

RESEARCH ARTICLE

Estimates of Genetic Variability, Heritability and Genetic Advance in Rice (*Oryza sativa* L.) Under Sodic Soil

Shiv Prakash Shrivastav¹*, Verma OP ¹, Kanhaiya Lal² and Durga Prasad²

¹Department of Genetics and Plant Breeding, Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya -224 229, India.

²Department of Genetics and Plant Breeding, C.S. Azad University of Agriculture and Technology, Kanpur, India. *Corresponding author Email: ms.shiv92@gmail.com

Received: 6th April, 2023; Accepted: 7th June, 2023

Abstract

The experiment was carried out to evaluate the genetic variability, heritability and genetic advance in rice under the sodic soil condition. Results revealed highly significant variations within parents and hybrids. The five characters *viz.*, number of spikelet's per panicle, grain per panicle, amylose content, flag leaf area and 1000-grain weight showed high estimates of heritability coupled with high estimates of genetic advance as well as less than one average degree of dominance and predictability ratio nearly one in F₁'s. This indicated that the inheritance of these five characters was governed by additive gene action and the direct selection for these characters would be rewarding.

Keywords: Rice (Oryza sativa L.), genetic variability, heritability, genetic advance and sodic soil

Introduction

Rice (Oryza sativa L.) is the most important staple food crop of the world. Asia is the leader in rice production accounting for about 90% of the world's production. India has the world's largest rice-growing area (45million hectares), and ranks second in overall production (130.29 million tonnes) after China, with an average yield of 2895 kg/hectare (Anonymous 2021-22). The success of any breeding programme mainly depends on the quantum of genetic variability and the extent to which the desirable characters are heritable (Tiwari et al., 2011). Heritability and genetic advance are the direct selection parameters, so correct knowledge of heritability and genetic advance is much more essential in formulation of selection strategy. Although the information on above aspects in rice is available, but most of these studies are based on irrigated and normal soil conditions and literature based on salinity conditions are quite meager. Therefore, further studies aimed at generating and comparing information on above aspects in rice, are warranted to facilitate the development of high yielding rice cultivars for above ecosystem.

Materials and Methods

This experiment was carried out at the Main Experimental Station of A.N.D. University of Agriculture and Technology, Narendra Nagar, Ayodhya, India. The experimental material was based on a line x tester set of 63 hybrids (F₁'s) developed by crossing 21 lines (females) with 3 testers (males). An attempt was made to make a sixty three cross combinations during *kharif* season 2017 to generate F₁'s. The 63 F₁'s along with parents and two checks, Jaya and CSR 43 were evaluated to find out the genetic variability, heritability and genetic advance effects of their various attributes on grain yield under the sodic soil in Randomized Complete Block Design with three replications during *kharif* 2018. Phenotypic



(PCV), genotypic (GCV) and environmental (ECV) coefficients of variation for different characters were estimated by formulae suggested by Burton and de Vane (1953). The estimates of heritability in narrow sense ($h_{(ns)}^2$) have been classified by Robinson (1966) into three categories *viz.*, high (> 30%), medium (10-30%) and low (<10%).

Results and Discussion

Analysis of variance

The analysis of variance for different characters of line \times tester set 24 parents and their F_1 , s under sodic soil are presented in **Table 1.** Highly significant variability was found for all the characters in studied materials. Similar finding has also been reported by earlier researchers (Jayasudha *et al.*, 2009; Rahimi *et al.*, 2010; Sanghera and Hussain 2012; Latha *et al.*, 2013; Kargbo *et al.*, 2019; Sarker *et al.*, 2020 and Kulsum *et al.*, 2022). The analysis of variance revealed that mean squares due to parents v/s crosses were highly significant or significant for all the characters except flag leaf area in F_1 's. Similar result has also been supported by earlier researchers (Rahimi *et al.*, 2010; Sanghera *et al.*, 2012; Bassuony *et al.*, 2021 and Mazal *et al.*, 2021).

Coefficients of variation

The phenotypic (PCV) and genotypic (GCV) coefficients of variation for the eighteen characters have been presented in **Table 2.** The magnitude of phenotypic coefficient of variation was higher than the corresponding genotypic coefficient of variation for all the traits. The high estimates of phenotypic and genotypic coefficient of variation (> 20%) were estimated for amylose content, grain per panicle, spikelet's per panicle, flag leaf area, grain yield per plant in F₁'s. Similar results have also been reported by earlier researcher (Khedikar *et al.*, 2003; Saxena *et al.*, 2005; Singh and Singh, 2005; Dhanwani *et al.*, 2013; Gyawali *et al.*, 2018; Hasan *et al.*, 2020; Chavan *et al.*, 2022).

Estimates of heritability and genetic advance

The estimates heritability in narrow sense and genetic advance in per cent of mean have been presented in **Table 3.** High estimates of heritability in narrow sense were recorded for flag leaf area (94.36), amylose content (89.86), protein content (84.15), 1000-grain weight (76.84), panicle bearing tillers per plant (75.92), spikelets per panicle (66.91), panicle length (56.17), grains per panicle (55.23) in F_1 generation. Similar result has also been reported by earlier research (Sanghera and Hussain. 2012).

High estimates of genetic advance per cent of mean were reported for spikelets/panicle, grain per panicle, amylose content, plant height, flag leaf area and 1000-grain weight in F₁ generation. Similar result has also been reported by earlier researchers (Kargbo *et al.*, 2019, Prasad *et al.*, 2017 and Jaiswal *et al.*, 2020).

Some of the characters *i.e.*, flag leaf area, panicle bearing tiller per plant, panicle length, spikelets per panicle, grain per panicle, 1000-grain weight, amylose content and protein content showed less than unity of average degree of dominance in F₁s, revealing lack of dominance. The predictability ratio was lesser than one for all the characters studied in F₁s and above mention traits *i.e.*, flag leaf area, panicle bearing tiller per plant, panicle length, 1000-grain weight, amylose content and protein content showed close to one predictability ratio, this finding state that these characters was governed by additive gene. The same finding have also been reported by earlier reporters (Awad-Allah *et al.*, 2016; Bassuony and Zsembeli 2021; Abo-Yousef *et al.*, 2022).

Conclusion

From the study, it could be concluded that most of the characters were governed by dominant gene action. The five characters, spikelets/panicle, grain per panicle, amylose content, flag leaf area and 1000-grain weight showed high estimates of narrow sense heritability



Table 1: Analysis of variance for 18 characters of line × tester set of crosses (F₁s) and their parents in rice under sodic soil

						Sources of	Sources of variation					
Characters	Replica- tions	Treatments	Parents	Parents (Line)	Parents (testers)	Line vs testers	Parents vs Crosses	Crosses	Lines Effect	Testers Effect	Lines × testers Effect	Error
d.f.	2	98	23	20	2	1	1	62	20	2	40	172
Days to 50% flow- ering	4.533	23.844**	19.196**	19.411**	3.111	47.056**	55.643**	25.055**	64.550**	1.466	6.488**	3.591
Chlorophyll content	0.124	13.149**	9.791**	8.740**	14.066**	22.281**	46.735**	13.853**	35.210**	11.142*	3.310**	0.244
Leaf nitrogen	0.001	0.019**	0.016**	0.013**	0.001	0.107**	0.023**	0.019**	0.046**	0.005	0.007**	0.001
Leaf temperature	0.128	12.051**	11.205**	3.043**	0.032	196.801**	360.198**	6.749**	12.214**	0.077	4.350**	0.123
Flag leaf area (cm²)	0.596*	147.160**	134.078**	149.315**	47.452**	2.612**	0.334	154.381**	477.493**	0.715	0.508**	0.158
Plant height (cm)	0.794	415.83**	520.247**	477.477**	583.108**	1249.920**	373.497**	377.788**	1114.465**	84.964*	24.091**	1.9523
Panicle bearing tillers/plant	0.002	13.517**	13.118**	13.428**	2.919**	27.314**	120.576**	11.938**	36.594**	0.021	0.206**	0.091
Panicle length (cm)	0.031	20.710**	25.136**	19.019**	3.969**	189.815**	45.582**	18.667**	56.134**	1.920	0.771**	0.446
Spikelets/panicle	5.107	4078.566**	1259.884**	1190.030**	2192.111**	792.508**	44748.580**	4468.238**	13596.620**	172.577	118.832**	5.561
Grains/panicle	24.969*	3472.527**	1397.688*	1390.316**	2072.444**	195.627**	26821.710**	3865.625**	11463.930**	1881.370**	165.687**	6.810
Spikelet fertility (%)	2.712	131.232**	116.838**	130.307**	19.6612**	41.815**	66.844**	137.610**	247.490**	435.496**	67.776**	3.992
Biological yield/ plant (g)	1.184	140,447**	137.447**	118.549**	387.111**	16.071**	3702.759**	84.104**	205.699**	135.894**	20.716**	2.180
Harvest index (%)	1.191	45.352**	61.207**	64.483**	58.461**	1.172	281.575**	35.660**	55.080**	181.603**	18.653**	2.338
L/B ratio	0.024	0.655**	0.781**	0.638**	2.491**	0.218**	0.106**	0.617**	1.581**	0.757**	0.128**	0.010
1000 -grain weight (g)	1.737*	24.200**	23.901**	26.424**	5.003**	11.241**	23.592**	24.321**	74.567**	0.302	0.398	0.369
Amylose content	0.000	200.271**	186.176**	211.551**	8.976**	33.090**	10.504**	208.561**	646.506**	0.001	0.016	0.001
Protein content (%)	0.001	0.512**	0.4523**	0.517**	0.025**	0.014**	0.315**	0.537**	1.655**	0.004	0.006**	0.001
Grain yield/plant (g)	0.048	33.619**	19.249**	16.884**	51.051**	2.947**	949.83**	24.172**	47.133**	99.290**	8.936**	0.081

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



coupled with high genetic advance as well as less than one average degree of dominance and predictability ratio in F₁ generations. This indicated very clearly that

the inheritance of these five characters was governed by additive gene action and the direct selection for these two characters would be rewarding.

Table 2: Estimates of general mean, phenotypic (PCV) and genotypic (GCV) coefficient of variation for 18 characters in rice under sodic soil

S. No.	Characters	General mean ±SE	Coefficient of	variation (%)
S. NO.	Characters	General mean ±SE	PCV	GCV
1	Days to 50% flowering	84.4944±SE1.0789	3.7800	3.0563
2	Chlorophyll content	13.0219±SE0.2813	16.5523	16.1190
3	Leaf nitrogen	0.5931±SE0.0143	13.7167	13.0572
4	Leaf temperature	35.0979±SE0.2004	5.8070	5.7211
5	Flag leaf area (cm ²)	32.7261±SE0.2258	21.3384	21.3045
6	Plant height (cm)	114.3304±SE0.7990	10.5977	10.5276
7	Panicle bearing tillers/plant	10.9906±SE0.1714	19.2656	19.0731
8	Panicle length (cm)	24.5035±SE0.3789	11.0447	10.7112
9	Spikelets/panicle	157.4007±SE1.3502	23.2804	23.2324
10	Grains/panicle	132.7453±SE1.6431	25.5728	25.4818
11	Spikelet fertility (%)	84.1179±SE1.2496	8.1508	7.7292
12	Biological yield/plant (g)	40.4981±SE0.8486	17.0131	16.6170
13	Harvest index (%)	39.1072±SE0.8772	10.3499	9.5840
14	L/B ratio	2.9280±SE0.0558	16.0935	15.7477
15	1000-grain weight (g)	24.4255±SE0.3451	11.7572	11.4968
16	Amylose content	18.8346±SE0.0155	43.0035	43.0033
17	Protein content (%)	6.2306±SE0.0199	6.5868	6.5632
18	Grain yield/plant (g)	15.8858±SE0.1621	20.9624	20.8868

Table 3: Heritability in narrow sense and genetic advance in per cent of mean for 18 characters in rice under sodic soil

Characters	Heritability	Genetic advance in	Average degree of dominance	Predictability ratio
Characters	$(h^2_{(ns)}^{0})$	per cent of mean	$\sqrt{\dot{6}^2 s/2\dot{6}^2 g}$	$26^2g/26^2g+6^2$
Days to 50% flowering	13.6550	0.4452	1.6804	0.2615
Chlorophyll content	14.9678	0.3512	2.2939	0.1597
Leaf nitrogen	9.4691	0.0097	2.9593	0.1025
Leaf temperature	2.9568	0.0745	5.6473	0.0304
Flag leaf area (cm ²)	94.3605	3.3689	0.2031	0.9604
Plant height (cm)	44.7904	3.5190	1.0643	0.4689
Panicle bearing tillers/plant	75.9264	0.8344	0.4202	0.8499
Panicle length (cm)	56.1769	0.8865	0.5741	0.7521
Spikelets/panicle	66.9151	15.0828	0.6865	0.6797
Grains/panicle	55.2367	12.6391	0.8815	0.5627
Spikelet fertility (%)	5.3870	0.5423	4.0656	0.0570
Biological yield/plant (g)	14.4625	0.8465	2.3004	0.1589
Harvest index (%)	4.7966	0.2525	4.1666	0.0545
L/B ratio	17.3950	0.0815	2.0960	0.1854
1000-grain weight (g)	76.8403	1.1987	0.1496	0.9781
Amylose content	89.8609	4.0346	0.0365	0.9987
Protein content (%)	84.1591	0.1871	0.3903	0.8678
Grain yield/plant (g)	8.6103	0.3202	3.2431	0.0868



References

- Abo-Yousef MI, Elseidy EH, Talha IA and Elnagar OA. 2022. Genetics studies of grain yield and related traits of agronomic importance using triple test cross analysis in rice. In 2nd International Conference on Sustainable Ecological Agriculture 2. Uluslararası Sürdürülebilir Ekolojik Tarm Kongresi (87).
- Anonymous. 2021-22. Directorate of Economics And Statistics, Dept. of Agriculture and Co-operation. Ministry of Agriculture, Government of India.
- Awad-Allah MMA, Wissa MT and Elmoghazy AM. 2016. Line× tester analysis and heterosis for grain quality characters of some parental lines of hybrid rice (*Oryza sativa* L.). *Minufiya Journal of Agriculture Research*, 41: 567-586.
- Bassuony NN and Zsembeli J. 2021. Inheritance of some flag leaf and yield characteristics by half-diallel analysis in rice crops (*Oryza Sativa* L.). *Cereal Research Communications*, 49: 503-510.
- Burton GM and de Vane EH. 1953. Estimating heritability in tall fescue (*Festucaarundinacea*) from replicated clonal material. *Agronomy Journal*, 45:471-481.
- Chavan BR, Dalvi VV, Kunkerkar RL, Mane AV and Gokhale NB. 2022. Studies on genetic variability for yield and yield contributing traits in aromatic rice (*Oryza sativa* L.). *The Pharma Innovation Journal*, 11: 1732-1735.
- Dhanwani RK, Sarawgi AK, Solanki A and Tiwari JK. 2013. Genetic variability analysis for various yield attributing and quality traits in rice (*O. sativa* L.). *The Bioscan*, 8: 1403-1407.
- Gyawali S, Poudel A and Poudel S. 2018. Genetic Variability and Association Analysis in Different Rice Genotypes in Mid-Hill of Western Nepal. *Acta Scientific Agriculture*, 2: 69-76.

- Hasan JM, Kulsum UM, Majumder RR and Sarker U. 2020. Genotypic variability for grain quality attributes in restorer lines of hybrid rice. *Genetika*, 52: 973-989.
- Jaiswal R, Gaur SC, Jaiswal SK and Kumar A. 2020. An estimate of variability, heritability and genetic advance for grain yield and yield components in bread wheat (*Triticum aestivum L.*). *Current Journal of Applied Science and Technology*, 39: 1-6.
- Jayasudha S and Sharma D. 2009. Combining ability and gene action analysis for yield and its components in rice (*Oryza sativa* L.). *Journal of Rice Research*, 2: 105-111.
- Kargbo SS, Showemimo F, Akintokun P and Porbeni J. 2019. Combining ability analysis and gene action for yield and yield related traits in rice (*Oryza sativa* L.) under saline conditions. *Journal of Plant Breeding and Genetics*, 7(2): 63-74.
- Kempthorne O. 1957. An introduction to genetic statistics. *John Willey and Sons, Inc. New York*, p.p. 468-471.
- Khedikar VP, Bharose AA, Sharma D and Khedikar YP. 2003. Study on genetic parameters in scented rice genotypes. *Journal of Soils and Crops*, 13 (2): 338-342.
- Kulsum U, Sarker U and Rasul MG. 2022. Genetic variability, heritability, and interrelationship in salt-tolerant lines of T. *Amanrice*. *Genetika*, 54: 761-776.
- Latha S, Sharma D and Sanghera GS. 2013. Combining ability and heterosis for grain yield and its component traits in rice (*Oryza sativa* L.). *Notulae Scientia Biologicae*, 5: 90-97.
- Mazal TM, ElShnawy MM, Anis GB and Hussein FA. 2021. Genetic analysis of some qualitative and quantitative traits in rice (*Oryza sativa* L.). *Journal of Plant Production*, 12: 577-583.



- Prasad KR, Radha Krishna KV, Bhave MHV and Subba-Rao LV. 2017. Genetic variability, heritability and genetic advance in boro rice (*Oryza sativa* L.) germplasm. *International Journal of Current Microbiology and Applied Sciences*, 6: 1261-1266.
- Rahimi M, Rabiei B, Samizadeh H and Kafi GA. 2010. Combining ability and heterosis in rice (*Oryza sativa* L.) cultivars. *Journal of Agricultural Science & Technology*, 12: 223-231.
- Robinson HF. 1966. Quantitative genetics in relation to breeding on the contentnial of the mendelism. *Indian Journal of Genetics*, 26A: 171-187.
- Sanghera GS and Hussain W. 2012. Heterosis and combining ability estimates using line x tester analysis to develop rice hybrids for temperate conditions. *Notulae Scientia Biologicae*, 4: 131-142.

- Sarker U. 2020. Variability, heritability, character association, and path coefficient analysis in advanced breeding lines of rice (*Oryza sativa* L.). *Genetika*, 52: 711-726.
- Saxena RR,Saxena RR,Motiramani NK, Nichal SS and Sahu RK. 2005. Studies on variability, heritability and genetic advance in scented rice germplasm accessions. *Journal of International Academicia*, 9: 487-489.
- Singh RK and Singh O. 2005. Genetic variation for yield and quality characters in mutants of aromatic rice. *Annals of Agricultural Research*, 26: 406-410.
- Tiwari R, Suresh BG, Mishra VK, Kumar A and Kumar A. 2011. Genetic variability and character association in direct seeded upland rice (*Oryza sativa* L.). *Environment and Ecology*. 29: 2132-2135.