



## African Journal of Biological Sciences



### Studies on genetic variability, Heritability, Genetic advance, Correlation, and path coefficient analysis in rice (*Oryza sativa* L.)

Siddheshwar Ravsaheb Korake, Shiv Prakash Shrivastav\* and Harmanpreet Kaur  
Department of Genetics and Plant Breeding, School of Agriculture, Lovely Professional University, Jalandhar - Delhi, Grand Trunk Rd, Phagwara, Punjab 144001.

\*e-mail: [shiva.26060@lpu.co.in](mailto:shiva.26060@lpu.co.in)

#### ABSTRACT

**Background:** Rice (*Oryza sativa* L.) is the most important staple food crop of the world. Rice is an essential source of nutrition for billions of people on the planet. there is immense need to development of high yielding coupled with quality, multiple resistance, and wider adaptive rice varieties to fulfill requirement and ensure food security. The yield is a complex trait that depends on various attributes. Therefore, the knowledge about genetic variability, Heritability and genetic advance and relationship of different attributes to yield is crucial for making efficient selection strategy.

**Methods:** The experiment was carried out to evaluate the genetic variability, heritability and genetic advance, correlation, and path coefficient analysis in rice. The experimental material was based on a line x tester set of 24 hybrids ( $F_1$ 's) developed by crossing 8 lines (females) with 3 testers (males). An attempt was made to make twenty-four cross combinations ( $F_1$ 's) during *Kharif* season 2022. The 24  $F_1$ 's along with parents and two check varieties *i.e.* PR-26 and Pusa Basmati 1121 were evaluated at the Main Experimental Station of Lovely Professional University, Punjab, India in Randomized Complete Block Design with three replications during *Kharif* 2023.

**Result:** The experimental result revealed highly significant variations for all traits except panicle length and the L/B ratio in parents and their crosses. For every trait under investigation, the phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV). The high estimates of phenotypic and genotypic coefficient of variation (> 20%) were estimated for panicle bearing tillers per plant (PCV=21.46%, GCV=20.93%), flag leaf area (PCV=21.39%, GCV=21.09%), grain yield per plant (PCV=20.57%, GCV=20.12%) in  $F_1$ 's. The estimates of heritability in broad sense ( $h^2_{(bs)}$ ) and genetic advance in percent of mean. High estimates of broad sense heritability (>75%) were recorded for the Days to 50% flowering, flag leaf area, panicle bearing tillers per plant, 1000-grain weight, spikelets per panicle, biological yield per plant, plant height, grains per panicle, grain yield per plant, spikelet fertility, harvest index in  $F_1$ 's crosses. The genetic advance in per cent of mean was found to be very high (>30%) for, flag leaf area (42.82%), panicle bearing tillers per plant (42.06%), biological yield per plant (35.01%), grain yield (40.54%) in  $F_1$ 's. The high estimates of genetic advance in per cent of mean (>20%) were recorded for spikelet per panicle (22.04%), grain per panicle (23.92%) 1000-grain weight (23.06%), in  $F_1$ 's crosses. The grain yield per plant exhibited highly significant and positive association at phenotypic level with L/B ratio (0.4187) followed by spikelets per panicle (0.4283), harvest index percent (0.5007), panicle bearing tillers per plant (0.5386), biological yield per plant (0.8685), in  $F_1$ 's.

**Key words:** Rice (*Oryza sativa* L.), genetic variability, heritability, genetic advance, correlation, and path coefficient analysis

## 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 largest area 46.38 million hectare constituting 28.26% of the land under rice in the world and rank second in total production 130.29 million tonnes next to China with an average productivity of 2809 Kg/hectare (DAC and FW, 2021-22). It is one of the major food crops of the developing world and forms the staple diet of about half of the world's population. More than 90 per cent of the world's rice is grown and consumed in Asia, known as the rice bowl of the world, where 60 per cent of the earth's people and two third of world's poor live (Khush and Virk, 2000). Asia is the leader in rice production accounting for about 90% of the world's production. About 75% of the world's supply is consumed by the people in Asian countries and thus, rice is of immense importance to food security of Asia. The demand for rice is expected to increase with continuous increase in global population.

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. 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

The experiment was carried out at the Main Experimental Station of Lovely Professional University, Punjab, India. The experimental material was based on a line x tester set of 24 hybrids ( $F_1$ 's) developed by crossing 8 lines (females) with 3 testers (males). An attempt was made to make twenty-four cross combinations ( $F_1$ 's) during *Kharif* season 2022. The 24  $F_1$ 's along with parents and two check varieties *i.e.* PR-26 and Pusa Basmati 1121 were evaluated to find out the genetic variability, heritability, genetic advance effects, correlation, and path coefficient analysis of their various attributes on grain yield in Randomized Complete Block Design with three replications during *Kharif* 2023. The observations were recorded on thirteen different traits *i.e.* days to 50% flowering, flag leaf area ( $\text{cm}^2$ ), plant height (cm), panicle bearing tillers/plant, panicle length (cm), spikelets/panicle, grains/panicle, spikelet fertility (%), biological yield/plant (g), harvest index (%), L/B ratio, and grain yield/plant (g) in rice (*Oryza sativa* L).

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 ( $h^2$  (ns)) have been classified by Robinson (1966) into three categories viz., high (>30%), medium (10-30%) and low (<10%). Estimates of correlation and direct and indirect influences were made for each of the thirteen characters. We computed the basic correlations ( $r$ ) between different features at the phenotypic ( $p$ ) and genotypic ( $g$ ) levels, as suggested by Searle (1961). We also carried out route coefficient analysis according to the guidelines provided by Dewey and Lu (1959). Furthermore, we estimated heritability in the narrow sense ( $h^2$  (ns)) using formulas by Johnson *et al.* (1955) and assessed genotypic and phenotypic coefficient of variations using techniques outlined by Singh and Chaudhary (1985) and Burton (1952). Lastly, we calculated genetic progress using methods from Allard (1960) and Johnson *et al.* (1955).

## RESULTS AND DISCUSSION

### Analysis of variance

The analysis of variance for thirty-five genotypes of line  $\times$  tester set comprising of twenty-four crosses and eleven parents is 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 replication non-significant for all characters except flag leaf area, panicle length, and 1000 grain weight these were showed significant variances in  $F_1$ 's. Similar researchers have found result Dey (2010); Kamboj *et al.*, (2018); Zewdu (2020); and Abdalla *et al.*, (2021).

The analysis of variance revealed that mean squares due to treatments and parents were highly significant for all the characters except L/B ratio in treatments. Similar studies have reported in the results Devi *et al.*, (2017); Dhurai *et al.*, (2014); Umarani *et al.*, (2017); Devi *et al.*, (2016); Sahu *et al.*, (2017); Aditya and Bhartiya (2015); and Dodake *et al.*, (2022) and panicle length and L/B ratio in parents of hybrids. The analysis of variance revealed that mean squares due to parents (lines) were highly significant for all the characters except panicle length and L/B ratio in  $F_1$ 's. Earlier studies have found in similar result Ratna (2009); and Panchal *et al.*, (2019). It further revealed that mean squares due to parents (tester) were highly significant for all the characters except non-significant variances for panicle length, spikelet per panicle, spikelet fertility harvest index and L/B ratio in  $F_1$ 's.

The analysis of variance revealed that mean squares due to line *vs* tester were highly significant for all the characters except non-significant variances for spikelet fertility, L/B

ratio and grain yield per plant in  $F_1$ 's. Previous investigators have likewise documented comparable findings (Singh *et al.* 2019; and Sanghera and Hussain, 2012).

The analysis of variance revealed that mean squares due to parents vs crosses were highly significant for all the characters except significant variances for panicle length and L/B ratio in  $F_1$ 's. Similar result has been supported by earlier researchers (Rahimi *et al.*, 2010; Sanghera *et al.*, 2012; Bassuony *et al.*, 2021; and Mazal *et al.*, 2021).

The analysis of variance revealed that mean squares due to crosses were highly significant for all the characters except significant variance panicle length and non-significant L/B ratio in  $F_1$ 's. Similar outcomes have been noted by prior researchers as well (Sultana *et al.*, 2016; Kamboj *et al.*, 2018; Singh *et al.*, 2019; and Dodake *et al.*, 2022).

The analysis of variance revealed that mean squares due to lines effect were non-significant for all the characters except highly significant variance panicle bearing tiller per plant and significant variance biological yield per plant in  $F_1$ 's. This observation has been confirmed by previous studies (Dar *et al.*, 2014; Devi *et al.*, 2017; Mishra *et al.*, 2019; Yadav *et al.*, 2020; and Rahman 2020).

The variances due to testers effect were highly significant for flag leaf area, plant height and panicle bearing tillers per plant except significant variances for spikelet per panicle, biological yield per plant and grain yield per plant in  $F_1$ 's. Earlier researchers have reported analogous results (Kumar 2016; Prakash *et al.*, 2018; Marri 2020; and Shrivastav *et al.*, 2022).

The analysis of variance revealed that mean squares due to line  $\times$  testers interaction were highly significant for all the characters except non-significant variances for panicle length and L/B ratio in  $F_1$ 's. This finding aligns with previous research conducted by others (Devi *et al.*, 2017; Singh and Diw 2017; Panchal *et al.*, 2019; Singh *et al.*, 2019; and Abawa 2022).

### **Coefficients of variation**

The phenotypic (PCV) and genotypic (GCV) coefficients of variation for the thirteen 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 panicle bearing tillers per plant (PCV=21.46%, GCV=20.93%), flag leaf area (PCV=21.39%, GCV=21.09%), grain yield per plant (PCV=20.57%, GCV=20.12%) in  $F_1$ 's. Similar results have also been reported by earlier researcher (Khedikar *et al.*, 2003; Saxena *et al.*, 2005; Dhanwani *et al.*, 2013; Gyawali *et al.*, 2018; Hasan *et al.*, 2020; Chavan *et al.*, 2022). The moderate estimates (10-20%) of PCV and GCV were recorded for Spikelets per panicle (PCV=10.85%, GCV=10.78%), Grains per panicle (PCV=11.58%, GCV=11.73%), Biological yield per plant (PCV=17.58%,

GCV=17.29 %), 1000-grain weight (PCV=12.18%, GCV=11.67%) in  $F_1$ 's. The moderate estimates of PCV and low estimates of GCV were recorded for harvest index (PCV=10.06%, GCV=9.71%) in  $F_1$ 's. The low estimates (<10%) PCV and GCV recorded for Days of 50% flowering (PCV=9.70%, GCV=9.58%) Plant height (PCV=9.22%, GCV=9.11%), Panicle length (PCV=7.85%, GCV=5.99%), Spikelet fertility (PCV=8.72%, GCV=8.49%) of  $F_1$ 's crosses.

### Estimates of heritability and genetic advance

The estimates of heritability in broad sense ( $h^2_{(bs)}$ ) and genetic advance in per cent of mean for thirteen characters have been depicted in Table 2. High estimates of broad sense heritability (>75%) were recorded for the Days to 50% flowering, flag leaf area, panicle bearing tillers per plant, 1000-grain weight, spikelets per panicle, biological yield per plant, plant height, grains per panicle, grain yield per plant, spikelet fertility, harvest index in  $F_1$ 's crosses. The moderate estimates of heritability (50-75%) were recorded for the Panicle length in  $F_1$ 's. The L/B ratio is the character showed low estimates of heritability (<50%) in  $F_1$ 's. Similar result has also been reported by earlier research (Sanghera and Hussain. 2012). The genetic advance in per cent of mean was found to be very high (>30%) for, flag leaf area (42.82%), panicle bearing tillers per plant (42.06%), biological yield per plant (35.01%), grain yield (40.54%) in  $F_1$ 's. Similar result has also been reported by earlier researchers (Prasad *et al.*, 2017; and Kargbo *et al.*, 2019). The high estimates of genetic advance in per cent of mean (>20%) were recorded for spikelet per panicle (22.04%), grain per panicle (23.92%) 1000-grain weight (23.06%), in  $F_1$ 's crosses. Moderate genetic advance in per cent of mean (10-20%) were noted for spikelet fertility (17.04%), Harvest index (19.29%) in  $F_1$ 's crosses. On the other hand, low estimates (<10%) were noted for days to 50% flowering (9.51%), panicle length (9.42%), L/B ratio (1.93) in  $F_1$ 's crosses.

### Estimation Correlation coefficients

The estimates of simple correlation coefficients at phenotypic and genotypic levels computed between thirteen characters under study are presented in Table 3 (a and b). The phenotypic correlation coefficients and genotypic correlation coefficients for thirteen traits were analyzed in the  $F_1$ 's of twenty-four cross combinations and their eleven parents. Differences in magnitude as well as in direction were observed for different traits. However, both genotypic correlation coefficient and phenotypic correlation coefficient exhibited similar signs with few exceptions. In general, both positive and negative character associations were observed among different traits. Further, it was also observed that the estimates of genotypic correlation coefficient were higher than the corresponding phenotypic correlations. The grain yield per plant exhibited highly significant and positive association at phenotypic level with followed by L/B ratio (0.4187), spikelets per panicle (0.4283), harvest index percent (0.5007), panicle bearing tillers per plant (0.5386), biological yield per plant (0.8685), in  $F_1$ 's. Previous investigations have shown a same result Jyothi (2002); Madhubabu (2017); Behera *et al.*, (2020); Gulati *et al.*, (2023); and Kumari *et al.*, (2023).

The grain yield per plant was found to be positive and significantly associated with grains per panicle (0.3336) in  $F_1$ 's. The significantly and negatively associated with panicle length (-0.3550) in  $F_1$ 's.

### CONCLUSION

The experiment on genetic variability, heritability, genetic advance, correlation, and path coefficient analysis in rice emphasizes that these factors play critical roles in traits selection and utilize further breeding program for rice improvement. The highly significant variations for all traits except panicle length and the L/B ratio in parents and their crosses. The high estimates of phenotypic and genotypic coefficient of variation (> 20%) were estimated for panicle bearing tillers per plant, flag leaf area, grain yield per plant in  $F_1$ 's. The high estimates of heritability in broad sense ( $h^2_{(bs)}$ ) and genetic advance in percent of mean (>75% and >20% respectively) were reported in the flag leaf area, panicle bearing tillers per plant, 1000-grain weight, spikelets per panicle, biological yield per plant, grains per panicle, and grain yield per plant. The high heritability with high genetic advance indicating the character is given due to consideration in further breeding program and selection for traits could be practiced with due care to achieve desirable level of yield potential in rice. The grain yield per plant exhibited a highly significant and positive association at phenotypic level with L/B ratio followed by spikelets per panicle, harvest index percent, panicle bearing tillers per plant, and biological yield per plant in  $F_1$ 's. The grain yield per plant was found to be positive and significantly associated with grains per panicle in  $F_1$ 's. These features might be considered during selection to increase grain yield.

### REFERENCES

- Abawa, A. (2022). Genetic variability and association of traits in upland rice (*Oryza sativa* L.) Genotypes under irrigation condition in mecha district, northwestern ethiopia (doctoral dissertation).
- Abdalla, A., Elmoghazy, A., and Foda, A. (2021). Genetic analysis of yield and some related traits in rice (*Oryza Sativa* L.) Using Line x Tester Design. Journal of Environmental Studies and Researches, 11(4), 348-368.
- Aditya, J. P., and Bhartiya, A. (2015). Combining ability analysis for yield and components traits in fine grain rice of Mid Hills of Uttarakhand.
- Bassuony, N.N., 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.
- Behera, P. P., Singh, S. K., and Singh, D. K. (2020). Genetic association study of rice (*Oryza sativa* L.) genotypes for yield and yield attributing traits over five different locations. Plant Archives, 20(2), 5191-5196.
- Burton, G.M., and de Vane, E.H. (1953). Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agronomy Journal, 45:471-481.

- Chavan, B.R., Dalvi, V.V., Kunkerkar, R.L., Mane, A.V., and Gokhale, N.B. (2022). Studies on genetic variability for yield and yield contributing traits in aromatic rice (*Oryza sativa* L.). The Pharma Innovation Journal, 11: 1732-1735.
- Dar, S. H., Rather, A. G., Najeeb, S., Zeerak, N. A., Shikari, A. B., Bhat, Z. A., and Hassan, G. (2014). Gene action and standard heterosis over environments in Rice (*Oryza sativa* L.). Electronic Journal of Plant Breeding, 5(3), 360-370.
- Devi, A., Kumari, P., Dwivedi, R., Dwivedi, S., Mishra, K. K., Verma, O. P., and Dwivedi, D. K. (2017). Combining ability analysis for yield and its quality traits in rice (*Oryza sativa* L.) Over environment. Journal of Pharmacognosy and Phytochemistry, 6(4), 35-42.
- Devi, A., Kumari, P., Dwivedi, R., Dwivedi, S., Verma, O. P., Singh, P. K., and Dwivedi, D. K. (2017). Gene action and combining ability analysis for yield and yield contributing traits in rice (*Oryza sativa* L.) Over environment. Journal of Pharmacognosy and Phytochemistry, 6(3), 662-671.
- Devi, K. R., Chandra, B. S., Lingaiah, N., Hari, Y., and Venkanna, V. (2017). Analysis of variability, correlation and path coefficient studies for yield and quality traits in rice (*Oryza sativa* L.). Agricultural Science Digest-A Research Journal, 37(1), 1-9.
- Devi, K. R., Parimala, K., Venkanna, V., Lingaiah, N., Hari, Y., and Chandra, B. S. (2016). Estimation of variability for grain yield and quality traits in rice (*Oryza sativa* L.). Int. J. Pure App. Biosci, 4(2), 250-255.
- Dewey, D.R., and Lu, K.H. (1959). Correlation and path coefficient analysis of crested wheat grass seed production, 51:515-518.
- Dey, S. R. (2010). Combining ability and heterosis in inter-ecotypic classes of rice (*Oryza sativa* L.) (doctoral dissertation, department of genetics and plant breeding, Sher-e-Bangla Agricultural University, Dhaka, Bangladesh).
- Dhanwani, R.K., Sarawgi, A.K., Solanki, A., and Tiwari, J.K. (2013). Genetic variability analysis for various yield attributing and quality traits in rice (*Oryza Sativa* L.). The Bioscan, 8: 1403-1407.
- Dhurai, S. Y., Bhati, P. K., and Saroj, S. K. (2014). Studies on genetic variability for yield and quality characters in rice (*Oryza sativa* L.) under integrated fertilizer management. The Bioscan, 9(2), 745-748.
- Dodake, M. M., Intwala, C. G., and Patel, P. B. (2022). Heterosis and combining ability studies for yield and yield component traits in rice (*Oryza sativa* L.). The Pharma Innovation Journal, 11(7), 1206-1210.
- Gulati, J. M. L., Sar, K., Chowdhury, M. R., Dash, S., Behura, A. K., and Behera, B. (2023). Phenotypic Correlation Coefficient and Path Analysis in Rice (*Oryza sativa* L.): An Overview.

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, J.M., Kulsum, U.M., Majumder, R.R., and Sarker, U. (2020). Genotypic variability for grain quality attributes in restorer lines of hybrid rice. *Genetika*, 52: 973-989.

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.

Johnson, H. W., Robinson, H. F., And Comstock, R. E. (1955). Estimation of genetic and environmental variability in soybean. *Agronomy Journal*, 47: 314-318.

Jyothi, R. (2002). Stability analysis of kunjukunju rice cultures (*Oryza sativa* L.) (Doctoral dissertation, Department of Plant Breeding and Genetics, College of Horticulture, Vellanikkara).

Kamboj, G., Kumar, P., and Singh, D. (2018). Estimates of genetic parameters for grain yield, various yield components and some quality traits in rice (*Oryza sativa* L.). *Journal of Applied and Natural Science*, 10(1), 459-465.

Kargbo, S.S., 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, V.P., Bharose, A.A., Sharma, D., and Khedikar, Y.P. (2003). Study on genetic parameters in scented rice genotypes. *Journal of Soils and Crops*, 13 (2): 338-342.

Khush, G. S., and Virk, P. S. (2000). Rice breeding: achievements and future strategies.

Kulsum, U., Sarker, U., and Rasul, M.G. (2022). Genetic variability, heritability, and interrelationship in salt-tolerant lines of T. Amanrice. *Genetika*, 54: 761-776.

Kumar, S. S., Kumar, Y. V., Pal, B. V., Chand, Y. M., and Minakshi, S. R. (2016). Wide Compatibility Gene Approaches and Heterosis Relationship in Japonica x Indica Hybrid Rice (*Oryza sativa* L.). *Molecular Plant Breeding*, 7.

Kumari, S., Sinha, S., Satyendra, Kumar, V., Singh, R. S., Kumar, A., and Singh, S. (2023). Estimation of genetic variability, correlation, and path analysis in elite rice genotypes (*Oryza sativa* L.).

Latha, S., Sharma, D., and Sanghera, G.S., (2013). Combining ability and heterosis for grain yield and its component traits in rice (*Oryza sativa* L.). *Notulae Scientia Biologicae*, 5: 90-97.



Madhubabu, P., Suman, K., Rathod, R., Fiyaz, R. A., Rao, D. S., Sudhakar, P., and Neeraja, C. N. (2017). Evaluation of grain yield, quality and nutrients content in four rice (*Oryza sativa* L.) Genotypes.

Marri, C. (2020). Development of doubled haploids for iron toxicity tolerance in rice (*Oryza sativa* L.) (Doctoral dissertation, Department of Plant Breeding and Genetics, College of Horticulture, Vellanikkara).

Mazal, T.M., Elshnawy, M.M., Anis, G.B., and Hussein, F.A. (2021). Genetic analysis of some qualitative and quantitative traits in rice (*Oryza sativa* L.). *Journal of Plant Production*, 12: 577-583.

Mishra, S., Verma, O. P., Srivastava, S. P., and Singh, K. P. (2019). Identifying superior parents and hybrids for certain quantitative traits in rice (*Oryza sativa* L.) Under sodic soils. *Journal of Pharmacognosy and Phytochemistry*, 8(3), 01-05.

Panchal, R. J., Mistry, P. M., Patel, P. B., and Raval, K. G. (2019). Evaluation of F1 hybrid for the assessment of combining ability for yield and its attributes in rice (*Oryza sativa* L.). *International Journal of Chemical Studies*, 7(5), 225-229.

Prakash, H. P., Verma, O. P., Chaudhary, A. K., and Amir, M. (2018). Correlation and path coefficient analysis in rice (*Oryza sativa* L.) For sodicity tolerance. *Int. J. Curr. Microbiol. App. Sci*, 7(7), 177-187.

Prasad, K.R., Radha Krishna, K.V., Bhave, M.H.V., and Subba-Rao, L.V., (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, G.A., (2010). Combining ability and heterosis in rice (*Oryza sativa* L.) Cultivars. *Journal of Agricultural Science and Technology*, 12: 223-231.

Rahman, M. A. (2020). Characterization and variability analysis of several advanced lines of boro rice (*Oryza sativa* L.) (doctoral dissertation, department of genetics and plant breeding).

Ratna, m. (2009). Yield and quality analysis of some advanced lines of basmati rice (doctoral dissertation, department of genetics and plant breeding, sher-e-bangla agricultural university, dhaka, bangladesh).

Robinson, H.F. (1966). Quantitative genetics in relation to breeding on the content of the mendelism. *Indian Journal of Genetics*, 26A: 171-187.

Sahu, P. K., Deepak Sharma, D. S., Suvendu Mondal, S. M., Vikash Kumar, V. K., Satyapal Singh, S. S., Samarth Baghel, S. B., and Das, B. K. (2017). Genetic variability for grain quality traits in indigenous rice landraces of Chhattisgarh, India.

Sanghera, G. S., and Hussain, W. (2012). Study on heterosis in relation to combining ability per se performanle in temperate rice (*Oryza Sativa* L.)

Sanghera, G.S., and Hussain, W. (2012). Heterosis and combining ability estimates using line x tester analysis to develop rice hybrids for temperate conditions. *Notulae Scientia Biologicae*.

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, R.R., Saxena, R.R., Motiramani, N.K., Nichal, S.S., and Sahu, R.K. (2005). Studies on variability, heritability, and genetic advance in scented rice germplasm accessions. *Journal of International Academia*, 9: 487-489.

Searle, S.R., (1961). Phenotypic, genotypic, and environmental correlations. *Biometrics*, 17:474-480.

Shrivastav, S. P., Verma, O. P., Jakhar, D. S., Singh, V., and Lal, K. (2022). Studies on component of genetic variance and heterotic response in rice (*Oryza sativa* L.) For high yield with quality and sodicity tolerance. *Indian journal of genetics and plant breeding*, 82(04).

Singh, R. K., & Chaudhary, B. D. (1985). Line x Tester analysis. *Biometrical methods in quantitative genetic analysis*, Ed, 3, 215-223.

Singh, R., Pandey, D. P., and Kumari, A. (2019). Combining ability and gene action studies in physiological, phenological and yield traits in rice (*Oryza sativa* L.). *Journal of Cereal Research*, 11(3), 231-241.

Singh, S. K., and Diw, A. K. (2017). *Analysis Of Variance for Yield a Rice (Oryza Sativa)*.

Singh, S. K., Bindal, S., Singh, A., and Srivastava, S. (2019). Combining ability effects for yield traits in rice (*Oryza sativa* L.) Under sodic soil. *Journal of Pharmacognosy and Phytochemistry*, 8(1), 281-283.

Sultana, R. A. Z. I. A., Ansari, N. A., Ramesha, M. S., Sankar, A. S., and Krishna, K. M. (2016). Generation mean analysis of quantitative traits in restorer lines of rice (*Oryza sativa* L.). *Annals of plant and soil research*, 586.

Tiwari, R., Suresh, B.G., Mishra, V.K., 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.

Umarani, E., Radhika, K., Padma, V., and Subbarao, L. V. (2017). Variability, heritability, and genetic advance for agro-morphological and grain quality parameters in landraces of rice (*Oryza sativa* L.). *Environment and Ecology*, 35(3), 1682-1687.

Yadav, V. P., Singh, P. K., and Verma, O. P. (2020). Genetic variation and heritability for quantitative traits in rice (*Oryza sativa* L.) under sodic soil. *The Indian Journal of Agricultural Sciences*, 90(2), 316-319.

Zewdu, Z. (2020). Combining ability analysis of yield and yield components in selected rice (*Oryza sativa* L.) genotypes. *Cogent Food & Agriculture*, 6(1), 1811594.

**Table 1: Analysis of variance for 13 characters of line × tester set of crosses (F1's) and their parents in rice.**

Characters	Sources of variation											
	Replications	Treatments	Parents	Parents (Line)	Parents (testers)	Line vs testers	Parents vs Crosses	Crosses	Lines Effect	Testers Effect	Lines × testers Effect	Error
<b>d.f.</b>	2	34	11	7	2	1	1	23	7	2	14	68
Days to 50% flowering	5.30	248.41**	463.88**	445.60**	643.11**	233.46**	977.72**	123.01**	189.17	198.93	79.09**	5.46
Flag leaf area (cm <sup>2</sup> )	15.78*	173.69**	261.84**	266.31**	362.52**	29.24*	232.19**	132.83**	135.48	685.67**	52.52**	4.96
Plant height (cm)	3.66	244.84**	306.28**	236.57**	243.90**	918.96**	2385.03**	125.08**	36.36	1088.59**	31.79**	6.31
Panicle bearing tillers/plant	1.85	20.04**	14.47**	7.47**	34.82**	22.72**	54.20**	20.98**	18.28**	149.98**	3.91**	0.99
Panicle length (cm)	15.90*	9.33**	8.26	7.02	4.77	24.00*	23.15*	9.19*	13.29	5.61	7.64	4.63
Spikelets/panicle	1.56	767.36**	659.57**	889.20**	30.51	310.25**	120.01**	842.37**	221.16	4044.17*	695.58**	10.69
Grains/panicle	12.39	636.49**	566.52**	760.75**	91.11**	157.72**	140.96**	688.46**	503.53	2072.56	583.20**	12.96
Spikelet fertility (%)	5.87	170.17**	92.31**	126.81**	15.69	4.04	180.73**	203.56**	267.30	77.83	189.66**	8.04
Biological yield/plant (g)	18.10	299.48**	302.49**	330.07**	131.44**	451.52**	2758.50**	191.26**	293.23*	462.89*	101.47**	11.62
Harvest index (%)	1.60	74.86**	38.00**	21.57**	14.80	199.43**	785.07**	60.00**	56.36	13.82	68.43**	5.97
L/B ratio	0.06	0.30	0.22	0.27	0.07	0.24	2.40*	0.25	0.23	0.01	0.29	0.30
1000 -grain weight (g)	6.73*	24.49**	31.21**	26.35**	53.90**	19.90**	36.49**	21.04**	13.49	63.52	18.75**	2.03
Grain yield/plant (g)	7.56	122.10**	48.96**	56.09**	43.88**	9.18	2005.05**	72.03**	86.98	189.85*	47.72**	5.77

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

**Table 2: Estimates of general mean, phenotypic (PCV) and genotypic (GCV) coefficient of variation, heritability in broad sense ( $h^2_{(bs)}$ ) and genetic advance in percent of mean for 13 characters in rice.**

S.N.	Characters	General mean $\pm$ SE	Coefficient of variation (%)		Heritability in broad sense (%)	Genetic advance in per cent of mean
			PCV	GCV		
		F1's	F1's	F1's	F1's	
1	Days to 50% flowering	92.29 $\pm$ SE1.37	9.70	9.58	98	9.51
2	Flag leaf area (cm <sup>2</sup> )	35.49 $\pm$ SE1.27	21.39	21.09	97	42.82
3	Plant height (cm)	95.43 $\pm$ SE1.41	9.22	9.11	97	18.51
4	Panicle bearing tillers/plant	11.84 $\pm$ SE0.56	21.46	20.93	95	42.06
5	Panicle length (cm)	23.90 $\pm$ SE1.21	7.85	5.99	58	9.42
6	Spikelets/panicle	145.10 $\pm$ SE1.85	10.85	10.78	99	22.04
7	Grains/panicle	121.65 $\pm$ SE2.05	11.85	11.73	98	23.92
8	Spikelet fertility (%)	84.10 $\pm$ SE1.65	8.72	8.49	95	17.04
9	Biological yield/plant (g)	59.89 $\pm$ SE1.92	17.58	17.29	97	35.01
10	Harvest index (%)	53.40 $\pm$ SE1.41	10.06	9.71	93	19.29
11	L/B ratio	3.02 $\pm$ SE0.31	10.85	3.19	9	1.93
12	1000 -grain weight (g)	23.37 $\pm$ SE0.80	12.18	11.67	92	23.06
13	Grain yield/plant (g)	31.99 $\pm$ SE1.36	20.57	20.12	96	40.54

Table 3(a): Estimates of phenotypic correlation coefficients (F1's) between 13 characters in rice.

Crosses	Days to 50% flowering g	Flag leaf area (cm <sup>2</sup> )	Plant height (cm)	Panicle bearing tillers/plant	Panicle length (cm)	Spikelets/panicle	Grains/panicle	Spikelet fertility (%)	Biological yield/plant (g)	Harvest index (%)	L/B ratio	1000 - grain weight (g)	Grain yield/plant (g)
Days to 50% flowering	<b>1.0000</b>	0.3026*	0.1535	-0.3052	0.1637	-0.1495	0.0812	0.2730	-0.1912	-0.0655	-0.1389	-0.0072	-0.1848
Flag leaf area (cm <sup>2</sup> )		<b>1.0000</b>	-0.1713	-0.2397	-0.1572	-0.0821	0.0281	0.1228	0.2725	-0.1303	0.0435	0.3970*	0.1639
Plant height (cm)			<b>1.0000</b>	0.1218	0.0096	0.2861	0.4269**	0.2157	-0.0681	-0.3211*	-0.1411	-0.2436*	-0.2288
Panicle bearing tillers/plant				<b>1.0000</b>	-0.3772*	0.5981**	0.3799*	-0.2042	0.4644**	0.2559	0.1480	0.0236	0.5286**
Panicle length (cm)					<b>1.0000</b>	-0.2249	-0.0613	0.1574	-0.3840*	-0.1105	-0.0879	-0.1883	-0.3550*
Spikelets/panicle						<b>1.0000</b>	0.6681**	-0.3072*	0.4321**	0.1244	-0.0192	-0.0270	0.4283**
Grains/panicle							<b>1.0000</b>	0.5007**	0.2941	0.1466	0.1105	-0.0647	0.3336*
Spikelet fertility (%)								<b>1.0000</b>	-0.1074	0.0292	0.1612	-0.0574	-0.0623
Biological yield/plant (g)									<b>1.0000</b>	0.0142	0.3133*	0.1679	0.8685**
Harvest index (%)										<b>1.0000</b>	0.2873	0.1288	0.5007**
L/B ratio											<b>1.0000</b>	-0.1368	0.4187**
1000 -grain weight (g)												<b>1.0000</b>	0.1883
Grain yield/plant (g)													<b>1.0000</b>

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

Table 3(b): Estimates of genotypic correlation coefficients (F1's) between 13 characters in rice.

Crosses	Days to 50% flowering	Flag leaf area (cm <sup>2</sup> )	Plant height (cm)	Panicle bearing tillers/plant	Panicle length (cm)	Spikelets/panicle	Grains/panicle	Spikelet fertility (%)	Biological yield/plant (g)	Harvest index (%)	L/B ratio	1000 - grain weight (g)	Grain yield/plant (g)
Days to 50% flowering	<b>1.0000</b>	0.3129*	0.1584	-0.3078*	0.2144	-0.1544	0.0815	0.2834	-0.1991	-0.0612	-0.4046**	0.0029	-0.1902
Flag leaf area (cm <sup>2</sup> )		<b>1.0000</b>	-0.1807	-0.2510	-0.2111	-0.0864	0.0276	0.1305	0.2876	-0.1266	0.1341	0.4111**	0.1808
Plant height (cm)			<b>1.0000</b>	0.1237	0.0010	0.2942	0.4393**	0.2242	-0.0711	-0.3369*	-0.4438**	-0.2703	-0.2375
Panicle bearing tillers/plant				<b>1.0000</b>	-0.5155**	0.6166**	0.3934*	-0.2136	0.4883**	0.2736	0.5364**	0.0170	0.5584**
Panicle length (cm)					<b>1.0000</b>	-0.3105	-0.0939	0.2124	-0.5480**	-0.1388	0.1718	-0.2507	-0.5023**
Spikelets/panicle						<b>1.0000</b>	0.6767**	-0.3029*	0.4424**	0.1341	-0.0280	-0.0265	0.4427**
Grains/panicle							<b>1.0000</b>	0.4950**	0.3000*	0.1502	0.4148**	-0.0720	0.3415*
Spikelet fertility (%)								<b>1.0000</b>	-0.1138	0.0201	0.5450**	-0.0669	-0.0713
Biological yield/plant (g)									<b>1.0000</b>	0.0125	1.3222*	0.1655	0.8718**
Harvest index (%)										<b>1.0000</b>	0.9940**	0.1377	0.4939**
L/B ratio											<b>1.0000</b>	-0.2970	1.6477**
1000 -grain weight (g)												<b>1.0000</b>	0.1901
Grain yield/plant (g)													<b>1.0000</b>

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

