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Genetic variability and character association studies for yield and yield related traits in rice (*Oryza sativa* L.)

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Abstract
Rice (*Oryza sativa* pv. *sativa*) holds paramount significance as a staple food crop, serving as the primary dietary staple for approximately half of the global population. The study titled "Identification of high-yielding, disease resistant lines with enhanced bran oil content in 3K rice genome subset panel" was conducted during the kharif season of 2022-23 at ICAR- Indian Institute of Rice Research, Rajendranagar, Hyderabad. In this study, forty germplasm lines from the 3k rice genome subset panel and eight varieties from Telangana were assessed for their resistance to bacterial leaf blight and blast, as well as genetic variability and the association of traits related to yield. The experiment was conducted using an Alpha Lattice Design with two replications. Data was recorded for twelve different characteristics, including days to 50 percent flowering, plant height, panicle length, panicle weight, total number of tillers per plant, number of productive tillers per plant, total number of grains per panicle, total number of filled grains per panicle, total number of unfilled grains per panicle, spikelet fertility, 1000 grain weight, and single plant yield. Variability studies indicated substantial differences in all characteristics across the genotypes examined. Plant height, total grains per panicle, total number of filled grains, and total number of unfilled grains, spikelet fertility, and single plant yield displayed notably high PCV (Phenotypic Coefficient of Variation) and GCV (Genetic Coefficient of Variation) values, along with high heritability and significant genetic advance as a percentage of the mean. Moreover, character association studies indicated a significant and positive correlation between yield and plant height, panicle weight, number of tillers per plant, number of productive tillers, and test weight. Based on these findings, selecting genotypes with these favorable traits, in addition to disease resistance, holds great promise for enhancing yield in future breeding programs.

Keywords: Genetic variability, genetic advance, heritability, correlation and rice

Introduction
Rice (*Oryza sativa* L.) is the major cereal crop in the developing world. Rice being main diet for more than 70% of Indians, it also provides a living for between 120 and 150 million rural households, hence rice is called as "Grain of Life". Given the expanding global population and the escalating effects of climate change, rice breeders face the imperative task of creating more sustainable varieties that offer increased yields, healthier grains, and diminished environmental impacts. (Stein *et al.*, 2018; Wang *et al.*, 2018) [29, 30]. India holds the position of being the foremost global exporter of rice and stands as the second-largest producer of this cereal. The total land area dedicated to rice cultivation in India spans 46.83 m ha, resulting in an annual production of 130.39 million tonnes and achieving a productivity rate of 2809 kg per hectare. (Directorate of Economics and Statistics, 2022). It is essential to boost output and productivity to feed the growing population. Due to the low heritability of yield, direct selection is often ineffective. Instead, employing indirect selection of component traits is preferred to enhance overall yield. The evaluation of genetic advance, heritability, and variability for these component traits, along with their associations with yield, has been recognized as highly significant.

Phenotypic variance is the sum of genetic and environmental influences as well as their interaction (G x E). Genotypic Genetic variability is assessed using Coefficient of Variation (GCV), heritability estimates, and genetic advance (GA). GCV quantifies the level of genetic variation present in the population, whereas heritability represents the proportion of variance that is heritable. Analyzing the connection between yield and these quantitative traits is crucial for identifying the factors that significantly impact yield. This valuable information is obtained through correlation analysis, which reveals the quantitative characteristics and their influence on yield.

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Prior to initiating any breeding program or implementing appropriate selection strategies, a thorough examination of the genetic variability within the target crop species is essential. (Shivani *et al.*, 2021) [27]. A frequent and established method for determining the genetic variations among genotypes is to measure phenotypic and genotypic variances in a field trial.

Material and Methods
Forty germplasm lines of 3K rice genome subset panel which were procured from International Rice Research Institute (IRRI), Philippines was maintained at ICAR-Indian Institute of Rice Research (ICAR-IIRR), Rajendranagar, Hyderabad and eight varieties of Telangana constitutes the experimental material and was employed in the present investigation during *kharif* 2022-2023. Seeds of all genotypes were sowed in nursery beds that were one meter wide and ten metres long and transplanted utilising an Alpha Lattice Design in the well-watered main field. All the recommended agronomic practices were carried out accordingly. Phenotypic observations were conducted on five randomly chosen plants from each genotype, encompassing various traits such as days to 50% flowering, plant height, panicle length, panicle weight, total number of tillers per plant, number of productive tillers per plant, number of filled grains per panicle, number of unfilled grains per panicle, total number of grains per panicle, spikelet fertility, test weight, and single plant yield. The data was analyzed using the alpha lattice design for the analysis of variance. Genotypic and phenotypic coefficients of variation were calculated employing Falconer's (1981) [12] formula. Heritability was determined using Allard's (1960) [3] formula, while genetic advance was computed using Burton's formula from 1952. Finally, correlation analysis was conducted following the methodology described by Johnson *et al.* (1955) [13].

Results and Discussion
Table 1 displays the analysis of variance results for various traits. The treatments, which represents the mean sum of squares due to genotype, exhibited significant differences (with a probability of < 0.001) for all the studied characters, as reported by Manivelan *et al.* (2022) [18].

Estimation of genetic variability
The most substantial estimates of PCV and GCV were recorded for of single plant yield, plant height, panicle weight, grains per panicle, number of filled grains per panicle, number of unfilled grains per panicle, and test weight, indicating that selection for these traits would be beneficial. On the other hand, panicle length, number of tillers per plant, number of productive tillers per plant, and spikelet fertility displayed moderate levels of PCV and GCV. Days to 50% flowering showed low GCV and PCV. These findings are consistent with the results reported by Nithya *et al.* (2020) [21], Nath and Kole (2021) [20], Ramya (2021) [25], Bhargavi *et al.* (2021) [5], Deepthi *et al.* (2022) [8], Faysal *et al.* (2022) [11], Chavan *et al.* (2022) [7], Demeke *et al.* (2023) [9].

Heritability and genetic advance
Plant height, panicle length, panicle weight, grains per panicle, number of filled grains per panicle, number of unfilled grains per panicle, spikelet fertility, test weight, and single plant yield demonstrated high heritability and high genetic advance as a percentage of the mean. These results align with the findings of Faysal *et al.* (2022) [11], Kulsum *et al.* (2022) [15], Demeke *et al.* (2023) [9].
On the other hand, plant height, number of tillers per plant, and number of productive tillers per plant exhibited high heritability with moderate genetic advance as a percentage of the mean, as reported by Manivelan *et al.* (2022) [18].

Correlation Studies Genotypic correlation
Correlation studies showed that grain yield per plant exhibited positive and significant associations with plant height (0.242*), panicle weight (0.427**), number of tillers per plant (0.357**), number of productive tillers per plant (0.511**), and test weight (0.443**), indicating a strong link between these traits and yield. On the other hand, there was a negative and significant association with days to 50% flowering (-0.212*), and a negative but non-significant association with the number of unfilled grains (-0.016). Panicle length (0.039), grains per panicle (0.02), number of filled grains (0.03), and spikelet fertility (0.045) showed positive but non-significant associations with grain yield. Similar results were validated by Nandeshwar (2010) [19], Rashid *et al.* (2014) [24], Prasad *et al.* (2017) [22], Shivani *et al.* (2018) [26], Nithya *et al.* (2020) [21], Lingaiah *et al.* (2020) [17], Lakshmi *et al.* (2021) [16] and Begum *et al.* (2021) [4].
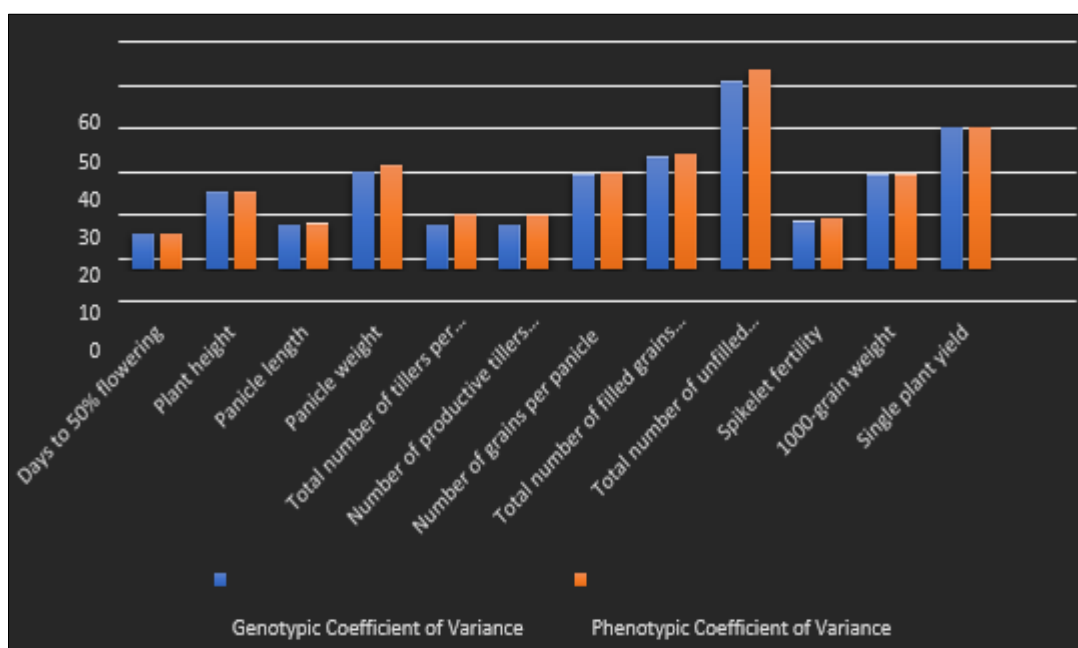
Phenotypic correlation
Grain yield per plant exhibited significant positive associations with plant height (0.24*), panicle weight (0.389**), number of tillers per plant (0.314**), number of productive tillers per plant (0.448**), and test weight (0.44**), indicating a robust link between these traits and yield. On the other hand, there was a significant negative association with days to 50% flowering (-0.21*), and a non-significant negative association with the number of unfilled grains (-0.022). Panicle length (0.035), grains per panicle (0.02), number of filled grains (0.033), and spikelet fertility (0.053) displayed positive but non-significant associations with grain yield. These findings are consistent with previous studies by Nandeshwar (2010) [19], Rahman *et al.* (2014) [23], Ahamed *et al.* (2021) [2], Begum *et al.* (2021) [4], Kulsum *et al.* (2022) [15], Sravani *et al.* (2022) [28], and Kiran *et al.* (2023) [14]. In conclusion, selecting for traits that show positive and significant associations with yield, such as plant height, panicle weight, number of tillers per plant, number of productive tillers per plant, and test weight, can be considered reliable for enhancing grain yield in rice breeding programs.

Table 1: Analysis of Variance

S. No.	Characters	Mean Sum of Squares			
		Replication	Genotypes	Block	Error
		DF = 1	DF = 47	DF = 5	DF = 42
1	Days to 50% flowering	0.26	136.73***	0.19	0.27
2	Plant height	0.2	1631.3***	0.1	0.3
3	Panicle length	0.055	17.106***	0.234	0.228
4	Panicle weight	0.280	1.076***	0.072	0.085
5	Total number of tillers per plant	2.344	5.131***	1.219	1.121
6	Number of productive tillers per plant	1.760	4.099***	0.310	0.933
7	Number of grains per panicle	1	3232***	28	44
8	Total number of filled grains per panicle	6	2656.9***	45.3	48.2
9	Total number of unfilled grains per panicle	12.8	702.4***	89.7	29.2
10	Spikelet fertility	1.45	200.33***	21.05	7.61
11	1000-grain weight	0.26	62.29***	0.18	0.13
12	Single plant yield	0.05	123.15***	0.89	0.79

*, **, *** Significant at 0.01, 0.001 and 0 level of probability
DF – degrees of freedom

Fig 1: Graphical representation of genotypic and phenotypic coefficient of variation
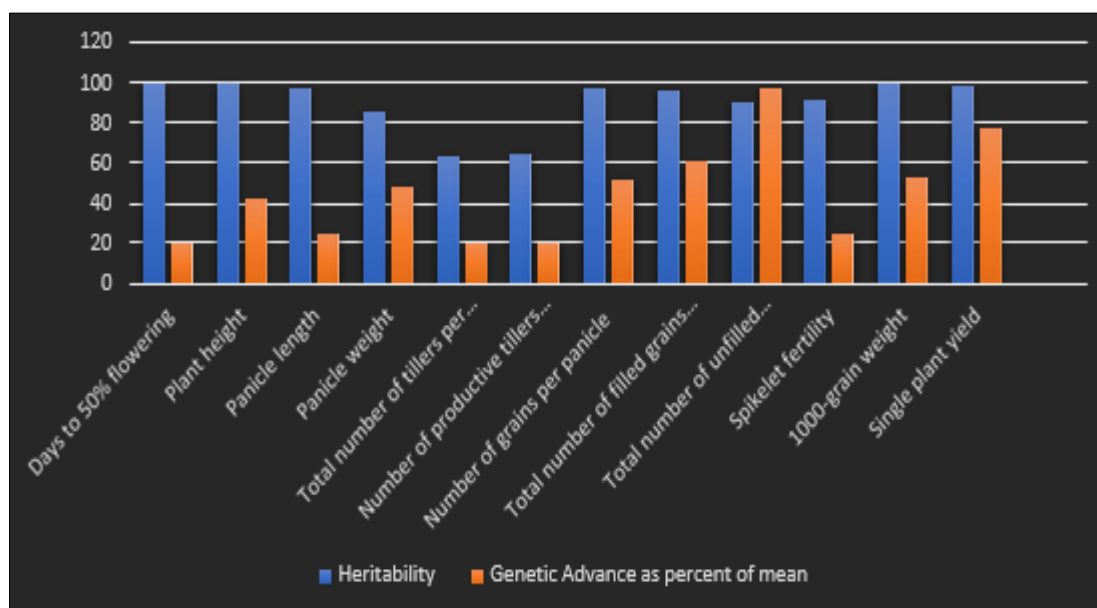
Fig 2: Graphical representation of heritability (broad sense) and genetic advance as percent of mean (5%)

Table 2: Estimates of mean, range, genetic variability, heritability and genetic advance for yield and yield attributing

Characters	Mean	Standard Error Mean	Minimum	Maximum	Genotypic Coefficient of Variance	Phenotypic Coefficient of Variance	Heritability	Genetic Advance as percent of mean
DFF	86.99	0.360	73	103	9.4960231	9.5141261	99.619814	19.524493
PH	138.479	0.385	85.5	191.4	20.622121	20.625872	99.963636	42.473896
PL	24.364	0.338	18.3	31.7	11.923247	12.0839	97.358716	24.234887
PW	2.757	0.204	1.66	5.97	25.547013	27.617988	85.565005	48.687535
NT	11.844	0.751	6	15	11.940589	14.940021	63.877681	19.658863
NPT	10.594	0.658	6	14	12.000216	14.874176	65.089708	19.943538
GPP	156.927	4.611	79	250	25.445676	25.782854	97.401581	51.732617
NFG	120.396	4.893	56	205	29.999258	30.544993	96.458603	60.694259
NUFG	36.531	4.220	10	105	49.982587	52.585783	90.344302	97.867682
SF	76.483	2.126	47.5	93.854	12.786988	13.377651	91.364362	25.178184
TW	22.113	0.002	9.414	31.812	25.415	25.415007	99.999943	52.355427
SPY	20.791	0.633	7.04	41.06	37.619158	37.865329	98.703981	76.989798

Where,

DFF- Days to 50% flowering
PH- Plant height (cm)
PL- Panicle length (cm)
PW- Panicle weight (g)

NT- Total number of tillers per plant
NPT- Number of productive tillers per plant
NFG- Number of filled grains per panicle
NUFG- Number of unfilled grains per panicle

TG- Total number of grains per panicle
SF- Spikelet fertility
TW- Test weight (g)
SPY- Single plant yield (g)

Table 3: Character association studies on yield and yield related traits

		DFF	PH	PL	PW	NT	NPT	GPP	NFG	NUFG	SF	TW	SPY
DFF	Genotypic	1.0000	0.047	0.064	-0.176	-0.057	-0.064	0.118	0.095	0.07	-0.011	-0.23*	-0.212*
	Phenotypic	1.0000	0.047	0.066	-0.17	-0.032	-0.045	0.117	0.094	0.067	-0.01	-0.23*	-0.21*
PH	Genotypic		1.0000	0.57**	0.208*	-0.12	-0.146	0.039	-0.054	0.192	-0.184	0.329**	0.242*
	Phenotypic		1.0000	0.563**	0.192	-0.095	-0.116	0.038	-0.054	0.183	-0.177	0.329**	0.24*
PL	Genotypic			1.0000	0.038	-0.136	-0.104	0.015	-0.038	0.108	-0.164	0.265**	0.039
	Phenotypic			1.0000	0.041	-0.092	-0.081	0.009	-0.04	0.096	-0.154	0.261*	0.035
PW	Genotypic				1.0000	0.221*	0.292**	0.187	0.227*	-0.041	0.181	0.474**	0.427**
	Phenotypic				1.0000	0.147	0.182	0.171	0.2	-0.023	0.147	0.438**	0.389**
NT	Genotypic					1.0000	0.952**	0.341**	0.314**	0.124	0.052	0.083	0.357**
	Phenotypic					1.0000	0.827**	0.27**	0.256*	0.077	0.063	0.066	0.314**
NPT	Genotypic						1.0000	0.323**	0.34**	0.035	0.159	0.039	0.511**
	Phenotypic						1.0000	0.252*	0.288**	-0.021	0.177	0.031	0.448**
GPP	Genotypic							1.0000	0.889**	0.428**	0.099	-0.366**	0.02
	Phenotypic							1.0000	0.881**	0.421**	0.092	-0.361**	0.02
NFG	Genotypic								1.0000	-0.033	0.531**	-0.331**	0.03
	Phenotypic								1.0000	-0.06	0.541**	-0.325**	0.033
NUFG	Genotypic									1.0000	-0.834**	-0.146	-0.016
	Phenotypic									1.0000	-0.841**	-0.139	-0.022
SF	Genotypic										1.0000	-0.047	0.045
	Phenotypic										1.0000	-0.045	0.053
TW	Genotypic											1.0000	0.443**
	Phenotypic											1.0000	0.44**
SPY	Genotypic												1.0000
	Phenotypic												1.0000

Where,

DFF- Days to 50% flowering
PH- Plant height (cm)
PL- Panicle length (cm)
PW- Panicle weight (g)

NT- Total number of tillers per plant
NPT- Number of productive tillers per plant
NFG- Number of filled grains per panicle
NUFG- Number of unfilled grains per panicle

TG- Total number of grains per panicle
SF- Spikelet fertility
TW- Test weight (g)
SPY- Single plant yield (g)

Conclusion

The study's findings indicated notable positive correlations between grain yield and specific traits such as plant height, panicle weight, number of tillers per plant, number of productive tillers per plant, and test weight, both at the phenotypic and genotypic levels. High heritability and substantial genetic advance were observed in traits like plant height, panicle length, panicle weight, grains per panicle, number of filled grains per panicle, number of unfilled grains per panicle, spikelet fertility, test weight, and single plant yield. These findings support the effectiveness of phenotypic selection to enhance various traits in rice breeding programs. Overall, the study suggests the potential for implementing selection strategies to genetically improve rice grain yield based on the identified associations and variability among the studied traits.

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