Original Research Article

Genetic Evaluation of Recombinant Inbred Lines of rice derived from Swarna-Sub1 x AC 20431B for yield related traits

ABSTRACT

Submergence is the third most important abiotic stress hugely affecting yield and productivity in rice. There are many wild varieties and landraces available which are tolerant to submergence stress. These genotypes can be utilized as donors in different breeding programs. The population derived from such germplasms are subjected to genetic evaluation for yield and yield related attributes for development of lines that are high yielding as well as tolerant to submergence. The present investigation was executed in 120 Recombinant Inbred Lines (RIL) population (F_{10}) derived from Swarna-Sub1 x AC 20431B along with four land races and Swarna-Sub1 to elucidate the association existing between yield and yield attributing characters. Apart from this, Correlation and path analysis was also employed to study direct and indirect effect on grain yield.Observations for agro-morphological traits such as days to 50% flowering, plant height, panicle length, total number of tillers, number of effective tillers per plant, number of filled grains and Spikelet fertility, test weight, grain yield per plant, biomass per plant and harvest index were recorded and analyzed for various variability parameters. Correlation and path coefficient analysis were also carried out.High heritability and genetic advance values were observed for days to 50% flowering, plant height, panicle length, total number of tillers per plant, effective tillers per plant, filled grains per panicle, spikelet fertility, test weight, grain yield and biomass per plant. Among all the characters; filled grains per panicle, biomass and harvest index per plant showed significant correlation with grain yield. Effective number of tillers per plant has the highest positive direct effect on grain yield.

***Keywords**: Submergence, recombinant inbred lines, agro-morphological traits, heritability, correlation, path coefficient analysis.*

1. INTRODUCTION

Rice (*Oryza sativa* L.) or ‘Global Grain’ is one of the cereals of immense significance as it has been a staple diet of many civilizations across the world since time immemorial. It has formed a basis for global food security and socioeconomic stability, especially in Asian countries which account for 90% of global rice production. Rice production in India is predicted to be around 124.0 million metric tonnes for the year 2022-23 (USDA report, 2022). There has been a decline in productivity in rice production owing to various abiotic and biotic stresses affecting rice. Submergence is the third most significant abiotic stress altering the growth and productivity of the cereal crop especially in eastern India (Sarkar *et al*., 2006). It directly affects over 22-million-hectare area cultivated with rice which further leads to yield loss of over 600 million to 1 billion dollars (Kumar *et al.,* 2021). Maximum damage by submergence is caused during germination and seedling stage which are found to be highly intolerant to the stress (Ismail et al., 2009). Submergence impairs the gaseous exchange in the crop, adversely affect the plant growth and productivity by disrupting the source-sink relationships, causes oxidative stress in plants, decreases the chlorophyll contents and photosynthesis rate leading to leaf senescence and hence diminishes the metabolic performance and survival rates in the rice plants (Mahmood *et al.*, 2019).The existence of many landraces, wild relatives and cultivated varieties in the world is a fortune as this vast genetic variability can be explored to find genes conferring submergence tolerance in rice and can be utilized in different plant breeding programs. One such landrace is FR13A which is hugely exploited due to its ability to show tolerance when completely submerged for two weeks. Other landraces such as AC 38575, AC 37887, IC258990, IC258830, AC 42087 and AC 20431-B showed survival rate of more than 80% even after 20 days (Sarkar *et al*., 2011). Other recommended rice varieties for deep water conditions include Sabita, Ambika, Saraswati and Hangseswari which showed increased yield even under deep-waterlogged conditions (Oladosu *et al.*, 2020).These traditional rice varieties and landraces have evolved tolerance to submergence owing to different physiological and morphological responses shown by them such as presence of hydrophobic wax on leaves that creates a gas film which in turn assists in respiration and photosynthesis, ability to maintain non-structural carbohydrates leading to rapid post-recovery stress, control of reactive oxygen species (ROS) and rapid recovery and regeneration after stress (Sarkar, 1998; Singh *et al.*,2009; Chakraborty *et al.*,2020).However, these landraces have low yield and poor quality in the farmers’ fields thus delimiting its cultivation on larger scale. Yet, the landraces can be used as parents in breeding programs along with popular varieties to develop lines having desirable combination of high yield and tolerance to submergence stress. This further necessitates the study of genetic variability, heritability and genetic advance for grain yield and yield attributing characters in developed population so as to produce improved genotypes with high yield potential. Thus, the present investigation was carried out in population consisting of 120 recombinant inbred lines (RIL) developed from Swarna-Sub1 x AC 20431B. The nobility of the RIL population is that the male parent, AC 20431B is a weedy rice whereas the other parent, Swarna-Sub1 is a cultivated rice. Therefore, the objective of this study was to evaluate variability and other important genetic parameters of yield and yield attributing traits such as heritability and genetic advance to predict the gain under selection. Moreover, the other parameters such as correlation and path analysis decide the association between yield and its determinants which determine their direct and indirect effects with grain yield. This type of analysis can assist the breeder in choosing applicable selection strategies to increase grain yield.

2. MATERIAL AND METHODS

The experiment was conducted on a RIL population (F_{10} generation)derived from Swarna-Sub1(susceptible parent for 21 days submergence stress) x AC 20431B (susceptible parent for 21 days submergence stress) consisting of 120 lines.Along with it, four landraces AC 38575, AC 42088, AC 42087 and FR13A available in ICAR-NRRI were also taken. The entries were planted in a randomized complete block design (RCBD)at ICAR-National Rice Research Institute (NRRI), Cuttack, Odisha during *kharif* season of 2022. The lines were planted in two blocks and two parents were used as checks. All the agronomic practices adopted for rice cultivation were followed.

Observations were recorded for three randomly selected plants for agro-morphological traits such as days to 50% flowering, plant height, panicle length, total number of tillers, number of effective tillers per plant, number of filled grains and Spikelet fertility, test weight, grain yield per plant, biomass per plant and harvest index. The recorded observations were analyzed through genetic variability components such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (broad sense), genetic advance and genetic advance as a percent of mean (Allard, 1960; Burton, 1952; Hanson *et al*., 1956) using variability package of R software version 4.3.0.The outputs obtained after each analysis were further grouped as high, medium and low on basis of values of PCV and GCV (Sivasubramanium and Menon,1973), heritability (Robinson *et al.*, 1949) and genetic advance as a percent of mean (Johnson *et al.*,1955). The correlation and path coefficient analysis were carried out using variability package of R program to study the degree of correlation between yield and its components and also to assess the direct and indirect effects of yield attributing characters on yield.

3. RESULTS AND DISCUSSION

3.1Estimation of variability parameters

For a successful breeding program, presence of genetic variability is a necessity as it allows selection of superior genotypes over existing cultivars. Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance as a percent of mean (GAM) are shown in Table 1. The phenotypic coefficient of variation (PCV) was found to be higher than genotypic coefficient of variation (GCV) in all the parameters except Plant height and Test weight implying the influence of environment on the expression of these characters.Highest GCV and PCV values were observed for Harvest Index (54.24 and 70.83), biomass per plant (48.58 and 54.08), grain yield per plant (49.98 and 51.97), number of filled grains per panicle (42.14 and 45.3), number of effective tillers per plant (38.31 and 49.19) and total tillers per plant (38.83 and 49.19) respectively.Moderate GCV and PCV values were found for days to 50% flowering (17.71 and 18.27), plant height (13.5 and 13.79), spikelet fertility (11.62 and 13.81) and test weight (19.39 and 19.74) and low values of GCV and PCV were seen in panicle length (7.07 and 8.09).The results were similar to the findings reported by Shivani *et al.* (2018) for grain yield per plant, number of filled grains per panicle, plant height, test weight and panicle length. In plant breeding programs genetic variability augmented with heritability is important for selection of superior genotypes. Heritability is the portion of phenotype variability that can be attributed to genetic variation (Bansidhar *et al*., 2019). High broad sense heritability was found in test weight (96.47%), plant height (95.81%), days to 50% flowering (93.93%), grain yield per plant (92.47%), filled grains per panicle (86.51%), biomass per plant (80.6%), panicle length (74.99%), spikelet fertility (70.75%), total number of tillers per plant (62.68%), total number of effective tillers per plant (60.67%). Medium heritability was observed in harvest index (58.64%). Since, selection intensity, phenotypic variability and heritability determines genetic advance, heritability estimates along with genetic advance will be adequate in predicting the response to selection (Johnson et al., 1955). Genetic advance as a percent of mean was found to be high for grain yield per plant (99%), biomass per plant (89.89%), harvest index (85.57%), number of filled grains per panicle (80.74%), number of tillers per plant and effective tillers per plant (63.34% and 61.48%), test weight (39.23%), days to 50% flowering (35.36%), plant height (27.22%) and spikelet fertility (20.13%) and medium for panicle length (12.5%). These findings were in agreement with Bansidhar *et al.* (2019) for panicle length and Ratnam *et al.* (2023) for days to 50% flowering, plant height, effective tillers per plant, number of filled grains per panicle and test weight.

Table 1. Estimates of range, mean and genetic parameters for yield in RIL population (F_{10})

CHARACTERS	RANGE		MEAN	Coefficient of Variance		h^2 (%)	GAM (%)
	MAX	MIN		GCV	PCV		
Days to 50% flowering	100	30	62.42	17.71	18.27	93.93	35.36
Plant height	151.4	72.5	119.19	13.5	13.79	95.81	27.22
Panicle length	32	19	24.19	7.07	8.09	74.99	12.5
Total tillers/ plant	22	2	7.03	38.83	49.05	62.68	63.34
No. of effective tillers/plant	19	2	6.67	38.31	49.19	60.67	61.48
No. of filled grains/panicle	207	11	82.22	42.14	45.3	86.51	80.74
Spikelet fertility (%)	98.5	27.02	80.77	11.62	13.81	70.75	20.13
Testweight	42.3	10.02	26.06	19.39	19.74	96.47	39.23
Grain yield/ plant	60.29	3.23	16.86	49.98	51.97	92.47	99
Biomass/plant	152.2	7.25	46.5	48.58	54.08	80.6	89.89
Harvest Index	395.34	8.5	45.09	54.24	70.83	58.64	85.57

PCV- Phenotypic coefficient of variation, GCV-Genotypic coefficient of variation, h^2 - broad sense heritability (%), GAM- Genetic Advance as percent of Mean (5%)

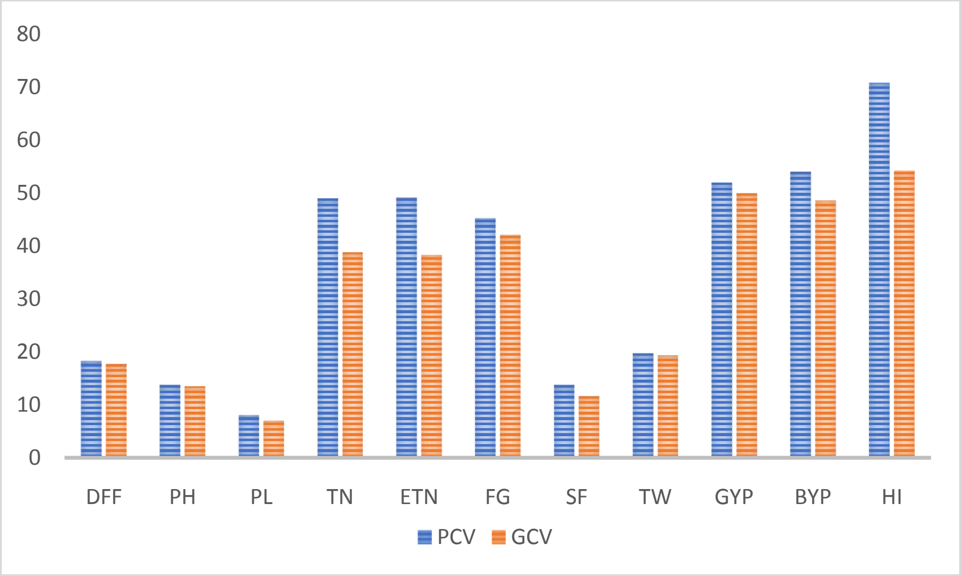

Figure1. Comparison of Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) among RIL population (F_{10})

DFF-Days to 50% flowering, PH-Plant height, PL-Panicle length, TN-Tiller number, ETN-Effective tiller number, FG-filled grains per panicle, SF-Spikelet Fertility, TW-Test weight, GYP- grain yield per plant, BYP-Biomass yield per plant, HI-Harvest Index

3.2 Correlation Studies

Correlation studies between yield and yield attributing characters is important in recognizing the important traits that can be further exploited for selection of superior lines and designing of apt breeding programs. Phenotypic and genotypic correlations were calculated for different attributes viz, days to 50% flowering, plant height, panicle length, total number of tillers and effective tillers per plant, filled grains per panicle, spikelet fertility, test weight, grain yield per plant, biomass per plant and harvest index for the RIL population. The results are presented in Table 2. The correlation analyses showed that genotypic correlation coefficients were higher than the phenotypic correlation coefficients implying that the relationships between different traits were due to genetic causes and hence phenotypic expression of correlations is reduced under the influence of the environment. This was in conformity with the findings of Singh *et al.* (2022).Grain yield per plant was found to be positively significant with filled grains per panicle, biomass and harvest index. Test weight was found to be positively significant with plant height, filled grains per panicle and spikelet fertility. Other yield components viz, days to 50% flowering, total number of tillers, number of effective tillers and test weight showed non-significant positive association with grain yield.

Table 2. Genotypic and Phenotypic Correlation coefficients among 11 characters in RIL Population (F_{10})

TRAITS	DFF	PH	PL	TN	PN	FG	SF	TW	GYP	BYP	HI
DFF	1	0.0582	-0.1024*	0.0223	0.0181	0.0293	0.0369	0.0853	0.0343	0.1264*	-0.0969
PH	0.0629	1	0.3138**	-0.1283*	-0.0961	-0.0044	0.1068*	0.2349**	-0.0271	0.0286	-0.0925
PL	-0.1262	0.3648**	1	-0.1111	-0.0977	-0.0728	-0.0698	0.0516	-0.0467	-0.1051*	0.0745
TN	0.0302	-0.1581	-0.1642	1	0.9712**	0.0396	0.0629	0.0396	0.0921	-0.0353	0.1194*
ETN	0.0226	-0.1211	-0.1588	0.9967**	1	0.03	0.0517	0.0351	0.0853	-0.0345	0.1114*
FG	0.0385	0.0013	-0.098	0.0271	0.0141	1	0.4355**	0.2114**	0.1427**	0.1863**	-0.0117
SF	0.0654	0.141	-0.1201	0.0383	0.0101	0.5114**	1	0.2111**	-0.0565	0.1335**	-0.125*
TW	0.0861	0.2424**	0.053	0.0524	0.0507	0.2335**	0.2535	1	0.0641	0.1087*	-0.0702
GYP	0.043	-0.0323	-0.0586	0.1057	0.1109	0.1521	-0.0872	0.0635	1	0.2839	0.4775**
BYP	0.1545	0.0254	-0.14	-0.043	-0.047	0.2227	0.183*	0.1184	0.3233**	1	-0.509**
HI	-0.1462	-0.1172	0.1022	0.1516	0.1618	-0.0157	-0.2194*	-0.0854	0.5762**	-0.517	1

, indicate significance at 5% and 1% levels respectively; DFF-Days to 50% flowering, PH-Plant height, PL-Panicle length, TN-Tiller number, ETN-Effective tiller number, FG-filled grains per panicle, SF-Spikelet Fertility, TW-Test weight, GYP- grain yield per plant, BYP-Biomass yield per plant, HI-Harvest Index*

3.3 Path coefficient analysis

Path coefficient analysis allows partition of genotypic correlations into direct and indirect effects which further allows differentiating the direct and indirect effects through additional attributes by apportioning the correlations (Wright, 1923). The relationship between the yield and the character is true only if the correlation between yield and the observed trait is due to direct effects of the trait. In the present investigation, genotypic path coefficient was studied using grain yield per plant as the dependent variable for all the agromorphological traits taken. The path coefficient analysis is given in Table 3. Effective tiller number has the highest direct positive effect on grain yield per plant (0.45495), followed by filled grains per panicle (0.25363) and test weight (0.05781) and days to 50% flowering (0.03814).Bhargava *et al.*,2021 also reported that productive tiller number exerted maximum direct positive effect on grain yield per plant (0.6380) followed by grain number per panicle(0.2974) in a F_2 population in rice.

Table 3. Path analysis of direct and indirect effects for grain yield in rice

TRAITS	DFF	PH	PL	TN	ETN	FG	SF	TW
DFF	0.03814	-0.00009	0.00575	-0.01081	0.01028	0.00976	-0.01506	0.00498
PH	0.00240	-0.00145	-0.01633	0.05655	-0.0551	0.00033	-0.03245	0.01401
PL	-0.00481	-0.00053	-0.04557	0.05873	-0.07225	-0.02487	0.02765	0.00307
TN	0.00115	0.00023	0.00748	-0.35769	0.45346	0.00686	-0.00882	0.00303
ETN	0.00086	0.00018	0.00724	-0.35652	0.45495	0.00358	-0.00232	0.00293
FG	0.00147	0	0.00447	-0.00968	0.00642	0.25363	-0.11771	0.0135
SF	0.0025	-0.0002	0.00547	-0.01371	0.00459	0.1297	-0.23019	0.01465
TW	0.00329	-0.00035	-0.00242	-0.01874	0.02307	0.05923	-0.05835	0.05781

4. CONCLUSION

The present investigation showed the existence of diversity among 120 RIL lines, four landraces FR13A, AC38575, AC42087, AC42088 and one variety Swarna-Sub1. High heritability in broad sense was observed for all the attributes viz, days to 50% flowering, plant height, panicle length, total number of tillers per plant, effective tillers per plant, filled grains per panicle and spikelet fertility, test weight and grain yield per plant. This proves that these characters if employed for selection in hybridization program could be successfully inherited by the progeny. The correlation analysis exhibited that traits such as days to 50% flowering, total number of tillers and effective tillers per plant, filled grains per panicle, spikelet fertility and test weight showed positive contribution to plant yield and harvest index. Among these characters filled grains per panicle, biomass and harvest index per plant showed significant correlation with grain yield. Effective number of tillers per plant has the highest positive direct effect on grain yield. So, these traits may be regarded as selection criteria for improvement of grain yield in breeding programs in rice.

REFERENCES

1. Allard RW. Principles of Plant Breeding. Publishers by John Wiley and Sons Inc., New York, USA; 1960.
   Available: https://ipad.fas.usda.gov/highlights/2022/12/India/index.pdf
2. Bansidhar, Jaiswal P, Singh MK, Deo I. Estimation of Genetic Parameters for Yield and Related Traits in Advanced Recombinant Lines of Kalanamak Rice (*Oryza sativa* L.). International Journal of Current Microbiology and Applied Sciences.2019; 8(9): 2052-2059.
3. Bhargava K, Shivani D, Pushpavalli SNCVL, Sundaram RM, Beulah P, Senguttuvel P. Genetic variability, correlation and path coefficient analysis in segregating population of rice. Electronic Journal of Plant Breeding. 2021;12(2): 549-555.
4. Burton GW. Quantitative inheritance in grasses. Proceeding on 6th International Grassland Congress Journal. 1952;1: 277-283.
5. Chakraborty K, Guru A, Jena P, Ray S, Guhey A, Chattopadhyay K, Sarkar R. Rice with a SUB1 QTL possesses greater initial leaf gas film thickness leading to delayed perception of submergence stress. Annals of Botany.2020; 1-15.
6. Hanson G, Robinson HF, Comstock RE. Biometrical studies on yield in segregating population of Korean Lespedeza. Agronomy Journal.1956; 48:268-274.
7. Ismail AM, Ella ES, Vergara GV, Mackill DJ. 2009. Mechanisms associated with tolerance to flooding during germination and early seedling growth in rice (*Oryza sativa*). Annals of Botany.2009; 103: 197–209.
8. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean. Agronomy Journal. 1955;47 (7): 314- 318.
9. Kumar A, Nayak AK, Hanjagi PS, Kumari K, Vijayakumar S, Mohanty S, Tripathi R, Panneerselvam P. Submergence stress in rice: Adaptive mechanism, coping strategies and future research needs. Environmental and Experimental Botany. 2021;186.https://doi.org/10.1016/j.envexpbot.2021.104448.
10. Mahmood U, Hussain HA, Hussain S, Ashraf U, Khaliq A, Hussain S. Submergence Stress in Rice: Physiological Disorders, Tolerance Mechanisms, and Management. 2019; https://doi.org/10.1007/978-3-030-06118-0_7.
11. Oladosu Y, Rafil MY, Arolu F, Chukwu SC, Muhammad I, Kareem I, Salisu MA,Arolu IW. Submergence tolerance in rice: review of mechanism, breeding and future prospects. Sustainability.2020; 12(4):1632.
12. Ratnam TV, Kumar BNVSRR, Subba Rao LV, Srinivas T, Kumar ADVSLPA, Suneetha Y. Genetic analysis for zinc rich landraces for yield, quality and nutritional traits in rice (*Oryza sativa* L.). Journal of Environmental Biology. 2023; 44:840-854.
13. Robinson HF, Comstock RE, Harvey PH. Estimation of heritability and the degree of dominance in corn. Agronomy Journal. 1949; 41: 353-359.
14. RStudio Team. 2020. RStudio: Integrated Development for R. RStudio, PBC, Boston, MA http://www.rstudio.com.
15. Sarkar RK, Bhattacharjee B. Rice Genotypes with *SUB1* QTL Differ in Submergence Tolerance, Elongation Ability during Submergence and Re-generation Growth at Re-emergence. Rice. 2011; 5: 7.
16. Sarkar RK, Reddy JN, Sharma SG, Ismail AM. Physiological basis of submergence tolerance in rice and implications for crop improvement. Current Science. 2006; 91:899–6.
17. Sarkar RK. Saccharide content and growth parameters in relation with flooding tolerance in rice. Biol. Plant. 1998;40: 597–603.

18. Shivani D, Cheralu C, Neeraja CN, Gouri Shankar V. Genetic Variability Studies in Swarna X Type 3: Ril Population of Rice (*Oryza sativa* L.). International journal of pure and applied bioscience. 2018; 6(2): 384-392.
19. Singh S, Mackill DJ, Ismail AM. Responses of SUB1 rice introgression lines to submergence in the field: yield and grain quality. Field Crops Res.2009; 113:12-23.
20. Singh SK, Jagadev PN, Katara JL, Jeughale K, Samantaray S, Bastia DN, Parameswaran C. Correlation study of yield and yield related traits of doubled haploid rice lines (*Oryza sativa* L.). The Pharma Innovation. 2022; 11(2):468-471.
21. Sivasubramanian S, Madhavamenon P. Combining ability in rice. Madras Agricultural Journal. 1973; 60: 419-42.
22. USDA. 2022. Commodity Intelligence Report.
23. Wright S. Theory of path coefficients. Genetics. 1923; 8:239-255.