

APPRAISAL OF GENETIC ARCHITECTURE OF YIELD AND ITS CONTRIBUTING TRAITS IN RICE GERMPLASM

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ABSTRACT

The field experiment was carried out during wet season 2013 at Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, Uttar Pradesh to evaluate one hundred thirty four rice germplasm to assess the genetic component of variability for yield and yield attributing characters. The high estimates of GCV and PCV were observed for grain yield per plant, filled grains per panicle, number of effective tillers per plant, total number of filled grain per panicle and panicle weight indicating importance in selection for improving the rice yield. High value of heritability was obtained for all the characters except spikelet fertility percentage. High heritability coupled with high genetic advance as per cent of mean was observed for the grain yield per plant, number of filled grains per panicle, total number of grains per panicle, number of effective tillers per plant, panicle weight, test weight, plant height and days to 50% flowering indicating the less influence of environmental variance in the inheritance of these traits, which can be further improved by simple selection.

Keywords: Variability, heritability, genetic advance, inheritance.

INTRODUCTION

Rice is a cereal crop belongs to genus *Oryza* of family Poaceae. *Oryza sativa* is a cultivated diploid species having 24 chromosomes of AA genome. The *sativa* rice germplasms of the world are commonly divided into three sub-species i.e. Indica, Japonica and Javanica grown in tropical, temperate and in intermediate climate respectively. Rice is a short day self-pollinated crop, needs a hot humid climate with average temperature 21 to 37°C throughout the life period of crop. Rice is grown, particularly in India with a wide range of agro climatic situations, from high altitude Himalayan valleys to the tropical coastal areas of Kerala. Detection and utilization of the genetic variability in crop genomes has been one of the most important tasks for plant geneticists and breeders for understanding the genome architecture and also devising strategies for crop modification and improvement (Varshney *et al.* 2008). Genetic variability is prerequisite for plant improvement to develop high yielding varieties of crops. Evaluation of germplasm has played a wider role in crop improvement and helps in understanding the nature and magnitude of variability for yield and its attributing traits. If this variability is not available naturally then the variability needs to be created by artificially induced mutation. Selection is an effective tool if there exist a real or statistical difference among the performance of the different genotypes. The genotypic coefficients of variation (GCV), phenotypic coefficients of variation (PCV), heritability and genetic advance will play an important role in

exploiting future research projection of rice improvement. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone. The knowledge of genetic variability in a given crop species for characters under improvement is important in any plant breeding programme. Heritability with genetic advance is more helpful in predicting the gain under effective selection. Therefore, the present study was conducted with the objective to determine the level and distribution of genetic variability in diverse rice germplasm for appraisal of genetic architecture of yield and its contributing traits on the basis of different genetic parameters.

MATERIALS AND METHODS

The present investigation was carried out during wet season 2013 at Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi. The experimental seed materials were collected from IRRI, Philippines; NBPGR, New Delhi; CRRI, Cuttack; NDUAT, Faizabad; NRCPB, New Delhi and BHU, Varanasi. The nursery was sown on 09 June 2013, about 21 days old seedlings were used for transplanting in the main field. All entries were grown in a randomized block design with three replications. Each plot consisted of five rows of 1.5 m length with spacing 15×20 cm. Observations were recorded for the attributes *viz.* days to 50% flowering (DF), days to maturity (DM), plant height (cm) (PH), panicle length (cm) (PL), number of effective tillers per plant (ET),

panicle weight (PW), total number of grains per panicle (TG), filled grains per panicle (FG), spikelet fertility percentage (SF), test weight (g) (TW), kernel length (mm) (KL), kernel breadth (mm) (KB), kernel length/breadth ratio (L/B), kernel length after cooking (mm) (KLAC), grain elongation ratio (GER) and grain yield per plant (g) (GYP). The experimental data were compiled by taking mean value over randomly selected plants from all the replications and subjected to the following statistical analysis *viz.* analysis of variance (Panse and Sukhatme 1961), genotypic and phenotypic coefficient of variation

(Burton, 1952), heritability (Lush, 1940), genetic advance as per cent of mean (Johnson *et al.*, 1955).

RESULTS AND DISCUSSION

It is evident from the analysis of variance that the germplasm differed significantly for all the sixteen traits under study (Table 1). Significant variability for various traits in the rice genotypes were also reported by Yaqoob *et al.* (2012) and Chouhan *et al.* (2014). Considerably high range of variation was observed for most of the traits in the present set of accessions suggesting a positive scope of improvement through simple selection.

Table 1: Analysis of variance for sixteen traits in 134 rice germplasm

Source of variation	Df	Mean sum of squares							
		DF	DM	PH	PL	ET	PW	FG	TG
Replicate	2	48.60	257.63	2391.04	246.13	37.78	1.88	2582.41	3094.59
Treatments	133	2191.52**	2329.73**	1729.01**	23.65**	19.91**	1.12**	2981.16**	3501.09**
Error	266	34.39	40.07	60.05	1.89	0.43	0.02	16.60	19.69

Table 1: cont.

Source of variation	Df	Mean sum of squares							
		KL	KB	TW	SF%	LB	KLAC	GER	GYP
Replicate	2	1.6105	0.22	144.7	0.26	0.03	3.32	0.004	587.45
Treatments	133	1.39**	0.196**	76.29**	15.26**	0.58**	2.19**	0.03**	128.71**
Error	266	0.03	0.01	0.67	2.717	0.02	0.1	0.0007	2.82

**Significant at 1% level of significance

Genetic variability: In present investigation, it was observed that the estimates of PCV were slightly higher than GCV for all traits. The differences between the values of PCV and GCV were small. Similar observations were also made by Veerabhadhiran *et al.* (2009), and Paikhomba *et al.* (2014). Both PCV and GCV were higher for grain yield per plant followed by filled grains per panicle, number of effective tillers, total grain, panicle weight and days to 50% flowering (Table 2), indicating these traits are under the major influence of genetic control and less variable due to environmental factors. Therefore, such traits could be relied upon and simple

selection can be practiced for further improvement. The present findings are in consonance with the report made by Anjaneyulu *et al.* (2010) and Singh *et al.* (2014). Plant height, days to maturity, panicle length, kernel length, kernel breadth, kernel length-breadth ratio and kernel length after cooking exhibited moderate PCV and GCV value. Low PCV and GCV estimates was exhibited by spikelet fertility percentage followed by elongation ratio, kernel length after cooking, kernel length, kernel breadth, and panicle length indicating that selection for these traits would not be the more effective in comparison with other traits.

Table 2: Average performance of sixteen quantitative and qualitative traits in 134 rice germplasm

Traits Parameter	DF	DM	PH	PL	ET	PW	FG	TG	KL	KB	TW	SF%	LB	KLAC	ER	GYP	
Range	Max	183.00	213.67	186.11	28.15	15.61	4.89	191.16	208.30	8.42	3.05	36.70	95.17	4.51	10.66	1.70	34.69
	Min	72.33	81.00	83.66	14.35	1.75	1.45	45.68	51.58	4.74	1.63	10.56	81.37	1.91	6.39	1.00	5.96
Grand mean		133.36	168.96	128.21	22.47	8.20	2.32	96.14	107.63	6.19	2.34	21.20	89.08	2.69	8.19	1.33	16.53

Heritability: The GCV provides a measure of comparison of variability and sometimes gives some indication regarding validity of traits for selection. However it does not provide clear picture of the extent of genetic gain to be expected from selection of phenotypic traits, unless heritable function of variation (heritability) is known (Burton 1952). In

present investigation high value of heritability was obtained for days to 50% flowering, days to maturity, plant height, panicle length, number of effective tillers per plant, panicle weight, total number of grains per panicle, filled grains per panicle, test weight, kernel length, Kernel breadth, kernel length/breadth ratio, kernel length after cooking, grain

elongation ratio and grain yield per plant (Table 3). High heritability indicates the scope of genetic improvement of these characters through selection. Similar results have been reported by Panwar *et al.* (1997), Sarawgi *et al.* (2000) and Minnie *et al.* (2013). **Genetic advance:** Genetic advance as percent of mean was high for grain yield per plant, number of filled grains per panicle, total number of grains per panicle, number of effective tillers per plant, panicle

weight, test weight, plant height and days to 50% flowering (Table 3). Genetic advance as percent of mean was medium for days to maturity and kernel length breadth ratio. Genetic advance as percent of mean was lowest for spikelet fertility percentage followed by grain elongation ratio, kernel length after cooking and panicle length these results were in accordance with Dutta *et al.* (2013).

Table 3: Genetic parameters for sixteen quantitative and qualitative traits in 134 rice germplasm

Traits Parameter	DF	DM	PH	PL	ET	PW	FG	TG	KL	KB	TW	SF%	LB	KLAC	ER	GYP
SE of mean (\pm)	3.39	3.65	4.47	0.79	0.38	0.09	2.35	2.56	0.10	0.07	0.47	0.95	0.09	0.18	0.02	0.97
Phenotypic variance	753.4	803.3	616.37	9.14	6.92	0.39	1004.79	1180.16	0.48	0.07	25.88	6.90	0.21	0.80	0.01	44.79
Genotypic variance	719.0	763.2	556.32	7.26	6.50	0.36	988.19	1160.47	0.45	0.06	25.21	4.18	0.18	0.70	0.01	41.96
Environmental variance	34.4	40.07	60.05	1.89	0.43	0.02	16.60	19.69	0.03	0.01	0.67	2.72	0.02	0.10	0.00	2.82
PCV (%)	20.6	16.78	19.36	13.46	32.07	26.86	32.97	31.92	11.20	11.65	24.00	2.95	16.93	10.90	8.27	40.48
GCV (%)	20.1	16.35	18.40	11.99	31.07	26.01	32.70	31.65	10.86	10.59	23.68	2.30	15.95	10.21	8.02	39.18
ECV (%)	4.40	3.75	6.04	6.11	7.95	6.73	4.24	4.12	2.73	4.86	3.86	1.85	5.67	3.82	2.00	10.16
C.V. (%)	4.40	3.75	6.04	6.11	7.95	6.73	4.24	4.12	2.73	4.86	3.86	1.85	5.67	3.82	2.00	10.16
Heritability (%)	95.4	95	90.3	79.4	93.9	93.7	98.3	98.3	94.1	82.6	97.4	60.6	88.8	87.7	94.2	93.7
Genetic advance at K = 2.06	53.96	55.47	46.16	4.94	5.09	1.20	64.22	69.59	1.34	0.46	10.21	3.28	0.83	1.61	0.21	12.92
Gen. Adv. as % of Mean	40.46	32.83	36.00	22.00	62.00	51.86	66.80	64.66	21.70	19.82	48.15	3.68	30.95	19.70	16.03	78.13

The high heritability coupled with high genetic advance as percent of mean was observed for the grain yield per plant (93.7, 78.13), number of filled grains per panicle (98.3, 66.80), total number of grains per panicle (98.3, 64.66), number of effective tillers per plant (93.9, 62), panicle weight (93.7, 51.86), test weight (97.4, 48.15), days to 50% flowering (95.4, 40.46) and plant height (90.3, 36) (Table 2), showing the less influence of environmental variance in the inheritance of trait. Similar results were observed by Sabesan *et al.* (2009) and Mazid *et al.* (2013) and Singh *et al.* (2014). The high heritability coupled with high

genetic advance as percent of mean was observed for grain yield per plant, total grains per panicle and filled grains per panicle indicating these traits were less influenced by environment and phenotypic estimates of such traits would be very close to their actual genetic potential. Thus, these characters were under the influence of additive gene action and a satisfactory selection programme for agronomic improvement is possible.

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