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Exploring Genetic Variability in Rice for Yield Improvement under Low Phosphorus Soil Conditions

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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 an essential macronutrient for all living organisms. P deficiency in soils is a major limiting factor for crop growth in rice and reduces yield. Understanding genetic variability for low P tolerance is crucial for improvement of rice genotypes for this stress. This study was conducted

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under low soil P and normal conditions to evaluate genetic variability in yield and its associated traits among rice genotypes. The experimental material consists of 91 $F_{2:3}$ mapping population along with two checks, planted in a low P and normal plot at ICAR-IIRR, Hyderabad. Traits assessed included days to 50% flowering, plant height, total number of tillers, number of productive tillers per plant, flag leaf length, flag leaf width, panicle length, total number of grains per panicle, spikelet fertility, single plant yield, shoot length, root length, root volume, dry root weight, dry shoot weight and root to shoot ratio. ANOVA analysis suggested, mean sum of squares due to test genotypes were significant ($p<0.01$) for most of the traits under study. Plant height, number of tillers per plant, number of productive tillers per plant, flag leaf length, number of grains per panicle, spikelet fertility, single plant yield, shoot length, root volume, shoot dry weight, root dry weight and root to shoot ratio possessed high GCV and PCV values under low P condition. Genetic advance as *per cent* of mean for all traits possessed high genetic advance as *per cent* mean except for days to 50% flowering which showed medium GAM under low P condition. The genotypes showed varied response to genetic variability, heritability and genetic advance as *per cent* mean for days to 50% flowering (low), plant height (high), number of productive tillers per plant (high), panicle length (medium to high), flag leaf length (high), flag leaf width (medium to high), number of grains per panicle (high), spikelet fertility (high), single plant yield (high), root volume (high), shoot dry weight (high), root dry weight (high) and root to shoot ratio (high) under low P condition. This study identified these traits with high genetic variability and heritability, which are useful for developing P efficient rice cultivars and selection based on these traits would improve the rice for low soil P tolerance.

Keywords: Rice; variability; diversity; phosphorus deficiency, phenotyping.

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 an important cereal crop in ensuring global food security and occupies a second prominent position in global agriculture. The global rice demand by 2050 is expected to be around 827 million tons. Hence, enhancing food production is vital to meet the needs of the ever-growing population and ensure food security for the future. Rice production is constantly affected by various biotic and abiotic stresses. Among the various abiotic stresses, drought, salinity and nutrient deficiencies play an important role in limiting rice production. Among the nutrients, Phosphorus (P) is a vital nutrient required for the growth and development of rice plants, as it is a vital component of enzymes, nucleic acids, cell membranes and other metabolic activities (Cordell et al., 2009). Concerns are being expressed that limited P resources may lead to a scarcity of P fertilizers and there is no alternative available for P fertilizers to substitute its role in plant growth and development (Correll, 1998). India is the biggest importer of phosphorus-based fertilizers with a 90% dependency (Webeck et al., 2014; Swamy et al., 2019). Cultivated plants use only approximately 20-30% of the applied P fertilizer and they are rapidly immobilized owing to fixation and microbial activity. In acidic soils, free iron and aluminium oxides bind to native and applied P, whereas in calcareous soils, the abundant calcium and magnesium compounds binds inorganic phosphates into forms, that are highly unavailable to plants (Kirk et al., 1998 and Vance et al., 2003). 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. The application of additional phosphate fertilizers can increases the costs of fertilizers for poor farmers. Plants cope with low P availability in the soil by developing adaptive changes at morphological, physiological, biochemical and molecular levels for enhanced P uptake and increased internal P use efficiency (Raghothama, 1999; Abou-Seed et al., 2020 and Marzouk et al., 2024). Therefore, enhancing phosphorus efficiency in crops would play a crucial role in promoting the sustainability of agroecosystems and developing cultivars with enhanced ability to thrive and yield in low soil P conditions is an important goal in modern plant breeding. Understating adaptive mechanisms to low-phosphate stress will be helpful for effective breeding and genetic engineering strategies to produce highly phosphate-efficient crops (Lopez-Arredondo et al., 2014). Genetic variability is a crucial resource for plant breeders aiming to improve plant performance. This variability within populations arises from genetic diversity, environmental factors, and the interaction between genetic and environmental influences. The presence of genetic variability in crop germplasm facilitates the efficient selection of high-yielding, well-adapted crop plants, which can either be directly introduced as new varieties or incorporated as parental lines in breeding programs targeting crop improvement. For plant breeders, understanding the extent of genetic variability present in the gene pool of crop species is fundamental to initiating an effective and well-informed breeding program. Genetic variability for low P tolerance is essential for the success of any plant breeding program aimed at developing phosphorus-efficient cultivars, as it reflects genomic differences in P efficiency. Consequently, investigating the genetic variability among rice genotypes for low P tolerance through screening of various yield-related traits under low P stress conditions becomes crucial. The present study was therefore designed to evaluate the genetic variability of yield and its associated traits in rice genotypes under low P conditions.

2. MATERIALS AND METHODS

The experimental material for the current investigation comprised 91 rice genotypes ($F_{2:3}$ mapping population) with 2 checks. Improved Sambha Mahsuri was used as a low P sensitive check and LR 279 was used as a low P tolerant check in the study. The present study was conducted using an augmented block design with three replication at ICAR-Indian Institute of Rice Research (IIRR), Hyderabad during the *Rabi* season in 2022. Twenty-four days old seedlings of 91 rice lines and checks were transplanted in a low P screening plot (available P < 2 kg ha^{-1}) to evaluate their performances in low P stress condition. The recommended dose of nitrogen (100 kg/ha), 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 16 traits such as days to 50% flowering, plant height (cm), the total number of tillers per plant, number of productive tillers per plant, panicle length (cm), flag leaf length (cm), flag leaf width (cm), total number of grains per panicle, single plant yield (g), spikelet fertility (%), shoot length (SL), root length (RL), root volume (RV), dry root weight (DRW), dry shoot weight (DSW) and root to shoot ratio (R/S), For recording observations, five randomly selected plants within each genotype were used and mean data was subjected to statistical analysis. The analysis of variance (ANOVA), phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), broad-sense heritability (h^2) (bs), and genetic advance as percentage of mean (GAM) were computed using the Augmented RCBD package in R studio version 4.3.1 of R software (Aravind et al., 2023).

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance (ANOVA)

The ANOVA results for yield and its attributing traits in low soil P conditions were presented in Table 1. The MSS due to treatments were found to be significant for all traits except for days to fifty per cent flowering, panicle length, flag leaf width, number of grains per panicle, per cent spikelet fertility, root length and root to shoot ratio. The MSS due to Treatment vs Checks were detected to be significant for all traits except days to fifty per cent flowering, flag leaf length, root dry weight and root to shoot ratio. The variability found among the lines for various yield traits under low P conditions helps the breeders in the identification of low P tolerant lines, which could serve as donors for low P tolerance breeding. Under normal P conditions, the ANOVA revealed that, the MSS due to treatments were found to be significant for most of the traits. The ANOVA for normal P condition were presented in Table 2. The overall results from the ANOVA revealed that, MSS due to treatments, treatments *vs* checks were significant at ($p<0.01$and $p<0.05$) for most of the traits under low P and normal P conditions, indicating that traits were significantly influenced by low P treatment followed by genotypic effect under investigation [Kale et al., 2021; Swamy et al. (2019 and 2020)]. Variability among the genotypes was significant for all yield and yield attributing traits, especially under low P and these findings confirm the presence of significant differences in the experimental material and offer scope for further investigations.

3.2 Mean Performance, PCV, GCV, h^2 (bs) and GAM of Rice Genotypes

In any crop improvement programs, especially in rice for low soil P breeding program, the number of productive tillers, plant yield and root traits are highly desirable. Genetic variability arising from differences among individuals within a plant population due to genetic makeup is essential for successful plant breeding programs. This diversity enables breeders to select optimal candidates from a varied pool of materials,

Table 1. Analysis of variance for yield and yield attributing traits of F_3 population under low soil P during *Rabi* 2022-23

Source	Df	Mean sum of squares															
		DFF	**PH**	**NT**	**NPT**	**PL**	**FL**	**FW**	**NGP**	**SF**	**SPY**	**RL**	**SL**	**RV**	**RDW**	**SDW**	**R/S**
Block (ignoring Treatments)	2	84.32^{ns}	440.62^{**}	4.45^{**}	1.15^{**}	28.73^{*}	33.25^{ns}	0.04^{*}	378^{ns}	456.75^{ns}	14.07^{**}	4.27^{ns}	466.07^{**}	30.74^{**}	0.96^{**}	21.15^{**}	0.01^{ns}
Treatment (eliminating Blocks)	92	123.18^{ns}	464.48^{**}	9.97^{**}	6.2^{**}	12.09^{ns}	155.96^{*}	0.03^{ns}	683.38^{ns}	267.99^{ns}	6.3^{**}	17.74^{ns}	191.89^{**}	18.94^{**}	0.25^{**}	3.94^{**}	0.01^{ns}
Checks	1	416.67^{*}	2242.67^{**}	37.5^{**}	24^{**}	4.17^{ns}	322.67^{*}	0.11^{*}	29.04^{ns}	656.6^{*}	50.46^{**}	170.67^{*}	337.5^{**}	148.01^{**}	0.63^{*}	3.56^{**}	0.01^{ns}
Test and Test vs. Check	91	119.96^{ns}	444.94^{**}	9.67^{**}	6^{**}	12.18^{ns}	154.13^{*}	0.03^{ns}	690.57^{ns}	263.72^{ns}	5.82^{**}	16.06^{ns}	190.29^{**}	17.52^{**}	0.25^{*}	3.94^{**}	0.01^{ns}
Treatment (ignoring Blocks)	92	122.57^{ns}	472.3^{**}	10.1^{**}	6.22^{**}	12.7^{ns}	156.65^{*}	0.03^{ns}	691.59^{ns}	277.17^{ns}	6.61^{**}	17.8^{ns}	200.98^{**}	19.61^{**}	0.27^{*}	4.4^{**}	0.01^{ns}
Treatment vs. Check	1	49.06^{ns}	148.67^{**}	25.5^{**}	0.22^{**}	78.19^{**}	2.37^{ns}	0.03^{*}	2184.6^{*}	547.36^{*}	0.11^{**}	313.85^{*}	98.07^{*}	19.99^{**}	0^{ns}	0.46^{**}	0^{ns}
Treatments	90	120.12^{ns}	456.23^{**}	9.59^{**}	6.09^{**}	12.07^{ns}	156.52^{*}	0.03^{ns}	682.36^{ns}	269.95^{ns}	6.19^{**}	12.81^{ns}	200.6^{**}	18.18^{**}	0.27^{*}	4.45^{**}	0.01^{ns}
Block (eliminating Treatments)	2	112.67^{ns}	80.67^{**}	0^{ns}	0^{ns}	0.67^{ns}	1.5^{ns}	0^{ns}	0.33^{ns}	34.72^{ns}	0.01^{**}	1.5^{ns}	48.17^{*}	0^{ns}	0^{ns}	0^{ns}	0^{ns}
Residuals	2	16.67	0.67	0	0	0.67	4.17	0	57.66	24.13	0	4.17	1.5	0.01	0.01	0	0
$CD_{0.05}$ A		25	12.42	2.89	46.2	5.23	6.15	5	4.97	0.34	0.5	12	0.5	0.84	29.9	7	2.41
$CD_{0.05}$ B		14	7.17	3.12	26.68	4.89	5.23	3	2.87	0.68	0.29	7	0.29	0.38	17.3	4	3.53
$CD_{0.05}$ C		30	15.21	2.45	56.59	4.12	5.48	6	6.08	0.82	0.61	15	0.61	0.94	36.6	9	1.84
$CD_{0.05}$ D		25	12.42	3.69	46.2	3.71	4.0	5	4.97	0.46	0.5	12	0.5	0.7	29.9	7	2.72

ns P > 0.05; * P <= 0.05; ** P <= 0.01

***DFF:** Days to 50% flowering, **PH:** Plant height (cm), **NT:** Number of tillers per plant, **NPT:** Number of productive tillers per plant, **PL:** Panicle length (cm), **FL:** Flag leaf length (cm), **FW:** Flag leaf width (cm), **NGP:** Number of grains per panicle, **SF:** Spikelet fertility (%), **SPY:** Single plant yield (g), **RL:** Root length (cm), **SL:** Shoot length (cm), **RV:** Root volume (ml), **SDW:** Shoot dry weight (g), **RDW:** Root dry weight (g), **R/S:** Root-to-shoot ratio*

Table 2. Analysis of variance for yield and yield attributing traits of F_3 population under control soil P during *Rabi* 2022-23

Source	DF	Mean sum of squares															
		DFF	**PH**	**NT**	**NPT**	**PL**	**FL**	**FW**	**NGP**	**SF**	**SPY**	**RL**	**SL**	**RV**	**RDW**	**SDW**	**R/S**
Block (ignoring Treatments)	2	163.71^{ns}	47.2^{ns}	1.55^{ns}	0.47^{ns}	0.62^{ns}	30.32^{**}	0.01^{ns}	1374.66^{**}	253.51^{*}	127.16^{**}	9.06^{ns}	65.83^{ns}	135.8^{*}	15.05^{**}	646.3^{**}	0.02^{**}
Treatment (eliminating Blocks)	92	79.95^{ns}	373.11^{*}	5.33^{ns}	4.7^{ns}	5.04^{ns}	46.65^{**}	0.08^{ns}	1783^{**}	211.1^{ns}	53.72^{**}	34.34^{ns}	372.12^{*}	121.16^{*}	7.42^{**}	121.3^{**}	0.02^{**}
Checks	1	216^{ns}	140.17^{ns}	0.67^{ns}	0.67^{ns}	6^{ns}	130.7^{**}	0.03^{ns}	28.17^{ns}	353.96^{*}	0.2^{ns}	104.17^{*}	54^{ns}	541.5^{**}	8.17^{**}	138.2^{**}	0.03^{**}
Test and Test vs. Check	91	78.45^{ns}	375.67^{*}	5.39^{ns}	4.75^{ns}	5.03^{ns}	45.73^{**}	0.08^{ns}	1802.28^{**}	209.53^{ns}	54.3^{**}	33.57^{ns}	375.6^{*}	116.54^{*}	7.41^{**}	121.1^{**}	0.02^{**}
Treatment (ignoring Blocks)	92	83.5^{ns}	374.09^{*}	5.34^{ns}	4.7^{ns}	4.96^{ns}	47.09^{**}	0.08^{ns}	1808.81^{**}	216.46^{ns}	56.35^{**}	34.36^{ns}	373.02^{*}	123.76^{*}	7.74^{**}	135.3^{**}	0.02^{**}
Treatments vs. Checks	1	39.92^{ns}	16.51^{ns}	37.6^{*}	18.9^{*}	1.63^{ns}	130.2^{**}	0.11^{ns}	11155.7^{**}	298.85^{*}	233.35^{**}	476.01^{**}	4.35^{ns}	450.57^{**}	24.5^{**}	61.34^{**}	0.11^{**}
Treatments	90	82.51^{ns}	380.66^{*}	5.04^{ns}	4.58^{ns}	4.98^{ns}	45.23^{**}	0.08^{ns}	1724.74^{**}	214.02^{ns}	55.01^{**}	28.68^{ns}	380.66^{*}	115.48^{*}	7.55^{**}	136.1^{**}	0.02^{**}
Block (eliminating Treatments)	2	0.17^{ns}	2.17^{ns}	1.17^{ns}	0.67^{ns}	4.5^{ns}	10.17^{*}	0.08^{ns}	187.17^{*}	7.17^{ns}	5.78^{*}	8.17^{ns}	24.5^{ns}	16.17^{ns}	0.33^{ns}	3.26^{*}	0^{ns}
Residuals	2	21.5	16.17	1.17	0.67	0.5	0.17	0.05	7.17	12.5	0.19	2.17	4.5	1.5	0.05	0.14	0
$CD_{0.05}$A		28	2.48	1	16.29	5	6.57	24	4.3	0	1.31	9	7.45	2	21.5	13	2.63
$CD_{0.05}$B		16	1.43	1	9.4	3	3.79	14	2.48	0	0.76	5	4.3	1	12.4	7	1.52
$CD_{0.05}$C		35	3.04	2	19.95	6	8.05	30	5.27	0	1.61	11	9.13	3	26.4	16	3.22
$CD_{0.05}$D		28	2.48	1	16.29	5	6.57	24	4.3	0	1.31	9	7.45	2	21.5	13	2.63

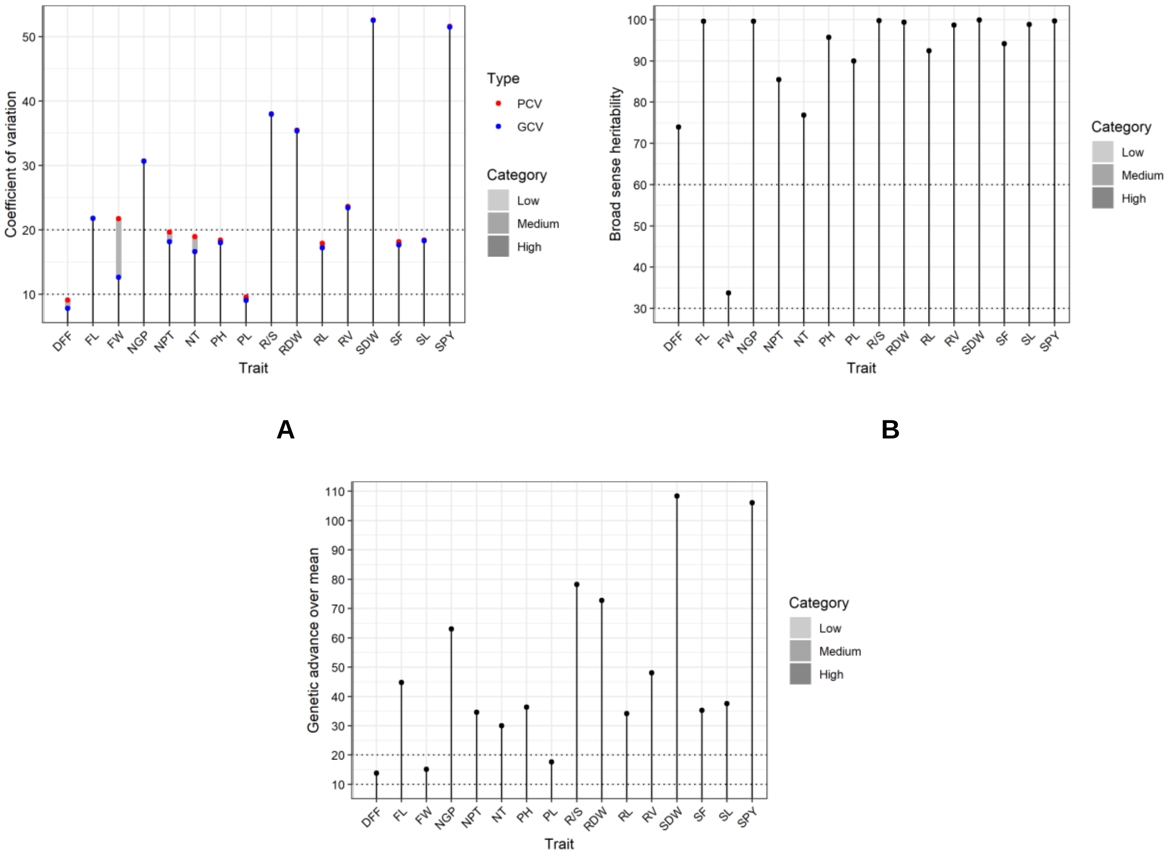
ns P > 0.05; * P <= 0.05; ** P <= 0.01

***DFF:** Days to 50% flowering, **PH:** Plant height (cm), **NT:** Number of tillers per plant, **NPT:** Number of productive tillers per plant, **PL:** Panicle length (cm), **FL:** Flag leaf length (cm), **FW:** Flag leaf width (cm), **NGP:** Number of grains per panicle, **SF:** Spikelet fertility (%), **SPY:** Single plant yield (g), **RL:** Root length (cm), **SL:** Shoot length (cm), **RV:** Root volume (ml), **SDW:** Shoot dry weight (g), **RDW:** Root dry weight (g), **R/S:** Root-to-shoot ratio*

Table 3. Genetic variability parameters for yield and yield attributing traits of F_3 lines under Control and low soil P condition during *Rabi* 2022-23

Trait	Mean		Min.		Max.		GCV		PCV		ECV		hBS		GAM	
	Control	**P_0**	**Control**	**P_0**	**Control**	**P_0**	**Control**	**P_0**	**Control**	**P_0**	**Control**	**P_0**	**Control**	**P_0**	**Control**	**P_0**
DFF	100.26	152.87	64.67	106.67	115.17	170.67	7.79	7	9.06	7	4.62	3	73.94	86.12	13.82	13
PH	106.19	98.44	61.33	55.33	144.83	145.33	17.98	22	18.37	22	3.79	1	95.75	99.85	36.29	45
NT	11.84	8.58	5.33	3.00	16.83	15.00	16.61	36	18.95	36	9.12	0	76.83	100	30.04	74
NPT	10.90	5.19	5.67	1.00	16.67	12.00	18.15	48	19.64	48	7.49	0	85.46	100	34.62	98
PL	23.46	20.47	17.5	9.33	30.50	30.33	9.03	17	9.52	17	3.01	4	89.97	94.48	17.66	33
FL	30.86	31.65	18.17	12.5	54.17	63.00	21.75	39	21.79	40	1.32	6	99.63	97.34	44.8	79
FW	1.28	0.89	0.78	0.32	2.18	1.22	12.61	18	21.72	19	17.69	5	33.69	94.22	15.1	37
NGP	135.38	86.25	60.67	39.93	296.67	201.13	30.61	29	30.68	30	1.98	9	99.58	91.55	63.02	57
SF	80.55	76.24	34.17	29.68	99.96	101.25	17.62	21	18.16	22	4.39	6	94.16	91.06	35.28	40
SPY	14.38	7.23	2.50	2.77	38.6	14.57	51.50	34	51.59	34	3.01	0	99.66	100	106.07	71
RL	29.94	18.68	18.83	10.00	43.00	31.33	17.20	16	17.89	19	4.92	11	92.44	67.47	34.12	27
SL	105.99	53.69	59.5	7.83	140.5	82.83	18.30	26	18.41	26	2	2	98.82	99.25	37.53	54
RV	45.55	7.16	21.67	2.00	85.17	28.00	23.44	60	23.59	60	2.69	1	98.7	99.96	48.04	122.87
RDW	7.75	0.64	3.37	0.10	16.57	3.70	35.37	80	35.48	81	2.79	13	99.38	97.53	72.75	162.69
SDW	22.19	2.48	6.30	0.31	63.2	13.78	52.55	85	52.57	85	1.69	1	99.9	99.97	108.35	175.38
R/S	0.40	0.29	0.18	0.10	0.91	0.72	37.97	36	38.01	38	1.85	13	99.76	89.02	78.23	71

***DFF:** Days to flowering, **PH:** Plant height (cm), **NT:** Number of tillers, **NPT:** Number of productive tillers, **PL:** Panicle length (cm), **FL:** Flag leaf length (cm), **FW:** Flag leaf width (cm), **NGP:** Number of grains per panicle, **SF:** Spikelet fertility (%), **SPY:** Single plant yield (g), **RL:** Root length (cm), **SL:** Shoot length (cm), **RV:** Root volume (ml), **SDW:** Shoot dry weight (g), **RDW:** Root dry weight (g), **R/S:** Root-to-shoot ratio, **GCV:** Genotypic coefficient of variance, **PCV:** Phenotypic coefficient of variance, **ECV:** Environmental coefficient of variance, **hBS:** Heritability (broad sense), **GAM:** Genetic advance as percentage of mean*

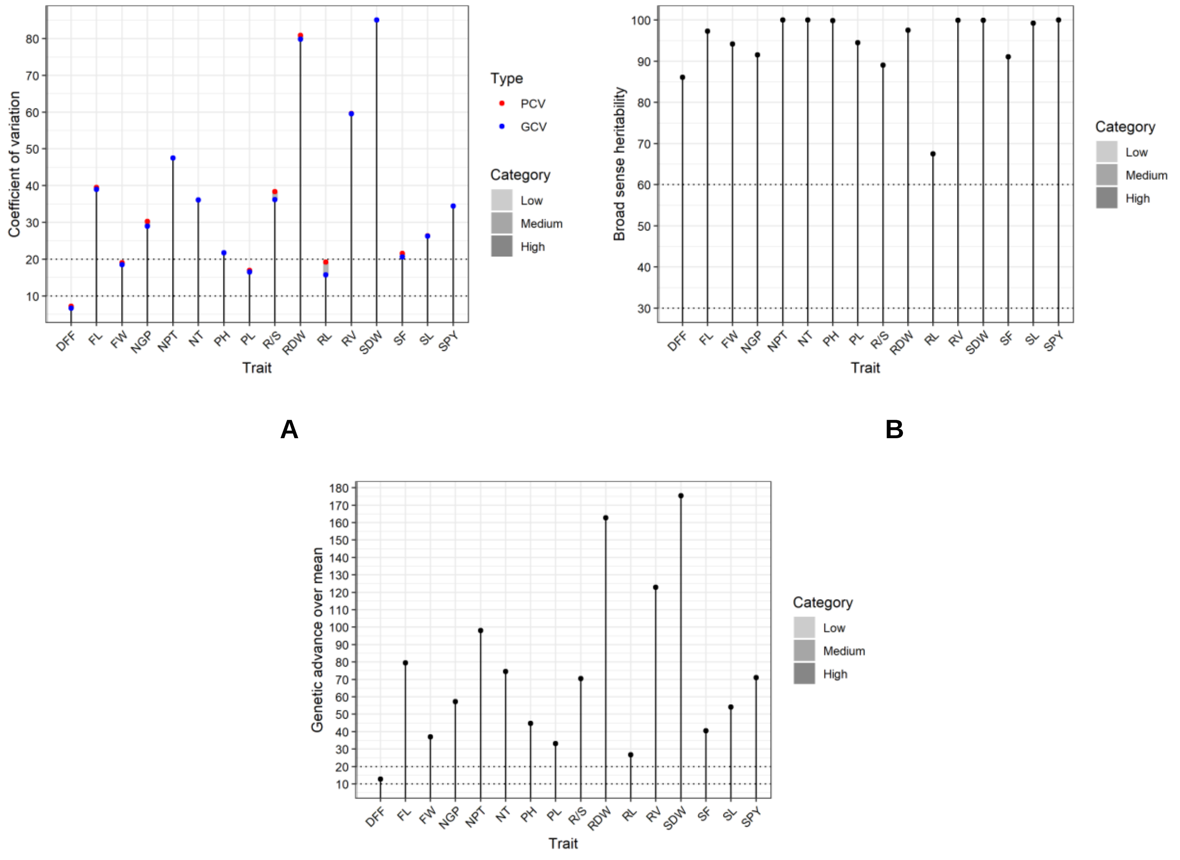


A

B

C

Fig. 1. Genetic variability parameters of F_3 population evaluated in control conditions. Graphs representing the (A) Phenotypic and genotypic coefficient of variation. (B) Broad-sense heritability, and (C) Genetic advance as percentage of mean



A

B

C

Fig. 2. Genetic variability parameters of F_3 population evaluated in low P condition. Graphs representing the (A) Phenotypic and genotypic coefficient of variation. (B) Broad-sense heritability, and (C) Genetic advance as percentage of mean

underscoring the importance of understanding genetic variability within populations for initiating effective and strategic breeding efforts. The genetic variability parameters *viz*., mean, maximum, minimum, GCV (%), PCV (%), h2 (bs) (%) and GAM for each trait were compiled in the following table and figures (Table 3; Fig. 1; Fig. 2).

3.3 Mean Performances of Rice Genotypes

In Rice, especially for low soil P breeding programs, the number of productive tillers, plant yield and root traits are highly desirable traits. Genetic variability, which arises from differences among individuals within a plant population due to genetic composition, is crucial for the success of plant breeding programs. This variability enables breeders to identify and select optimal candidates from a diverse pool of genetic materials, emphasizing the need for a thorough understanding of genetic variability within populations to initiate effective and strategic breeding programs.

Phenotypic variation for days to fifty *per cent* flowering under control (recommended dose of P application) and low P (available P<2.0 kg ha^{-1}) condition ranged from (64.67 to 115.17) and (106.67 to 170.67) days with an overall mean of (100.26) and (152.87) days, respectively. From the study, it was observed that mean values for days to fifty *per cent* flowering under low P were more as compared to the control condition indicating the critical role of P requirement in flowering and imparting stress conditions during the flowering stage. It is predicted to be an adaptive mechanism of plants that leads to increased P acquisition and utilization, helping the crop plants to attain maximum reproductive biomass. Plant height is an important morphological character because it is associated with light interception efficiency, lodging and dry matter production. Plant height in study varied from (61.33 to 144.83) cm and (55.33 to 145.33) cm with an average of (106.19) and (98.44) cm under control and low P conditions respectively. The number of tillers and productive tillers per plant are important for yield attributing characters and these traits were used as key indices for breeding/screening of rice cultivar tolerance to stress conditions, like low P stress to know the variability existing for these traits become prime important under P stress environment. Phenotypic variation for the total number of tillers per plant ranged from (5.33 to 16.83) and (3 to 15) with an overall mean of (11.84) and (8.58). Panicle length per plant varied from (17.5 to 30.5) and (9.33 to 30.33) with an overall mean of (23.46) and (20.47). Flag leaf length per plant varied from (18.17 to 54.17) cm and (12.5 to 63) with an overall mean of (30.86) and (31.65) similarly, flag leaf width varied from (0.78 to 2.18) cm and (0.32 to1.22) with an overall mean of (1.28) and (0.89). The total number of grains per panicle varied from (60.67 to 296.67) and (39.93 to 201.13) with an overall mean of (135.38) and (86.25). *Per cent* spikelet fertility per plant varied from (34.17 to 99.96) and (29.68 to 101.25) with an overall mean of (80.55) and (76.24). Grain yield per plant under study varied from (2.50 to 38.60) and (2.77 to 14.57) with an overall mean of (14.38) and (7.23). Root length under study varied from (18.83 to 43) and (10 to 31.33) with an overall mean of (29.94) and (18.68). Shoot length under study varied from (59.50 to 140.50) and (7.83 to 82.83) with an overall mean of (105.99) and (53.69). Root volume under study varied from (21.67 to 85.17) and (2 to 28) with an overall mean of (45.55) and (7.16). Root dry weight under study varied from (3.37 to 16.57) and (0.1 to 3.7) with an overall mean of (7.75) and (0.64). Root to shoot ratio under study varied from (0.18 to 0.91) and (0.1 to 0.72) with an overall mean of (0.40) and (0.29) under control and low P conditions (Aluwihare et al., 2016; Vejchasarn et al., 2016; Swamy et al., 2019; Kale et al., 2021; Anila et al., 2022; Anandan et al., 2022; Vishnupriya et al., 2024 and Harisha et al., 2024). The most reliable metrics for evaluating low P tolerance are the number of productive tillers, grain yield and root traits. The considerable diversity observed in these traits among the lines suggests a strong potential for identifying novel sources to improve these characteristics under low P conditions. Additionally, the presence of sufficient genetic variation across all traits studied in the rice genotypes indicates that these materials could serve as valuable donors in breeding programs aimed at enhancing low P tolerance.

3.4 PCV, GCV, h^2 (bs) and GAM

GCV and PCV for days to 50% flowering were (7.79 and 9.06) % and (7 and 7) % while heritability and GAM were (73.94 and 13.82) % and (86.12 and 13) % respectively for control and low P conditions. GCV and PCV for plant height were (17.98 and 18.37) % and (22 and 22) % while, heritability and GAM were (95.75 and 36.29) % and (99.85 and 45) % respectively. GCV and PCV for the total number of tillers per plant was (16.61 and 18.95) %, and (36 and 36) % while, heritability and GAM were (76.83 and 30.04) % and (100 and 74) %, similarly GCV and PCV for the number of productive tillers per plant was (18.15 and19.64) % and (48 and 48) % whereas, heritability and GAM was (85.46 and 34.62) % and (100 and 98) % respectively. GCV and PCV for panicle length were (9.03 and 9.52) %, and (17 and 17) % while, heritability and GAM were (89.97 and 17.66) % and (94.48 and 33) %. GCV and PCV for flag leaf length were (21.75 and 21.79) %, and (39 and 40) % while, heritability and GAM were (99.63 and 44.8)% and (97.34 and 79)% similarly, GCV and PCV for flag leaf width were (12.61 and 21.72)%, and (18 and 19)% while, heritability and GAM was (33.69 and 15.1)% and (94.22 and 37)%. GCV and PCV for the total number of grains per panicle were (30.61 and 30.68) % and (29 and 30) % while, heritability and GAM were (99.58 and 63.02) % and (91.55 and 57) %. GCV and PCV for *per cent* spikelet fertility were (17.62 and 18.16) % and (21 and 22) % while heritability and GAM were (94.16 and 35.28) % and (91.06 and 40) %. GCV and PCV for grain yield per plant were (51.5 and 51.59) % and (34 and 34) % while heritability and GAM were (99.66 and106.07) % and (100 and 71) %. GCV and PCV for root length were (17.2 and 17.89) %, and (16 and 19) % while heritability and GAM were (92.44 and 34.12) % and (67.47 and 27) %. GCV and PCV for shoot length were (18.3 and 18.41) % and (26 and 26) % while heritability and GAM were (98.82 and 37.53) % and (99.25 and 54) %. GCV and PCV for root volume this trait were (23.44 and 23.59) %, and (60 and 60) % while, heritability and GAM were (98.7 and 48.04) % and (99.96 and 122.87) %. GCV and PCV for root dry weight were (35.37 and 35.48)%, and (80 and 81)% while heritability and GAM were (99.38 and 72.75)% and (97.53 and 162.69)% and GCV and PCV for shoot dry weight trait were (52.55 and 52.57)%, and (85 and 85)% while, heritability and GAM were (99.9 and 108.35)% and (99.97 and 175.38)%. GCV and PCV for root to shoot ratio were (37.97 and 38.01) %, and (36 and 38) % while, heritability and GAM were (99.76 and 78.23) % and (89.02 and 71) % under control and low P condition.

The GCV and PCV provide a measure to compare the variability present among the traits. In the present study, the traits *viz*., plant height, number of tillers per plant, number of productive tillers per plant, flag leaf length, number of grains per panicle, spikelet fertility, single plant yield, shoot length, root volume, shoot dry weight, root dry weight, root-to-shoot ratio possessed high GCV and PCV values and showed small difference between GCV and PCV values and further these traits were used indicator for low P condition in several studies, which indicate that these traits could be more useful in improvement of rice under low soil P condition (Wissuwa & Ae, 2001; Wissuwa, 2005; Aluwihare et al., 2016; Vejchasarn et al., 2016; Swamy et al., 2019 and Kale et al., 2021).

Genetic advance as *per cent* of mean for all traits possessed high genetic advance as *per cent* mean except for days to 50% flowering which showed medium GAM (Ameenal et al., 2016 and Abebe et al., 2017). High heritability accompanied by high genetic advance shows that the character is governed by additive gene action and selection may be rewarding for improvement of such a trait. The lines showed high genetic variability and high heritability coupled with high genetic advance as *per cent* mean for most of the traits. Selection based on these traits would greatly improve the rice genotypes for low soil P tolerance.

4. CONCLUSION

P resources are recognized as one of the limiting resources in future. Thus, the identification and utilization of low soil P tolerant crop genotypes will be an important aspect of plant breeding in order to saving cost of cultivation, reduce fertilizer import costs and also limit the environmental contaminations caused by P fertilizer runoffs. The present study is important in the context of genetic variability studies for low soil P tolerance and these kind of efforts can positively contribute to reduce application of P fertilizers and optimize their use in future, thus saving valuable foreign exchange for countries like India.

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 the writing or editing of this manuscript.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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