Mysore J. Agric. Sci., 56 (2) : 194-199 (2022)

Phenotypic Evaluation of Genetic Variability and Selection of Yield Contributing Traits in Recombinant Inbred Lines of Rice (*Oryza sativa* L.) under Submerged Condition

R. LAKSHMEESHA[1], K. M. HARINIKUMAR[2] AND H. B. MAHESH[3]
[1 & 2] Department of Biotechnology, College of Agriculture, UAS, GKVK, Bengaluru - 560 065
[3] Department of Genetics and Plant Breeding, V. C. Farm, Mandya - 571 405
e-Mail : maheshbg@gmail.com

ABSTRACT

Investigation and better understanding regarding the genetic variability existing in a base population of crop is pivotal for crop improvement, so that it can be exploited by plant breeders. The objective of the current study was to estimate the magnitude of genetic variability, heritability and genetic advance of yield and its contributing traits in recombinant inbred lines (RILs) of rice evaluated in a submerged condition. The RIL population was derived from an inter-specific cross between BPT5204 and HPR14 parents. 1255 RILs and parents were evaluated for their performance for various important agronomical traits. Phenotypic data were subjected for descriptive statistical analysis *viz.,* mean, range, standard deviation, coefficient of variation. Preliminary evaluation of RILs showed presence of genotype by environment (G×E) interactions for nine quantitative traits. For few traits higher values of genotypic coefficient of variation (GCV) (18.92- 59.38%), phenotypic coefficient of variation (PCV) (19.42- 69.41%), heritability (73.2-94.84%) and genetic advance as a percentage of mean (GAM) (48.84-70.81%) were observed for plant height, total number of tillers, nonproductive tillers, productive tillers, test weight, five panicle weight and single plant yield. Similarly, higher heritability (h^2) coupled with higher GAM for majority of the traits indicated existence of additive gene action. Low PCV, GCV, GAM and moderate h^2 were observed for days to 50 per cent flowering and panicle length indicating presence of non-additive gene action and can be used for exploitation of heterosis. High GCV and PCV was observed for non productive tillers, single plant yield and test weight indicating that these characters could be used as selection for crop improvement. The Pearson correlation analysis showed that single plant yield was positively correlated with all the traits except plant height.

Keywords : Rice breeding, PCV, GCV, Heritability

RICE, *Oryza sativa* L., is the world's most important staple crop, feeding more than half of the world's population. It is a self-pollinated, short-day, C_3 plant that belongs to the Poaceae family and is originated in South East Asia (Meghana *et al*, 2015). It is a healthy cereal crop that provides 20 per cent of calories and 15 per cent of protein and is consumed by half of the world's population. Rice is also the most important and dependable food crop in India, feeding more than two-thirds of the population. The slogan 'Rice is Life' is most appropriate for India because this crop provides a living for millions of rural households. In India, rice is grown in an area of 43 million ha with the production of 118.43 million tons and average productivity of 2.75 t ha^{-1} (Anon, 2020). Currently, the world's population of around six billion is expected to exceed eight billion by 2030, necessitating a 40 per cent increase in rice productivity to meet the population growth (Khush and Brar, 2002; Bhavsar *et al*., 2017). The development of new genotypes requires knowledge on the genetic variability present in the germplasm of the crop to design efficient breeding program. The knowledge about genetic variability is helpful to understand if these variations are heritable or non-heritable. The magnitude of variation due to heritable component is very important because, it would be a guide for selection of parents for crop improvement (Dutta *et al*,.2013). Therefore, selection for high yield requires knowledge about genetic variability and good understanding of correlation between yield and yield components regarding the genetic material. Genetic variability for agronomic traits is the key component of breeding program for broadening the gene pool of any crop for that matter (Dutta *et al.,* 2013). The success of breeding program depends upon the quantum of genetic variability available for use and the extent to which the desirable characters are heritable. Variability refers to the presence of differences among the individuals of plant population. Variation results due to difference either in genetic constitution of the individual of a plant population or in environment, they have grown. Recombinant inbred lines (RILs) can serve as a powerful tool for genetic mapping. RILs are developed by crossing two inbred lines followed by repeated selfing or sib mating to create a new inbred whose genome is a mosaic of the parental genomes. As each RIL is an inbred and so can be propagated eternally, a panel of RILs has a number of advantages for genetic mapping. Also, the breakpoints in RILs are more dense than those that occur in any one meiosis, greater mapping resolution can be achieved. The existence of genetic variability is essential for improvement of genetic material. Selection is also effective when there is significant amount of genetic variability among the individuals in breeding materials.

MATERIAL AND METHODS

Plant Materials

Parents with diverse genetic background *viz.,* BPT-5204 (good grain qualities and high yield) and HPR14 (high protein content) (Hittalmani, 1990) were crossed to develop 1255 segregating lines and selections were carried out based on phenotypic parameters in RILs of rice.

Experimental Site and Layout

The RIL population along with parents was planted in an augmented design at college of agriculture V.C. Farm, Mandya, during summer 2020 and observations were recorded on individual lines and used for statistical analysis. Twenty one days seedlings were transplanted with 20cm x 10cm spacing and minimum of 15 plants maintained in each line. Recommended cultural practices for rice cultivation were carried out to ensure uniform crop stand as per the package of practices. Phenotypic data was collected for a total of 1255 RILs related to yield and yield contributing traits like days to 50 per cent flowering (DFF) was recorded as the number of days from germination to 50 per cent of plants with initiation of flowering based on visual observation of the each RIL, plant height (PH) was recorded at maturity stage (cm) from base of the plant at soil surface to the panicle tip of main tiller and averaged over 5 plants, number of tillers per plant (TN) was measured by counting total number of tillers per plant at harvesting stage and averaged over five plants, panicle length (PL) (cm) measured from the panicle neck to the tip (excluding awn) at reproductive stage, panicle weight (PW) was calculated by total weight of 5 panicles and averaged, thousand grain weight (TW) (grams) measured by weighing 1000 filled grains from each plant (Mohanty *et al*., 2018).

Statistical Analyses

The data points recorded on the above mentioned traits were statistically analyzed using Excel and R studio. Analysis of variance (ANOVA) was computed for individual genotype. To estimate the contribution made by each factor to variation, broad sense heritability, GAM and Pearson correlation coefficients analysis between yield and its component were computed in order to determine the relationship between the examined traits and yield.

RESULTS AND DISCUSSION

Phenotypic Assessment of RIL Population

ANOVA revealed highly significant and exploitable variability among all the genotypes for nine traits (Table 2). Vast amount of genetic variability in the initial breeding material ensures better chance of producing desired recombinants for improvement of the crop. Significant differences were also observed for GEI variance for all the traits. This suggests the presence of variation among the genotypes for all

TABLE 1

ANOVA (Treatment adjusted) for recombinant inbred lines of rice

Source	Df	1.P.L	5. P. W	DFF	NPT	PH	PT	S. P. Y	TT	TW
Block (ignorig Treatm)	6	8.15 *	13.49 ns	12.14 ns	98 **	606.16 **	95.01 **	50.6 **	344.75 **	1014.39 **
Treatmet (eliminang Blocks)	887	3.6 ns	4 ns	19.14 ns	1.32 ns	176.47 **	10.47 *	20.49 **	15.16 *	16.55 *
Treatment : Check	1	8.64 *	137.97 **	1828.57 **	2.57 ns	7130.31 **	151.14 **	20.64 *	193.14 **	3.02 ns
Treatment : Test and Test vs. Check	886	3.59 ns	3.85 ns	17.09 ns	1.32 ns	168.62 **	10.31 *	20.49 **	14.96 *	16.57 *
Residuals	9	1.64	8.73	11.98	0.53	8.85	2.68	2.73	4.56	4.48

DFF- Days to 50% flowering, PH- Plant height (cm), TT- Total number of tillers, NPT- Number of non-productive tillers, PT- Number of productive tillers. TW- Test weight (gm), 5 P W- 5 Panicle weight (gm), 1 P L- One panicle length, SPY- Single plant yield. ns P > 0.05; * P <= 0.05; ** P <= 0.01

these traits evaluated. This suggested that there were inherent genetic differences among the genotypes.

Genetic Variability, Heritability and Genetic Advance

The PCV and GCV for nine traits are presented in Table 3 and Table 4, respectively. A trend of higher magnitude of PCV than that of GCV, indicating the influence of environmental factors on the expression of the traits evaluated in the study. Higher estimates of PCV (>30%) was recorded for non-productive tillers (69.41), single plant yield (37.63) productive tillers (35.78) and total number of tillers (36.8). Moderate estimates (10 to 30%) of PCV was recorded for test weight (29.53), five panicle weight (27.8) and plant height (19.42), while single panicle length (9.45) and days to 50 per cent flowering (4.53) showed lower estimate (<10%) of PCV.

Higher estimates of GCV (>50%) was recorded for non-productive tillers (59.38), single plant yield (34.73), total number of tillers (31.56) and productive tillers (31.08). Moderate estimates (10 to 30 %) of GCV was recorded for test weight (26.55), five panicle weight (25.46) and plant height (18.92). However single panicle length (7.01) and days to 50 per cent flowering (2.33) traits showed low estimate (<10%). The results were in conformity with Shashidara *et al.* (2019).

High estimate of broad sense heritability (h^2b) (>80%) was recorded for plant height (94.84), single plant yield (85.17), five panicle weight (86.5), test weight (80.85), productive tillers (75.42), total number of tillers (73.54) and non-productive tillers (73.2), whereas low estimate of (<60%) h^2b was recorded in single panicle length (55.06) and days to 50 per cent flowering (26.58) which are in conformity with the findings of Ramesh *et al.* (2020) and Adhikari *et al.* (2018).

The GAM for all the traits varied from 2.48 to 70.81 per cent and the value of GAM was moderately high for all the traits, except days to 50 per cent

TABLE 2

Pre-harvest genetic parameters estimated in RIL population for phenotypic characters

Traits	Mean	Std. Error	Std. Deviation	Range		PCV (%)	GCV (%)	h^2	GAM
				Min	Max				
DFF	89.22	0.15	4.43	75.57	108	4.53	2.33	26.58	2.48
PH	67.44	0.44	13.24	27.73	105.9	19.42	18.92	94.84	38.01
TT	11.29	0.14	4.28	2.67	34.77	36.8	31.56	73.54	55.83
NPT	2.02	0.05	1.61	0	9.04	69.41	59.38	73.2	70.81
PT	9.23	0.12	3.5	0.93	27.68	35.78	31.08	75.42	55.68

DFF- Days to 50% flowering, PH- Plant height (cm), TT- Total number of tillers, NPT- Numberof non-productive tillers, PT- Number of productive tillers. ns P > 0.05; * P <= 0.05; ** P <= 0.0

TABLE 3

Post-harvest genetic parameters estimated in RIL population for phenotypic characters

Traits	Mean	Std. Error	Std. Deviation	Range		PCV (%)	GCV (%)	h^2	GAM
				Min	Max				
TW	16.38	0.16	4.83	7.86	45.82	29.53	26.55	80.85	49.25
5 P W	6.57	0.1	2.85	2.48	15.7	27.8	25.46	86.5	48.84
P L	20.19	0.07	2.05	13.28	26	9.45	7.01	55.06	10.73
SPY	11.41	0.15	4.43	2.28	34.74	37.63	34.73	85.17	66.12

TW- Test weight (gm), 5 P W- 5 Panicle weight (gm), P L- panicle length, SPY- Single plant yield.
ns P > 0.05; * P <= 0.05; ** P <= 0.0

TABLE 4

Phenotypic correlation coefficient among different traits in RILs

PL	5PW	DFF	NPT	PH	PT	SPY	TT	TW
5PW	0.32 ***	0.22 ***	0.07 *	0.27 ***	“0.02	0.12 ***	0.02	0.18 ***
DFF		0.29 ***	0.23 ***	0.11 ***	0.01	0.38 ***	0.09 **	0.00
NPT			0.19 ***	-0.44 ***	-0.10 **	0.09 **	-0.01	0.04
PH				-0.03	0.25 ***	0.05	0.61 ***	-0.25 ***
PT					0.02	0.09 **	0.02	0.06
SPY						0.36 ***	0.90 ***	-0.18 **
TT							0.33 ***	0.08 *
TW								-0.24 **

DFF- Days to 50% flowering, PH- Plant height (cm), TT- Total number of tillers, NPT- Number of non-productive tillers, PT- Number of productive tillers. TW- Test weight (gm), 5 P W- 5 Panicle weight (gm), 1 P L- One panicle length, SPY- Single plant yield. ns P > 0.05; * P <= 0.05; ** P <= 0.0

Plate 1 : General view of the RILs of rice from seedlings stage to reproductive stage

flowering and panicle length. The GAM was high (>60%) for non-productive tillers (70.81), for single plant yield (66.12), while moderate estimates for (>30%) total number of tillers (55.83), productive tillers (55.68), test weight (49.25), plant height (38.01) and low (<20%) for single panicle length (10.73) and days to 50 per cent flowering (2.48) were observed. High heritability coupled with high GAM was observed for the all the characters except single panicle length and days to 50 per cent flowering also recorded by Ramesh *et al.* (2020). High heritability along with high genetic advance was observed for traits *viz.,* non-productive tillers, single plant yield, total number of tillers, productive tillers, test weight, plant height, indicating that these characters are largely controlled by additive gene action, which indicates that improvement in these characters is possible through mass selection and progeny selection. Days to 50 per cent flowering and single panicle length exhibited high level of heritability along with low estimates of genetic advance. These results indicate the role of non-additive genes in inheritance of these characters; hence improvement of these traits through heterosis breeding rather than selection could be adopted. Therefore, selection could be postponed for these characters or these characters could be improved by inter mating of superior genotypes of segregation population. Vanisree *et al.* (2013) also reported non additive gene action for plant height and days to 50 per cent flowering.

The worth of independent secondary traits in the selection process can be understood by their significant association with a dependent trait like yield. Results of yield trait association exhibited significantly high positive correlation with days to 50 per cent flowering, five panicle weight, single panicle length, non-productive tillers except plant height (Table 4).

From the present study, it can be concluded that there is adequate genetic variability in the material studied. High GCV and PCV were observed for nonproductive tillers, single plant yield and test weight indicating the importance of these characters in selection for crop improvement. High heritability along with high genetic advance for plant height, single plant yield and non-productive tillers, indicated that these characters are largely controlled by additive gene action and can be improved by the mass selection and progeny selection. Also, the results suggests that the single plant yield, plant height, non-productive tillers and test weight are important yield contributing traits and selection based on these traits would be most effective to realize higher genetic gain in yield levels.

REFERENCES

ADHIKARI, B. N., JOSHI, B. P., SHRESTHA, J. AND BHATTA, N. R., 2018, Genetic variability, heritability, genetic advance and correlation among yield and yield components of rice (Oriza sativa L.). *J. Agric. Natural Res.*, **1** (1) : 149 - 160.

ANONYMOUS, 2020, ICAR-NRRI Annual Report, 2020.

BHAVSAR, S., SOLANKI, T., AMIN, S. AND JAIN, N., 2017, Assessment of genetic purity of parental lines of hybrid rice using DNA-based markers. *On Lin. J. Bio. Sci.*, **15** (2) : 59.

DUTTA, P., DUTTA, P. N. AND BORUA, P. K., 2013, Morphological traits as selection indices in rice : A statistical view. *Univ. J. Agric. Res.*, **1** (3) : 85 - 96.

KHUSH, G. S. AND BRAR, D. S., 2002, Biotechnology for rice breeding: progress and impact. In: sustainable rice production for food security. *Proceedings of the 20th Session of the International Rice Commission*. Bangkok, Thailand, July, 23 - 26.

KUMAR, S., CHAUHAN, M. P., TOMAR, A. AND KASANA, R. K., 2018, Coefficient of variation (GCV & PCV), heritability and genetic advance analysis for yield contributing characters in rice (*Oryza sativa* L.). *J. Pharm. and Phytochem.*, **7** (3) : 2161 - 2164.

MEGHANA, H. S., SHAILAJA, H., GANDHI, R. V. AND MEERA, N., 2015, Phenotypic screening for salt tolerance at germination and seedling stage and SSR marker validation in rice (*Oryza sativa* L.). *Mysore J. Agric. Sci.*, **49** (4) : 686 - 692.

MOHANTY, S., KUMAR, J., MOHANTY, N., GOUDA, G., PRADHAN, S. K., DASH, S. K. AND BEHERA, L., 2018, Assessment of genetic variability in recombinant inbred lines of rice (*Oryza sativa* L.) using phenotypic traits and molecular markers. *New Agriculturist*, **29** (1) : 1 - 12.

RAGVENDRA, T., SURESH, B. G., MISHRA, V. K., ASHUTOSH, K. AND ASHOK, K., 2011, Genetic variability and character association in direct seeded upland rice (*Oryza sativa*). *Environ. and Ecology*, **29** (4A) : 2132 - 2135.

RAMESH, C., PRASAD, S. R., RAMANAPPA, T. M., DEVARAJU, P. J. AND SIDDARAJU, R., 2020, Estimation of genetic variability parameters in germplasm accessions of rice (*Oryza sativa* L.). *Mysore J. Agric. Sci.*, **54** (2) : 59 - 66.

SHAILAJA HITTALMANI, SHASHIDHAR, H. E. AND SHIVASHANKAR, G., 1990, Purple Puttu a new high yielding protein rice selection. *Curr. Res.*, **18** : 110 - 111.

SHASHIDHARA, N., BIRADAR, H. AND HITTALMANI, S., 2019, Qualitative and quantitative genetic variations in the F_2 Inter varietal cross of rice (*Oryza sativa* L.) under aerobic condition and parental polymorphism survey. *Int. J. Curr. Micro. App. Sci.*, **6** : 2215 - 2225.

VANISREE, S., SWAPNA, K., RAJU, C. D., RAJU, C. S. AND SREEDHAR, M., 2013, Genetic variability and selection criteria in rice. *J. Biol. and Scientific Opinion*, **1** (4) : 341 - 346.

(*Received :* May 2022 *Accepted :* June 2022)