Plant Archives Vol. 26, Supplement 1, 2026 pp. 1548-1556 e-ISSN:2581-6063 (online), ISSN:0972-5210

Plant Archives

Journal homepage: http://www.plantarchives.org

DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2026.v26.supplement-1.208

GENETIC STUDIES IN RICE (*ORYZA SATIVA* L.) GENOTYPES UNDER DIRECT SEEDED CONDITIONS

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(Date of Receiving : 21-09-2025; Date of Acceptance : 03-12-2025)

ABSTRACT

The present research work was conducted on 50 rice (*Oryza sativa* L.) genotypes including eleven checks during *Kharif* season, 2024 at rice research farm of Birsa Agricultural University, Ranchi, Jharkhand to assess the extent of genetic variability, correlation, and path coefficient analysis for yield and yield attributing traits under upland direct seeded conditions. The genotypes were sown in alpha lattice design. Results of analysis of variance revealed significant differences among the genotypes for all the studied traits, indicating sufficient genetic variability. High PCV and GCV were recorded for traits such as yield per plant, yield per plot and proline content. Yield per plant showed positive and significant correlation with traits such as days to fifty percent flowering, plant height, tillers per plant, panicle length, total number of spikelets per panicle, number of filled spikelets, 1000 grain weight, yield per plot, harvest index and chlorophyll content. Path analysis revealed that traits such as, filled spikelets per panicle, unfilled spikelet per panicle, and spikelet fertility exerted the highest direct positive effect on yield per plant. These findings suggest that these traits can be effectively used as selection criteria in breeding programs aimed at improving rice productivity under upland direct seeded conditions.

***Keywords* :** Rice, Upland, Direct seeded rice, Genetic variability, Correlation, Path coefficient.

Introduction

Rice (*Oryza sativa* L.) is considered as one of the most important staple cereal crops worldwide, feeding more than half of the global population. In Jharkhand, rice cultivation is predominantly dependent on rainfall, where productivity is often constrained by drought stress, and erratic rainfall patterns. For upland direct seeded rice cultivation, unpredictable and irregular distribution of rainfall during the cropping season significantly impacts seed germination, vegetative growth, flowering and ultimately reduces the grain yield. Therefore, increasing rice productivity under such conditions is a challenge for breeders. Genetic variability is the foundation for any crop improvement programmes, as it provides a base for selecting superior genotypes. Parameters like genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, and genetic advance as percent of mean provide insights into the extent and nature of variation present among genotypes. Additionally, correlation analysis is combined with path analysis to identify traits influencing grain yield positively or negatively and to understand how much each trait contributes to yield directly or indirectly. This study was conducted to explore genetic variability, correlation, and path coefficient among 50 rice genotypes under upland direct-seeded conditions, aiming to identify important traits contributing for yield improvement.

Materials and Methods

The experimental material consisted of 50 rice genotypes including 11 checks collected from diverse origins. The research was carried out in the Rice Research farm of Birsa Agricultural University, Kanke, Ranchi, Jharkhand during *kharif* season of year 2024. The experiment was carried out in alpha lattice design with two replications and two blocks in each replication. Each plot consisted of 4 meters length of five rows, occupying the area of 4 m^2 per plot. The total experimental area was 800 m^2. The collected seeds were directly used for line sowing in dry soil. The fertilizer dose of nitrogen, phosphorus and potassium were applied in the ratio of 14:11:4 kg for 800 m^2. Observations were recorded for seventeen characters including thirteen quantitative traits *viz*., seedling emergence at 10 days after sowing (TDAE), days to fifty percent flowering (DFF), plant height (PH), number of tillers per plant (TPP), panicle length (PL), total number of spikelets per panicle (TSPP), number of unfilled spikelets per panicle (USPP), number of filled spikelets per panicle (FSPP), spikelet fertility (SF), thousand grain weight (TGW), grain yield per plant (YPP), grain yield per plot (YPPLOT), and harvest index (HI) and four bio-chemical traits which are namely chlorophyll content (CHL), proline content (PRO), iron (Fe) and zinc content (Zn). The recorded data were analyzed using R-Studio, appropriate for the alpha lattice design to ensure accuracy and minimize experimental error. The ANOVA (Fisher, 1925), genotypic and phenotypic variance (Burton and Devane, 1953), GCV and PCV (Burton, 1952), broad sense heritability (Lush, 1949 and Allard, 1960), range of heritability (Robinson *et al.,* 1949), genetic advance (Jhonson, 1955) and correlation analysis (Miller, 1958) was calculated. The path coefficients analysis (Dewey and Lu, 1959) was performed by considering yield per plant as a dependent variable.

Results and Discussion

Analysis of Variance

Analysis of variance (Table 1) revealed highly significant differences ($P < 0.01$) among genotypes for all the traits studied except spikelet fertility, which exhibited significant differences ($P < 0.05$) indicating the presence of considerable genetic variability. Such significant differences confirm that the evaluated genotypes possess sufficient variability, which can be exploited in selection and breeding programmes.

Mean Value

Wide differences were observed in the mean values among all genotypes for the studied traits, indicating the presence of considerable variability in the experimental material. Estimates of variability parameters along with minimum and maximum range of mean value among genotypes for all characters are presented in Table 2. The minimum seedling emergence at 10 DAS was noted in genotype BVD 111 (72.02), whereas genotype IR22EL1485 reported the maximum value (86.68). The minimum mean value for days to 50% flowering was recorded in genotype IR22EL1031 (74 days), while the maximum was observed in genotype IRRI 154 (93 days). Plant height ranged from 74 cm in genotype IR22EL1031 to 93 cm in genotype IRRI 154, with a mean of 93.22 cm across genotypes. The maximum number of tillers per plant was noted in genotype DRR Dhan 44 with 12.5 tillers, whereas genotype IR22EL1031, reported with only 5.8 tillers. Panicle length varied from 18.7 cm in genotype TBR 13 to 25.6 cm in genotype IR22EL1493, with an overall mean of 22 cm. Genotype IR22EL1156 and IR22EL1408 showed the highest number to total spikelets, and filled spikelets whereas highest spikelet fertility and lowest unfilled spikelets was observed in Anjali. The lowest 1000-grain weight was observed in genotype IR22EL1268 (20.85g), whereas the highest was obtained in genotype IR22EL1493, with 31.75 g. Grain yield per plant ranged from 7.2 g in genotype IR22EL1268 to 26.3 g in IR22EL1101, with a mean of 15.95 g across the genotypes. The overall average yield per plot among all the genotypes under study was 1.26 kg. The highest yield per plot was recorded in genotype IR22EL1156, with 1.81 kg, while the lowest was recorded in genotype IR22EL1031, with 0.8 kg yield per plot. The overall mean value of the harvest index among all genotypes was recorded 35.39% with highest in genotype IR22EL1156 with 40.05 %, while the lowest was observed in genotype IR22EL1031, with 30.40 %. Minimum chlorophyll content was recorded in genotype BKR 270 (1.22) highest in genotype IR22EL1421 (1.65). Genotype IR22EL1485 recorded minimum (0.95) proline content whereas IR22EL1089 (1.45) recorded maximum amount of proline. Genotypes IR22EL1385 and IR22EL1076 reported minimum (5.00) iron content whereas DRR Dhan 44 (10.50) reported highest iron content. Zinc content was minimum genotype IR22EL1146 (15.00) while maximum (23.50) in four genotypes namely IR22EL1031, BKR 270, TBR 13, and BVD 111.

Although mean performance gives an initial indication of superiority among genotypes, it does not necessarily reflect its true genetic potential. It alone cannot be considered as a reliable criterion for selection, since it is highly influenced by environmental factors. Selection based only on genotypes with better mean performance may lead t biased results, as genotypes performing well under one environment may not perform similarly under different environmental conditions. Hence, for effective selection, mean performance should be considered in conjunction with genetic parameters such as heritability, a genetic advance as percent of mean.

Genetic parameters

Genetic parameter of seventeen characters are presented in Table 2. Genotypic coefficients of variation ranged from 2.317% for spikelet fertility to 34.548% for proline content. GCV was high (more thn 20%) for traits such as proline content (32.548%), yield per plant (24.860%), and yiel per plot (21.450%). Traits like unfilled spikelet per panicle (19.223%), filled spikelet per pecil (19.18%), total spikelet per panicle (18.5%), iron content (14.378%) and tillers per plan(14.089%) exhibited moderate GCV (10-20%) performance while thousand grain weigt (8.55%), plant height (8.03%), harvest index (6.998%), panicle length (6.232%), seedling mergence at ten days after sowing (4.306%), days to fifty percent flowering (3.135%),zinc content (8.662)and spikelet fertility (2.317%) recorded low GCV (less than 10%). Phenotypic coefficients of variation ranged from 4.079% for spikelet fertility to 34.468 for proline content. Traits such as, total spikelet per panicle (20.876%), unfilled spikelet per panicle (25.158%), filled spikelet per panicle (22.585), yield per plant (27.97%) and yield per plot (22.145%) recorded high PCV (> 20%) while traits like iron (19.542%), zinc (12.746%) and tillers per plant (17.293%) reported moderate PCV value (10-20%). Traits namely thousand grain weight (8.86%), plant height (9.828%), harvest index (7.481%), pnicle length (6.232%), chlorophyll content (5.964%), seedling emergence at ten days after sowing (4.306%), days to fifty percent flowering (3.135%) and spikelet fertility (2.317%) reported low value for PCV. High GCV value along with high PCV (Graph 1) were recorded for grain yield per plant, proline content and grain yield per plot, whereas tillers per plant and iron content exhibited moderate GCV and PCV, indicating significant genetic variation and suggesting these traits can be effectively improved through selection. High PCV but moderate GCV were recorded for unfilled spikelet per panicle, filled spikelet per panicle, and total spikelet per panicle suggesting direct selection based on phenotype may be less effective unless heritability is also high. The relatively smaller difference observed between PCV and GCV for traits such as, seedling emergence at ten days after sowing, days to fifty percent flowering, plant height, panicle length, total spikelet per panicle, spikelet fertility, thousand grain weight, yield per plot, proline, chlorophyll and harvest index reflecting that these characters are less influenced by environmental factors and that the observed variation is largely genetic in origin so direct selection based on phenotype will be effective for these key traits. On the other hand, traits such as tillers per plant, yield per plant, iron, zinc content, filled and unfilled spikelets per panicle, showing a wider gap between PCV and GCV indicate greater environmental effect and require careful selection. Similar findings were also reported by Kumar *et al.* (2018), Kumar *et al.* (2014), Bhor *et al.* (2020), Rajasekhar *et al.* (2022), Sravan *et al.* (2012), Seyoum *et al.* (2012), Acharjee *et al.* (2021), Zeleke and Woerde (2021), and Singh *et al.* (2018).

Heritability provides an estimate of the proportion of total variability that is heritable and thus determines the effectiveness of selection. The range of heritability (broad sense–h^2b) recorded from 32.270% for spikelet fertility to 93.820% for grain yield per plot. The high heritability (> 61%) was observed for yield per plot (93.82%), thousand grain weight (93.133%), harvest index (87.505%), yield per plant (78.998%), total number of spikelet per panicle (78.155%), seedling emergence at ten days after sowing (72.237%), number of filled spikelet per panicle (72.142%), panicle length (67.785%), plant height (66.753%), chlorophyll (70.56), proline content (89.17) and number of tillers per plant (66.380%). The moderate heritability (30 to 60%) was observed for unfilled spikelet per panicle (58.381%), iron (54.13%), zinc content (46.178%), days to fifty percent flowering (53.255%), and spikelet fertility (32.270%). High heritability for these traits indicates that phenotypic selection will be effective, whereas low heritability suggests a greater environmental influence and phenotypic selection may not truly effective. The significance of broad sense heritability lies in its role in predicting the expected response to selection when used in combination with genetic advance.

The range of genetic advance as per cent of mean (GAM) was ranged from 2.712% for spikelet fertility to 63.314% for proline content. High genetic advance as per cent of mean (> 20%) was observed for yield per plant (45.518%) followed by yield per plot (42.801%), total spikelet per panicle (33.610%), filled spikelet per panicle (33.559%), unfilled spikelet per panicle (30.257%), iron content (21.791%), proline content (63.314%) and tillers per plant (23.647%). Moderate GAM (10-20%) was exhibited by thousand-grain weight (16.998%) followed by plant height (13.515%), harvest index (13.484%), chlorophyll (10.321%), zinc content (12.125%), and panicle length (10.570%). Low genetic advance as percent of mean (< 10%) was reported for seedling emergence at ten days after sowing (7.540%), followed by days to fifty percent flowering (4.7135%), and spikelet fertility (2.712%). High GAM recorded for the traits provides a relative measure of the expected genetic gain under selection pressure. High heritability along with high genetic advance as percent of mean (Graph 2) was observed for characters, tillers per plant, total spikelets per panicle, filled spikelets per panicle, yield per plant, yield per plot and proline content implying these traits are strongly influenced by genetics and could be effectively improved through selection. These results agree with the findings of Kumar *et al.* (2014), Kumar *et al.* (2018), Manickavelu *et al.* (2006), Nath and Kole (2021), Rajasekhar *et al.* (2022), Sala *et al.* (2015), Sala and Geetha (2015), Seyoum *et al*. (2012), and Singh *et al*. (2018).

Table 1 : Analysis of variance with mean sum of squares of 17 characters

Sources of variation (d.f) /Traits	Replication (1)	Block (2)	Genotype (49)	Error (47)
Seedling emergence at 10 DAS	0.04	5.49	28.12**	4.49
Days to fifty percent flowering	40.96	3.73	22.08**	6.86
Plant height (cm)	6.71	31.31	139.96**	27.76
Tillers per plant	0.02	0.32	4.79**	1.00
Panicle length (cm)	2.35	2.52	4.65**	0.82
Total number of spikelets/ panicle	1.83	24.20	598.85**	75.52
Unfilled spikelets/panicle	2.03	0.63	14.82**	4.03
Number of filled spikelets/ panicle	7.73	31.35	502.54**	83.45
Spikelet fertility (%)	5.42	2.45	16.26*	8.58
Thousand grain weight (g)	1.03	0.07	9.96**	0.37
Grain yield per plant (g)	27.56	9.44	35.63**	3.96
Grain yield per plot (kg)	0.00	0.01	0.15**	0.00
Harvest index (%)	107.85	0.58	13.14**	0.89
Chlorophyll content (mg/g fw)	1.12	0.00	0.02**	0.00
Proline content (µmol/g fw)	0.69	0.01	0.99**	0.06
Iron content (ppm)	3.24	3.15	3.00**	0.80
Zinc content (ppm)	24.01	0.26	9.34**	3.57

Table 2 : Estimates of genetic parameters in 50 rice genotypes for seventeen characters

Traits	Range				GCV (%)	PCV (%)	Heritability (%)	GA	GAM (5%)
	Min.	Genotype	Max.	Genotype					
TDAE	72.02	BVD 111	86.68	IR22EL1485	4.306	5.067	72.237	6.012	7.540
DFF	74.00	IR22EL1031	93.50	IRRI 154	3.135	4.296	53.255	4.164	4.713
PH	72.30	TBR 13	108.80	BKR 270	8.030	9.828	66.753	12.598	13.515
TPP	5.80	IR22EL1031	12.50	DRR Dhan 44	14.089	17.293	66.380	2.321	23.647
PL	18.70	TBR 13	25.60	IR22EL1493	6.232	7.570	67.785	2.326	10.570
TSPP	57.70	Anjali	145.50	IR22EL1156	18.455	20.876	78.155	29.518	33.610
USPP	4.30	Anjali	19.10	IR22EL1493	19.223	25.158	58.381	3.679	30.257
FSPP	52.20	IR22EL1268	131.30	IR22EL1156	19.180	22.582	72.142	25.392	33.559
SF	78.29	TBR 13	92.51	Anjali	2.317	4.079	32.270	2.331	2.712
TGW	20.85	IR22EL1268	31.75	IR22EL1493	8.550	8.860	93.133	4.358	16.998
YPP	7.20	IR22EL1268	26.30	IR22EL1101	24.860	27.970	78.998	7.261	45.518
YPPLOT	0.80	IR22EL1031	1.81	IR22EL1156	21.450	22.145	93.820	0.541	42.801
HI	30.40	IR22EL1031	40.05	IR22EL1156	6.998	7.481	87.505	4.772	13.484
CHL	1.22	BKR 270	1.65	IR22EL1421	5.964	7.101	70.560	0.147	10.321
PRO	0.95	IR22EL1485	1.45	IR22EL1073	32.548	34.468	89.170	1.331	63.314
Fe	5.00	IR22EL1382, IR22EL1076	10.50	DRR Dhan 44	14.378	19.542	54.130	1.556	21.791
Zn	15.00	IR22EL1146,	23.50	IR22EL1031, BKR 270, TBR 13, BVD 111	8.662	12.746	46.178	2.404	12.125

Correlation coefficient

The result of correlation analysis is presented in Table 3. Correlation analysis revealed that for all the characters genotypic correlation was higher than phenotypic correlation suggesting a strong inherent relationship between different traits and that environmental factors have not played much role in transmission of these traits. Yield per plant exhibited highly significant and positive phenotypic correlation with thousand grain weight (0.413), yield per plot (0.544), harvest index (0.425), chlorophyll content (0.318), filled spikelets per panicle (0.420), days to fifty percent flowering (0.269), plant height (0.444), tillers per plant (0.460), panicle length (0.545), total number of spikelets per panicle (0.423) whereas, highly significant and negative phenotypic correlation with iron content (-0.315), it whereas exhibited significant and negative phenotypic correlation with zinc content (-0.242). On the other hand, non-significant and positive phenotypic correlation with unfilled spikelet per panicle (0.187), spikelet fertility (0.187), whereas, non-significant and negative phenotypic correlation with proline content (-0.083), seedling emergence at ten days after sowing (-0.131). Yield per plant exhibited highly significant and positive correlation at genotypic level with days to fifty percent flowering (0.386), plant height (0.542), tillers per plant (0.651), panicle length(0.591), total number of spikelets per panicle(0.510), filled spikelets per panicle (0.529), spikelet fertility (0.333), thousand grain weight (0.472), yield per plot (0.605), harvest index (0.546), and chlorophyll content (0.414) whereas, highly significant and negative correlation with iron content (-0.455) and zinc content (-0.399). Unfilled spikelet per panicle (0.249) exhibited significant and positive correlation. On the other hand, non-significant and negative genotypic correlation found with seedling emergence at ten days after sowing (-0.176) and proline content (-0.094). Genotypic and phenotypic correlations for yield per plant were significant and positive with traits such as days to fifty percent flowering, plant height, tillers per plant, panicle length, total number of spikelets per panicle, number of filled spikelets, 1000-grain weight, yield per plot, harvest index and chlorophyll content whereas spikelet fertility exhibited significant positive correlation at genotypic level only (Graph 3). This result says that improvement in these traits is likely to result in a simultaneous increase in grain yield under upland direct-seeded conditions. Comparable results were made by Abarshar *et al.* (2011), Belete *et al.* (2022), Farheen *et al.* (2023), Rajasekhar *et al.* (2022), Seyoum *et al.* (2012), Zeleke and Woerde (2021).

Path coefficient analysis

Results of path analysis revealed that characters such as filled spikelet per panicle, unfilled spikelet per panicle and spikelet fertility had the highest positive direct effect on yield (Table 4). Similarly, panicle length showed a high positive direct effect whereas traits such as, days to fifty percent flowering exhibited moderate positive direct effect on yield per plant, suggesting its favourable role in yield determination. On the other hand, seedling emergence at ten days after sowing, tillers per plant, total spikelet per panicle, thousand grain weight, proline and chlorophyll content showed a negative direct effect on yield under the studied conditions implying that these characters may not be suitable for direct selection for yield improvement. The residual effect was 0.1413, indicating that the traits included in the model explained approximately 85.87% of the variability in yield per plant. This suggests that most of the variation is accounted for, and only a small portion is due to other unmeasured factors. These findings are supported by Belete *et al.* (2022), Bhor *et al.* (2020), Chandra and Nilanjaya (2017), Farheen *et al.* (2023), Kumar *et al.* (2014), Kumar *et al.* (2018), Rajasekhar *et al.* (2022), Sala and Geetha (2015), Seyoum *et al.* (2012), Singh *et al.* (2022), Umarani *et al.* (2019), Zeleke and Woerde (2021), Khatun *et al.* (2015), Eargram *et al.* (2021), Abarshahr *et al.*(2011) and Singh *et al.* (2018).

Conclusion

By collectively analysing the results of genetic variability, traits such as yield per plant, yield per plot, and proline content exhibited high value for GCV, PCV, heritability and genetic advance as percent of mean whereas, traits like tillers per plant, total spikelet per panicle, and filled spikelet per panicle expressed moderate to high GCV and PCV with high heritability along with high genetic advance as percent of mean. This indicates that wide variability is present among the genotypes for these traits, and direct selection based on phenotype will be effective in breeding programs, as improvements achieved in one generation are likely to be passed on to the next generation. Characters such as panicle length, filled spikelets per panicle and spikelet fertility showed positive and significant correlation with grain yield at both the genotypic and phenotypic levels and result of path analysis also confirmed that these traits had high positive direct effect on yield indicating a strong inherent genetic contribution. Based on the result of this investigation it is recommended that direct selection based on these key traits, either individually or in combination, will accelerate genetic improvement and facilitate the development of high-yielding and stable rice varieties.

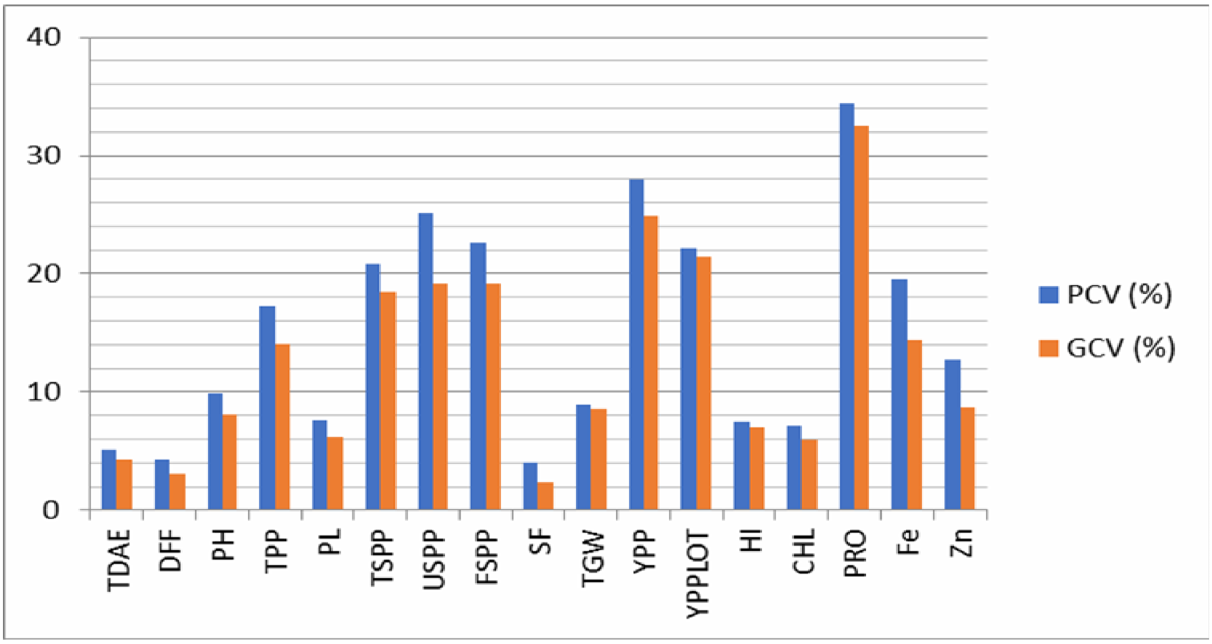

Fig. 1 : Trait-wise minimum and maximum estimates of GCV and PVC

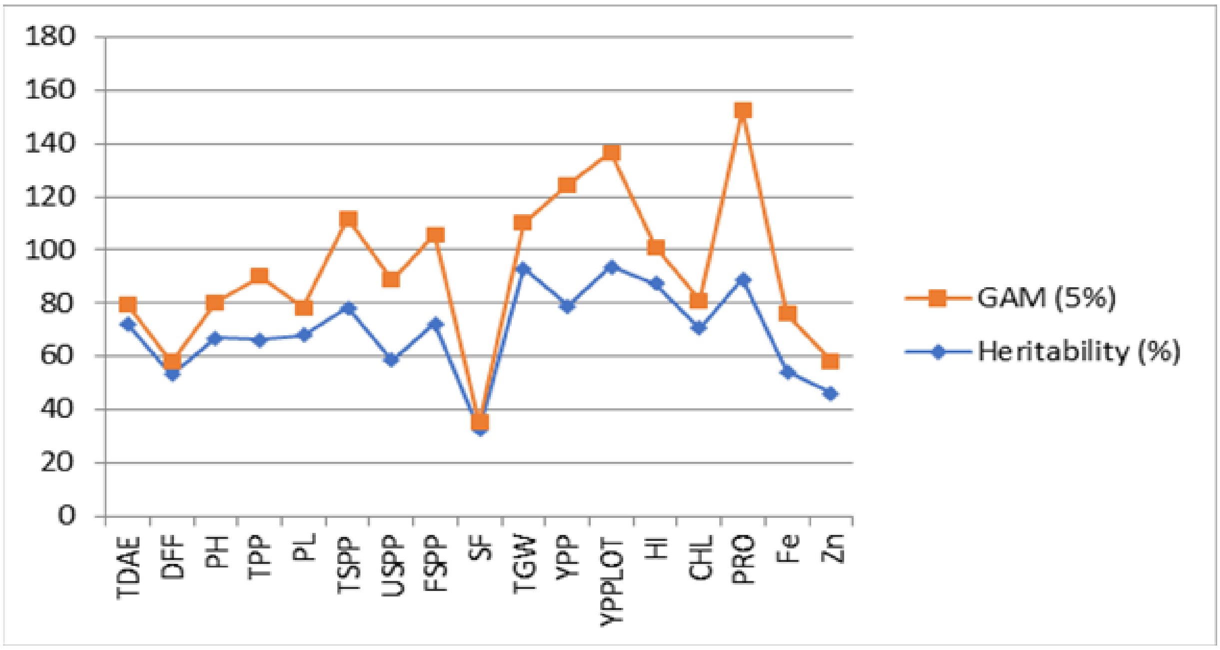

Fig. 2 : Trait-wise contribution of heritability and GAM

Table 3 : Genotypic (above diagonal) and Phenotypic (below diagonal) correlation coefficient

	TDAE	**DFF**	**PH**	**TPP**	**PL**	**TSPP**	**USPP**	**FSPP**	**SF**	**TGW**	**YPP**	**YPPLOT**	**HI**	**CHL**	**PRO**	**Fe**	**Zn**
TDAE	1.000	0.075	-0.180	0.088	0.180	0.090	0.127	0.080	-0.135	-0.048	**-0.176**	0.157	0.246*	0.237*	-0.179	-0.080	0.033
DFF	0.018	1.000	0.214*	0.434**	0.188	0.429**	0.271**	0.435**	0.110	0.157	**0.386****	0.450**	0.405**	0.277**	-0.073	-0.031	-0.384**
PH	-0.103	0.121	1.000	0.332**	0.512**	0.440**	0.320**	0.440**	0.124	0.486**	**0.542****	0.384**	0.335**	0.305**	-0.036	-0.428**	-0.078
TPP	0.014	0.256*	0.246*	1.000	0.548**	0.889**	0.413**	0.926**	0.580**	0.496**	**0.651****	0.898**	0.818**	0.523**	0.021	-0.221*	-0.537**
PL	0.119	0.177	0.491**	0.311**	1.000	0.573**	0.497**	0.560**	0.059	0.532**	**0.591****	0.554**	0.561**	0.258**	-0.207*	-0.404**	-0.153
TSPP	0.096	0.272**	0.319**	0.587**	0.398**	1.000	0.760**	0.994**	0.118	0.520**	**0.510****	0.973**	0.866**	0.627**	-0.095	-0.460**	-0.519**
USPP	0.106	0.186	0.205*	0.318**	0.326**	0.477**	1.000	0.687**	-0.541**	0.387**	**0.249***	0.566**	0.562**	0.244*	-0.271**	-0.369**	-0.247*
FSPP	0.084	0.258**	0.305**	0.573**	0.369**	0.988**	0.333**	1.000	0.219*	0.518**	**0.529****	0.996**	0.877**	0.661**	-0.063	-0.455**	-0.540**
SF	-0.064	0.004	0.071	0.163	0.010	0.280**	-0.690**	0.424**	1.000	0.184	**0.333****	0.418**	0.281**	0.442**	0.292**	-0.069	-0.383**
TGW	-0.046	0.103	0.358**	0.374**	0.410**	0.466**	0.256*	0.454**	0.154	1.000	**0.472****	0.555**	0.599**	0.259**	-0.040	-0.469**	-0.361**
YPP	**-0.131**	**0.269****	**0.444****	**0.460****	**0.545****	**0.423****	**0.187**	**0.420****	**0.187**	**0.413****	1.000	**0.605****	**0.546****	**0.414****	**-0.094**	**-0.455****	**-0.399****
YPPLOT	0.132	0.311**	0.331**	0.709**	0.492**	0.852**	0.454**	0.833**	0.207*	0.518**	**0.544****	1.000	0.929**	0.583**	-0.135	-0.506**	-0.560**
HI	0.153	0.286**	0.278**	0.603**	0.447**	0.678**	0.379**	0.660**	0.145	0.506**	**0.425****	0.828**	1.000	0.437**	-0.135	-0.480**	-0.333**
CHL	0.166	0.205*	0.180	0.333**	0.132	0.436**	0.215*	0.430**	0.119	0.229*	**0.318****	0.461**	0.361**	1.000	-0.151	-0.427**	-0.608**
PRO	-0.140	-0.009	-0.063	-0.016	-0.167	-0.089	-0.246*	-0.052	0.203*	-0.033	**-0.083**	-0.145	-0.111	-0.100	1.000	0.209*	0.175
Fe	-0.074	-0.103	-0.246*	-0.069	-0.337**	-0.305**	-0.159	-0.298**	-0.077	-0.296**	**-0.315****	-0.342**	-0.353**	-0.211*	0.153	1.000	0.443**
Zn	-0.002	-0.148	-0.107	-0.273**	-0.040	-0.258**	-0.093	-0.260**	-0.164	-0.233*	**-0.242***	-0.338**	-0.217*	-0.273**	0.139	0.241*	1.000

Where, ‘*’ - significant at 5%, ‘**’ - highly significant at 1%; Above diagonal value is genotypic and below diagonal value is phenotypic.

Where, **TDAE** – seedling emergence at 10 days after sowing, **DFF** - days to fifty percent flowering, **PH** - plant height (cm), **TPP** - number of tillers per plant, **PL** - panicle length (cm), **TSPP** - total number of spikelets per panicle, **USPP** - number of unfilled spikelets per panicle, **FSPP** - number of filled spikelets per panicle, **SF** - spikelet fertility (%), **TGW** - thousand grain weight (g), **YPP** - grain yield per plant (g), **YPPLOT** - grain yield per plot (kg), **HI** - harvest index (%), **CHL** - chlorophyll content (mg/g FW), **PRO** - proline content (µmol/g FW), **Fe** - iron content (ppm), and **Zn** - zinc content (ppm).

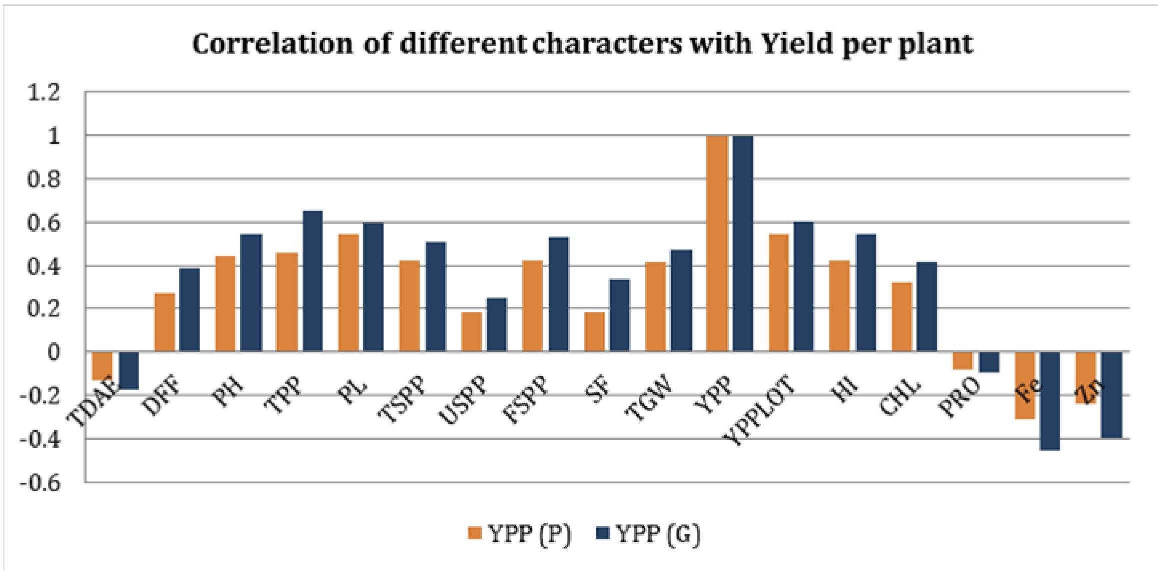

Fig. 3 : Genotypic and Phenotypic correlation coefficient for seventeen characters under studied

Table 4 : Estimates of path analysis at genotypic level

	TDAE	DFF	PH	TPP	PL	TSPP	USPP	FSPP	SF	TGW	HI	CHL	PRO
TDAE	-0.173	0.018	-0.028	-0.028	0.061	-1.214	0.418	0.902	-0.182	0.005	0.033	-0.006	0.017
DFF	-0.013	0.234	0.033	-0.136	0.063	-5.799	0.893	4.922	0.149	-0.016	0.054	-0.007	0.007
PH	0.031	0.050	0.156	-0.104	0.173	-5.951	1.054	4.975	0.168	-0.051	0.045	-0.007	0.003
TPP	-0.015	0.102	0.052	-0.313	0.185	-12.023	1.362	10.474	0.785	-0.052	0.109	-0.013	-0.002
PL	-0.031	0.044	0.080	-0.172	0.337	-7.756	1.639	6.337	0.079	-0.056	0.075	-0.006	0.020
TSPP	-0.016	0.100	0.069	-0.279	0.193	-13.528	2.504	11.249	0.160	-0.054	0.115	-0.015	0.009
USPP	-0.022	0.063	0.050	-0.130	0.168	-10.277	3.296	7.775	-0.732	-0.040	0.075	-0.006	0.026
FSPP	-0.014	0.102	0.069	-0.290	0.189	-13.454	2.266	11.311	0.296	-0.054	0.116	-0.016	0.006
SF	0.023	0.026	0.019	-0.182	0.020	-1.597	-1.783	2.477	1.352	-0.019	0.037	-0.011	-0.028
TGW	0.008	0.037	0.076	-0.156	0.179	-7.033	1.277	5.862	0.248	-0.104	0.080	-0.006	0.004
HI	-0.043	0.095	0.052	-0.256	0.189	-11.716	1.854	9.916	0.379	-0.063	0.133	-0.011	0.013
CHL	-0.041	0.065	0.048	-0.164	0.087	-8.478	0.804	7.473	0.598	-0.027	0.058	-0.024	0.015
PRO	0.031	-0.017	-0.006	-0.007	-0.070	1.289	-0.893	-0.710	0.395	0.004	-0.018	0.004	-0.097

Acknowledgement

Authors acknowledge with thanks to the Vice Chancellor, Birsa Agricultural University, Ranchi for providing necessary facilities during the M. Sc. (Ag.) course of investigation. The first author also extends gracious gratitude to the Dr. Vikas Kumar Singh, Coordinator, IRRI-South Asia Hub, Hyderabad for providing experimental materials.

References

Abarshahr, M., Rabiei, B. and Lahigi, H. S. (2011). Genetic variability, correlation and path analysis in rice under optimum and stress irrigation regimes. *Notulae Scientia Biologicae*, **3**(4), 134-142.

Acharjee, S., Chakraborty, N. R. and Das, S. P. (2021). Screening of rice landraces for potential drought tolerance through comparative studies of genetic variability and principal component analysis. *Electronic Journal of Plant Breeding*, **12**(4): 1091-1101.

Allard, R. W. (1960). Principles of Plant Breeding. *John Willy & Sons, New York.*

Belete, D. A., Tewachew, A., Bitew, M. and Mulualem, T. (2022). Correlation and path coefficient studies for yield and its components of upland rice (*Oryza sativa* L.) in North Western Ethiopia. *Journal of Scientific Agriculture*, **6**: 14-19.

Bhor, T. J., Kashid, N. V. and Kadam, S.M. (2020). Genetic variability, character association and path analysis studies for yield component traits in promising rice (*Oryza sativa*

L.) genotypes. *Journal of Pharmacognosy and Phytochemistry*, **9**(4): 1953-1956.

Burton, G.W. (1952). Quantitative inheritance of grasses. *Proceedings of 6th International Grassland Congress,* **1:** 277-283.

Burton, G. W. and De, Vane, E.H. (1953). Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal,* **45:** 478-481.

Chandra, K. (2017). Path coefficient analysis of yield components of rice under normal and aerobic conditions. *International Journal of Bio-resource and Stress Management*, **8**(6): 832-837.

Dewey, D. R. and Lu, K. H. (1959). A Correlation and Path-Coefficient Analysis of Components of Crested Wheatgrass Seed Production. *Agronomy Journal,* **51**(9): 515–518.

Eragam, A., Srividhya, A., Latha, P., Reddy, E. R., & Vemireddy, L. R. (2021). Identification of drought tolerant mutant lines based on genetic variability and diversity studies in rice (*Oryza sativa* L.). *The Journal of Research ANGRAU*, **49**(1): 1-17.

Farheen, M., Murthy, K., Mohan, Y. C. and Kumar, J. H. (2023). Studies on correlation and path analysis for yield and morpho-physiological traits in elite rice (*Oryza sativa* L.) genotypes under dry DSR system. *International Journal of Bio-resource and Stress Management*, **14**(4): 546-553.

Fisher, R. A. (1925). Statistical Methods for Research Workers. *Oliver and Boyd, Edinburgh.*

Johnson, H. W., Robinson, H. F. and Comstock, R. W. (1955). Estimates of Genetic and Environmental Variability in Soybeans. *Agronomy Journal,* **47**(7), 314–318.

Kumar, G., Dwivedi, D. K., Shivani, P. Y. and Chhavi, P. S. (2018). Analysis of genetic variability (PCV, GCV, heritability and genetic advancement) among thirteen different rice genotypes in north India. *Journal of Pharmacognosy and Phytochemistry*, **7**(3): 3514-3516.

Kumar, N. N., Babu, G. S. and Reddy, P. A. (2014). Studies on Correlation and Path Analysis in Upland Rice Germplasm. *Trends in Biosciences*, **7**(1): 46-50.

Lush, J. L. (1949). Heritability of quantitative characters in farm animals. *Hereditas (suppl.),* 356-375.

Manickavelu, A., Nadarajan, N., Ganesh, S. K., Gnanamalar, R. P. and Chandra Babu, R. (2006). Drought tolerance in rice: morphological and molecular genetic consideration. *Plant Growth Regulation*, **50**(2): 121-138.

Miller, P. A., Williams, J. C., Robinson, H. F. and Comstock, R. E. (1958). Estimates of Genotypic and Environmental Variances and Covariances in Upland Cotton and Their Implications in Selection. *Agronomy Journal,* **50**(3): 126-131.

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

Rajasekhar, J., Lavanya, G. R., Purushotham, G. and Kumar, D. P. (2022). Character Association and path coefficient analysis in upland rice (*Oryza sativa* L.) for grain yield and quality characters. *International Journal of Plant & Soil Science*, **34**(23): 410-419.

Robinson, H. F., Comstock, R. E., and Harvey, P. H. (1949). Breeding procedure designed to make maximum use of both general and specific combining ability. *Agronomy Journal,* **41**(8): 360–367.

Sala, M. and Geetha, S. (2015). Correlation and path analysis for iron and zinc content in segregating the population of rice. *Rice Genomics and Genetics*, **6**.

Seyoum, M., Alamerew, S. and Bantte, K. (2012). Genetic variability, heritability, correlation coefficient and path analysis for yield and yield related traits in upland rice (*Oryza sativa* L.). *Journal of Plant Sciences*, **7**(1): 13-22.

Singh, S. K., Singh, M., Vennela, P. R., Singh, D. K., Kujur, S. N. and Kumar, D. (2018). Studies on genetic variability, heritability and genetic advance for yield and yield components in drought tolerant rice (*Oryza sativa* L.) landraces. *International Journal of Current Microbiology and Applied Sciences,* **7**(3): 299-305.

Singh, S., Dixit, S., Tarkeshwar, K. Y. and Dutt, A. (2022). Direct and indirect effect computed between different phenotypic and genotypic levels of yield relatable traits in rice (*Oryza sativa* L.) under sodic soil. *The Pharma Innovation Journal*, **11**(7): 692-697.

Sravan, T., Rangare, N. R., Suresh, B. G. and Kumar, S. R. (2012). Genetic variability and character association in rainfed upland rice (*Oryza sativa* L.). *Journal of Rice Research*, **5**(1): 2.

Tuhina-Khatun, M., Hanafi, M. M., Rafii Yusop, M., Wong, M. Y., Salleh, F. M., & Ferdous, J. (2015). Genetic variation, heritability, and diversity analysis of upland rice (*Oryza sativa* L.) genotypes based on quantitative traits. *BioMed research international*, (1): 290861.

Umarani, E., Hemalatha, V., Subbarao, L. V., Neeraja, C. N., Suneetha, K. and Reddy, N. S. (2019). Studies on character association and path coefficient analysis for anaerobic germination traits, yield and its contributing characters in rice (*Oryza sativa* L.). *International Journal of Current Microbiology and Applied Sciences*, **8**(4): 355-362.

Zeleke, B. and Worede, F. (2021). Correlation and path analysis for yield and related traits in upland rice (*Oryza sativa* L.) Varieties. *Black Sea Journal of Agriculture*, **4**(1): 18-24.