GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS STUDIES IN EARLY TRANSPLANTED RICE

ABSTRACT

Aims: The aim of this study was to evaluate the genetic variation, heritability, and direct and indirect effects of various traits on grain yield in 64 rice genotypes under early transplanted conditions.
Study Design: The study utilized a randomized block design with two replications.
Place and Duration of Study: The research was conducted at the Agricultural Research Station in Sakoli, District Bhandara during the Kharif season of 2022.
Methodology: The experimental material comprised 64 rice genotypes along with the regional check Sakoli-6. Observations were recorded on the following traits: days to 50% flowering, days to maturity, plant height, number of panicles per square meter (panicles/m²), and grain yield. Data were analyzed for genetic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, genetic advance, correlation, and path analysis to determine the direct and indirect effects of these traits on grain yield in early transplanted condition.
Results: High GCV and PCV were observed for grain yield, with moderate values for the number of panicles/m², indicating significant variability conducive to improvement.Grain yield, number of panicles/m², and plant height exhibited high heritability and genetic advance. Whereas,correlation analysis showed significant positive correlations between the number of panicles/m² and grain yield, and significant negative correlations between days to 50% flowering and days to maturity with grain yield.Path analysis indicated that days to 50% flowering, followed by the number of panicles/m² and plant height, had the highest positive direct effects on grain yield.
Conclusion: The study identified the number of panicles/m² as a critical trait for selecting superior genotypes. Based on these findings, the rice genotypes RP 6496-JB 202-4-6-1-1-1-1, OR 2800-4, and KNM 13557 were recommended for further breeding programs under early transplanted conditions.

KEYWORDS*- Genetic variability, Correlation analysis, PATH analysis, Rice, Earlytransplanting*

1. INTRODUCTION

Rice is a staple food of world as well as in India, whereas India ranks first in area and second in production after China. Rice is a self-pollinated crops belonging to genus *Orzya* of the family Poaceae having chromosome number 2n = 24 comprising two species,*O.sativa* and *O. glaberrima. Oryza sativa* is cultivated in all countries worldwide whereas *Oryza glaberrima* specifically cultivated in West African countries [1]. The demand for food will be doubled by the year 2025 and tripled by 2050 [2]. In 2022-23, rice occupied an area of around 47,000 ha, resulting in a production of 2 lakh tons, indicating a productivity of 4.3 tons ha^{-1} [3]. With rising food security, various climate changes and increasing population pressure, improving rice yield becomes a critical challenge for breeders. In addition to solving the problem by understanding genetic variability, correlationand path analysis of agronomically important characters holds prime importance.

Early transplanting is the cultural practice aimed at exploiting favorable environmental conditions, which have the potential for resource utilization and significant improvement in yield [4]. However, the effectiveness of early transplanted rice highly depends on the genetic composition of the varieties, as different varieties respond differently in various environments.

The advancement in breeding for yield and yield contributing characters in any crop is governed by polygenic inheritance and also affected by environmental influence which is determined by the extent and nature of their genetic variability [5,6]. Heritability is the extent to which a trait can be transmitted in further generations, whereas for crop improvement in any crop the knowledge of heritability of the character holds prime importance that too in association with genetic advance which states genetic gain under selection along with heritability of the trait [7]. Character association revels the relative influence of the attributing characters on grain yield. Path analysis revels the influence of each contributing trait to yield directly as well as indirectly and also enable the breeders to rank the genetic attributes according to their contribution [2].

Considering all above points, the present investigation was undertaken to understand genetic variability, correlation and path analysis of yield and yield contributing characters in rice genotypes in early transplanted condition.

2. MATERIALS AND METHODS

The present investigation was carried out at research farm of Agriculture Research Station, Sakoli, Bhandara district, Maharashtra during *kharif* 2022 using 64 rice genotypes with the help of randomized block design in two replications in early transplanted condition. The nursery was sown in raised beds and healthy nursery was raised following uniform package of practices. Twenty-one days old seedlings were transplanted at spacing of 20 cm x 15 cm and observations were recorded on five randomly selected plants *viz*., days to 50% flowering, days to maturity, plant height (cm), number of panicles per meter square and grain yield (kg/ha). The experimental materials for experiment were comprised of 63 genotypes (Table. 1) along with one regional check Sakoli-6. Fertilizer dose of 100 kg N, 50 kg P_2O_5 and 50 kg K_2O was applied. The standard agronomic practices were adopted for normal crop growth.

Table 1: List of Genotypes under study

Code No.	Designation	Code No.	Designation
3601	RP 6112- MS-M-4-11-5-3-7- 9-4-1	3633	RP 6496-JB 202-4-6-1-1-1-1
3602	Pusa 2091-26	3634	KNP-241
3603	JGL 28639	3635	CR 3506-1-2-3-1-2-1
3604	CR 4075-1341-3-3-2-2-1-4-3	3636	R 1902-97-1-77-1
3605	CR 4401-1-7-IR117834-10-1 RGA-1 RGA-1RGA-1	3637	WGL 1719
3606	CSR AP10	3638	OR 2800-4
3607	CSR M1-4	3639	KPS-10321
3608	RNR 35105	3640	CR 4388-RGA-245
3609	KNM 12509	3641	HKR 18-32
3610	CR 3745-3-2-1-2-1-1	3642	RCPR 95-IR 97046-39-2-1-2
3611	CB 18611	3643	Sahbhagidhan
3612	RP 6468-JB 396-9-7-2-1-1-1	3644	CRR-DH8
3613	NVSR 3211	3645	RP 5599-240-B-7-3 (PSV-56)
3614	NWGR-16032	3646	CR 4386-RGA-134
3615	AD 19215	3647	TRC H2N 422-B-B-7-4
3616	CR 4396-1-13-11	3648	HURS 19-9-IR 128773-4-3-1-4-B
3617	TRC B3N 693-B-B-9-4	3649	UPR 4304-12-1-1-1
3618	CO-51 (NC)	3650	RP-6529-1780-28-7-16
3619	RCPR 94-IR97030-7-2-2-2	3651	CB 17529
3620	RP 6166-47-1-23	3652	MTU 1390 (IR17M1172)
3621	CSR M1-5	3653	CR 3842-62-5-1-1-1
3622	CR 3516-11-2-2-1-15	3654	NWGR-16034
3623	KJTR 4	3655	IIABR-10 / IIAB-309/IR 13T144
3624	IIABR-9/IIAB-54/IR 16A3098	3656	CRR - DH6
3625	WGL 1720	3657	RP 6680- RMS-1703-55-89-66
3626	AD (Bio) 13060	3658	NVSR 750
3627	ORJ 1345 (TP 30531)	3659	RNR 35109
3628	KNM 13557	3660	RP 6420-C10-269-12
3629	CR 3843-22-2	3661	NDR 8806-TFR-3
3630	BRR 0156	3662	RDR-2747
3631	UPR 4546-4-1-1-1	3663	CRR 778-B-B-2-2
3632	AD 18028	3664 (LC)	SKL-6

The data underwent statistical analysis as recommended by Panse and Sukhatme, 1967 [8] for analysis of variance using a randomized block design. Meanwhile, parameters of genetic variability, including mean, range, genotypic, and phenotypic coefficient of variation, were computed following the method outlined by Burton and Devane, 1953 [9]. Broad-sense heritability for grain yield and its components was determined using the formula proposed by Burton and Devane, 1953 [9]. Genetic advancement was calculated using the method suggested by Johnson *et al*., 1955 [10]. Genotypic and phenotypic correlation coefficients for all possible comparisons were computed according to the formula provided by Johnson *et al*., 1955 [10]. The partitioning of genotypic and phenotypic correlation coefficients into direct and indirect effects was carried out using the procedure outlined by Dewey and Lu, 1959 [11].

3. RESULTS AND DISCUSSION

3.1 Analysis of variance

Analysis of variance revealed significant differences for all traits studied (Table 2). Variance due to genotype was highly significant for all the traits indicating the presence of significant variability in all 64 genotypes under study. The estimates of genetic variability parameter showed that phenotypic variability is higher than genotypic variability indicating the influence of environment on expression of the traits.

Table 2. Analysis of variance for grain yield and yield contributing characters of rice

Source of variation	Degrees of freedom	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of panicles per m^2	Grain yield (g)
Replication	1	1.76	1.76	0.13	132.03	65868.72
Treatment	63	73.93**	73.93**	94.65**	4010.82**	1732667.30**
Error	63	0.52	0.52	0.49	77.68	277523.68

*, ** Significant at 5% and 1% level of significance

3.2 Genetic variability

Among the yield attributes, maximum PCV and GCV was depicted by grain yield (23.97, 20.40) having high GCV and PCV *i. e.* above 20% followed by number of panicles /m^2 (17.96, 17.62) which reported into moderate level ranged between 10 – 20% and in low variability (<10%) for the trait's days to 50% flowering (6.68, 6.64), plant height (6.48, 6.44) and days to maturity (5.03, 4.99) (Table 3). A close resemblance of phenotypic and genotypic variation for all the characters indicates stable expression of attributes and absence of high environmental influence. In the present study, grain yield and number of panicles /m^2 reported high variation in these traits and predicting greater scope for improvement of these traits. Similarly, Williams *et al.*, 2021 [1] reported higher estimates for number of panicles per hill and grain yield.

Table 3. Estimates of heritability, genotypic and phenotypic coefficient of variation, and genetic advance and genetic advance as per cent of mean in rice genotypes

Characters	Heritability	GCV	PCV	GA	GAM
Days to 50% flowering	98.60	6.64	6.68	12.39	13.58
Days to maturity	98.60	4.99	5.03	12.39	10.22
Plant height	98.97	6.44	6.48	14.06	13.20
Number of panicles per m^2	96.20	17.62	17.96	89.60	35.60
Grain yield	72.39	20.40	23.97	1495.12	35.75

The highest heritability (%) was recorded for plant height (98.97%) followed by days to 50% flowering, days to maturity (98.60%) and number of panicles /m^2 (96.20%). Similar results were exhibited by Akinwale *et al.,* 2011 [12] for rice genotypes with high heritability for days to heading, days to maturity, plant height, grain yield and number of panicles /m^2. The higher genetic advance as per cent of mean observed for grain yield (35.75) followed by number of panicles per m^2 (35.60) which is followed by days to 50% flowering (13.58) and plant height (13.20) indicating high genetic advance as per cent of mean. Whereas, days to maturity (10.22%) reported moderate level of genetic gain as per cent of mean. Since high heritability do not always indicate high genetic gain, heritability with genetic advance considered together should be used in predicting the ultimate effect for selecting superior varieties [12]. In the present investigation, all the traits showed high heritability with high genetic gain except for days to maturity reporting moderate gain as per cent of mean. For selection, it can be concluded that on the basis of variation, heritability and genetic advance as per cent of mean, the characters grain yield, number of panicles /m^2 and plant height holds prime importance. Similar results were also reported by Akinwale *et al.* 2011 [12], Sheena and Lavanya, 2023 [2] and Kavyashree *et al.,* 2022 [13].

3.3 Correlation analysis

In the study, genotypic correlation coefficient was higher in magnitude for almost all traits than phenotypic coefficient indicating the depression of phenotypic expression by environmental influence (Table 4). Number of panicles per m^2 showed highly positive significant correlation with grain yield followed by positive correlation with plant height in early transplanted situation. However, days to 50% flowering and days to maturity showed negative significant correlation with grain yield. Whereas, days to 50% flowering and days to maturity showed highest positive correlation between them and number of panicles per m^{2}reported negative significant correlation with days to 50% flowering and days to maturity. Similar results were reported by Ogunbayo*et al.,* 2014 [14], where grain yield showed highly positive correlation with number of panicles per m^2. Kavyashree *et al.* 2022 [13] also reported negative correlation between grain yield and days to 50% flowering along with flag leaf length. Kiran *et al.* 2023 [15] reported days to maturity as negatively correlated to grain yield.

Table 4. Estimates of genotypic correlation (above diagonal) and phenotypic correlation (below diagonal) for all the traits

Characters	Days to 50% flowering	Days to maturity	Plant height	Number of panicles per m^2	Grain yield
Days to 50% flowering	1.00	1.00**	-0.02	-0.30*	-0.51**
Days to maturity	1.00**	1.00	-0.02	-0.30*	-0.51**
Plant height	-0.02	-0.02	1.00	-0.07	0.05
Number of panicles per m^2	-0.29*	-0.29*	-0.07	1.00	0.87**
Grain yield	-0.44**	-0.44**	0.05	0.73**	1.00

(*, ** Significant at 5% and 1% level of significance)

3.4 Path analysis

Path analysis offers plant breeders to study direct and indirect effects simultaneously with multiple independent and dependent variables. In the present investigation, direct and indirect effect was represented in Table 5. The residual effect was found to be 0.1683which reveals that sufficient characters were included in the path coefficient and hence the information drawn can be used. Direct effect of any character on yield gives an idea about effective selection of traits that can be made to bring improvement in breeding programme. The indirect effect indicates the inter-relationship of component characters towards contribution of yield [16]. Days to 50% flowering (0.8619) exhibited highest direct effect on seed yield followed by number of panicles per m^2 (0.7933) and plant height (0.0986) whereas negative effect was reported by the trait days to maturity (-1.1362). In indirect effect on grain yield reported highest by number of panicles per m^2(0.8671) followed by plant height (0.0460) and negative effect was reported in relation with days to50% flowering (-0.5126) and days to maturity (-0.5114). Sheena and Lavanya 2023 [2] reported positive direct effect of number of panicles per hill, panicle length, test weight, number of spikelets per panicle, biological yield with grain yield per plant and negative direct effects with days to 50% flowering, days to maturity, number of tillers per hill, flag leaf width and harvest index. Results were also supported by Madishetty*et al.* 2023 [17] in findings showed negative effect between days to maturity and days to 50% flowering with grain yield.

Table 5. Direct and indirect effect of different characters in grain yield at genotypic level in rice (R = 0.1683)

Characters	Days to 50% flowering	Days to maturity	Plant height	Number of panicles per m^2	Grain yield
Days to 50% flowering	**0.8619**	-1.1367	-0.0020	-0.2358	-0.5126
Days to maturity	0.8623	**-1.1362**	-0.0020	-0.2355	-0.5114
Plant height	-0.0178	0.0234	**0.0986**	-0.0583	0.0460
Number of panicles per m^2	-0.2562	0.3372	-0.0072	**0.7933**	0.8671

*Values in the bold are the direct effect

4. CONCLUSION

In the present investigation, based on high GCV, PCV, high heritability along with genetic advance, positive significant genotypic correlation with yield and path coefficient analysis studied in this experiment, suggested only one character *i.e.,* number of panicle /m^{2}was useful under selection in early transplanted condition. Considering this character, RP 6496-JB 202-4-6-1-1-1-1, OR 2800-4 and KNM 13557are isolated as superior genotypes over all the genotypes for further rice breeding programme in early transplanted condition.

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