



Selection of superior phosphorus starvation tolerant rice (*Oryza sativa*) genotypes using parent offspring regression and MGIDI

AANANTHI N^{1*}, RAIZA CHRISTINA G¹, S K MOHAMED YASEEN¹, V NIRUBANA¹
and J RAMALINGAM¹

Agricultural College and Research Institute (Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu),
Killikulam, Tamil Nadu 628 252, India

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ABSTRACT

The study was carried out during 2019–20 winter (*rabi*) (Oct–Jan) and late *rabi* 2020 (Jan–May) seasons at Agricultural College and Research Institute, Killikulam, Tamil Nadu to evaluate F₃ and F₄ segregating populations of the cross Anna (R) 4 × IR 64 *Pup1* for phosphorus use efficiency, grain yield and related agronomic traits in rice (*Oryza sativa* L.). Significant genetic variability was observed for key traits, including grain yield, plant height, shoot phosphorus content and acid phosphatase activity. Estimates of phenotypic and genotypic coefficients of variation, heritability and genetic advance indicated moderate to high scope for genetic improvement, particularly for grain yield and phosphorus use efficiency. Skewness and kurtosis patterns across generations revealed shifts in genetic architecture, suggesting ongoing segregation and response to selection. Traits such as shoot phosphorus content and grain length-breadth ratio exhibited high heritability and strong intergenerational correlations, reflecting their stability across generations. Multi trait selection using the Multi trait Genotype Ideotype Distance Index (MGIDI) identified 10 superior genotypes, with AI- 48 showing the most desirable overall trait profile. Overall, the study demonstrates the potential for developing phosphorus efficient rice cultivars through the combined action of additive and non-additive genetic effects. The findings provide valuable insights for breeding programmes targeting high yielding rice genotypes adapted to phosphorus limited environments, thereby supporting more sustainable rice production.

Keywords: MGIDI, Parent-Offspring Regression, Phosphorus starvation tolerance, Rice

Rice (*Oryza sativa* L.) is an important food crop commonly cultivated in humid and temperate areas of the world for its high agronomic and nutritional importance. Phosphorus (P), referred as "King-Pin" in Indian agriculture essential for normal growth and development of crop plants which becomes least available to plants due to its interaction with high Ca ions in basic soils and high Al and Fe in acidic soils to form insoluble compounds (Dey *et al.* 2017).

Phosphorus deficiency is a major limiting factor affecting rice production in upland and lowland conditions and almost 50 per cent rice soils are P deficient (Vinod and Heuer 2012). Though application of phosphatic fertiliser enhances yield, but increases production cost and environmental pollution. "*Phosphorus uptake 1*" (*Pup1*), a major quantitative trait locus was identified in "*aus*" rice cultivar *Kasalath* in chromosome 12 related to the efficient use of soil P in rice plants (Wissuwa *et al.* 2002). Many of the present day rice cultivars are deficient in *Pup1*. Hence,

developing phosphorus deficient tolerant rice varieties via introgression of *Pup1* into superior rice cultivars is an alternative strategy for profiting the rice farmers.

In selection process, segregating population offers maximum variability of gene expression of various traits, heritability estimates are crucial for trait inheritance. Skewness and kurtosis measures gene number and gene interaction type for the expression of a particular trait for fixing selection strategies. Calculation of parent offspring regression (Lush 1940) reveals reduced environmental influence, specifying true genetic potentiality of the genotypes encourages selection (Kumar *et al.* 2020). Intergenerational correlation, measures how far the genetic potential of yield and yield attributing traits can be carried to the next generation.

Multi Trait Genotype Ideotype Distance Index (MGIDI) represents the ideal combination of desirable trait values, allows breeders to evaluate multiple traits by calculating distance index between genotype and ideotype (Olivoto and Nardino 2021). In the F₄ generation, MGIDI provides identification of genotypes with best overall performance, facilitates advancement of superior lines. Hence, the present investigation was designed primarily to study the genetic

¹Agricultural College and Research Institute (Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu), Killikulam, Tamil Nadu. *Corresponding author email: aananthi.n@tnau.ac.in

parameters of F_3 and F_4 generations of the cross Anna (R) 4 × IR 64 *Pup1* and to identify the desirable segregants coupled with high yield and phosphorus starvation tolerance.

MATERIALS AND METHODS

The present study was carried out during 2019–20 winter (*rabi*) (Oct-Jan) and late *rabi* 2020 (Jan-May) seasons at Agricultural College and Research Institute, Killikulam (8°46'N, 77°42'E; at an elevation of 40 m amsl), Tamil Nadu. The study intended to measure the genetic potential in the F_3 and F_4 generations of the cross Anna (R) 4 × IR 64 *Pup1* for yield and yield contributing traits. Anna (R) 4, a high yielding, short duration, semi dwarf, non-lodging, drought tolerant rice variety and having deficiency in phosphorus starvation was used as a female parent in this study. IR 64 *Pup1* was used as the donor parent for the introgression of phosphorus starvation tolerance genes. Eighty-seven genotypes from this cross were forwarded to F_3 generation. The F_3 progenies were raised along with their parents in a non-replicated trial since it was a segregating material. The recommended agronomic practices and plant protection methods were adopted during the crop growth period to obtain healthier crop. Foreground selection for *Pup 1* QTL was carried out in 87 F_3 progenies and 71 positive plants for *Pup1* QTL along with high yield performance was forwarded to F_4 generation for further analysis. Seventy-one families were planted with a row to row spacing of 20 cm and 10 cm between plants with each family had six rows of 15 single plants each. Biometrical observations like Days to 50% flowering (DFF) (days); Plant height (PH) (cm); Number of tillers per panicle (NTPP); Number of productive tillers per panicle (NPTP); Panicle length (PL) (cm); Number of filled grains per panicle (NFGPP); Hundred seed weight (HSW) (g); length-breadth ratio (LB); shoot phosphorus (SP) (mg/g of shoot weight) and acid phosphatase activity (AP) (molar of para nitrophenol released /min/mg of fresh weight) (Sadasivam 1996); Grain yield per plant (GYP) (g) were made on 10 randomly selected plants in both F_3 and F_4 progenies and their average values were used for further analysis, including Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) (Burton and De Vane 1953), broad sense heritability (H^2) (Lush 1940), Genetic advance percent of mean (GAM) (Johnson *et al.* 1955), skewness and kurtosis (Snedechor and Cochran 1989), intergenerational correlation parent progeny regression, and narrow sense heritability (h^2) (Smith and Kinman 1965) and employing Microsoft Excel and R software for data processing and graphing.

$$\text{Narrow sense heritability: } h^2 = \frac{b_{yx}}{2r_{xy}} \times 100$$

Where b_{yx} , Regression coefficient of F_4 upon the parent values of F_3 generation calculated for the respective trait; r_{xy} , Intergeneration correlation coefficient between the parent F_3 and F_4 generation.

MGIDI is based on the principle of rescaling of variables, factorial analysis of BLUP (Best Linear Unbiased

Prediction) values, ideotype planning and MGIDI estimation. The MGIDI was estimated based on the formula given below:

$$MGIDI_i = \sqrt{\sum_{j=1}^f (F_{ij} - F_j)^2}$$

Where F_{ij} is i^{th} genotype score for j^{th} factor ($i = 1, 2, \dots, g$; $j = 1, 2, \dots, f$), g and f are a number of genotypes and their factors. The MGIDI were analysed by using “metan” package version 1.18.0 (Olivoto and Nardino 2021) in R studio 4.2.1. with the ‘gamem’ and ‘mgidi’ functions.

RESULTS AND DISCUSSION

Rice is an ancient and the second most consumed cereal crop after wheat, providing over 70% of daily calories and serving as a key income source for farmers. Mineral deficiency and water limitation are major abiotic stresses affecting rice productivity. Under intensive cultivation, phosphorus (P) deficiency can severely limit rice production, further exacerbated by the use of superior varieties. Developing cultivars with enhanced P starvation tolerance is a sustainable alternative to reliance on fertilisers, as phosphate reserves decline and cultivation costs rise. Crop improvement relies on efficient selection from segregating populations. Variability is essential for selecting the best progenies, with F_2 being ideal for maximum segregation and recombination, while F_3 and F_4 are equally critical for selection.

Mean estimates help eliminate undesirable genotypes, and crosses with favourable mean values for multiple traits enhance selection efficiency (Finkner *et al.* 1973). This study revealed significant variation in F_3 and F_4 generations. Days to 50% flowering ranged from 68–98 days (mean: 79). Plant height varied from 94.5–119.04 cm (mean: 105.16), and 100 seed weight from 1.98–2.86 g. Shoot phosphorus content ranged from 0.225–0.18 mg/g, while acid phosphatase activity varied from 0.208–0.362 molar para nitrophenol/min/mg. Grain yield ranged from 13.3–37.11 g/plant (mean: 24.93). In F_4 , plant height varied from 80.90–106 cm, shoot phosphorus from 0.112–0.179 mg/g, and acid phosphatase activity from 0.225–0.356 molar para nitrophenol/min/mg. Grain yield ranged from 18.11–38.43 g/plant (mean: 28.27) (Supplementary Table 1 and 2). These diverse phenotypes form a strong base for selection, particularly for improving yield, phosphorus efficiency, and plant architecture, aligning with findings by (Nirubana *et al.* 2019) in F_2 of Anna (R) 4 × IR 64 *Pup1*.

Genetic variability estimates for yield and component traits offer essential information which helps in selecting superior segregants. PCV and GCV values are useful for ascertaining the role of environment effects on various biometrical traits (Akinwale *et al.* 2011). In both F_3 and F_4 generations, traits like number of filled grains per panicle, number of tillers per plant, number of productive tillers per plant, acid phosphatase activity, shoot phosphorus content, grain yield per plant recorded moderate PCV and GCV which indicates good potential for selection and

improvement. Additionally, grain yield per plant exhibited high PCV and GCV in the F_4 generation alone recommends a wider possibility for improvement. These results are in agreement with the outcomes of (Dhidhi 2021, Yadav and Pitha 2022, Demeke *et al.* 2023). Heritability gives the relative magnitude of heritable portion of the variation, and it signifies the fundamental role for exercising selection of elite genotypes in a breeding programme (Tripathi *et al.* 2018). High heritability and genetic advance as per mean were exhibited by number of tillers per plant, number of productive tillers per plant, number of filled grains per panicle, acid phosphatase activity and grain yield per plant in both the generations (F_3 and F_4). In the F_4 generation alone, days to fifty per cent flowering displayed high heritability and genetic advance as per mean (Table 1). These results indicate strong genetic control and lesser environmental influence on these traits and therefore selection for these traits will be highly effective. These results were in concordance with the findings (Chamar *et al.* 2021, Dhidhi 2021, Faysal *et al.* 2022).

Skewness and kurtosis studies have prime importance in the analysis of segregating breeding populations, as they provide insight into the genetic architecture and can imply the nature of the gene action controlling the trait. The F_3 generation exhibited positive skewness for the traits like days to 50% flowering (1.38), plant height (0.22), number of tillers per plant (0.09), number of productive tillers per plant (0.67), panicle length (0.42) and shoot phosphorus (0.677), while negative skewness was displayed by number of filled grains per panicle (-0.33), hundred seed weight (-0.32), length-breadth ratio (-0.49), acid phosphatase activity (-0.32) and grain yield per plant (-0.04). In the F_4 generation, days to 50% flowering (0.40), number of productive tillers per plant (0.16), panicle length (0.87),

number of filled grains per panicle (0.21), hundred seed weight (0.15), shoot phosphorus content (0.30) and grain yield per plant (0.26) showed positive skewness. Conversely, negative skewness was seen for the traits like plant height (-0.86), number of tillers per plant (-0.006), length-breadth ratio (-1.30) and acid phosphatase activity (-0.47) (Table 1, Fig. 1). The changing pattern of skewness over generations for key traits such as grain yield, number of filled grains per panicle, and plant height would indicate that genetic segregation is still existing and/or there is a response to selection pressures. The findings were in accordance with (Mamata *et al.* 2018, Rao *et al.* 2020).

In the F_3 generation, leptokurtic curve was observed for days to 50% flowering (5.13) and platykurtic curve was shown by the traits plant height (-0.45), number of tillers/plant (-0.15), number of productive tillers/plant (0.40), panicle length (0.12), number of filled grains/panicle (0.30), hundred seed weight (-0.36), length-breadth ratio (0.41), acid phosphatase activity (-0.36), shoot phosphorus content (0.13) and grain yield per plant (0.37). The F_4 generation displayed leptokurtic curve for panicle length (1.16) and length-breadth ratio (4.64) whereas days to 50% flowering (-0.69), plant height (0.43), number of tillers/plant (-0.60), number of productive tillers/plant (-1.07), number of filled grains/panicle (-1.50), hundred seed weight (-0.78), acid phosphatase activity (-0.34), shoot phosphorus content (-0.78) and grain yield/plant (-1.09) showed a platykurtic curve (Table 1). The leptokurtic curve indicated the contribution of major genes and significant epistatic interactions. Most traits in the successive generations were predominantly platykurtic in nature that indicated a relatively flatter, more uniform distribution of genetic effects, offering greater scope for selection. Generational shift in skewness and kurtosis revealed evolutionary response of

Table 1 Genetic variability, heritability, and genetic advance parameters for various traits in F_3 and F_4 generations of rice

Traits	F_3 generation						F_4 generation					
	PCV	GCV	H ²	GAM	S _k	K	PCV	GCV	H ²	GAM	S _k	K
DFP	5.27	5.02	90.67	9.85	1.38	5.13	11.20	11.09	98.08	22.63	0.40	-0.69
PH	5.06	4.96	96.09	10.02	0.22	-0.45	4.92	4.81	95.6	9.69	-0.86	0.43
NTTP	15.35	14.76	92.47	29.25	0.09	-0.15	13.4	12.65	89.17	24.61	-0.01	-0.60
NPTP	18.64	17.99	93.17	35.77	0.67	0.40	15.25	14.42	89.43	28.09	0.16	-1.07
PL	9.67	9.00	86.61	17.25	0.42	0.12	13.19	12.59	91.05	24.75	0.87	1.16
NFGPP	17.87	16.86	89.08	32.79	-0.33	0.30	11.86	11.12	88.03	21.5	0.21	-1.50
HSW	9.51	9.14	92.32	18.08	-0.32	-0.36	15.61	15.23	95.17	30.61	0.15	-0.78
LB ratio	5.05	4.83	91.70	9.53	-0.49	0.41	6.59	6.42	94.9	12.89	-1.30	4.64
AP	13.09	12.15	86.2	23.24	-0.32	-0.36	14.43	13.8	91.43	27.18	-0.47	-0.34
SP	11.36	10.84	91.02	21.3	0.68	0.13	9.75	9.50	94.85	19.06	0.30	-0.79
GYP	19.83	19.37	95.45	38.99	-0.04	0.37	27.94	27.41	96.26	55.41	0.26	-1.09

DFP, Days to 50% flowering (days); PH, Plant height (cm); NTTP, No. of tillers/plant; NPTP, No. of productive tillers/plant; PL, Panicle length (cm); NFGPP, No. of filled grains/panicle; HSW, 100-seed weight (g); LB ratio, Length-breadth ratio; AP, Acid Phosphatase (molar para nitro phenol released/min/mg of fresh weight); SP, Phosphorus content in shoot (mg/g shoot weight); GY, Grain yield/plant (g); PCV, Phenotypic coefficient of variation; GCV, Genotypic coefficient of variation; H², Broad-sense heritability; GAM, Genetic advance as percent of mean; S_k, Skewness; K, Kurtosis.

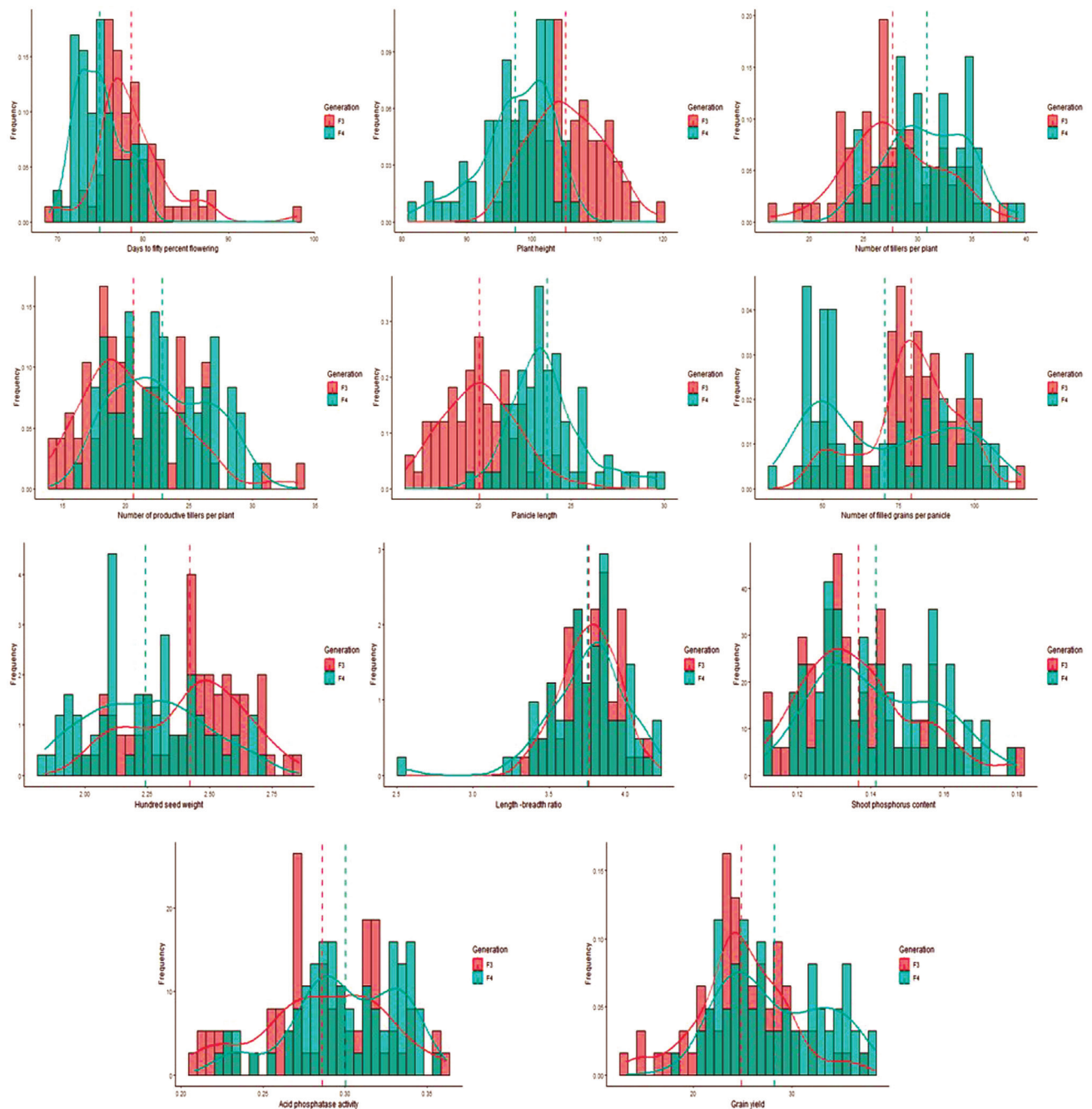


Fig 1 Combined frequency distribution pattern of quantitative traits in F_3 and F_4 generations.

trait to selection and thus helping breeders to modify their strategy by intensifying the selection for positively skewed traits, and likewise by creation of new genetic variability for those traits which showed negative kurtosis and low kurtosis. The studies of (Seeli *et al.* 2021, Kumari *et al.* 2024, Singh *et al.* 2025) corroborated these results on rice traits in segregating populations.

Intergenerational correlation studies are vital for assessing how much of a trait's genetic potential is transmitted to next generations. In this study, among the eleven traits analysed only two traits, viz. shoot phosphorus content (0.368) and length breadth ratio (-0.281) displayed highly significant correlation coefficients. While other traits

like days to 50% flowering (0.126), number of productive tillers/plant (0.083), panicle length (0.073), number of filled grains/panicle (0.132), hundred seed weight (0.100), acid phosphatase activity (0.104) and grain yield (0.054) exhibited positive correlation. Negative correlation was recorded for plant height (-0.066) and number of tillers per plant (-0.066) (Table 2).

The parent-offspring regression analysis provided information about the significant relationship of traits in both F_3 and F_4 generations, with some traits displaying highly significant regression coefficients ($p < 0.01$). Like intergenerational correlation coefficients, significant regression values were recorded only for two traits, viz.

Table 2 Intergenerational correlation, parent-progeny regression, and narrow-sense heritability of biometrical traits in rice

Traits	Intergenerational correlation	Parent progeny regression	Narrow sense heritability (%)
Days to 50% flowering	0.126	0.075	29.65
Plant height (cm)	-0.066	-0.056	43.01
Number of tillers/plant	-0.066	-0.056	43.01
Number of productive tillers/plant	0.083	0.077	46.87
Panicle length (cm)	0.073	0.072	48.9
Number of filled grains/panicle	0.132	0.197	74.61
Hundred seed weight (g)	0.100	0.105	52.72
Length breadth ratio	-0.281*	-0.404*	71.87
Acid phosphatase activity (molar of para-nitrophenol released/min/mg of fresh weight)	0.104	0.089	42.52
Shoot phosphorus content (mg/g of shoot weight)	0.368**	0.380**	51.57
Grain yield (g)	0.054	0.061	56.08

* and ** indicate significance at 5% and 1% levels, respectively.

shoot phosphorus content (0.380) and length-breadth ratio (-0.404). Highest regression coefficients were displayed by shoot phosphorus content (0.380) followed by number of filled grains/panicle (0.197) and hundred seed weight (0.105). Traits like plant height (-0.056), number of tillers/plant (-0.056), grain yield (0.061), days to 50% flowering (0.075) and number of productive tillers/plant (0.077) exhibited low regression coefficients in this study (Table 2, Supplementary Fig. 1). The highly significant correlations and regressions obtained in shoot P content and the length-breadth ratio confirm their genetic control and consistent transmission, highlighting their reliability as selection targets. Low values of correlation and regression coefficients with respect to grain yield and flowering time might indicate their polygenic nature and also their susceptibility to environmental influence. The results found were similar to the findings of Seeli *et al.* (2021), Anushya *et al.* (2025).

Narrow-sense heritability (h^2) that can be estimated using parent offspring regression values refers to the proportion of phenotypic variance that is due to additive genetic variance, which is the genetic variance that can be attributed to the sum of the effects of individual alleles. Number of filled grains per panicle (74.61%) and length-breadth ratio (71.87%) displayed high narrow sense heritability revealed that these traits are mainly controlled by additive gene action and have the potential for rapid improvement through simple selection methods such as mass selection, pedigree selection, and single seed descent methods. Moderate heritability between 30 and 50% were observed for the traits plant height (43.01%), number of tillers/plant (43.01%), acid phosphatase activity (42.52%), number of productive tillers/plant (46.87%), panicle length (48.9%), shoot phosphorus content (51.57%), hundred seed weight (52.72%) and grain yield (56.08%) indicates that the environmental factors and non-additive gene effects, in addition to additive ones, exhibited considerable influence on trait expression. Therefore, effective genetic

improvement of these traits demands successive cycles of selection using methods such as progeny testing, bulk pedigree, and recurrent selection with progeny selection to secure significant progress (Table 2). Similar findings was reported by Viswabharathy *et al.* (2023) and Sood *et al.* (2024). The studies suggested a breeding strategy that concentrates on highly heritable traits with significant intergenerational correlations, and simultaneously applies molecular markers or intensified selection to moderately heritable traits with weak correlations.

In both the F_3 and F_4 generations, traits such as days to 50% flowering, plant height, number of tillers/plant, number of productive tillers/plant, panicle length, number of filled grains/panicle, hundred seed weight, length breadth ratio, acid phosphatase activity, shoot phosphorus content and grain yield exhibited high broad sense heritability. While estimating narrow sense heritability using parent progeny regression analysis, traits like number of filled grains/panicle and length-breadth ratio that showed high narrow sense heritability along with high broad sense heritability. This indicated that these characters are mainly governed by additive gene action and therefore, respond well to simple selection methods. Conversely, the traits that showed high broad sense heritability displayed only moderate narrow sense heritability percentages, specifically for the traits like plant height, number of tillers/plant, acid phosphatase activity, number of productive tillers/plant, panicle length, shoot phosphorus content, hundred seed weight and grain yield (Fig. 2). This contrast reflects the overriding influence of non-additive genetic effects such as dominance and epistasis in their control. In cases of traits related to grain yield, plant height, and tiller number, breeders would more likely have to consider the application of methods that capture additive and non-additive genetic effects, which includes hybrid breeding and recurrent selection (Hill *et al.* 2008).

Principal Component Analysis (PCA), Factor

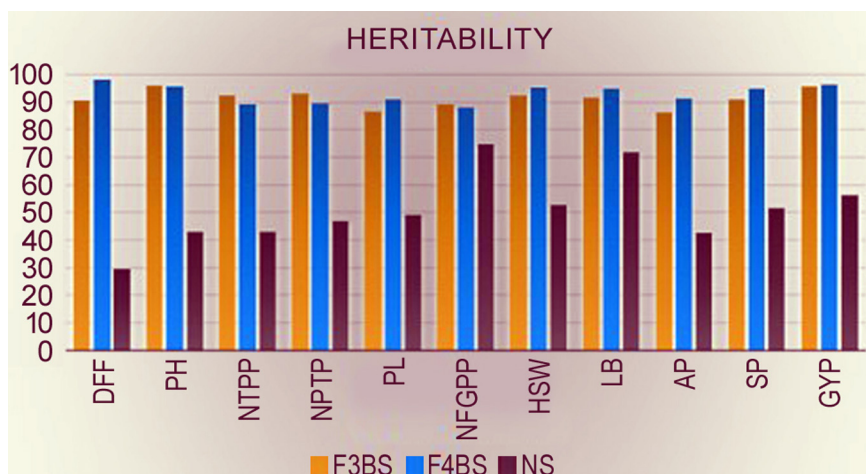


Fig. 2 Comparison of broad sense and narrow sense heritability of biometrical traits of the cross.

DFF, Days to 50% flowering (days); PH, Plant height (cm); NTPP, No. of tillers/plant; NPTP, No. of productive tillers/plant; PL, Panicle length (cm); NFGPP, No. of filled grains/panicle; HSW, 100-seed weight (g); LB ratio, Length-breadth ratio; AP, Acid Phosphatase (molar para nitro phenol released/min/mg of fresh weight).

relationships (Table 3). The MGIDI selection is based on the factorial analysis and includes the correlation of component variables for selection. The factor analysis revealed that a total of five different factors were grouped from 11 variables. The FA1 includes NFGPP, SP, AP; FA2 includes NPTP, NTPP, DFF; FA3 includes GY, PL; FA4 includes HSW, LB; FA5 includes PH. The heritability percent varied from 4% (DFF) to 100% (AP) indicated the fact that not all plant traits are under the same level of genetic control and all the variables exhibited greater heritability except DFF, HSW and LB. The estimation of selection gain for individual variables is possible by MGIDI selection index and also to know the strengths and weaknesses of individual traits for the selection of

Analysis (FA), and Multi-trait Genotype-Ideotype Distance Index (MGIDI) enable breeders to conduct an analysis on complex data sets of multiple traits by reducing the dimensionality and identifying the key patterns or relationships among the traits and genotypes. PCA revealed that the first five components had eigen values greater than one and together accounted for 69.41% of the cumulative variance would indicate a high level of complexity in the trait

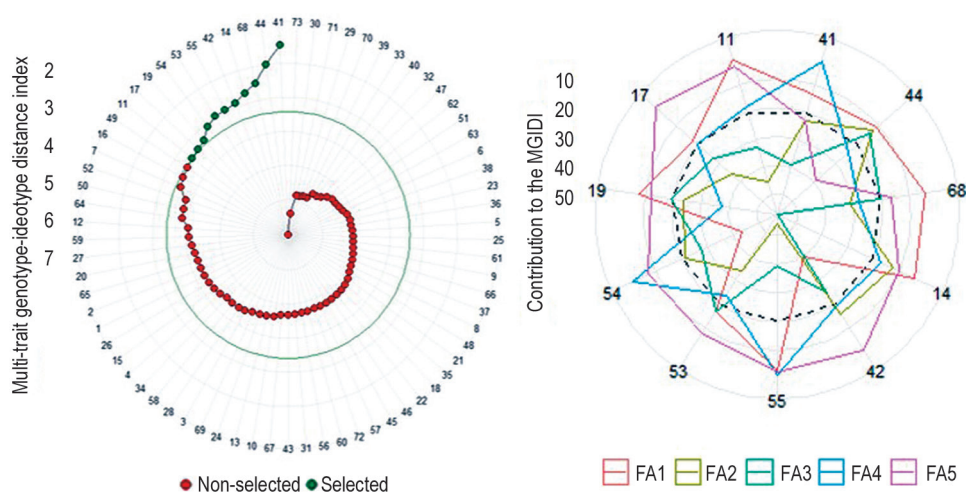


Fig. 3 MGIDI based genotypes selection and its strength-weakness plot of selected genotypes.

Table 3 MGIDI selection index-Factor analysis

PC	Eigen values	Variance	Cumulative variance	Variables	Factor	h ²	SG
PC1	2.75	24.96	24.96	DFF	FA2	4	0.26
PC2	1.48	13.43	38.39	PH	FA5	48	4.06
PC3	1.26	11.5	49.89	NTPP	FA2	41	7.22
PC4	1.13	10.24	60.14	NPTP	FA2	88	19.6
PC5	1.02	9.27	69.41	PL	FA3	68	8.00
PC6	0.94	8.59	78	NFGPP	FA1	25	10.96
PC7	0.72	6.55	84.55	HSW	FA4	20	2.82
PC8	0.68	6.15	90.7	LB	FA4	16	1.60
PC9	0.38	3.47	94.17	SP	FA1	63	9.42
PC10	0.34	3.05	97.22	AP	FA1	100	15.85
PC11	0.31	2.78	100	GY	FA3	68	17.34

SG, Selection gain.

superior genotypes. In the present study, all the variables exhibited positive selection gain and differed from 0.26% (DFF) to 19.6% (NPTP) illustrates the potentials for improvement across all these traits (Table 3).

The selection intensity of 15% was engaged for the selection of superior performing genotypes among the 73 F₄ rice progenies. The MGIDI score selected 10 genotypes like AI- 48, AI-53, AI-84, AI-14, AI-49, AI-71, AI-64, AI-70, AI-19 and AI-17(Fig. 3) as superior performing genotypes for 11 studied variables. According to Al-Ashkar *et al.* (2023), the genotype with the least score of MGIDI had greater performance and was selected as a superior genotype. In this study, genotype AI-48 had least MGIDI score of about 1.471 recommends this line as possessing the best combination of characteristics in the assessed parameters.

The selection of genotypes primarily depends on the selection with correlated variables. The strength and weakness view of selected genotypes (Fig. 3) is useful to know the different variables which contribute for the selection. The FA line located near the centre is said to be a greater contributing variable and *vice versa* (Olivoto and Nardino 2021). According to this, FA3 occupies the middle of the factor analysis plot, reflecting a very high contribution to superior genotype selection. This agrees with the fact that the improvement in yield potential is usually the main objective of most rice breeding programmes. In case of considering individually selected genotype AI-48 had the greatest strength of FA4 and weakness of FA3. It means this genotype, though with desirable plant architecture, is not that powerful in its yield potential. Similarly, genotype AI-11, AI-19, AI-14, AI-84 and AI-53 had strength of FA1 indicates their potential in high yields at yield components. These findings point out the necessity of a multivariate approach in plant breeding. Even as some genotypes may exhibit excellence in certain combinations of traits, they may need improvement with respect to other traits.

This study highlights the importance of developing phosphorus efficient rice cultivars to address phosphorus deficiency in intensive farming systems. The evaluation of F₃ and F₄ populations revealed significant genetic variability and heritability for key traits, including grain yield and phosphorus efficiency, supporting effective selection of superior genotypes. The application of the Multi trait Genotype Ideotype Distance Index (MGIDI) identified ten promising genotypes, with genotype AI-48 standing out as the most favourable for breeding. The findings emphasise the potential for breeding phosphorus efficient, high yielding rice varieties through targeted selection, offering a sustainable solution to improving rice productivity in phosphorus deficient soils.

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