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Exploring Genetic Variability for Yield and Its Attributing Traits in Rice (*Oryza sativa* L.) under Low Soil Phosphorous Condition

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Authors' contributions

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

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ABSTRACT

Phosphorus (P) is a vital macro-nutrient essential for the growth and development of all crop plants including rice. Inadequate availability of P in the soils hinders crop growth, resulting in reduced rice yields. Genetic variability for low P tolerance is of utmost importance to understand the genetics and improvement of rice genotypes for the trait. The present study was conducted under low soil P condition to assess the genetic variability for yield and its attributing traits in rice genotypes. The experimental material consists of 245 rice genotypes along with six checks which were planted in low P plot at ICAR-IIRR, Hyderabad using augmented block design and phenotyped for the traits viz., days to 50% flowering, plant height, total number of tillers, number of productive tillers per plant, panicle length, single plant yield, thousand grain weight and spikelet fertility. ANOVA analysis revealed that MSS due to test genotypes were significant ($p<0.01$) for all the traits under study. PCV and GCV were found to be high for single plant yield, total number of tillers and number of productive tillers while, plant height, thousand grain weight and spikelet fertility showed moderate PCV and GCV. Genetic advance as percentage of mean coupled with heritability was observed to be higher for all the traits except panicle length, which was moderate in nature. These results signify that there was sufficient amount of genetic variability for all the studied traits under low P in the studied genotypes. Therefore, genetic improvement through selection for these traits would be more rewarding and could be useful for developing genotypes tolerant to low P stress.

Keywords: Rice; genetic variability; phosphorous; heritability; genetic advance.

1. INTRODUCTION

Rice (*Oryza sativa* L.) serves as a primary staple diet for over half of the world's population and plays a crucial role as a cereal crop in ensuring global food security. The anticipated global rice demand by 2050 is expected to be around 584 million tons or lower [1]. Hence, enhancing food production is vital to meet the needs of the ever-growing population and ensure food security for future. Rice production is constantly hit by various biotic and abiotic stresses, posing challenges to increased productivity. Low available soil phosphorous (P) is one among those challenges significantly affecting the rice growth and development at every stage of the crop [2].

Among the nutrients, P is one of the important nutrients essential for growth and development of rice crop as it is a vital component of enzymes, nucleic acids, cell membranes, and other metabolic activities [3]. A lack of sufficient available P in soil due to its high fixation and low solubility nature, rice plant exhibits stunted growth, reduced grain yield, reduced biomass, delayed flowering and maturity [4]. The application of additional phosphate fertilizers can address these issues, but the rising costs of fertilizers pose a significant challenge for poor farmers and also demands increasing import [5]. Therefore, enhancing phosphorus efficiency in crops would play a crucial role in promoting the sustainability of agroecosystems [6] and developing cultivars with enhanced ability to thrive and yield in low soil P conditions is an important goal in modern plant breeding [7,8,9]. Plants exhibit diverse adaptive responses to cope with low P stress. They develop mainly two mechanisms to overcome these stress conditions by: (a) enhancing phosphorus acquisition efficiency through modifications in root morphology, root exudation and phosphorus uptake pathways, and (b) optimizing phosphorus utilization efficiency through internal mechanisms that improve the efficient use of absorbed phosphorus at the cellular level [10].

Genetic variability serves as the fundamental asset for plant breeders seeking to enhance plant performance. This variability within a population arises from genetic diversity, environmental influences, and the interaction between genetics and the environment. The presence of genetic variability in crop germplasm assists in efficiently selecting high-yielding, well-adapted crop plants which can be utilized either by directly introducing it as a new variety or by incorporating it as one of the parents in breeding programs aimed at developing improved crop varieties. An insight into the magnitude of genetic variability present in the gene pool of a crop species is of utmost importance to a plant breeder for starting a judicious plant-breeding program.

Genetic variability for low phosphorous tolerance is key for the success of any plant-breeding program aimed at developing of phosphorous efficient cultivars. It reflects differences at genomic level for the level of phosphorous efficiency [11]. Thus, it is crucial to investigate the genetic variability among the rice genotypes for low phosphorous tolerance by screening various yield attributing traits under low P stress condition. The present investigation was thus aimed to assess the genetic variability of yield and its attributing traits of rice genotypes in low P condition.

2. MATERIALS AND METHODS

The experimental material for the current investigation comprised of 245 rice genotypes (advanced breeding lines of large number of crosses, few varieties and landraces) with six check varieties. Swarna, Kasalath and Rasi were low P tolerant checks whereas, Tanu, Improved sambha mahsuri and IR-64 were low P sensitive checks used in the study. The present study was conducted at ICAR-Indian Institute of Rice Research (IIRR), Hyderabad during *Rabi* season 2021 using augmented block design with five blocks, where each block accommodated 45 rice genotypes along with six checks distributed randomly within block. Twenty-four days old seedlings of 245 rice genotypes and checks were transplanted in low P screening plot (Available $P < 2$ kg ha^{-1}) for evaluating their performances in low phosphorous stress condition. Recommended dose of nitrogen (100 kg/ha) and potash (60 kg/ha) and zero P fertilizers were applied to raise a good crop and all the recommended agronomic practices were followed. The phenotypic data was taken for 8 traits such as days to 50% flowering, plant height (cm), total number of tillers per plant, number of productive tillers per plant, panicle length (cm), single plant yield (g), thousand grain weight (g) and spikelet fertility (%). For recording observations, five randomly selected plants within each genotype were used and mean data was subjected to statistical analysis. The analysis of variance, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) calculated using the method of Burton and De-Vane [12], heritability by Lush [13] and genetic advance by Johnson et al. [14] were computed using Augmented RCBD package in R studio version 4.3.1 of R software [15].

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance

The ANOVA results for yield and its attributing traits in low soil P conditions were presented in Table 1. The results revealed that mean sum of squares (MSS) due to treatments (test genotypes + checks) were highly significant ($p<0.01$ and $p<0.05$) for the traits under investigation. The MSS due to test genotypes were also found to be highly significant ($p<0.01$ and $p<0.05$) for all the eight traits studied, indicated that the sufficient variability was present among the rice genotypes for the studied traits in low phosphorous condition. Similar findings were reported by Deng et al. [16]. The variability found among studied genotypes for various yield traits under low P stress facilitates breeders in identification of low P tolerant lines, which could be potentially serve as donors in low P tolerance breeding.

3.2 Mean Performances of Rice Genotypes

In any crop improvement programs, especially in rice, early flowering is one of the highly desirable traits. Genetic variability, arising from differences among individuals within a plant population due to genetic makeup or environmental factors, is essential for successful plant breeding programs. This diversity enables breeders to select optimal candidates from a varied pool of materials, underscoring the importance of understanding genetic variability within populations for initiating effective and strategic breeding efforts Basavaraj et al. [17]. The genetic variability parameters *viz*., mean, maximum, minimum, CV (%), GCV (%), PCV (%), h^2(bs) (%) and GAM for each trait were compiled in Table 2.

The phenotypic variation for days to 50% flowering (DFF) ranged from 73.47 to 137.13 days. The average value for DFF trait was 122.07 days as it is represented in Table 2. The variation for the trait plant height ranged from 54.23 cm to 126.56 cm with a mean of 81.79 cm (Table 2). The mean of plant height was reduced in rice genotypes compared to tolerant checks indicated that the effect of low P stress on growth of the rice crop. Maximum and minimum values for number of total tillers per plant was 13.79 and 2.62 respectively with mean for the trait was 6.92 (Table 2). Similarly, the average value for number of productive tillers per plant under low P was 5.46 and the maximum and minimum value for the trait was 11.01 and 2.11 respectively.

The panicle length was varied from 16.53 cm to 30.24 cm with the average of 20.76 cm for the trait. The phenotypic variation for the single plant yield ranged from 1.08 g to 13.69 g with the mean of 6.29 g (Table 2). Thousand grain weight was varied from 11.22 g to 25.78 g with a mean of 19.43g. Spikelet fertility had a maximum value of 98.66% while minimum value was 19.06% with the average performance of 75.94%. The present study uncovered the presence of sufficient genetic variation for all the traits under study in the rice genotypes used and the materials could be used for association mapping and donors for low P tolerance breeding.

3.3 Phenotypic (PCV) and Genotypic Coefficient of Variation (GCV)

The extent of variability within available genotypes can be evaluated using the PCV and GCV. The values of PCV and GCV of each trait were graphically represented in Fig. 1a. High GCV and PCV obtained for total number of tillers (23.05% and 26.06%), number of productive tillers per plant (24.86% and 28.77%) and single plant yield (41.72% and 42.27%). In contrast, GCV and PCV was found to be low for days to 50% flowering (7.29 and 7.52) and panicle length (6.92% and 9.20%). Moderate GCV and PCV were exhibited by plant height (13.96% and 14.56%), thousand grain weight (14.60% and 15.21%) and spikelet fertility (16.64% and 19.27%) (Table 2). Our research findings are in agreement with the previous results of Basavaraj et al. [17], Yaseen et al. [18] and Basavaraj et al. [19]. All traits examined showed higher PCV relative to GCV, suggesting considerable influence from environmental factors on these traits. Nonetheless, a narrow range of difference between PCV and GCV indicated that less influence of environmental factors on the trait expression. Similar results presented by Adhikari et al. [20], Faysal et al. [21] and Chacko et al. [22]. Therefore, selection based on phenotype can be effective for improving traits with moderate to high levels of PCV and GCV.

3.4 Heritability and Genetic Advance as Percentage of Mean

Broad sense heritability ranged from 56.64% (panicle length) to 97.42% (single plant yield). Broad sense heritability of each trait was graphically represented in Fig. 1b. High broad sense heritability estimates were obtained for all traits except panicle length which was moderate, indicating minimal influence of environmental factors on trait expression. This facilitates breeders in effective selection of superior genotypes based on their phenotypic performance. Genetic advance was varied from 10.75 (panicle length) to 84.96 (single plant yield). High genetic advance was observed for plant height, total number of tillers, number of productive tillers per plant, single plant yield, thousand grain weight and spikelet fertility whereas, moderate values were found for days to 50% flowering and panicle length. Genetic advance over mean of each trait was graphically represented in Fig. 1c.

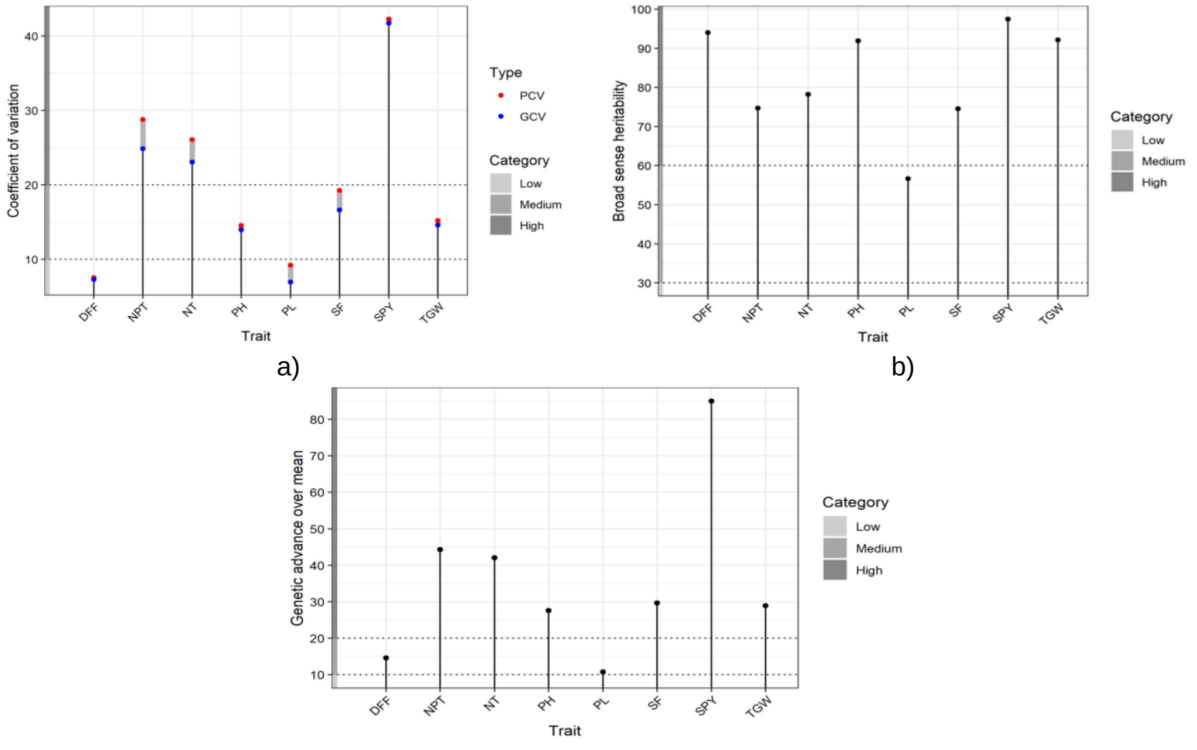
The combination of genetic advance and heritability estimates generally provides a more precise estimation of the gain under selection than relying solely on heritability estimates. High heritability coupled with high genetic advance as percentage of mean was observed for the traits *viz*., total number of tillers, number of productive tillers per plant, single plant yield, thousand grain weight and spikelet fertility while, moderate heritability along with moderate genetic advance was seen in panicle length. This suggests the predominance of additive genetic variance, enabling the direct phenotypic selection of promising genotypes in breeding programme would be rewarding. Our results are consistent with the earlier reports Nirubana et al. [4], Basavaraj et al. [17] and Abebe et al. [23].

Table 1. Analysis of variance for yield and yield attributing traits in rice genotypes during *Rabi* 2021 under low phosphorous condition

Sources	***d.f.***	**DFF**	**PH**	**NT**	**NPT**	**PL**	**SPY**	**TGW**	**SF**
Treatment	250	111.59 **	168.61 **	3.52 **	2.68 **	3.9 *	7.8 **	9.41 **	215.63**
Check	5	1344.59 **	1491.43 **	13.76 **	11.8 **	16.7 **	40.02 **	43.93 **	269.85 **
Test genotypes	244	84.21 **	141.76 **	3.26 **	2.47 **	3.65 *	7.07 **	8.73 **	214.08**
Test vs. Check	1	628.53 **	105.03 **	15.77 **	9.27 **	1.61	25.42 **	2.58	324.48*
Block	4	4.97	8	0.72	1.42	2.01	1.07 **	0.32	57.72
Residuals	20	5.03	11.47	0.71	0.63	1.58	0.18	0.69	54.45

*Significance level: *P<0.05 and **P<0.01, d.f. degrees of freedom*

DFF- Days to 50 per cent flowering (days), PH- Plant height (cm), NT- Number of tillers per plant (no.) NPT- Number of productive tillers per plant (no.), PL- Panicle length (cm), SPY- single plant yield (g), TGW-Thousand grain weight (g), SF- spikelet fertility (%)



a)

b)

c)

Fig. 1. Graphical representation of variability of different traits in the rice genotypes a) coefficient of variation b) broad sense heritability and c) genetic advance over mean

Table 2. The genetic variability parameters *viz*., mean, maximum, minimum, CV (%), GCV (%), PCV (%), h^2(bs) (%) and GAM for each trait in rice genotypes under low P condition

Traits	**Range**		**Mean**	**CV (%)**	**Genetic variability**		**h^2(bs)**(%)	**GAM**
	Min	**Max**			**GCV** (%)	**PCV** (%)		
DFF	79.74	139.84	122.07	1.84	7.29	7.52	94.03	14.58
PH	54.23	126.56	81.79	4.13	13.96	14.56	91.91	27.60
NT	2.62	13.79	6.92	12.29	23.05	26.06	78.20	42.04
NPT	2.11	11.01	5.46	14.62	24.86	28.77	74.67	44.32
PL	16.53	30.24	20.76	6.05	6.92	9.20	56.64	10.75
SPY	1.08	13.69	6.29	6.87	41.72	42.27	97.42	84.96
TGW	11.22	25.78	19.43	4.27	14.60	15.21	92.15	28.92
SF	19.06	98.66	75.94	9.68	16.64	19.27	74.56	29.64

DFF- Days to 50 per cent flowering (days), PH- Plant height (cm), NT- Number of tillers per plant (no.) NPT- Number of productive tillers per plant (no.), PL- Panicle length (cm), SPY- single plant yield (g), TGW-Thousand grain weight (g), SF- spikelet fertility (%)

4. CONCLUSIONS

Enhancing the development and adoption of crops tolerant to low soil phosphorus (P) is gaining prominence, acknowledging P resources as a critical future limitation. Additionally, improving varietal tolerance to low soil P in crops such as rice aids in reducing production costs, lessening import dependence, and mitigating environmental contamination from fertilizer runoff. The current study underscores the significance of these points by indicating the potential for enhancing rice genotypes with low soil P tolerance. It highlights the presence of substantial genetic variability among the rice genotypes under study for yield and its attributing traits related to low soil P tolerance. It opens the way for breeders to study further and utilizing these resources for mapping experiments.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declares 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.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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