



ISSN (E): 2277- 7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2022; 11(1): 1386-1389
© 2022 TPI

www.thepharmajournal.com

Received: 19-10-2021

Accepted: 29-12-2021

PK Yadav

Department of Genetics and
Plant Breeding, Narendra Deva
University of Agriculture and
Technology, Kumarganj,
Ayodhya, Uttar Pradesh, India

PK Singh

Department of Genetics and
Plant Breeding, Narendra Deva
University of Agriculture and
Technology, Kumarganj,
Ayodhya, Uttar Pradesh, India

OP Verma

Department of Genetics and
Plant Breeding, Narendra Deva
University of Agriculture and
Technology, Kumarganj,
Ayodhya, Uttar Pradesh, India

Corresponding Author:

PK Yadav

Department of Genetics and
Plant Breeding, Narendra Deva
University of Agriculture and
Technology, Kumarganj,
Ayodhya, Uttar Pradesh, India

Estimating genetic variability, heritability and genetic advance in rice (*Oryza sativa* L.) for yield and its components under sodic soil

PK Yadav, PK Singh and OP Verma

Abstract

The experimental materials of rice for this investigation was comprised of 22 genotypes as lines (female) and three testers (male) viz., Narendra Usar 3, NDR 359 and CSR 36. Each of three testers was crossed with 22 lines during *kharif*, 2013. The experiment was based on evaluation of a line × tester set of 66 hybrids (F₁s) along with their 22 parents and two check varieties viz., Narendra Usar 3 and Arize 6444, in order to assess twelve characters viz., days to 50% flowering, flag leaf area, (cm²), plant height (cm), panicle bearing tillers per plant, panicle length (cm), spikelets per panicle, spikelet fertility (%), biological yield per plant (g), harvest index (%), L:B ratio, 1000-grains wt. (g) and grain yield per plant (g) under salt affected soil following randomized block design with three replications. The analysis of variance revealed that all the treatments, parents, parent vs crosses, crosses, lines and lines x testers were highly significant for majority of the yield and its contributing traits which indicated sufficient variation among the treatment/materials under study. In general, PCV were higher than the GCV for all the characters under salt affected soil which indicated influence of environment. High heritability coupled with high genetic advance in per cent of mean were observed for flag leaf area, panicle bearing tillers per plant, spikelets per panicle, grains per panicle, biological yield per plant, L:B ratio and grain yield per plant it indicating the preponderance of additive gene action. Hence, emphasis should be given to select these quantitative traits to enhance the yield potential of rice (*Oryza sativa* L.) under salt affected soil.

Keywords: Estimating, variability, heritability, genetic, *Oryza sativa* L.

Introduction

Rice, *Oryza sativa* L. (2n=24) is the staple food for nearly half of the world's population (Garris *et al.* 2005; FAO, 2017) [11, 9]. It is the third highest worldwide produced crop after maize and sugarcane with annual production of 758.8 million tones (503.6 million tons of milled rice) (FAOSTAT, 2015) [10]. Overall production in the Asia has already reached 686.1 million tones (455.3 million tones, milled basis) (FAO, 2017) [9]. It is grown under diverse agro-climatic conditions and over wide geographical range (Cheng *et al.*, 2005) [7]. Salinity as an abiotic stress widely limits the crop production severely (Shannon, 1998) [26]. A saline soil is usually the reservoir of a number of soluble salts such as Ca²⁺, Mg²⁺, Na⁺ and anions SO₄²⁻, Cl⁻, HCO₃⁻ with exceptional amounts of K⁺, CO₃²⁻, and NO₃⁻. A soil can be termed as saline if its EC is 4 dS/m or more (USDA-ARS 2008) [32], (equivalent to approximately 40 mM NaCl) with an osmotic pressure of approximately 0.2 MPa. Salinity is the condition when the EC is sufficient to cause yield reduction of most crops. The pH of saline soils generally ranges from 7- 8.5 (Mengel *et al.* 2001) [17]. Water scarcity, declining water quality for irrigation and soil salinity are problems which are becoming more acute. It is estimated that 20% of all cultivated land and nearly half of irrigated land is affected by salt, greatly reducing the yield of crops to well below their genetic potential. There is limited evidence at present that remediation of saline soils enhance crop yield stability (Tester and Devenport, 2003). Salinity-stress effects on crop grown are manifested by impairment of photosynthetic capacity. High amounts of sodium in the soil solution impair cell metabolism and photosynthesis by imposing an osmotic stress on cell water relations and by increasing the toxicity of sodium in the cytosol. Heritability is the proportion of observed differences on a trait among individuals of a population that are due to genetic differences. Factors including genetics, environment and random chance can all contribute to the variation between individuals in their observable characteristics. Genetic variability is a measure of the tendency of individual genotypes in a population to vary from one another. Variability is different from genetic diversity, which is the amount of variation seen in a particular population. The variability of a trait describes how

much that trait tends to vary in response to environmental and genetic influences. Therefore, present investigation was undertaken with the view of to find out genetic variability in the study materials.

Materials and Methods

The experiment was conducted during *Kharif*, 2014 at the Research Farm of Genetics & Plant Breeding, N.D. University of Agriculture and Technology, Kumarganj, Ayodhya. The experimental materials of rice for this investigation comprised of 22 genotypes as lines (female) and three testers (male) Narendra Usar 3, NDR 359 and CSR 36. Each of three testers was crossed with 22 lines during *Kharif* 2013. Thus, total number of 66 hybrids (F_1) were obtained. The total set of ninety-three genotypes were grown during *Kharif*, 2014 and evaluated along with their parents and two check varieties (Narendra Usar 3 and Arize 6444) in Randomized complete block design with three replications, with the spacing of 20 cm row to row and 15 cm plant to plant. The pH, EC and ESP of were 8.9, 0.28 dSm^{-1} and 68%, respectively for saline soil. Observations were recorded on randomly selected five plants from each entry in each replication. The data were recorded on days to 50% flowering, flag leaf area (cm^2), plant height (cm), panicle bearing tillers per plant, panicle length (cm), spikelets per panicle, spikelet fertility (%), biological yield per plant (g), harvest index (%), L:B ratio, 1000-grains wt. (g) and grain yield per plant (g). Recommended cultural practices were adopted to raise good crop. The mean data of different traits were subjected to analyze by standard statistical and biometrical method for Line x Tester analysis. Analysis of variance was done based on RBD (Panse and Sukhatme, 1961) [23] for each of the characters separately. The phenotypic and genotypic coefficient of variance, heritability in broad sense (Burton and de Vane, 1953) [5] and Genetic advance was estimated (Allard, 1960) [1].

Results and Discussion

The Presence of genetic variability is pre-requisite for selection of superior genotypes during crop improvement programme. Therefore, assessment of extent of variation present in the genetic material is important to estimate the magnitude of improvement that can be achieved in breeding material for various characters. The analysis of variance indicated highly significant mean sum of squares due to treatment for all the 12 characters at 1% level of significance (Table 1). This reveals high variability among the genotypes providing ample scope of selection for different quantitative traits under salt affected soil. Significant variation for various quantitative traits were also reported by Bekele *et al.*, (2013) [4], Nilman *et al.*, (2014) [19], Sandhya *et al.*, (2015) [28] and Saha *et al.*, 2019) [16].

Estimates of phenotypic variances were higher than genotypic variance for all the studied quantitative traits indicating the influence of environmental factors on these traits. Highest phenotypic and genotypic variances were observed for spikelets per panicle (757.64, 782.24) and biological yield per plant (113.95, 117.79) followed by flag leaf area (55.53, 59.59) and plant height (44.97, 46.32) (Table 3). Therefore, selection of desirable genotypes in breeding programme for these traits is favourable. Anjaneyulu *et al.*, (2010) [2] and Idris (2012) [8] also observed similar results during their

experiment in rice. In the present study it was found that there is close correspondence of genotypic variance to phenotypic variance for most of the traits specifying that phenotypic variability is a reliable measure of genotypic variability.

Coefficient of variation estimates i.e. GCV and PCV revealed that phenotypic coefficient of variation (PCV) was slightly higher than genotypic coefficient of variation (GCV) for all the traits revealing very less influence of environment on the expression of traits and selection through phenotype alone could be successful. High estimates of GCV and PCV (> 20%) was recorded for flag L:B ratio (27.65, 24.70) and flag leaf area (24.94, 24.70) indicating large scope of selection for these characters, while other characters had moderate (10-20%) or low GCV and PCV values indicating less variability and need for creation of variation through hybridization and mutation in salt stress soil. Limbani *et al.*, (2017) [10], Prasad *et al.*, (2017) and Saha *et al.*, 2019 [30] also observed close estimates of GCV and PCV for different traits in rice and values of PCV were slightly higher than GCV.

Coefficient of variations measures the amount of variability present in the characters but it alone is not sufficient to determine the expected progress that could be made in quantitative traits (Falconer, 1981) [7]. It has been suggested that estimates of GCV and heritability together provide a better portrait of amount of genetic gain expected under phenotypic selection (Burton and Devane, 1953) [5]. Heritability is a useful quantitative parameter, which considers the role of heredity and environment determining the expression of a trait (Allard, 1960) [1]. In the present study, high estimates of heritability in broad sense (>75%) was observed for all the twelve characters under study, which exhibited moderate heritability (50-75%). Similar observation were made by Padmaja *et al.*, (2008) [22] and Sumanth *et al.*, (2017) [17] having high heritability for various quantitative traits in rice.

The genetic advance is a useful indicator of the progress that can be expected as a result of exercising selection (Vanniarajan *et al.*, 1996) [19]. Since it is dependent on phenotypic variability and heritability in addition to selection intensity, the heritability estimates in conjunction with genetic advance will be more effective and reliable in predicting the response to selection (Johnson *et al.*, 1955) [9]. Genetic advance in percent mean was observed highest (>20%) for grain yield per plant followed by biological yield per panicle, spikelets per panicle, panicle bearing tillers per plant and panicle length. On the other hand, moderate genetic advance (10-20%) was observed for plant height, harvest –index and Days to 50% flowering. Neeta *et al.* (2018) also reported high genetic advance in percent mean for L: B ratio and flag leaf area and under salt stressed soil.

L:B ratio, flag leaf area, grain yield per plant, biological yield per plant and spikelets per panicle characters possessed high heritability coupled with high genetic advance indicated the preponderance of additive gene action. These results are similar to those of Patil *et al.*, 2003 [13] and Saha *et al.*, 2019 [30]. These characters can be improved through simple method of selections. The characters showing high heritability along with moderate or low genetic advance can be improved by intermating superior genotypes of segregating population developed from recombination breeding (Samadia, 2005; Saha *et al.*, 2019) [30].

Table 1: Analysis of variance for randomized block design for 12 characters in rice

Characters d. f.	Source of variation		
	Replications	Treatments	Error
	2	90	180
Days to 50% flowering	0.27	50.98**	1.03
Flag leaf area(cm ²)	4.62*	156.53**	1.06
Plant height (cm)	0.84	131.01**	1.31
Panicle bearing tillers per plant	0.04	4.16**	0.42
Panicle length (cm)	1.91	25.15**	0.89
Spikelets per panicle	36.28	2279.06**	23.96
Spikelet fertility (%)	0.98	34.45**	3.06
Biological yield per plant (g)	17.42*	352.67**	4.01
Harvest-index (%)	3.29	19.77**	1.95
L/B Ratio	0.01	2.74**	0.00
1000- grain weight (g)	0.04	22.17**	0.54
Grain yield per plant (g)	0.71	64.52**	0.53

*,** Significant at 5% and 1% probability levels, respectively.

Table 2: Analysis of variance for 12 characters of line × tester set of crosses and their parents in rice

Characters d.f.	Sources of variation								
	Replications	Treatments	Parents	Lines	Testers	Lines vs testers	Parents vs Crosses	Crosses	Error
	2	90	24	21	2	1	1	65	180
Days to 50% flowering	0.27	50.98**	75.76**	77.54**	59.11**	71.76**	237.21**	38.96**	1.03
Flag leaf area(cm ²)	4.62*	156.53**	160.22**	140.41**	369.61**	157.38**	1695.52**	132.04**	1.06
Plant height (cm)	0.84	131.01**	190.50**	200.05**	4.69*	361.42**	1742.57**	84.26**	1.31
Panicle bearing tillers per plant	0.04	4.16**	2.12**	1.89**	5.55**	0.22	120.41**	3.12**	0.42
Panicle length (cm)	1.91	25.15**	8.46**	9.60**	0.63	0.04	748.05**	20.19**	0.89
Spikelets per panicle	36.28	2279.05**	1077.52**	1153.71**	415.50**	801.74**	84281.05**	1461.12**	23.96
Spikelet fertility (%)	0.98	34.45**	20.00**	19.88**	26.65**	9.24	1864.85**	11.63**	3.06
Biological yield per plant (g)	17.42*	352.67**	92.64**	83.62**	155.79**	155.89**	14536.62**	230.47**	4.01
Harvest-index (%)	3.29	19.77**	7.78**	6.98**	18.89**	2.40	46.73**	23.78**	1.95
L/B Ratio	0.01	2.73**	2.87**	3.05**	0.94**	2.91**	6.21**	2.63**	0.00
1000- grain weight (g)	0.04	22.17**	16.28**	15.08**	21.66**	30.75**	438.55**	17.93**	0.54
Grain yield per plant (g)	0.71	64.52**	13.38**	13.07**	12.69**	21.16**	2581.55**	44.68**	0.53

*,** Significant at 5% and 1% probability levels, respectively.

Table 3: Estimates of general mean, phenotypic (PCV) and genotypic (GCV) coefficient of variation, heritability in broad sense (h²b) and genetic advance in per cent of mean for 12 characters in rice

Characters	General mean ±SE	Coefficient of variation (%)		Heritability in broad sense (%)	Genetic advance in per cent of mean
		PCV	GCV		
Days to 50% flowering	102.08±0.58	4.11	3.98	94.12	7.97
Flag leaf area(cm ²)	30.06±0.59	24.94	24.70	98.13	50.42
Plant height (cm)	92.86±0.66	7.31	7.20	97.08	14.62
Panicle bearing tillers per plant	9.28±0.37	14.58	12.82	77.26	23.22
Panicle length (cm)	24.40±0.54	12.27	11.65	90.17	22.79
Spikelets per panicle	169.36±2.82	16.50	16.24	96.85	32.93
Spikelet fertility (%)	87.48±1.01	4.23	3.74	78.06	6.80
Biological yield per plant (g)	57.31±1.15	18.96	18.64	96.66	37.75
Harvest-index (%)	39.53±0.80	7.12	6.19	75.50	11.08
L/B Ratio	3.46±0.04	27.65	27.54	99.25	56.53
1000- grain weight (g)	23.29±0.42	11.83	11.40	92.91	22.65
Grain yield per plant (g)	22.65±0.42	20.41	20.16	97.56	41.03

Conclusion

The results reflect that certain landraces of rice has the potential for incorporating some of the important and valuable traits for sustainability. In the present experiment, considering the evaluation of important variability parameters i.e. Coefficient of variation, heritability and genetic advance together, it was revealed that flag leaf area, grains per panicle, panicle bearing tillers per plant, spikelet per panicle and plant height are most important characters because they have high heritability coupled with high genetic advance. This indicates involvement of additive gene action in controlling these traits.

Therefore, these characters could be improved through selection in segregating generations. The traits with high heritability and low genetic advance e.g. days to 50% fertility, spikelet fertility and harvest index indicated that they are governed by non-additive action and can be improved by intermating superior genotypes of segregating population developed from recombination breeding. These traits may prove rewarding for breeders.

Reference

1. Allard RW. Principles of Plant Breeding. Publishers by

- John Wiley and Sons Inc. New York, USA. 1960, 485.
2. Anjaneyulu M, Reddy DR, Reddy KHP. Genetic variability, heritability and genetic advance in rice (*Oryza sativa* L.). *Research on Crops*. 2010;11(2):415-416.
 3. Basavaraja T, Asif M, Mallikarjun SK, Gangaprasad S. Variability, heritability and genetic advance for yield and yield attributing characters in different local rice (*Oryza sativa* L.) cultivars. *Asian J. of Bio. Sci.* 2013;8(1):60-62.
 4. Bhattacharya RK. Estimates of genetic parameters of some quantitative characters in rice under stress soil (saline condition). *Oryza*. 1978;15:146-150.
 5. Burton GW, Devane EW. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal*. 1953;45:478-481.
 6. Bekele BD, Rakh S, Naveen GK, Kundur PJ, Shashidhar HE. Estimation of genetic variability and correlation studies for grain zinc concentrations and yield related traits in selected rice (*Oryza sativa* L.) genotypes. *Asian Journal of Biological Sciences*. 2013;4(3):391-397.
 7. Cheng SH, Cao LY, Zhan XD. Techniques for hybrid rice seed production. *Jindun Publishing House*, Beijing, 2005.
 8. Gopikannan M, Ganesh SK. Investigation on combining ability and heterosis for sodicity tolerance in rice (*Oryza sativa* L.). *African J. Agril. Res.* 2013;8(32):4326-4333.
 9. FAO. Rice Market Monitor/July 2017. pp 3-4. (http://www.fao.org/fileadmin/templates/est/COMM_MAR_KETS_MONITORING/Rice/Images/RMM/RMM-Jul17). 2017.
 10. FAOSTAT. World's crop production. Food and agricultural organization. 2015.
 11. Garris AJ, Tai TH, Coburn J, Kresovich S, McCouch S. Genetic structure and diversity in *Oryza sativa* L. *Genetics*. 2005;169:1631-1638. <https://doi.org/10.1534/genetics.104.035642>
 12. Idris AE, Justin FJ, Dagash YMI, Abuali AI. Genetic variability and inter relationship between yield and yield components in some rice genotypes. *American Journal of Experimental Agriculture*. 2012;2(2):233-239.
 13. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. *Agron.* 1955;47:314-318.
 14. Kempthorne O. An introduction to genetical statistics. John Wiley and Sons Inc. New York, 1957, 468-471.
 15. Kumar A, Verma OP. Genetic variability, heritability and genetic advance studies in rice (*Oryza sativa* L.) under sodic soil. *Res. Environ and Life Sci.* 2016;9(2):149-151.
 16. Limbani PL, Gangani MK, Pandya MM. Genetic variability, Heritability and Genetic advance in Rice (*Oryza sativa* L.) *International Journal of Pure and Applied Bioscience*. 2017;5(6):1364-1371.
 17. Mengel K, Kirkby EA, Kosegarten H, Appel T. Principles of plant nutrition. Kluwer, Dordrecht. 2001.
 18. Mall AK, Babu JDP, Babu GS. Estimation of genetic variability in rice. *J. Maharashtra Agric. Univ.* 2005;30(2):166-168.
 19. Nilamani D, Natarajan S, Das AB. Genotypic variations in agromorphological and physico-chemical traits in ethnic aromatic rice (*Oryza sativa*) landraces of Odisha. *Indian Journal of Agricultural Sciences*. 2014;84(8):987-992.
 20. Panwar A, Dhaka RPS, Kumar V. Genetic variability and heritability studies in rice. *Adv. in Plant Sci.* 2007;20(1):47-49.
 21. Prasad S, Verma OP, Tripathi N, Ashish, Yadav PK. Combining ability for yield and its contributing traits in rice (*Oryza sativa* L.) Under salt affected soil. *Int. J. Sci. and Res.* 2015;4(9):1050-1054.
 22. Padmaja D, Radhika K, Subba Rao LV, Padma V. Studies on variability, heritability and genetic advance for quantitative characters in rice (*Oryza sativa* L.). *Journal of Plant Genetic Resources*. 2008;21:3.
 23. Panse VG, Sukhatme PV. Statistical methods for agricultural workers, 2nd Edition ICAR, New Delhi. 1961, 361.
 24. Patil PV, Sarawgi AK, Shrivastava MN. Genetic analysis of yield and quality traits in traditional aromatic accessions of rice. *Journal of Maharashtra Agriculture University*. 2003;28(3):255-258.
 25. Robinson HF, Comstock RE, Harvey PH. Estimates of heritability and degree of dominance in corn. *Agro. J.* 1949;41:353-359.
 26. Shannon MC. Adaptation of plants to salinity. *Adv Agron* 1998;60:75-120.
 27. Sumanth V, Suresh BG, Ram J, Srujana G. Estimation of genetic variability, heritability and genetic advance for grain yield components in rice (*Oryza sativa* L.) *Journal of Pharmacognosy and Phytochemistry*. 2017;6(4):1437-1439.
 28. Sandhya, Babu SG, Kumar R. Genetic Variability, Interrelationship and Path Analysis for Yield Improvement of Rice Genotypes. *The Bioscan*. 2014;9(3):1161-1164.
 29. Samadia DK. Genetic variability studies in Lasora (*Cordiamyxa* Roxb.). *Indian Journal of Plant Genetic Resources*. 2005;18(3):236-240.
 30. Setu Rani, Saha, Lutful Hassan, Md. Ashraful Haque, Mirza Mofazzal Islam, Md. Rasel. Genetic variability, heritability, correlation and path analyses of yield components in traditional rice (*Oryza sativa* L.) landraces *J Bangladesh Agril Univ* 2019;17(1):26-32.
 31. Tripathi N, Verma OP, Singh PK, Rajpoot P. Studies on Genetic Variability, Heritability and Genetic Advance in Rice (*Oryza sativa* L.) for Yield and Its Components under Salt Affected Soil. *International journal of current microbiology and applied sciences*. 2018;7:5316-5324.
 32. USDA-ARS. Research Databases Bibliography on Salt Tolerance. George E. Brown, Jr. Salinity Lab. US Dep. Agric., Agric. Res. Serv. Riverside, CA. 2008.
 33. Vanniarajan C, Rangasamy P, Ramalingam J, Nadarajan N, Arumugampillai. Studies on genetic variability in hybrid rice derivatives. *Crop Research*. 1996;12(1):24-27.