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Genetic deciphering of various morphological and agronomic traits under DSR conditions in Rice (*Oryza sativa* L.)

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Abstract

Water scarcity, labor shortages, and climate variability threaten the sustainability of conventional transplanted rice cultivation, necessitating the adoption of alternative establishment methods such as dry direct seeded rice (DDSR). The success of DDSR depends largely on the availability of rice genotypes possessing traits that ensure early crop establishment and stable yield performance under aerobic soil conditions. The present study aimed to assess genetic variability and identify key yield-contributing traits among rice genotypes suitable for DDSR environments. Thirty rice genotypes comprising varieties and advanced cultures of PJTAU, Telangana, were evaluated during *Kharif*, 2021 at Agricultural Research Station, Kampasagar, using a randomized block design with three replications. Observations were recorded for nine quantitative traits, and estimates of phenotypic and genotypic coefficients of variation, heritability, and genetic advance were computed using standard statistical procedures. Analysis of variance revealed significant differences among genotypes for all traits studied, indicating substantial genetic variability. Phenotypic coefficient of variation exceeded genotypic coefficient of variation for all characters, reflecting environmental influence on trait expression. High variability was observed for seed vigour index, number of grains per panicle, and test weight. High heritability coupled with high genetic advance as percent of mean was recorded for seed vigour index, grains per panicle, test weight, and number of effective tillers per square meter, suggesting the predominance of additive gene action and effectiveness of selection. The results indicate that these traits can serve as reliable selection criteria for improving grain yield under dry direct seeded rice conditions.

Keywords: Rice, DSR, GCV, PCV, heritability, genetic advance

Introduction

Rice (*Oryza sativa* L.) is a major food crop that forms the dietary foundation for more than half of the global population and is mostly grown under submerged soil conditions and requires more water compared to other crops. Erratic rainfall patterns, increasing scarcity of resources especially water and labor during critical operations, deterioration of soil health, changing climate, emerging energy crisis and the rising cost of cultivation has lead to marked shift of rice cropping system from puddled transplanting to direct seeding in majority of rice growing areas (Ladha *et al.*, 2009) [8]. The need to develop alternative rice establishment techniques has intensified due these challenges and in this context, direct seeded rice (DSR) is increasingly being adopted as a resource-efficient alternative to conventional puddled transplanted rice (Singh *et al.*, 2024) [19] and has become regular practice under rainfed situations (Ladha *et al.*, 2009) [8]. Its wider acceptance is attributed to its operational simplicity and multiple agronomic and environmental advantages.

Sustainable food production requires reducing greenhouse gas emissions from agriculture and improving the ability of farming systems to cope with climate-related risks (Ahmed *et al.*, 2025) [1]. Flooded rice systems are major emitters of methane (CH₄) and nitrous oxide (N₂O), greenhouse gases with high radiative forcing and global warming potential (Xu *et al.*, 2022) [22]. Paddy rice cultivation contributes approximately 10% of total agricultural greenhouse gas emissions and nearly 20% of methane emissions from agriculture, highlighting the need for climate-smart establishment methods such as direct seeded rice (IPCC, 2014; Smartt *et al.*,

2016)^[5, 21]. Additionally, DSR enhances soil physical properties for succeeding crops, minimizes methane emissions, offers greater flexibility within diverse cropping systems, and presents a promising pathway for improving water use efficiency and long-term environmental sustainability (Singh *et al.*, 2024)^[19]. In order to increase the area of cultivation and yield potential under water scarce area, it is essential to develop new plant types which are suitable for dry direct seeded rice conditions and requires more efforts to understand the genetic background of the material being handled on the part of the plant breeder. The present investigation has been carried out to evaluate and identify rice varieties/cultures suitable for dry direct seeded rice (DDSR) with specific traits like seed vigour index, grain filling percentage (%), test weight (g) and grain yield/plant (kg/ha).

Materials and Methods

The experimental material for the present investigation comprised of 30 rice genotypes which include varieties/advanced cultures of PJTAU Telangana, were evaluated in a complete randomized block design with three replications during *Kharif*, 2022 at Agricultural Research Station, Kampasagar, situated between 16.8536 N latitude and 79.4569 longitudes at 152 m above mean sea level, Telangana state, India. In each replication each genotype was grown in a plot size of 10.5 m² with a spacing of 20 x 15 cm under dry direct seeded condition using the fertilizer @ 120:60:40 kg (N: P: K) per ha. The data were recorded on five randomly selected plants from each replication for nine quantitative traits except days to 50% flowering which was computed on plot basis. Estimates of phenotypic and genotypic coefficients of variation according to Burton & De Vane (1952)^[3], heritability estimates in broad sense according to Lush (1940)^[10] and genetic advance as suggested by Johanson *et al.*, (1955) were calculated following standard statistical procedures.

Results and Discussion

The Analysis of variance carried out as per standard procedure of Panse and Sukhatme, (1985)^[13] has revealed a significant genotypic difference for all the traits studied indicating that a large amount of variability was present in the material. The results are in accordance with Mohan *et al.*, 2022^[12], Kumar *et al.*, 2017^[7] (Table-1). The substantial improvement of this crop is possible because of the presence of broad variability among the genotypes. Extent of variability was measured in terms of range, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) along with per cent heritability (h²), genetic advance and genetic advance over per cent mean and is presented in Table 2.

The mean data exhibited a wide range of variations among the characters studied (Table 2). Days to 50% flowering ranged between 76-116 days, plant height ranged from 71 to 138 cm, number of effective tillers/m² (347 to 733), Panicle length (cm) ranged from 17.6 to 29.6, for test weight the range is in between 10.3-34.2 g. No. of filled grains/panicle and grain filling percentage (%) recorded (55 to 202) and (56.2 to 101.3) respectively. Seed Vigour Index was ranged between 1350 to 3698 and grain yield had a range of 3465 to 6757 kg/ha.

Coefficient of variation indicates the amount of variability present in a character. The genotypic and phenotypic coefficients of variation are classified (low: less than 10%, moderate: 10-20% and high: more than 20%) as suggested by Sivasubramanian and Madhava Menon (1973)^[20]. The estimates

of the phenotypic coefficient of variation (PCV) was found higher than that of genotypic coefficient of variation (GCV) for all the traits, indicating the influence of the environment in governing the characters or expression of genotypes (Immanuel Antipas *et al.*, 2025 & Pravalika *et al.*, 2025)^[4, 11]. Phenotypic coefficient of variation and genotypic coefficient of variation was found to be high (>20%) for No. of filled grains/panicle (27.33%, 23.26%) test weight (25.82%, 21%) Seed Vigour Index (26.73%, 23.33%) respectively, indicating indicating more opportunity of selection for these characters. Moderate PCV and GCV recorded for days to 50% flowering, plant height, number of effective tillers/m² and grain yield indicates the presence of sufficient variability for these traits. The values are low for the characters, panicle length (cm), grain filling percentage (%) and selection for these characters will not be efficient because, variation is mainly influenced by environment (Table-2) These results are in similarity with the findings of Ramya Rathod *et al.*, 2020^[16].

The estimates of heritability are categorized as (low: less than 30%, moderate: 30-60% and high: more than 60%) as recommended by Johnson *et al.* (1955)^[6]. Heritability (in broad sense) estimates ranged from to 50.36% (grain filling percentage (%)) to 97.37% (No. of effective tillers/m²) (Table 2). High heritability was observed for no. of effective tillers/m² followed by days to 50% flowering, no. of grains per panicle, seed vigour index and test weight (g). All the other traits except panicle length and grain yield had heritability estimates of more than 60%, indicating the preponderance of additive gene action in the expression of these traits and they can be improved through individual plant selection.

The heritability value alone, however, does not provide any indication of the amount of genetic improvement that would results from selecting the best individuals. Limitations of heritability in broad sense include both the additive and non additive gene effects, which become reliable for selection if, coupled with high genetic advance (Ramanujan and Tirumalachar 1967)^[15]. High genetic advance estimates were obtained for characters, grain yield (1316.8) followed by Seed Vigour Index (977.83) and No. of effective tillers/m² (163.40). These findings are in accordance with Rashad Khan *et al.* 2023^[17] and Pavani *et al.* 2021^[14].

It might not be necessary to have traits with high heritability produce high genetic advance. High heritability should be accompanied by high genetic progress, according to Johnson *et al.*, 1955^[6]. Breeders need to be caution while analyzing heritability. The estimates of genetic advance as percent of mean is used for better prediction of characters since heritability estimates alone sometimes misleads interpretation of the data. Heritability alone fails to indicate the response to selection and a character having high heritability may not necessary give high genetic advance. Therefore, heritability should be always considered along with genetic advance as percent of mean to arrive at a more reliable conclusion. The range of genetic advance as percent of mean is classified (low: less than 10%, moderate: 10-20% and high: more than 20%) as suggested by Johnson *et al.* (1955)^[6]. High heritability coupled with high genetic advance as percent of mean was found for seed vigour index followed by no. of grains per panicle (Pravalika *et al.*, 2025, Immanuel Antipas *et al.*, 2025 & Lingaiah *et al.*, 2020)^[11, 4, 9], test weight (Pravalika *et al.*, 2025, Lingaiah *et al.*, 2020 & Shivani *et al.*, 2018)^[11, 9, 18] and no. of effective tillers/m² (Rashad Khan *et al.*, 2023)^[17] indicating the preponderance of

additive gene action for the expression of these characters with minor influence of environment and selection may be effective for improving these characters. High heritability accompanied with moderate genetic advance as percent of mean was observed for the traits days to 50% flowering and plant height (cm).

Moderate heritability with high genetic advance was found for grain yield (kg/ha), reflected the preponderance of non-additive gene action and selection for these traits may not be rewarding (Akinola *et al.*, 2019 & Lingaiah *et al.*, 2020) [2, 9]

Table 1: Analysis of variance for mean squares of nine morphological traits in rice

Variables	df	DFF	PH	NET	PL	NFG	TW	GFP	SVI	GY
Replication	2	0.164	1.98	22.5	7.9748	15.99	0.363	30.1	12000	975667
Genotype	29	290.965***	471.45***	19558.7***	19.942***	2589.34***	68.104***	226.777***	980388***	2701805**
Residuals	58	5.588	66.32	174.1	4.3964	291.36	8.991	56.059	92690	1106653
SE		1.36	4.70	7.62	1.21	9.86	1.73	4.32	175.77	607.36
CD 5%		3.86	13.31	21.56	3.43	27.90	4.90	12.24	497.59	1719.34
CD 1%		5.14	17.71	28.69	4.56	37.12	6.52	16.28	662.05	2287.59

Df: degree of freedom, DFF: Days to 50% flowering, PH: Plant Height (cm), NFG: No. of effective tillers/m², PL: Panicle length (cm), NFG: No. Of filled grains/panicle, TW: Test weight (g), GFP: Grain filling percentage, SVI: Seed Vigour Index, GY: Grain yield (kg/ha),

Note: *, ** and *** significant at 5%, 1% and 0.1% levels respectively.

Table 2: Estimates of variability and genetic parameters for nine traits in rice.

S. No.	Character	Range		Mean	Coefficient of Variation (%)		H (bs) (%)	G.A.	G.A. as % of mean
		Min.	Max.		GCV	PCV			
1	Days to 50% flowering	76	116	91.65	10.64	10.95	94.44	19.52	21.3
2	Plant height (cm)	71	138	100.47	11.56	14.12	67	19.60	19.51
3	No. of effective tillers/m ²	347	733	514.50	15.62	15.83	97.37	163.40	31.76
4	Panicle length (cm)	17.6	29.6	23.31	9.9	13.59	53.1	3.45	14.87
5	No. of filled grains/panicle	55	202	118.95	23.26	27.33	72.44	48.52	40.79
6	Test weight (g)	10.3	34.2	20.32	21	25.82	66.67	7.24	35.47
7	Grain filling percentage (%)	56.2	101.3	83.01	9	12.83	50.36	11.02	13.28
8	Seed Vigour Index	1350	3698	2331.4	23.33	26.73	76.14	977.83	41.94
9	Grain yield (kg/ha)	3465	6757	5483.7	15.46	20.5	56.85	1316.8	24.00

GCV- Genotypic coefficient of variation, PCV- Phenotypic coefficient of variation, H-Heritability, G.A. Genetic Advance

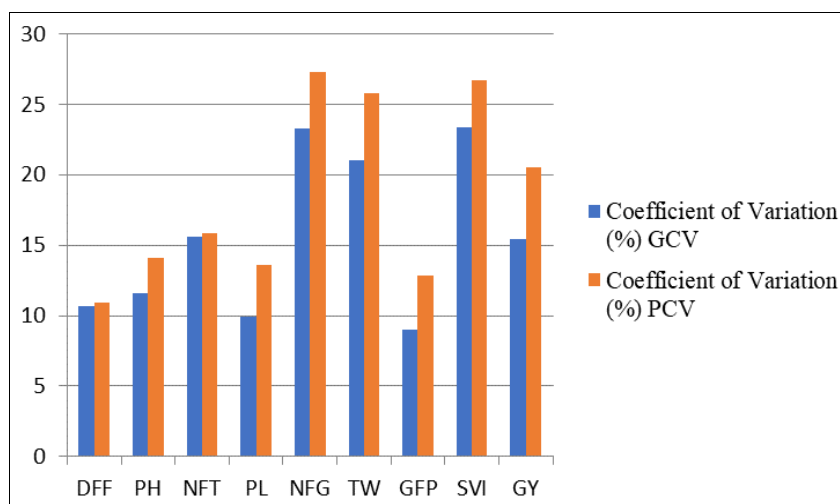


Fig 1: Genotypic and phenotypic coefficients of variation

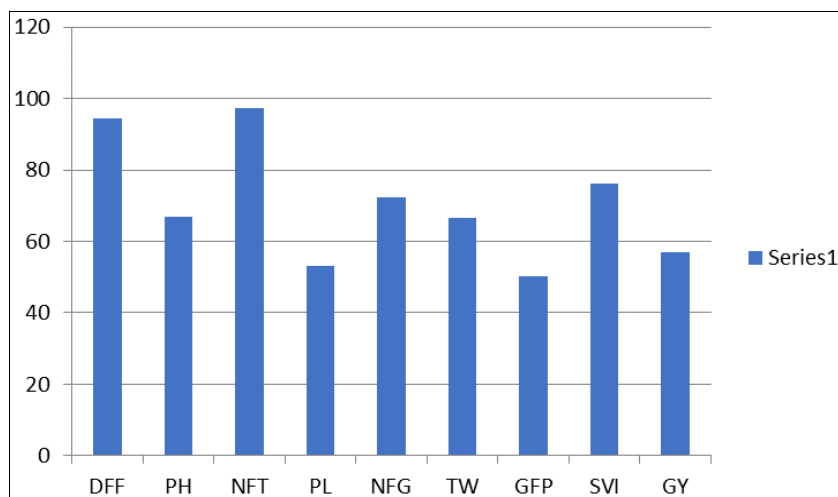


Fig 2: Broad-sense heritability

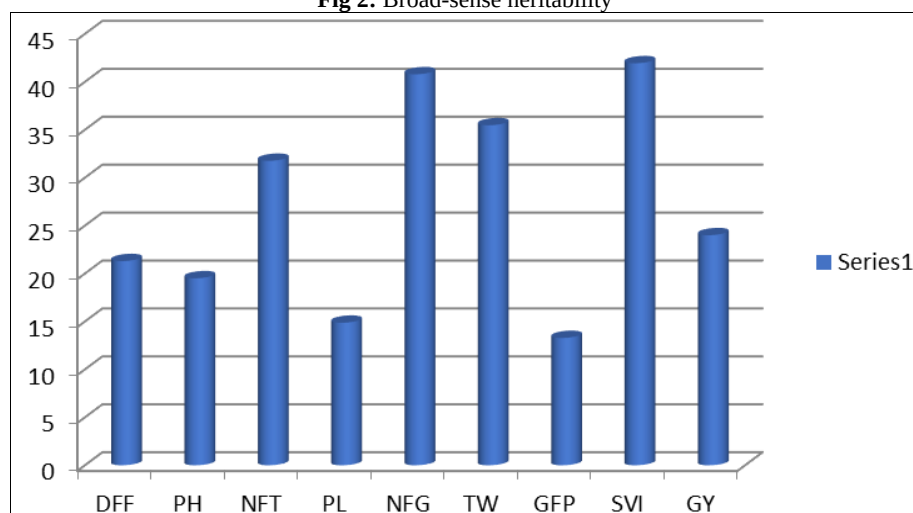


Fig 3: Genetic advance expressed as a percentage of the mean

Conclusion

The study revealed substantial genetic variability among rice genotypes under dry direct seeded conditions. High heritability and genetic advance for seed vigour index, number of filled grains per panicle, test weight, and number of effective tillers per square meter indicate their usefulness in selection for yield improvement. Focusing on these traits will accelerate the development of high-yielding rice genotypes adapted to DDSR environments.

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