance as percent of mean was medium in single plant yield (11.53%).

Table-4 Variability parameters for various biometrical traits

Characters	Range	Mean	GV	PV	GCV	PCV	Heritability (%)	GA (%)OF MEAN
DFF (days)	74.00-102.67	91.49	112.52	122.77	11.59	12.11	91.65	22.87
PH (cm)	86.33-146.67	105.00	511.41	536.58	21.54	22.06	95.31	43.31
NPT (no.)	11.00-22.00	15.33	14.15	15.90	24.54	26.01	89.03	47.70
PL (cm)	21.00- 31.67	24.30	9.74	10.84	12.85	13.55	89.89	25.09
NG (no.)	114.00-270.67	154.03	1810.89	2354.09	27.63	31.50	76.93	49.92
1000GWT (g)	13.60-22.23	18.52	5.47	8.44	12.64	15.70	64.85	20.97
SPY (g)	22.67-28.14	24.74	2.84	4.21	6.82	8.30	67.46	11.53

PH: Plant height, NPT: Number of productive tillers, PL: Panicle length, NG: Number of grains per panicle, 1000GW: Thousand grain weight, SPY: Single plant yield.

Discussion

Assessment of variability for different yield contributing characters is essential before planning for an appropriate breeding programme. The analysis of variance disclosed significant difference among the parents for the seven characters studied. Amount of variability present in parents under study is assessed by using genetic parameters such as Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) for all the seven biometrical traits. For all the biometrical traits the difference between Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient Variation (PCV) was small which implies low environmental influence. Higher magnitude of GCV and PCV was recorded for plant height, number of productive tillers per plant and number of grains per panicle. The high GCV and PCV for these traits signify the scope for selection to develop superior genotypes. Similar findings were observed for these traits [13-15]. The traits viz., days to fifty percent flowering, panicle length and thousand grain weight recorded moderate level of GCV indicating considerable amount of variability expressed for these characters. [16, 17] reported moderate level of GCV values with respect to thousand grain weight.

Estimates of GCV and PCV are not sufficient to know the heritable variation. Higher level of precision can be obtained with heritability in conjunction with genetic advance study. For selection of best genotypes for various biometrical traits, heritability coupled with high genetic advance would be more useful. It helps in determining the influence of environment on the expression of the genotype and reliability of characters. In the present study, high heritability with moderate genetic advance as per cent of mean was observed for single plant yield, whereas higher heritability estimates with high genetic advance as percent of mean was recorded for remaining six characters. This study revealed that seven traits would respond to selection. Comparable finding was previously reported by [18]. [19] was reported high genetic advance as per cent of mean for number of grains per panicle

Conclusion

Among the resistant donors for Blast and Bacterial blight genes, Zenith for Blast (Pi_z) and IRBB 60 ($Xa21$, $xa5$, $xa13$) for Bacterial blight were selected and used for hybridization programme.

Conflict of Interest: None declared

References

- [1] Shalini T., Govintharaj P., Ameen M., Manonmani S. and Robin S. (2016) *International Journal of Agricultural Science and Research*, 6(5), 339-346.
- [2] Dai S. and Roger N. B. (2009) *In vitro Cell Development Biology*, 45, 517-524.
- [3] Zhang Q. (2009) *Rice Science*, 16, 83-86.
- [4] Jones D.G and Clifford B.C. (1978) Cereal diseases: Their pathology and

control. BASF, 279.

- [5] Singh U. S., Mukhopadhyay A.N., Kumar J. and Chaube H.S. (1992) In: Plant diseases of international importance- Diseases of cereals and pulses. Prentice-Hall, Inc. 93-98.
- [6] Trench T.N., Wilkinson D.J. and Esterhuysen S.P. (1992) South African plant disease control handbook. Farmer Support Group
- [7] Narayanan N. N., Baisakh N., Oliva N P., VeraCruz C.M., Gnanamanickam S.S., Datta K. and Datta S. K. (2004) *Molecular Breeding*, 14, 61-71.
- [8] Perez L.M., Redoria E.D., Mendioro M.S., Vera Cruz C.M. and Leung H. (2008) *Euphytica*, 164(3), 627-636.
- [9] Johnson H.W., Robinson H.F. and Comstock R.E. (1955) *Agronomy Journal*, 47(4), 314-318.
- [10] Sivasubramanian S. and Menon M. (1973) *Madras Agricultural Journal*, 60, 11-39.
- [11] Lush J.L. (1940) *Proc. Amer. Soc. Animal Production*, 33(3), 293-301.
- [12] Robinson H.F., Comstock R.E. and Harvey P.H. (1949) *Agronomy Journal*, 41, 353-359.
- [13] Mamta Singh K. K. and Singh R.P. (2007) *Oryza*, 44(1), 160-162.
- [14] Ananad Rao S.D., Singh C.M., Suresh, B.G. and Lavanya G.R. (2011) *The Allahabad Farmer*, 67(1), 63-68.
- [15] Idris A. E., Justin F.J., Dagash Y. M. I. and Abuali A. I. (2012) *American Journal of Experimental Agriculture*, 2, 233-239.
- [16] Michael Gomez S. and Kalamani A. (2003) *Plant Archives*, 3 (1), 77-79.
- [17] Kundu A., Senapati B.K., Bakshi A. and Mandal G.S. (2008) *Oryza*, 45(4), 320-323.
- [18] Verma U. (2010) Genetic diversity analysis in exotic rice genotypes. M.Sc thesis. Dept. of GPB, Alhabed
- [19] Prajapati M., Singh C.M., Suresh V., Lavanya G.R. and Jadhav P. (2011) *Electronic Journal of Plant Breeding* 2(2), 235-238.