Estimates of Genetic Parameters for Yield Attributing Characters in Restorer Lines of Rice (*Oryza sativa* L.)

Comment [NSN1]: Corrected

ABSTRACT

Comment [NSN2]: Corrected

The present investigation was carried out to study the genetic variability, correlation and path coefficient analysis for eight yield and yield attributing traits in 47 (40 improved parental lines + 7 checks) lines of rice. Analysis of variance revealed significant differences among all the treatments under study. High values of PCV and GCV for traits like number of filled grains per panicle and single plant yield while moderate PCV and GCV recorded for Plant height, number of productive tillers per plant, spikelet fertility and 1000 grain weight. High heritability coupled with high genetic advance as percent of mean was observed for the traits namely number of filled grains per panicle, plant height and single plant yield. The traits productive tillers per plant, panicle length, number of filled grains per panicle, spikelet fertility % and 1000-grain weight exhibited significant and positive association with single plant yield. Number of filled grains per panicle, 1000-grain weight, number of productive tillers per plant, plant height and panicle length exhibited positive direct effect on single plant yield indicating that direct selection for these traits could lead to improvement in single plant yield.

Keywords: Genetic variability; heritability; Correlation; path coefficient analysis; Rice

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1. INTRODUCTION

Comment [NSN4]: Number section added

Rice (*Oryza sativa* L.) is the primary staple food for one third of the world population and is often referred as “Global Grain” (Ajmera *et al.*, 2017). It constitutes approximately 20% of the global dietary energy supply, making it a significant contributor in meeting the world's nutritional needs. Rice production and research have encountered significant challenges in recent times. Some major rice-producing nations have experienced a plateau in yield and total production for many years (Shetty *et al*., 2013). In current scenario, rice productivity is increasing at a rate of 1% per year which is less than the required rate of 2.4% per year to double the global production by 2050 (Dhonde *et al*., 2020). To meet the increased demand, many countries are actively seeking to leverage hybrid rice technology, which has the potential to enhance rice production and productivity. Restorer lines play a crucial role in hybrid rice breeding and by enhancing restorer lines, breeders can introduce greater genetic diversity into hybrid development, resulting in the creation of superior hybrids.

Grain yield is influenced by various component traits, with some directly impacting yield and others exerting indirect effects. Hence, to enhance grain yield, it is essential to identify the traits that directly or indirectly contribute to it. In such conditions a comprehensive study on the genetic variability of a population, character association and the path coefficient analysis for the grain yield and its attributing traits play a crucial role in improving crop productivity (Jan *et al*., 2017). The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) provide an idea about the magnitude of variability. Heritability estimates along with genetic advance are more helpful in predicting the genetic gain under selection. Analyzing correlations between crop yield and its attributing traits offers valuable insights towards the relationship between yield and its components (Dhavaleshwar *et al*., 2019). Additionally, path analysis aids in determining the direct and indirect causes of association and formulation of effective breeding strategies for development of better genotypes.

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Therefore, the present investigation was carried out with the aim of assessing the variability parameters, character association and path coefficient analysis for grain yield and its attributing traits.

2. MATERIALS AND METHODS

Comment [NSN6]: Number section added

The research was carried out during *kharif*, 2022 at Research farm, ICAR- Indian Institute of Rice Research (IIRR), Hyderabad, located at an altitude of 542 m above mean sea level on 17º 19’’ N latitude and 78º 23’’ E longitude in Southern Zone of Telangana State.

The material for the present genetic study comprised of 47 entries of which 40 are improved parental lines derived from the cross between AR 9-18 and yield enhancing donor YPK 198, through forward breeding, seven checks i.e., four maintainer lines (APMS6B, IR58025B, IR79156B, CRMS32B), two parents (AR 9-18, YPK 198) and a National Check (CR-DHAN-201). The experiment was laid out in Randomized Complete Block Design (RBD) in two replications.

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Phenotypic data was recorded for eight yield and its attributing traits *viz*., days to 50% flowering, plant height (cm), number of productive tillers per plant, panicle length (cm), spikelet fertility (%), number of filled grains per panicle, weight of 1000 grains (g) and single plant yield (g) on all the lines based on flowering duration and maturity. During the experiment to raise a healthy nursery and main crop, we diligently adhered to the recommended cultural practices and implemented essential crop protection measures.

Statistical analysis was done for the data recorded on eight yield and its attributing traits *viz*., genotypic coefficient of variation (GCV), phenotypic coefficient of Variation (PCV), broad sense heritability and genetic advance as per cent of mean. GCV and PCV were determined using the method described by Burton and Dewane (1953). The range of variability was categorized as follows: high (> 20%), moderate (10-20%) and low (< 10%) in accordance with the classification proposed by Sivasubramanian and Madhavamenon (1973). Lush (1949) and Hanson *et al.* (1956) proposed that broad sense heritability h^2(bs) was determined by taking the ratio of genotypic variance to the total variance and expressed in per cent. As per the classification proposed by Robinson *et al.* (1949) heritability estimates are categorized into three groups: high (> 60%), moderate (30-60%) and low (0-30%).

Genetic advance was calculated and then categorized into different levels: high (> 20%), moderate (10-20%) and low (< 10%) as suggested by Johnson *et al.* (1955). For the calculation of simple correlations, the formula given by Weber and Moorthy (1952) was used while for computation of path analysis, the method described by Dewey and Lu in 1959 was utilized.

3. RESULTS AND DISCUSSION

Comment [NSN8]: Number section added

The Analysis of Variance (ANOVA) indicated that the mean sum of squares due to genotypes was highly significant for all the characters, which further ascertain that there is considerable amount variability in the material and ample scope for the improvement in the investigated traits (Table 1).

The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) provide an idea about the magnitude of variability. Number of filled grains per panicle (28.91 % and 26.54 %) and single plant yield (24.13% and 21.12%) recorded high PCV and GCV values (Table 2, Figure 1), indicating the presence of considerable variability thus selection may be useful for improvement of these traits. Similar results were reported by Hasan-Ud-Daula and Sarker (2020). In variability study, moderate PCV and GCV was recorded for Plant height, number of productive tillers per plant, spikelet fertility and 1000 grain weight as also observed by Sandeep *et al.* (2018) for plant height, productive tillers per plant,1000-grain weight and Tiwari (2017) for spikelet fertility. Panicle length recorded moderate PCV and low GCV, similar results were reported by Ali *et al.* (2018). Low PCV and GCV estimates was exhibited by days to 50% flowering. These findings are consistent with the results reported Singh *et al*. (2020). The small differences observed between phenotypic coefficient of variation and genotypic coefficient of variation on most of the traits indicate the presence of sufficient genetic variability for the traits which may facilitate selection.

Number of filled grains per panicle (84.24 % and 50.17 %), plant height (77.4 % and 22.67 %) and single plant yield (76.56% and 38.06%) recorded high heritability and high genetic advance as a percentage of the mean (Table 2, Figure 2). This is indicating the presence of additive gene action thus selection may be effective for these traits. These results align with the findings of Lakshmi *et al*. (2020), Kiruthikadevi *et al.* (2020), Patra *et al.* (2020), Kumar *et al.* (2020) and Nath and Kole (2021). The traits spikelet fertility (73.30 % and 18.28 %) and 1000 grain weight (65.15% and 17.23%) exhibited high heritability with moderate genetic advance as a percentage of the mean, as reported by Hassan *et al*. (2020) and Awad *et al.* (2022) whereas, days to 50% flowering (71.30 % and 7.41 %) showed high heritability with low genetic advance as percent of mean as that reported by Dhavaleshvar *et al.* (2019). Moderate levels of heritability and genetic advance as percent of mean is recorded in number of productive tillers per plant (40.40 % and 14.12 %) and panicle length (55.42% and 14.79%) similar with that of Parvathi *et al.* (2011) and Singh *et al*. (2020) results.

At phenotypic level, number of productive tillers per plant (0.382^{**}), panicle length (0.238^{*}), number of filled grains per panicle (0.619^{**}), spikelet fertility % (0.232^{*}) and 1000-grains weight (0.604^{**}) exhibited significant and positive association with single plant yield hence, direct selection for these characters would improve the yield wherein, other yield components *viz.*, days to 50% flowering (0.032), plant height (0.073) had shown positive non-significant association (Table 3). Similar results were reported by Santhipriya *et al*. (2017) and Singh *et al.* (2020) for single plant yield with number of productive tillers per plant, panicle length and 1000-grain weight; Saha *et al.* (2019), Kiruthikadevi *et al.* (2020), Shrivatsav *et al.* (2020), Hasan-Ud-Daula and Sarker (2020) for number of filled grains per panicle; Shrivastav *et al*. (2020) and Buelah *et al.* (2022) for spikelet fertility %.

Considering grain yield as effect and other quantitative traits as causes the correlation coefficient between grain yield per plant and various component characters were partitioned into measure of direct and indirect effects through path analysis. It was observed that the direct and indirect association through other characters by path analysis revealed that number of filled grains per panicle (0.4495) exhibited highest positive direct effect on single plant yield (Table 4, Fig. 3) followed by 1000 grain weight (0.3778), number of productive tillers per plant (0.2006), plant height (0.0503) and panicle length (0.0105) while the trait days to 50% flowering (-0.0809) exhibited negative direct effect followed by spikelet fertility (-0.0277). These results are in accordance with Kiruthikadevi *et al.* (2020) for filled grains per panicle, 1000-grain weight and productive tillers per plant and panicle length and Gunasekaran *et al*. (2017) for plant height. The residual effect of path coefficient analysis was 0.6475. High value of residual effect could be due to the influence of other traits which were not included in this study.

4. CONCLUSION

Comment [NSN9]: Number section added

The estimates of PCV and GCV were notably high for traits such as number of filled grains per panicle and single plant yield implying that direct selection for these traits may lead to genetic improvement. Furthermore, it was noted that traits like plant height, number of filled grains per panicle and single plant yield both high heritability and a substantial genetic advance as a percentage of the mean. This indicates the predominance of additive gene action in their genetic control. Through correlation and path coefficient analysis, it was evident that among the examined yield traits, characteristics such as number of filled grains per panicle, 1000-grain weight, productive tillers per plant, panicle length were considered as most critical ones as they exhibited higher correlation coefficients and direct effects in association with single plant yield.

COMPETING INTERESTS

Comment [NSN10]: Name section added

Authors have declared that no competing interests exist.

Comment [NSN11]: Added

Table 1. Analysis of variance (ANOVA) for eight yield and yield attributing traits in rice

Comment [NSN12]: Corrected

Source of Variations		Replication	Treatment	Error
d. f.		**2**	**46**	**92**
Mean Sum of Squares	DFF	26.596	45.791**	7.661
	PH	225.11	451.09**	57.4
	PTPP	2.6111	2.5011**	1.0604
	PL	0.3102	14.3035**	4.1029
	FG	233.02	2982.49**	255.1
	SF	0.856	161.506**	24.879
	TGW	0.1755	9.5835**	2.0223
	SPY	0.013	32.979**	4.379

**** Significant at 1% level**
DFF- Days to 50% flowering, **PH**- Plant height (cm), **PTPP**-Number of productive tillers per plant, **PL**-Panicle length (cm), **FG**- Number of filled grains per panicle, **SF**-Spikelet fertility (%), **TGW**- 1000 grains weight (g), **SPY**- Single plant yield (g).

Table 2. Estimates of variability, heritability and genetic advance for yield and yield attributing traits in rice

Comment [NSN13]: Corrected

S. No	Characters	Mean	Range		PCV (%)	GCV (%)	Heritability in broad sense (h^2) (%)	Genetic Advance as % of mean
			Min	Max				
1	**DFF**	102.46	91.00	116.00	5.05	4.26	71.30	7.41
2	**PH**	112.10	72.33	146.67	14.21	12.51	77.40	22.67
3	**PTPP**	7.88	5.00	12.00	16.94	10.78	40.40	14.12
4	**PL**	23.42	17.00	31.00	12.95	9.64	55.42	14.79
5	**FG**	139.16	76.67	267.00	28.91	26.54	84.24	50.17
6	**SF**	79.76	42.69	92.85	12.10	10.36	73.30	18.28
7	**TGW**	18.76	13.72	25.01	12.83	10.36	65.15	17.23
8	**SPY**	17.91	9.04	24.65	24.13	21.12	76.56	38.06

DFF- Days to 50% flowering, **PH**- Plant height (cm), **PTPP**-Number of productive tillers per plant, **PL**-Panicle length (cm), **FG**- Number of filled grains per panicle, **SF**-Spikelet fertility (%), **TGW**- 1000 grains weight (g), **SPY**- Single plant yield (g).

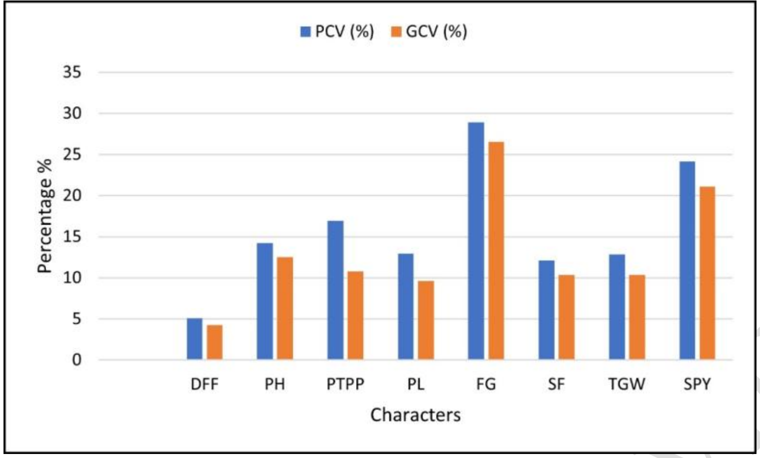

Fig. 1. Histogram of Phenotypic Coefficient of Variation and Genotypic Coefficient of Variation

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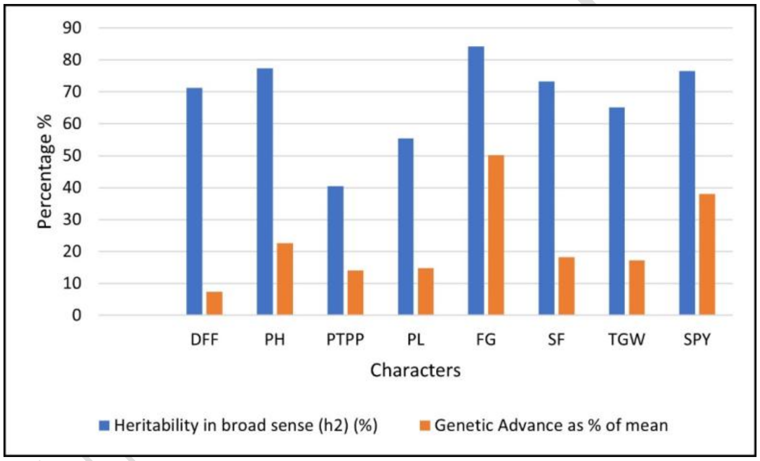

Fig. 2. Histogram of h2 (broad sense) and Genetic advance as per cent of mean

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Table 3. Correlation coefficients of yield and its attributing traits in rice

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Traits	DFF	PH	PT	PL	FG	SF	TGW	SPY
DFF	1	0.0269	-0.0067	0.0562	0.2636 *	-0.1516	-0.0262	0.0325
PH		1	-0.0081	0.3291 **	0.0323	-0.0233	0.0220	0.0735
PTPP			1	0.248 *	0.2068 *	-0.1117	0.2204 *	0.3826 **
PL				1	0.1875	-0.1198	0.2102 *	0.2387 *
FG					1	0.3503 **	0.4131 **	0.6196 **
SF						1	0.3052 **	0.2325 *
TGW							1	0.6046 **
SPY								1
*** Significant at 5% level, ** Significant at 1% level**								

DFF- Days to 50% flowering, **PH**- Plant height (cm), **PTPP**-Number of productive tillers per plant, **PL**-Panicle length (cm), **FG**- Number of filled grains per panicle, **SF**-Spikelet fertility (%), **TGW**- 1000 grains weight (g), **SPY**- Single plant yield (g).

Table 4. Phenotypic path analysis showing direct and indirect effects of yield attributing traits on single plant yield

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Traits	DFF	PH	PTPP	PL	FG	SF	TGW	SPY
DFF	**-0.0809**	0.0014	-0.0013	0.0006	0.1185	0.0042	-0.0099	0.0325
PH	-0.0022	**0.0503**	-0.0016	0.0035	0.0145	0.0006	0.0083	0.0735
PTPP	0.0005	-0.0004	**0.2006**	0.0026	0.0930	0.0031	0.0833	0.3826
PL	-0.0045	0.0166	0.0491	**0.0105**	0.0843	0.0033	0.0794	0.2387
FG	-0.0213	0.0016	0.0415	0.0020	**0.4495**	-0.0097	0.1560	0.6196
SF	0.0123	-0.0012	-0.0224	-0.0013	0.1575	**-0.0277**	0.1153	0.2325
TGW	0.0021	0.0011	0.0442	0.0022	0.1857	-0.0085	**0.3778**	0.6046

Bold values are direct effects **Residual effect = 0.6475**

DFF- Days to 50% flowering, **PH**- Plant height (cm), **PTPP**-Number of productive tillers per plant, **PL**-Panicle length (cm), **FG**- Number of filled grains per panicle, **SF**-Spikelet fertility (%), **TGW**- 1000 grains weight (g), **SPY**- Single plant yield (g).

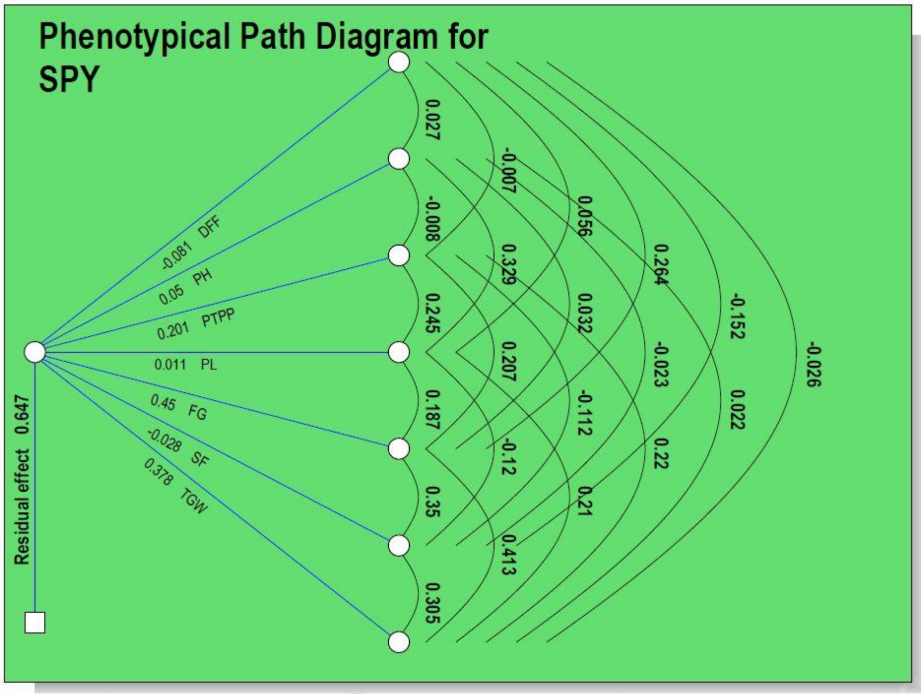

Fig. 3. Phenotypic path diagram

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