Genetic Variability Studies for Yield and its Attributing Traits in Rice F4 Mapping Population (*Oryza sativa* L.)

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Original Research Article

ABSTRACT

An experiment was conducted at ICAR-IIRR during the wet season of 2023 in a mapping population derived from the cross TI-128 X BPT-5204, along with five checks in an augmented block design with eight blocks. This study revealed that, significant variability was present among the population for all the traits examined. High genotypic coefficient of variation was observed for number of tillers per plant (29.68), number of productive tillers per plant (30.56) and total number of grains per

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panicle (29.66). High phenotypic coefficient of variation and genotypic coefficient of variation was observed for the trait grain yield per plant. High heritability coupled with high genetic advance as percent of mean was recorded for number of tillers per plant, number of productive tillers per plant, total number of grains per panicle and grain yield per plant showing that these traits are regulated by additive gene effects, making them suitable for selection criteria in rice breeding programs. The traits *viz.*, number of tillers per plant (0.42***), number of productive tillers per plant (0.41***), filled grains per panicle (0.20**), total number of grains per panicle (0.18**) and test weight (0.18**) exhibited significantly positive association with grain yield per plant.

1. INTRODUCTION

"With the continuously increasing global population and the challenges presented by changing climatic conditions, there is a heightened demand for rice varieties with improved yield, climate resilience, and nutritional value. Enhancing rice yield potential is crucial to meeting the food demands of the rapidly growing population and remains a primary breeding objective for researchers worldwide" [1]. One of the fundamental factors supporting the development of improved rice cultivars is the genetic variability within rice genotypes [2]. Assessing genetic variability in any crop species is crucial for selecting an appropriate breeding program. The effectiveness of selection relies on the extent of genetic variability within the plant population. Given that grain yield and its component traits are quantitative in nature, breeders must identify superior genotypes based on an understanding of the components of variation [3,4]. A key aspect is dividing the total variation into phenotypic and genotypic components, as the magnitude of these components for various traits indicates the type of gene action, which in turn aids in determining an appropriate breeding method for trait improvement. Typically, estimating genetic variability alone does not provide a definitive indication of the improvement achievable through simple selection. Therefore, it should be combined with heritability and genetic advance [5]. According to Hansen and Pélabon [6] heritability estimates aid in the prediction of a trait's expression in subsequent generations by providing information about a trait's potential for transmission to future generations. Genetic advance, however, shows how the mean genotypic characteristics of the selected group differ from those of the original population. When estimating the genetic gain under selection, heritability estimates combined with genetic advance are more accurate than heritability alone. Correlation analysis provides a good measure of the association between characters and helps to identify the most important character(s) to be considered for effective selection for increasing yield. Therefore, considering all these facts and recognizing the importance of genetic variability in plant breeding experiments, the present research work has been taken up in a F4 mapping population.

2. MATERIALS AND METHODS

The experimental material comprised a mapping population developed through cross between a selected high-yielding female parent mutant line (TI-128) and the original male parent (BPT-5204). The F_4 mapping population, consisting of 192 recombinant inbred lines (RILs), were evaluated for yield and yield-related traits under irrigated conditions at ICAR-IIRR (Fig. 1), Hyderabad, during the wet season of 2023 in augmented block design with eight blocks, each containing 24 lines along with the parent lines (TI-128 and BPT-5204) and five checks (CR Dhan-201, CR Dhan-202, MAS 946-1, Sabita, Sahbhagidhan), randomized within each block. Each line was sown in a single row of two-meter length with a spacing of 20 cm × 15 cm. Recommended agronomic practices and plant protection practices were implemented to raise a good crop stand for irrigated rice cultivation were followed, sowing of seeds in nursery beds and transplanting to the main field after 30 days under irrigated condition. Timely weeding was performed, and field maintenance adhered to standard agronomic practices [7].

"Observations were recorded for three plants on various traits viz. days to 50% flowering (DFF), plant height (PH in cm), number of tillers per plant (NT), number of productive tillers per plant (PT), panicle length (PL in cm), filled grains per panicle (FGPP), total number of grains per panicle, grain yield per plant (GYPP), and test weight (TW in g) at the reproductive maturity. Chlorophyll content was recorded using the Soil
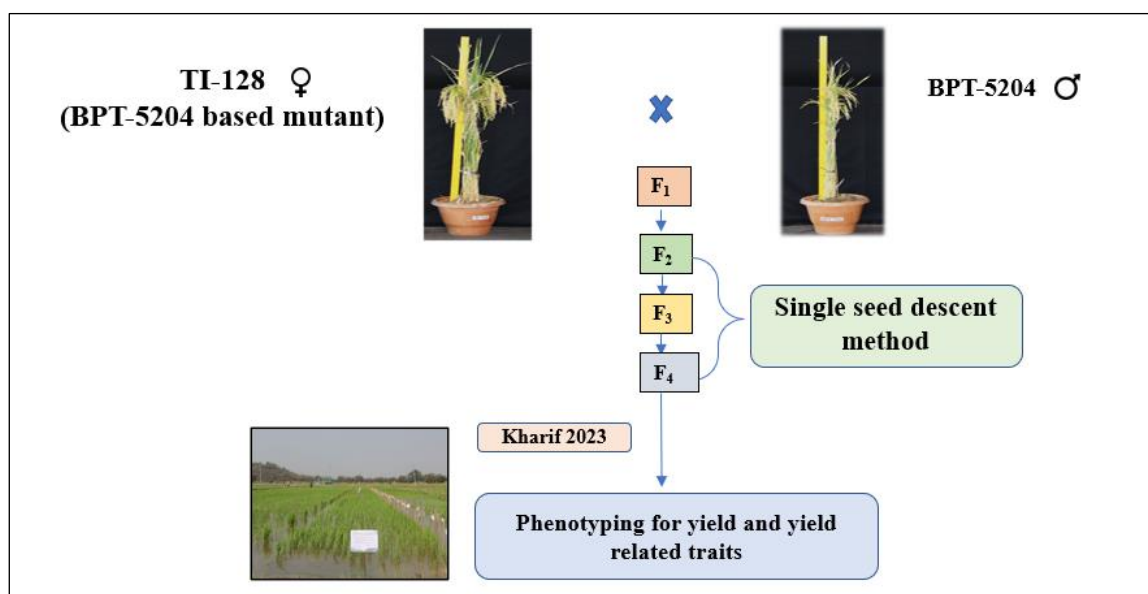
Fig. 1. Experimental flow chart

Plant Analysis Development (SPAD) chlorophyll meter (SPAD-502 plus Minolta, New Jersey, USA) in the morning hours between 7 to 9 am" [8]. Soil Plant Development Index (SPAD), Analysis of variance (ANOVA) and genetic variability studies were computed using R studio (version 3.5.2) with R-scripts) and the Pearson's method (1895) was used to perform correlation analysis.

3. RESULTS AND DISCUSSION

3.1 ANOVA of Augmented Block Design

The ANOVA indicated significant mean sum of squares for all traits across various sources of variation (Table 1). The source of variation for entries, excluding blocks, was significant for all traits analyzed, viz. days to 50% flowering, plant height (cm), number of tillers per plant, number of productive tillers per plant, SPAD, panicle length (cm), filled grains per panicle, total number of grains per panicle, grain yield per plant (g), and test weight (g). A wide range of variation for days to fifty percent flowering, plant height (cm), productive tillers per plant, panicle length (cm), grain yield per plant (g), test weight (g) was reported by Pathak et al. [9], Vilas et al. [10], and Kumar et al. [11]. Their research indicated that the lines exhibited significant variability for traits with substantial inherent genetic variation (80%). Genetic variability is crucial in breeding, particularly for desirable traits, as greater variability within a population enhances the potential for crop improvement.

3.2 Genetic Variability Parameters

The analysis of genetic variability parameters, including range, mean, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability, and genetic advance as a percentage of the mean, was conducted using the augmented RCBD package in R Studio (version 3.5.2). This analysis aimed to estimate the extent and magnitude of genetic variation for yield and yield-related traits in the mapping population. The mean performance of the traits exhibited a wide range of variation for most of the studied characteristics, with detailed findings presented in Table 2. Genetic parameters were categorized as follows: GCV and PCV into low (0-10%), moderate (10-20%), and high (>20%); heritability into low (0-30%), moderate (30-60%), and high (>60%); and genetic advance as a percentage of the mean into low (0-10%), moderate (10-20%), and high (>20%).

The study on variability demonstrated that the phenotypic and genotypic coefficients of variation were high for GYPP, NT, NPT, SPAD, NGPPF, and NGPPT. The genotypic coefficient of variation (GCV) was the highest for NPT at 30.56 and lowest for DFF at 5.27. Similarly, the phenotypic coefficient of variation (PCV) was the highest for NPT at 32.24 and lowest for DFF at 5.51. Additionally, the minimal difference

Table 1. Analysis of variance of augmented block design

Source	Df	Mean.Sq																		
		DFF		GYPP		PH		NT		NPT		SPAD		PL		FGPP		TNGPP		TW
Treatment (ignoring Blocks)	198	43.15	**	32.81	**	116.23	**	16.76	**	16.08	**	179.15	**	9.77	**	6469.94	**	17790.60	**	2.48 **
Treatment: Check	6	219.90	**	344.77	**	1474.21	**	30.41	**	33.32	**	388.55	**	79.80	**	29002.60	**	111197.41	**	21.50 **
Treatment: Test	191	35.34	**	21.69	**	63.10	**	16.31	**	15.53	**	166.62	**	6.61	**	4706.22	**	13572.56	**	1.85 **
Treatment: Test vs. Check	1	474.01	**	286.31	**	2116.48	**	20.64	**	17.31	**	1315.84	**	194.31	**	208144.42	**	262994.14	**	9.45 **
Block (eliminating Treatments)	7	1.05	ns	4.57	ns	5.29	ns	4.36	*	7.43	**	11.33	ns	2.07	ns	86.33	ns	548.39	ns	2.41 *
Residuals	42	2.98		3.45		3.65		1.50		1.58		19.06		2.75		398.37		913.59		0.91

*Significance levels: *P<0.05 and **P<0.01, d.f. degrees of freedom, DFF-Days to 50 percent flowering, PH-Plant height, NT-Number of tillers per plant, NPT-Number of productive tillers per plant, SPAD-Soil Plant Analytical Development, PL-Panicle length, FGPP- Filled grains per panicle, TNGPP- Total number of grains per panicle and TW-Test weight*

Table 2. Estimates of genetic variability parameters of mapping population in rice

S. No.	Character	Mean	Range		Coefficient of Variation		Heritability (broad	Genetic advance as
			Minimum	Maximum	PCV (%)	GCV (%)	sense) h^2(bs) (%)	per cent of mean
1	Days to fifty percent flowering	107.85	93.46	117.38	5.51	5.27	91.57	10.41
2	Plant height (cm)	111.77	85.23	132.84	7.11	6.90	94.21	13.81
3	Number of tillers per plant	12.97	6.11	26.87	31.15	29.68	90.81	58.35
4	Number of productive tillers per plant	12.22	6.02	26.74	32.24	30.56	89.84	59.75
5	SPAD	46.11	19.62	74.01	27.99	26.34	88.56	51.14
6	Panicle length	26.01	11.67	33.16	9.88	7.55	58.36	11.90
7	Filled grains per panicle	231.84	60.37	607.61	29.59	28.31	91.54	55.88
8	Total number of grains per panicle	379.39	126.00	1212.86	30.71	29.66	93.27	59.09
9	Grain yield per plant	17.06	8.44	32.93	27.29	25.03	84.07	47.34
10	Test weight	13.39	8.80	19.70	10.16	7.25	50.94	10.67

*Significance levels: *P<0.05 and **P<0.01, d.f. degrees of freedom, DFF-Days to 50 percent flowering, PH-Plant height, NT-Number of tillers per plant, NPT-Number of productive tillers per plant, SPAD-Soil Plant Analytical Development, PL-Panicle length, FGPP- Filled grains per panicle, TNGPP- Total number of grains per panicle and TW-Test weight*

between GCV and PCV for all traits indicated that environmental factors had a negligible effect on the expression of these characteristics.

Traits such as GYPP, NT, NPT, SPAD, NGPPF, and NGPPT exhibited both high heritability and high genetic advance. All traits examined in the study exhibited high heritability, except for PL and TW, which showed moderate heritability. The highest heritability was observed for PH at 94.21. GYPP, NT, NPT, SPAD, NGPPF, and NGPPT exhibited high genetic advance as a percentage of the mean (GAM). GYPP, DFF, PH, PL, and TW show moderate GAM. The trait NPT showed the highest GAM at 59.75.

Traits showing high GCV, PCV, heritability, and GAM suggest that these traits are influenced significantly by additive gene action. Selective breeding efforts targeting these traits could yield beneficial improvements. Similar findings were reported by Demeke et al. [12]. Comparable results were observed by Mamata et al. [13]. and Shaikh et al. [14] who noted high heritability paired with substantial genetic advance for traits such as the number of tillers, number of productive tillers, and number of grains per panicle. Heritability estimates of a trait reflect the reliability of predicting its phenotypic value. High heritability enhances the effectiveness of

selecting specific traits, thereby making their improvement particularly beneficial.

3.3 Estimates of Correlation Coefficients for Yield and Yield Related Traits

To determine the degree of association between the traits, a correlation analysis was done. The graphical representation of these correlations is presented in Fig. 2. The traits *viz.*, number of tillers per plant, number of productive tillers per plant, filled grains per panicle, total number of grains per panicle, test weight exhibited significantly positive association with grain yield per plant similar results were obtained by (Sujitha et al ., 2020), (Saleh et al., 2020) .The inter-correlation among the traits revealed that plant height exhibited a significant positive correlation with panicle length (0.57***), panicle length with test weight (0.20**), and the total number of tillers per plant with the number of productive tillers per plant (0.99***). The results were in accordance with Reddy et al. [7] and Sadimantara et al. [15] who found a significant positive association between yield per plant and both the total number of grains per panicle and productive tillers per plant. Similarly, they observed a significant positive correlation between yield and traits such as panicle length, percentage of filled grains, and thousand grain
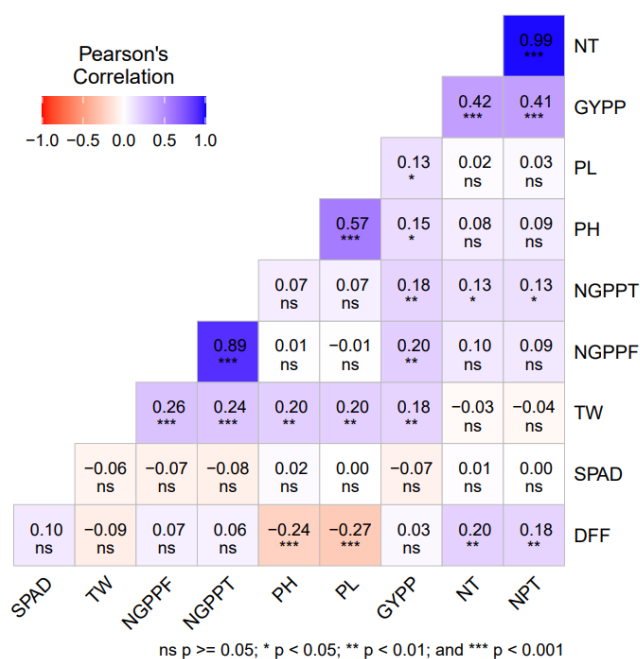

Fig. 2. Correlation analysis among yield and yield component traits in rice
DFF-Days to 50 percent flowering, PH-Plant height, NT-Number of tillers per plant, NPT-Number of productive tillers per plant, PL-Panicle length, FGPP- Filled grains per panicle, TNGPP- Total number of grains per panicle and TW-Test weight

weight. The trait of grain yield is not independent but is influenced by a complex network of associations with other traits that collectively impact the overall yield [3]. This indicates that these traits are major determinants of yield in rice. The significant positive correlations between yield and yield-related traits suggest that selecting for these traits could result in positive indirect selection, thereby enhancing grain yield improvement. The study identified the following lines as promising based on their yield performance:-KB-39-181, KB-39-146, KB-39-298, KB-39-188, and KB-39-195.

The high yielding lines under irrigated conditions can be further tested under aerobic [3] and low soil phosphorus condition [16,17], by using assessment of multiple tolerance indices to identify rice lines exhibiting less decrement of yield under both system of cultivation.

4. CONCLUSION

The analysis of variance revealed the presence of significant differences in the mapping population for all the traits studied. The current study concluded that grain yield per plant and the number of productive tillers per plant exhibited high coefficients of variation, making these traits effective targets for selection to transfer desirable characteristics to the next generation. High phenotypic and genotypic coefficients of variation, coupled with high heritability and high genetic advance as a percentage of the mean, were recorded for the number of tillers per plant, number of productive tillers per plant, filled grains per panicle, total number of grains per panicle and grain yield per plant. These findings indicate that direct selection is highly effective for these traits.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of manuscripts.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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