Environment and Ecology 40 (4) : 1981—1985, October—December 2022
ISSN 0970-0420

Study on Genetic Variability, Broad-Sense Heritability and Genetic Advance in Rice (*Oryza sativa* L.) for Yield and its Contributing Traits

Pushpanjali Kushawaha, Pooran Chand, L.K. Gangwar, S. K. Singh, Nirdesh kumar Chaudhary, Shiva Mohan

Received 10 June 2022, Accepted 7 July 2022, Published on 17 September 2022

ABSTRACT

Assessment of genetic variability, broad-sense heritability, and genetic advance in percent of mean were estimated in forty-five F_1^s, obtained by crossing ten genotypes of rice varieties using the half-diallel mating design in this study. The results revealed highly significant differences among the materials used in the current investigation for yield, their contributing traits and their quality characters. The mean sum of squares due to treatment was determined to be highly significant for all fourteen characteristics under study, suggesting that the materials had adequate variability. The difference between estimates of phenotypic or genotypic coefficient of variation was smaller, indicating that environmental influences on the inheritance of those traits were less significant. The result indicates that F_1^s possessed high heritability for traits like grain yield per plant, followed by biological yield per plant, harvest index, spikelet's per panicle, kernel length after cooking, 1000 grain weight, panicle length, grains per panicle, hulling percentage, days to maturity, L/B ratio and the plant height was recorded with the lowest heritability. High heritability coupled with high genetic advance as per cent of mean was observed for gel consistency. In comparison, high heritability coupled with moderate genetic advance was observed for harvest index, followed by grain yield per plant, days to 50% flowering, biological yield per plant, spikelet's per panicle and 1000 grain weight.

Keywords Rice, Coefficient of variation (phenotypic or genotypic), Heritability, Genetic advance.

INTRODUCTION

Rice is essential to the livelihood of billions of people around the world. Possibly the oldest domesticated grain (~10,000 years) belongs to the genus *Oryza* of the Poaceae family. The genus *Oryza sativa* (AA genome) contains both diploid (2n = 24) as well as tetraploid (2n = 48) of this species. All the varieties found in Asia, America, and Europe belongs to *Oryza*

Pushpanjali Kushawaha [1]*, Pooran Chand [2], L.K. Gangwar [3], S. K. Singh [4], Nirdesh Kumar Chaudhary [5], Shiva Mohan [6]
[1,5,6] PhD, [2] Professor, [3] Professor and Head, [4] Associate Professor
Genetics and Plant Breeding SVP University of Agriculture and Technology Meerut, India

Email: pushpanjali.kush@gmail.com
*Corresponding author

Table 1. Analysis of variance for 14 characters in 55 genotypes of rice.

Characters	Source of variation Repli-cation (df=2)	Treat-ment (df=54)	Error (df=108)
Days to 50% flow-ering	9.85	161.76**	11.11
Days to maturity	2.25	84.10**	19.1
Plant height (cm)	18.35	39.54**	10.52
Panicle length (cm)	0.25	5.17**	0.98
Spikelet's per pani-cle	3.38	166.41**	23.86
Grains per panicle	5.53	107.01**	22.57
1000-grain weight (g)	0.21	6.10**	1.14
Biological yield per plant (g)	1.54	44.36**	3.54
Harvest-index (%)	0.58	43.17**	5.14
Gel consistency (mm)	3.26	19.62**	0.88
Hulling percentage	1.86	12.44**	2.8
L/B ratio	0.06	0.13**	0.03
Kernel length after cooking (mm)	0.99	2.97**	0.54
Grain yield per plant (g)	0.1	10.31**	0.82

sativa. Rice varieties of the world are commonly grouped into three subspecies, viz. Indica (India), *Japonica* (Japan) and *Javanica* (Indonesia). Rice is sown under diverse conditions and production systems, but submergence in water is the most common method used worldwide. It is the primary food contributing approximately 40% to the total food grain production for more than 65% of the Indian population. It is the second most cultivated cereal globally and the most widely consumed staple food for about 60% of its population. Knowledge of genetic variability among genotypes is essential to start such a breeding effort aimed at varietal improvement. The extent of variability and its nature form the basis for all crop improvement programs. Estimation of genetic variability in conjunction with the estimates of heritability and genetic advance indicates the possible improvement achieved through selection. The magnitude of heritability, which assesses the relative amount of the heritable fraction of total variation and aids in the selection, determines the degree of success. Genetic advance (GA) under selection, on the other hand, indicates how much of the genetic gain was acquired as a result of selection. As a result, assessments of genetic variability, heritability, and genetic progress will be extremely useful in selecting and breeding high-yielding hybrids with good quality.

MATERIALS AND METHODS

Forty-five rice genotypes were grown in a Randomized Block Design with three replications during *kharif,* 2019-20 and 2020-21 at the technology park of Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut. Each genotype was sown in a three-meter long row with twenty-centimeter row spacing and ten-centimeter plant spacing. The data were recorded on five competitive plants taken from each replication for plant height at maturity (cm), panicle length (cm), spikelet's per panicle, grains per panicle, 1000-grain weight (g), biological yield per plant (g), harvest-index (%), gel consistency (mm), hulling percentage, L/B ratio, kernel length after cooking (mm) and grain yield per plant (g). While for characters, days to 50% flowering along with days to maturity were observed on the whole plot basis. The traits, viz. days to 50% flowering and days to maturity were noted down on a per plot basis. The analysis of variance is calculated. Heritability in the broad-sense (h^2b) is determined and divided into low (below 30%), medium (30–60%), and high (above 60%). Genetic advances in percent over the mean (at 5%) are computed and categorized into low (0-10%), moderate (10-20%), and high (20%). Estimates of PCV and GCV were calculated and categorized into low (below 10%), moderate (10-25%) and high (above 25%).

RESULTS AND DISCUSSION

Analysis of variance

The analysis of variance found extremely significant differences for all fourteen features evaluated among the genotypes in the current study, demonstrating that there is a lot of variation among the forty-five rice genotypes (Table 1). Maximum range of variation was observed for spikelet's per panicle, followed by days to 50% flowering, grains per panicle, days to maturity, biological yield per plant, harvest index,

Table 2. List of mean and range performance parents and hybrid.

Character	Mean	Minimum	Maximum
Days to 50% flowering	95.57	84.65 Pant Basmati - 2 × Pusa Basmati-1718	118.56 (Basmati – 386)
Days to maturity	131.22	122.29 (Vallabh Basmati - 24 × Pusa Basmati - 1637)	145.49 (Basmati - 386)
Plant height	112.26	102.08 (Pusa Basmati - 1 × Pusa Basmati - 1637)	119.37 (Pusa Basmati – 1509)
Panicle length	24.44	20.12 (Pant Basmati – 2)	26.56(Vallabh Basmati - 23 × Basmati – 386)
Spikelet's per panicle	136.86	119.00 (Pusa Basmati - 1)	151.83 (Pusa Basmati - 1121 × Pusa Basmati - 1637)
Grains per panicle	123.43	93.62 (Pant Basmati - 2)	133.55 (Pusa Basmati - 1121)
1000 grain weight	25.31	20.16 (Vallabh Basmati - 24)	28.35 (Pusa Basmati - 1 × Pusa Basmati – 1509)
Biological yield per plant	54.79	43.15 (Pusa Basmati – 1637)	63.89 (Pusa Basmati - 1637 × Pusa Basmati – 1718)
Harvest index (%)	36.59	31.38 (Vallabh Basmati 24 × Pusa Basmati 1121)	41.3 (Pusa Basmati 1 × Pusa Basmati 1718)
Gel consistency	21.98	10.17 (Basmati - 386)	25.61 (Pusa Basmati - 1 × Pusa Basmati – 112)
Hulling percentage	65.35	59.28 (Pusa Basmati - 1509)	68.52 (Basmati - 386 × Pusa Basmati – 1121)
L/B ratio	4.11	3.53 (Basmati CSR - 30)	4.50 (Basmati - 386 × Pusa Basmati – 1121)
Kernel length after cooking	18.59	15.69 (Vallabh Basmati - 24)	20.40 (Pusa Basmati - 1509 × Pusa Basmati – 1121)
Grain yield per plant (g)	20.02	16.41 (Pusa Basmati 1637)	25.45 (Pusa Basmati 1637 × Pusa Basmati 1718)

plant height, hulling percentage, L/B ratio, grain yield per plant, 1000-grain weight, panicle length, gel consistency and kernel length after cooking. These results were in agreement with the findings of Priyanka and Gauraha (2020), Bhargavi *et al.* (2021), Gupta *et al.* (2022).

Mean and range performance of genotypes

The mean and range performance of parents, including crosses for fourteen characters, have been presented in Table 2.

Coefficient of variation

The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) in general. However, the difference between PCV and GCV was smaller, indicating that environmental factors had less of an impact on phenotypic expression (Table 3). The genotypic and phenotypic coefficient of variation was low in traits, viz. harvest index, followed by grain yield per plant, day's to 50% flowering, biological yield per plant, 1000 grain weight, panicle length, kernel length after cooking, spikelet's per panicle, L/B ratio, grain per panicle, days to maturity, plant height and hulling percentage. A moderate coefficient of variation was recorded for gel consistency along with a high variance in grain yield per plant. Similar results were observed by Aditya and Bhartiya (2013), Paikhomba *et al.* (2014), Tripathi *et al*. (2018) and Singh and Verma (2018).

Heritability in the broad-sense

Heritability was recorded for all fourteen traits. The broad-sense heritability estimates for different characters are given in Table 2. In the present study, very high heritability was recorded for the characters, viz. gel consistency and days to 50% flowering. High heritability estimates were observed for grain yield per plant, followed by biological yield per plant, har-

Table 3. Mean, range, coefficients of variation, heritability (broad sense) and genetic advance as per cent of mean for yield attributing and physiological characters in 45 F_1s of rice genotypes.

Genotypes	Mean	Min	Max	Var (g)	Var (p)	Heri-tabi-lity (%)	GA mean 5%	GA mean 1%	GCV (%)	PCV (%)	ECV (%)
Days to 50% flowering	95.57	84.65	118.56	50.22	61.33	81.88	13.82	17.71	7.42	8.19	3.49
Days to maturity	131.22	122.29	145.49	21.67	40.76	53.16	5.33	6.83	3.55	4.87	3.33
Plant height (cm)	112.26	102.08	119.37	9.67	20.19	47.90	3.95	5.06	2.77	4.00	2.89
Panicle length (cm)	24.44	20.12	26.56	1.40	2.38	58.72	7.63	9.78	4.84	6.31	4.05
Spikelet's per panicle	136.86	119.00	151.83	47.52	71.38	66.57	8.47	10.85	5.04	6.17	3.57
Grains per panicle	123.43	93.62	133.55	28.14	50.72	55.49	6.60	8.45	4.30	5.77	3.85
1000-grain weight (g)	25.31	20.16	28.35	1.65	2.80	59.14	8.05	10.31	5.08	6.61	4.22
Biological yield per plant	54.79	43.15	63.89	13.61	17.15	79.35	12.36	15.83	6.73	7.56	3.43
Harvest-index (%)	43.25	36.55	53.08	12.68	17.81	71.16	14.31	18.33	8.23	9.76	5.24
Gel consistency (mm)	21.98	10.17	25.61	6.24	7.13	87.62	21.92	28.09	11.37	12.14	4.27
Hulling percentage	65.35	59.28	68.52	3.22	6.01	53.49	4.13	5.30	2.74	3.75	2.56
L/B ratio	4.11	3.53	4.50	0.03	0.06	51.70	6.48	8.31	4.38	6.09	4.23
Kernel length after cooking (mm)	18.59	15.69	20.40	0.81	1.35	60.23	7.75	9.94	4.85	6.25	3.94
Grain yield per plant (g)	23.60	20.37	28.70	3.16	3.98	79.41	13.83	17.73	7.54	8.46	3.84

vest index, spikelet's per panicle, kernel length after cooking, 1000 grain weight, panicle length, grains per panicle, hulling percentage, days to maturity, L/B ratio and the lowest heritability was recorded for plant height. Almost similar types of results were observed by Kumar *et al.* (2018), Roy and Shil (2020), Singh *et al.* (2021), Mahesh *et al.* (2022).

Genetic advance

The high expected genetic advance as percent of mean was recorded for gel consistency, whereas genetic advance as percent of mean was moderate for harvest index, followed by grain yield per plant, days to 50% flowering, biological yield per plant, spikelet's per panicle and 1000 grain weight, while low was noted for estimates of kernel length after cooking, followed by panicle length, grains per panicle, L/B ratio, days to maturity, hulling percentage and plant height.

Gel consistency had high heritability coupled with genetic advance as a percentage of the mean. While high heritability coupled with moderate genetic advance was observed for harvest index, followed by grain yield per plant, days to 50% flowering, biological yield per plant, spikelet's per panicle and 1000 grain weight. Similar results were shown by Hefena *et al.* (2016), Abebe *et al.* (2017), Akter *et al.* (2018), Adhikari *et al.* (2018), Singh and Verma (2018), Tripathi *et al.* (2018).

CONCLUSION

In the current investigation for yield, its contributing traits, and quality characters, highly significant differences among the materials are found. The mean sum of squares due to treatment was highly significant for all fourteen characteristics, suggesting that the materials had adequate variability. High heritability estimates were observed for characters like gel consistency, days to 50% flowering grain yield per plant, biological yield per plant, harvest index, spikelet's per panicle and kernel length after cooking, indicating that though the character is least influenced by the environmental effects, the selection for improvement for such character may not be useful, because broad-sense heritability is based on total genetic variance which includes both fixable (additive) and non-fixable (dominance and epistatic) variances. However, for some traits, like 1000 grain weight, panicle length, grains per panicle, hulling percentage, days to maturity, L/B ratio, and plant height, low heritability is found, which indicates that the character is highly influenced by environmental effects and genetic improvement through selection will be difficult due to masking effects of the environment on the genotypic effects. The high genetic advance for gel consistency, harvest index, grain yield per plant, days to 50% flowering, biological yield per plant, spikelet's per panicle and 1000 grain weight indicates that the traits are governed by additive genes, and selection will be valuable for improvement of such traits. However, the low genetic advance was noted for estimates of kernel length after cooking, followed by panicle length, grains per panicle, L/B ratio, days to maturity, hulling percentage, and plant height, indicating that the character is governed by non-additive genes in which heterosis breeding may be fruitful. High heritability coupled with high genetic advance as a percent of mean indicates that the most likely the heritability is due to additive gene effects, and selection may be effective. In the result high heritability coupled with high genetic advance as per cent of mean was observed for gel consistency.

REFERENCES

Abebe T, Alamerew S, Tulu L (2017) Genetic variability, heritability and genetic advance for yield and its related traits in rainfed low land rice (*Oryza sativa* L.). *Adv Crop Sci Tecnol* 5 (2) : 2—8.

Adhikari BN, Joshi BP, Shrestha J, Bhatta NR (2018) Genetic variability, heritability, genetic advance and correlation among yield and yield components of rice (*Oryza sativa* L.). *J Agric Natural Resour* 1 (1) : 149—160.

Aditya JP, Bhartiya A (2013) Genetic variability, correlation and path analysis for quantitative characters in rainfed upland rice of Uttarakhand Hills. *J Rice Res* 6(2): 24-34.

Akter N, Khalequzzaman M, Islam MZ, Mamun MAA, Chowdhury MAZ (2018) Genetic variability and character association of quantitative traits in *jhum* rice genotypes. *SAARC J Agric* 16 (1) : 193—203.

Bhargavi M , Shanthi P, Reddy VLN, Mohan Reddy D, Ravindra Reddy B (2021) Estimates of genetic variability, heritability and genetic advance for grain yield and other yield attributing traits in rice (*Oryza sativa* L.). *J Pharm Innov* 10 (5) : 507—511.

Gupta H, Purushottam GY, Yadav SK, Singh S, Kumar S (2022) Genetic variability, heritability and genetic advance for yield and its related traits in rainfed upland rice (*Oryza sativa* L.) genotypes. *The Pharmac Innov J* 11(2) : 2520—2524.

Hefena AG, Sultan MS, Abdel Moneam MA, Hammoud SA, Barutçular C, Sabagh ELA (2016) Assessment of genetic variability and correlation coefficient to improve some agronomic raits in rice. *J Experim Agric Int* 14 (5) : 1—8.

Kumar S, Chauhan MP, Tomar A, Kasana RK (2018) Coefficient of variation (GCV and PCV), heritability and genetic advance analysis for yield contributing characters in rice (*Oryza sativa* L.). *J Pharmacog Phytochem* 7(3) : 2161—2164.

Mahesh G, Ramesh T, Narendar Reddy S, Meena A, Fiyaz RA, Badri J, Jukanti AK (2022) Genetic variability, heritability, genetic advance and path coefficients for grain protein content, quality traits and grain yield in rice (*Oryza sativa* L.) germplasm lines. *The Pharmac Innov J* 11 (3) : 1836—1839.

Paikhomba N, Kumar A, Chaurasia AK, Rai PK (2014) Assessment of genetic parameters for yield and yield components in hybrid rice and parents. *J Rice Res* 2 : 117.

Priyanka AS, Gauraha D (2020) Genetic variability studies for yield and quality parameters in aromatic breeding lines of rice (*Oryza sativa* L.). *J Pharmacog Phytochem* 9 (6) : 1637-1640.

Roy SC, Shil P (2020) Assessment of genetic heritability in rice breeding lines based on morphological traits and caryopsis ultrastructure. *Scientific Rep* 10 : 78—30.

Singh B, Gauraha D, Sao A, Nair SK (2021) Assessment of genetic variability, heritability and genetic advance for yield and quality traits in advanced breeding lines of rice (*Oryza sativa* L.). *The Pharmac Innov* 10 (8) : 1627—1630.

Singh N, Verma OP (2018) Genetic variability, heritability and genetic advance in rice (*Oryza sativa* L.) under salt stressed soil. *J Pharmacog Phytochem* 7 (3) : 3114—3117.

Tripathi N, Verma OP, Singh PK, Rajpoot P (2018) Studies on genetic variability, heritability and genetic advance in rice (*Oryza sativa* L.) for yield and its Components under salt affected soil. *Int J Curr Microbiol Appl Sci* 7: 5316-5324.