Genetic Parameters and Association Studies for Yield and Grain Quality Traits in Rice Genotypes Derived from Distant Crosses

Chandra Bose GS[1], Krishna Veni B[2*], Rani Ch[3], Tushara M[4] and Ramesh D[5]

[1]Department of Genetics and Plant Breeding, Agricultural College, ANGRAU, Bapatla,

[2]Agricultural Research Station, ANGRAU, Bapatla,

[3]Agricultural Research Station, ANGRAU, Lam, Guntur,

[4]Agricultural Research Station, ANGRAU, Bapatla,

[5]Department of Agricultural Statistics and Computer applications, ANGRAU, Bapatla.

*Corresponding author E-mail: b.krishnaveni@angrau.ac.in

Abstract

In the current study, 49 rice genotypes were studied for thirteen yield and grain quality traits to estimate the variability parameters and character associations. Number of filled grains per panicle and grain yield/plant recorded high phenotypic and genotypic coefficients of variation and most of the characters studied manifested high heritability estimates except for ear bearing tillers/plant and kernel breadth. Grain yield/plant exhibited high estimates for all genetic parameters indicating the predominance of additive gene action in the inheritance of this trait. The results of correlations revealed that, days to 50% flowering, plant height, ear bearing tillers/ plant, number of primary branches/panicle, number of filled grains/panicle and test weight exhibited positive and significant correlation with grain yield. The outcome of path coefficient analysis concluded that days to 50% flowering, plant height, ear bearing tillers/plant, number of primary branches/panicle, number of filled grains/panicle and test weight manifested positive direct effects as well as significant positive association with grain yield, and hence direct selection of these traits would improve grain yield/plant.

Key words: Rice, variability, correlation, distant crosses, yield components

Introduction

Rice is the world's most important staple food crop, accounting for nearly half of the global population's dietary intake. Rice is grown on 44.16 million hectares in India, with an annual production of 118.87 million tons and an average productivity of 2.65 tons of milled rice per hectare (Ministry of Agriculture, 2019-20). Modern rice cultivars have limited genetic base which is becoming a major bottleneck for crop improvement efforts. Utilization of crop wild relatives (CWRs) is a promising approach to enhance genetic diversity in cultivated crops for yield and other important characteristics. To address food insecurity, particularly in developing countries, immediate attention must be paid to break the yield plateau. To date, majority of the increased yields have come from manipulating traits to meet future demands, which will necessitate the use of novel genetic resources. Many traits have been identified as possessing the potential to improve yield and high expression of these traits has been found in germplasm collections. For planning and execution of a successful breeding programme, the most essential pre-requisite is the availability of desirable genetic variability. Knowledge of the relationship between grain yield and its component characters will be useful for improving the grain yield.

Materials and Methods

The present investigation was conducted at Agricultural College Farm, Bapatla of Acharya N. G. Ranga Agricultural University (ANGRAU) during *kharif,* 2021. The experimental material comprised of 49 advanced rice genotypes derived from multiple crosses and back cross breeding material involving popular rice varieties and some wild rice genotypes. The details of the designation and the parentage of the genotypes used in the study are presented in **Table 1.** The experiment was laid out in Simple Lattice Design with two replications. Each genotype was raised in five rows of three-meter length with a spacing of 20 x 15 cm between and within the rows, respectively. Standard agronomic practices and recommended fertilizer doses were adopted for normal crop growth. Data was collected on five plants per replication on 13 yield components and grain quality traits *viz.*, days to 50% flowering, plant height (cm), ear bearing tillers/plant, flag leaf length (cm), flag leaf width (cm), panicle length (cm), number of primary branches/panicle, number of fertile grains/panicle, kernel length (mm), kernel breadth (mm), L/B ratio, test weight (g) and grain yield per plant (g) by following standard procedures. Mean data was utilized for statistical

Table 1: Details of the rice genotypes studied in the present investigation

S. No	Genotype	Cross combination	S. No	Genotype	Cross combination
01	BPT 2782	NLR145/MTU2077- released variety used as check			
02	BPT 2841	Swarna / IRGC18195 // MTU1081	26	BPT 3234	BPT5204/Ramappa
03	BPT 2848	RPBio226*1 / IRGC48493	27	BPT 3263	MTU7029 / IRGC18195// MTU1081
04	BPT 2858	RPBio226*1 / IRGC48493	28	BPT 3269	RPBIO226*1 / IRGC23385 // Nidhi / MTU1081
05	BPT 2955	MTU1010/IR50	29	BPT 3270	RPBIO226*1/IRGC23385//Nidhi/MTU1081
06	BPT 3111	MTU7029/ IRGC18195// MTU1081	30	BPT 3276	Cult.011120305 /cult.0910025-7
07	BPT 3136	RPBio226*1/ IRGC48493	31	BPT 3278	RPBio226*1/IRGC48493
08	BPT 3137	RPBio226*1/ IRGC48493	32	BPT 3279	RPBio226*1 /Jarava
09	BPT 3140	MTU7029/IRGC18195 //MTU1081	33	BPT 3281	Cult.01120305/ cult.0910025-7
10	BPT 3141	RPBio226*1/ IRGC30983	34	BPT 3286	Cult.01120305/cult.0910025-7
11	BPT 3143	RPBio2268*1/IRGC48493	35	BPT 3391	Cult.01120305/cult.0910025-7
12	BPT 3145	RPBio226*1/IRGC48493	36	BPT 3401	Cult.01120305/cult.0910025-7
13	BPT 3149	RPBIO226*1/IRGC23385//Nidhi/MTU1081	37	BPT 3409	RPBIO226*1/IRGC23385//Nidhi/MTU1081
14	BPT 3151	RPBio226*1/Jarava	38	BPT 3415	MTU7029/IRGC18195//MTU1081
15	BPT 3152	BPT5204*2/ *O. longistaminata*//B-95-1/SwarnaSub-1	39	BPT 3520	Cult.01120305/Cult.0910025-7
16	BPT 3157	MTU7029/IRGC18195//MTU1081	40	BPT 3521	Cult.01120305/Cult.0910025-7
17	BPT 3158	BPT5204*2/ *O. longistaminata*//B-95-1/SwarnaSub-1	41	BPT 3522	MTU7029/IRGC18195//MTU1081
18	BPT 3159	Cult.0910023/ RPBio226*1// Cult. 09100238// BPT5204/Tetep	42	BPT 3523	Cult.01120305/Cult.0910025-7
19	BPT 3164	B-95-1/RPHR1005//B-95-1	43	BPT 3524	MTU7029/ IRGC18195// MTU1081
20	BPT 3166	BPT5204*2/*O. longistaminata*//B-95-1/SwarnaSub-1	44	BPT 3525	RPBIO226*1/ IRGC30983
21	BPT 3167	RPBio226*1/ IRGC18195//MTU1081	45	BPT 3526	Cult.01120305/ Cult.0910025-7
22	BPT 3178	Cult.01120305/ cult.0910025-7	46	BPT 3527	MTU7029/ IRGC18195// /MTU1081
23	BPT 3217	Cult.01120305/ cult.0910025-7	47	BPT 3528	MTU7029/ IRGC18195//MTU1081
24	BPT 3220	Cult.01120305/ cult.0910025-7	48	BPT 3529	MTU7029 /IRGC18195//MTU1081
25	BPT 3227	(RPBio226*1/IRGC23385) // (Nidhi/MTU1081)	49	BPT 3530	MTU7029 /IRGC18195//MTU1081

analysis. The genotypic and phenotypic variance was calculated as per the formulae of Singh and Chaudhary (1977) and classified as described by Sivasubramanian and Madhava Menon (1973). Estimate of heritability inbroad sense ($h^2(b)$) and genetic advance as percent of mean were calculated by the formulae given by Johnson *et al.,* (1955). Phenotypic and genotypic correlations were calculated by using the formulae given by Falconer (1964). Path coefficient analysis proposed by Wright (1921) and developed by Dewey and Lu (1959) was used to compute the direct and indirect contribution of various traits to yield.

Results and Discussions

Analysis of variance (ANOVA) for morphological, yield attributing and grain quality traits revealed highly significant mean squares due to genotypes for all traits, indicating the existence of sufficient variation among the genotypes for morphological and yield component traits studied. Estimates of mean, range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2 broad sense) and genetic advance as percent of mean (GAM) for morphological and yield component traits studied in the current study were depicted in **Table 2.** Results on performance *per se* for morphological and yield related traits of the rice varieties studied, genotypes BPT 3276, BPT 3137, BPT 3151, BPT 3152, BPT 2841, BPT 3523 and BPT 3525 exhibited high grain yield accompanied by better yield attributing traits. All these entries recorded more flag leaf length, panicle length, more number of filled grains/panicle and test weight resulting in production of higher grain yield.

Table 2: Mean, range and variability parameters for morphological and yield related traits in rice

| S. No | Character | Mean | Range | | Coefficient of variation | | Heritability (%) | Genetic advance as percent of mean |
			Minimum	Maximum	GCV (%)	PCV (%)		
1	Days to 50% flowering	95.8	87	113.0	7.6	7.9	91.2	15.0
2	Plant height (cm)	134.4	105.3	169.0	10.9	11.5	90.5	21.5
3	Ear bearing tillers/ plant	8.24	6.0	10.5	7.8	9.9	15.6	3.2
4	Flag leaf length (cm)	40.0	24.6	56.6	19.9	19.9	99.4	40.9
5	Flag leaf width (cm)	2.63	2.2	4.2	15.2	16.1	89.0	29.4
6	Panicle length (cm)	25.7	22.1	32.3	8.1	9.1	80.0	15.0
7	Number of primary branches/ panicle	13.5	10.0	18.0	12.9	13.5	92.5	25.7
8	Number of filled grains/ panicle	198	142.9	293.0	21.0	21.6	94.4	12.7
9	Kernel length (mm)	5.71	4.88	6.4	8.6	8.6	99.2	17.6
10	Kernel breadth (mm)	1.98	1.69	2.51	19.6	21.1	13. 1	7.4
11	L/B ratio	2.91	2.6	3.36	13.6	16.5	68.1	23.1
12	Test weight (g)	16.3	12.5	20.0	10.9	11.4	93.2	21.8
13	Grain yield/ plant (g)	24.4	17.1	40.8	21.8	22.0	98.6	44.7

The estimates of phenotypic coefficient of variation for all the characters under study were higher than the estimates of genotypic coefficient of variation. Minimum phenotypic and genotypic coefficient of variations were observed for days to 50% flowering (7.9% and 7.6%) while maximum phenotypic and genotypic coefficient of variation was manifested by grain yield/plant (22.0% and 21.8%) indicating the existence of sufficient variation among the genotypes for potential yield improvement through selection. Other traits *viz.,* number of filled grains/panicle (21.6% and 21.0%) and kernel breadth (21.1% and 19.6%) also recorded high PCV and GCV. Similar findings were previously reported by Singh *et al.,* (2020) and Priyanka *et al.,* (2023) for days to 50% flowering and grain yield/plant.

Heritability is the measure of transmission of characters from generation to generation and estimates of heritability are helpful to the breeder in selecting superior individuals and successfully utilizing them in breeding programme(s) (Bharathi *et al.,* 2017). Except ear bearing tillers/plant (15.6%) and kernel breadth (13.1%), all other characters under study recorded high heritability estimates. Maximum heritability estimates were recorded for kernel length (99.2%) followed by flag leaf length (99.2%), grain yield/plant (98.6%), number of filled grains/panicle (94.4%), test weight (93.2%), number of primary branches/panicle (92.5%) and days to 50% flowering (91.2%). Similarly, high genetic advance as percent over mean, was manifested by grain yield per plant (44.7) followed by flag leaf length (40.9), flag leaf width (29.4) and number of primary branches per panicle (25.7) whereas ear bearing tillers (3.2) and kernel breadth (7.4) manifested low genetic advance as per cent over mean. These findings are in consonance with earlier reports of Babu (2020) for flag leaf length and flag leaf width; Islam *et al*., (2019) for number of primary branches/panicle; Nath and Kole (2021) and Sindhura *et al.,* (2022) for grain yield/plant, test weight and days to 50% flowering. Based on the results of variability parameters, it may be concluded that grain yield/plant exhibited high genotypic and phenotypic coefficients of variation along with high heritability and high genetic advance as per cent of mean whereas the characters *viz.,* flag leaf length, flag leaf width, number of primary branches/panicle and test weight manifested moderate PCV and GCV along with high heritability as well as high genetic advance as per cent of mean suggesting the predominance of additive gene action in the inheritance of these traits. Hence, simple selection will be highly rewarding for improving these characters.

Grain yield exhibited positive and significant correlation with days to 50% flowering (0.208*, 0.225*), plant height (0.201*), ear bearing tillers/plant (0.248*, 0.657**), number of primary branches/panicle (0.241*, 0.572**), number of filled grains/panicle (0.654**, 0.777**) and test weight (0.286**, 0.298**) indicating that grain yield will be improved simultaneously along with these characters **(Table 3)**. As a result, these traits should be prioritized when making selections for increased grain yield. These findings are in harmony with earlier findings of Kavitha *et al.,* (2020) and Nath and Kole (2021) for days to 50% flowering, plant height, number of primary branches/panicle and test weight; Saha *et al.*, (2019) for number of fertile grains/panicle. Further, studies on inter-character association between yield components and quality traits revealed significant and positive correlation of days to 50% flowering with number of primary branches/panicle (0.241*, 0.266**) suggesting that the genotypes possessing late duration manifested more number of primary branches/panicle. Hossain *et al.,* (2018) also reported similar association between the flowering duration and number of primary branches/panicle. Plant height manifested positive correlation with flag leaf length (0.473*, 0.500*), flag leaf width (0.351*, 0.418**), panicle length (0.435**,0.552**), number of filled grains/panicle (0.275**, 0.378**) and kernel length (0.199*, 0.203*) indicating that the genotypes with tall plant stature manifested more flag leaf length and width which produced longer panicles and more number of filled grains per panicle. Similar relationship was earlier reported by Ramya (2021). Flag leaf length and flag leaf width also inter-correlated with each other and both these traits exhibited significant and positive relationship with panicle length, number of filled grains/panicle, kernel breadth and test weight suggesting more flag leaf area of the plant aids in improvement of all these traits. Aditya and Bhartiya (2013) also found similar associations in their studies. Number of ear bearing tillers/plant manifested significant and negative relationship with

panicle length (-0.299**), kernel length (-0.331**), L/B ratio (-0.211*) and test weight (- 0.222*) at genotypic level suggesting that the genotypes with less number of tillers possessed longer panicles, slender grains and more test weight. It is interesting to note that number of primary branches/panicle manifested negative correlation with test weight (-0.435**) and significant negative relationship was recorded by kernel breadth with L/B ratio (-0.754**). These results suggest that the genotypes which possessed more number of primary branches/panicle manifested low test weight (slender grain type) and genotypes which possessed bolder grains (more kernel breadth) had less L/B ratio indicating the need for balanced selection while simultaneously improving these traits. Studies by Kumar *et al.,* (2017) and Herawati *et al*., (2021) revealed similar findings for number of ear bearing tillers per plant with panicle length and for number of primary branches/panicle with test weight respectively.

Selection based on characters with positive direct effect along with positive correlation with grain yield/ plant are needed to achieve fruitful results for yield improvement in breeding programmes. The results of path coefficient analysis revealed that number of

Table 3: Phenotypic and genotypic correlation coefficients for morphological and yield related traits in rice

Character		DFF	PH	EBT	FLL	FLW	PL	NPB/P	NFG/P	KL	KB	L/B	TW	GY/P
DFF	rp	1.000	0.059	0.059	-0.101	0.120	0.008	0.241*	0.092	-0.067	0.025	-0.054	0.108	0.208
	rg	1.000	0.067	0.387**	-0.107	0.124	-0.014	0.266**	0.168	-0.070	-0.028	-0.040	0.120	0.225*
PH	rp		1.000	-0.018	0.473**	0.351**	0.435**	0.162	0.275**	0.199*	0.078	0.082	-0.144	0.196
	rg		1.000	0.024	0.500**	0.418**	0.552**	0.178	0.378**	0.203*	0.226*	0.099	-0.133	0.201*
EBT	rp			1.0000	0.037	0.054	-0.186	0.213*	0.215*	-0.140	0.033	-0.108	-0.098	0.248*
	rg			1.0000	0.077	-0.083	-0.299**	0.580**	0.611**	-0.331**	-0.126	-0.211*	-0.222*	0.657*
FLL	rp				1.0000	0.195	0.509**	-0.088	0.204*	-0.033	0.098	-0.063	0.216*	0.044
	rg				1.0000	0.210*	0.575**	-0.092	0.266**	-0.035	0.284**	-0.080	0.222*	0.049
FLW	rp					1.0000	0.395**	0.197	0.110	-0.047	0.164	0.006	0.209*	0.012
	rg					1.0000	0.453**	0.220*	0.179	-0.038	0.488**	0.003	0.232*	0.030
PL	rp						1.0000	0.068	0.177	0.215*	0.091	0.168	-0.112	0.122
	rg						1.0000	0.091	0.193	0.243*	0.215*	0.249*	-0.156	0.141
NPB/P	rp							1.0000	0.264**	-0.115	0.060	-0.030	-0.435**	0.241*
	rg							1.0000	0.316**	-0.118	0.174	-0.037	-0.234*	0.572**
NFG/P	rp								1.0000	0.153	-0.038	0.133	0.018	0.654**
	rg								1.0000	0.198	0.620**	0.001	-0.020	0.777**
KL	rp									1.0000	-0.001	0.543**	0.278**	-0.025
	rg									1.0000	-0.000	0.654**	0.291**	-0.053
KB	rp										1.0000	-0.754**	0.217**	0.060
	rg										1.0000	-0.782**	0.348**	0.084
L/B	rp											1.0000	0.145	-0.033
	rg											1.0000	0.189	-0.050
TW	rp												1.0000	0.286**
	rg												1.0000	0.298**
GY/P	rp													1.0000
	rg													1.0000

**Significant at1 percent level of probability *Significant at5 per cent level of probability

DFF=Daysto50%flowering, **PH:** Plant height (cm), **EBT:** Ear bearing tillers, **FLL:** Flag leaf length (cm), **FLW:** Flag leaf width (cm), **PL:** Panicle length (cm), **NPB/P:** No. of primary branches/panicle, **NFG/P:** No. of fertile grains/panicle, **KL:** Kernel length (mm), **KB:** Kernel breadth (mm), **L/B:** Length/breadth ratio, **TW:** Test weight(g), **GY/P:** Grain yield/plant (g)

filled grains/panicle manifested high positive direct effect (0.679 and 0.607) on grain yield followed by panicle length (0.369 & 0.154), ear bearing tillers/plant (0.346 & 0.145), plant height (0.197 and 0.293) at both phenotypic and genotypic levels **(Table 4)**. Number of primary branches/panicle (0.455) and test weight (0.199) exhibited high positive direct effects at genotypic level. Devi *et al.,* (2017), Saha *et al.,* (2019) and Nath and Kole (2021) also reported similar findings in their studies. High positive direct effects of these traits appeared to be the main factor for their strong association with grain yield per plant. Hence, these traits should be considered as important selection criteria in rice improvement programmes.

Table 4: Direct and indirect effects of morphological and yield related traits on grain yield in rice

Character		DFF	PH	EBT	FLL	FLW	PL	NPB/P	NFG/P	KL	KB	L/B	TW
DFF	G	-0.056	0.023	0.259	0.052	-0.023	-0.005	-0.128	0.126	-0.001	-0.021	0.004	-0.003
	P	0.129	0.014	0.024	0.020	-0.013	0.001	-0.062	0.105	0.002	-0.001	-0.005	-0.004
PH	G	-0.004	0.293	-0.034	-0.236	-0.077	0.202	-0.087	0.137	0.011	0.015	0.007	-0.024
	P	0.009	0.197	-0.005	-0.096	-0.042	0.066	-0.043	0.105	-0.007	-0.001	0.015	0.009
EBT	G	-0.042	-0.029	0.346	0.025	0.019	-0.061	-0.297	0.431	-0.038	0.104	-0.032	0.230
	P	0.026	-0.007	0.145	0.009	-0.004	-0.020	-0.062	0.168	0.005	-0.006	0.004	-0.007
FLL	G	0.006	0.151	-0.019	-0.457	-0.035	0.219	0.037	0.111	-0.004	-0.027	0.013	0.054
	P	-0.013	0.093	-0.007	-0.202	-0.022	0.079	0.018	0.109	0.009	-0.006	0.069	-0.014
FLW	G	-0.007	0.122	-0.036	-0.088	-0.183	0.168	-0.104	0.072	0.002	0.002	0.015	0.066
	P	0.016	0.069	0.005	-0.038	-0.116	0.060	-0.048	0.069	-0.002	-0.008	0.003	-0.005
PL	G	0.008	0.161	-0.058	-0.270	-0.083	0.369	-0.049	0.077	0.009	-0.070	0.024	0.029
	P	0.009	0.085	-0.019	-0.104	-0.046	0.154	-0.019	0.074	0.002	-0.002	-0.062	-0.008
NPB/P	G	-0.016	0.057	0.226	0.037	-0.042	0.040	0.455	-0.191	-0.003	-0.046	0.019	0.036
	P	0.044	0.044	0.127	0.028	-0.012	0.032	-0.219	0.202	0.009	-0.002	0.009	-0.022
NFG/P	G	-0.012	0.066	0.246	-0.084	-0.022	0.047	-0.143	0.607	0.012	0.029	0.029	0.006
	P	0.019	0.030	0.036	-0.032	-0.012	0.017	-0.074	0.679	0.004	0.005	-0.013	-0.007
KL	G	0.002	0.059	-0.245	0.035	-0.007	0.066	0.022	0.131	-0.055	0.212	-0.143	-0.129
	P	-0.005	0.028	-0.014	0.004	-0.005	-0.007	0.011	-0.053	-0.032	0.005	0.029	0.019
KB	G	0.004	0.015	0.124	0.041	-0.001	-0.089	0.071	0.062	0.039	-0.291	0.154	-0.047
	P	-0.003	-0.003	-0.014	0.002	0.002	-0.005	0.017	0.055	-0.003	0.033	-0.029	0.007
L/B	G	-0.001	0.002	-0.051	-0.027	-0.014	0.042	-0.039	0.084	-0.036	0.208	-0.216	-0.003
	P	-0.005	0.016	0.005	-0.001	-0.003	-0.007	-0.002	-0.064	-0.010	-0.014	0.049	-0.002
TW	G	-0.009	0.083	-0.429	0.132	0.106	-0.039	0.098	-0.002	0.004	0.099	0.049	0.199
	P	-0.005	0.009	-0.005	0.029	0.087	-0.001	0.090	-0.022	-0.004	0.009	-0.004	0.099
GY/P	G	0.225*	0.201*	0.657*	0.049	0.030	0.141	0.572*	0.777*	-0.053	0.084	-0.050	0.298*
	P	0.208*	0.196	0.248*	0.044	0.012	0.122	0.241*	0.654*	-0.025	0.060	-0.033	0.286*

Residual effect: 0.2632(G), 0.4461(P); *Significantat1%level, **Significant at5%level

DFF: Days to 50% flowering, **PH**: Plant height (cm), **EBT**: Ear bearing tillers, **FLL**: Flag leaf length (cm), **FLW**: Flag leaf width (cm), **PL**: Panicle length(cm), **NPB/P**: No. of primary branches/panicle, **NFG/P**: No. of fertile grains/panicle, **KL**: Kernel length (mm), **KB**: Kernel breadth (mm), **L/B**: Length/breadth ratio, **TW**=Test weight(g), **GY/P**=Grain yield/plant (g)

References

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

Babu TB. 2020. Studies on genetic diversity of yield enhancing traits and gene linked markers among Elite rice lines. *M.Sc (Ag.) Thesis*. Acharya N.G. Ranga Agricultural University, Guntur, India.

Bharathi G, Krishna Veni B, Lal Ahamed M and Jaya Lalitha K. 2017. Genetic parameters for yield and yield components in rice (*Oryza sativa* L.) genotypes. *The Andhra Agricultural Journal,* 64(2): 357-359.

Devi KR, Chandra BS, 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*, 37(1): 1-9.

Dewey DR and Lu K H. 1959. A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agronomy Journal*, 51(9): 515-518.

Falconer DS. 1964. *An Introduction to Quantitative Genetics*. 2nd ed. pp. 312-324, Oliver and Boyd Publishing Co. Pvt. Ltd., Edinburgh.

Herawati R, Alnopri M and Widodo. 2021. Genetic analysis of panicle architecture traits in F_5 from single cross of local rice varieties for developing high yielding new type of upland rice. *International Journal of Agricultural Technology,* 17(1): 87-102.

Hossain S, Salim M, Azam MG and Noman S. 2018. Variability, correlation and path analysis in drought tolerant rice (*Oryza sativa* L.). *Journal of Bioscience and Agriculture Research,* 18(02): 1521-1530.

Islam MZ, Siddique MA, Akter N. 2019. Morpho-molecular divergence of restorer lines for hybrid rice (*Oryza sativa* L.) development. *Cereal Research Communications,* 47(3): 531-540.

Johnson HW, Robinson, HF and Comstock RE. 1955. Estimation of genetic and environmental variability in soybean. *Agronomy Journal*, 47(7): 314-318.

Kavitha B, Balakrishnan, D and Neelamraju S. 2020. Variability and correlation of yield traits in BIL x BIL populations derived from Swarna x *O. nivara*. *Journal of Rice Research*, 13(1): 1-8.

Kumar HRU, Gangaprasad S, Raghavendra P and Kumar BMD. 2017. Revealing genetic variability and trait association studies in landraces of rice (*Oryza sativa* L.) under controlled and drought conditions. *International Journal of Current Microbiology and Applied Sciences*, 6(8): 737-747.

Ministry of Agriculture and Farmers Welfare. 2019. Agricultural Statistics at a Glance: Rice-Major states-Area, production and yield along with coverage under irrigation, Department of Agriculture Cooperation and Farmers Welfare, Directorate of Economics and Statistics, Government of India, pp. 48-49.

Nath S and Kole PC. 2021. Genetic variability and yield analysis in rice. *Electronic Journal of Plant Breeding*, 12(1): 253-258.

Priyanka K, Krishna Veni B, Roja V and Jayalalitha K. 2023. Genetic parameters and association studies for morphological, physiological and quality traits in rice (*Oryza sativa* L.). *Journal of Rice Research,* 16(1): 48-56.

Ramya K. 2021. Studies on molecular characterization and stability for yield and quality traits in rice (*Oryza sativa* L.). *M.Sc (Ag.) Thesis*. Acharya N.G. Ranga Agricultural University, Guntur, India.

Saha SR, Hassan L, Haque MA, Islam MM and Rassel M. 2019. Genetic variability, heritability, correlation and path analyses of yield components in traditional rice (*Oryza sativa* L.) landraces. *Journal of Bangladesh Agricultural University*, 17(1): 26-32.

Sindhura NRH, Ravi Kumar BNVSR, Dayal Prasad Babu J and Raju MRB. 2022. Assessment of genetic variability, heritability and genetic advance for grain yield and other yield attributing traits in elite lines of rice (*Oryza sativa* L.). *Journal of Rice Research,* 15(2): 34-40.

Singh KS, Suneetha Y, Kumar GV, Rao VS, Raja DS and Srinivas T. 2020. Variability, correlation and path studies in coloured rice. *International Journal of Chemical Studies*, 8(4): 2138-2144.

Singh RK and Chaudhary BD. 1977. Biometrical Methods in Quantitative Genetic Analysis. pp. 215-218. *Kalyani Publishers,* New Delhi.

Sivasubramanian S and Madhava Menon P. 1973. Genotypic and phenotypic variability in rice. *Madras Agricultural Journal,* 60(9-13): 1093-1096.

Wright S. 1921. Correlation and causation. *Journal of Agricultural Research*, 20: 557-585.