

Variability and Association Studies for Yield Components in *OsPSTOL 1* gene Introgressed Backcross Inbred Lines (BILs) of Rice

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ABSTRACT: Globally rice is considered to be one of the most significant staple food. It is a member of the family Poaceae and holds a unique position among domesticated crop species. Abiotic stress causes 50 percent of yield losses worldwide. Phosphorus is the second-most critical component after nitrogen and it is considered a key factor for optimum crop productivity on arable land all over the world. Phosphorus deficiency is a major constraint in India, with approximately 60 percent of the rice-growing areas in South India suffering it. Genetic variability, correlation, and path analysis for yield contributing traits were studied on 12 backcross populations consisting of 120 plants. The high PCV and GCV were observed for plant height followed by single plant yield, number of productive tillers, the total number of tillers, and filled grains per panicle indicating the influence of the environment exhibiting a high degree of variation. The characters *viz.*, plant height, single plant yield, number of productive tillers per plant, the total number of tillers per plant, and filled grains per panicle showed high heritability coupled with high genetic advance as percent of mean which shows that these traits have additive gene action and are suitable for the selection of elite genotypes. Correlation analysis revealed that the number of productive tillers per plant showed the highest direct correlation followed by the number of tillers per plant, filled grains per panicle, spikelet fertility, plant height, and single plant yield. Thus these traits have a direct association with the yield of the plant. Path analysis revealed that there exists a high and direct positive effect for the number of filled grains per panicle, hundred-grain weight, and the number of productive tillers per plant on single plant yield. The traits that showed as highly correlated should be considered during selection for obtaining improved grain yield with phosphorus starvation tolerance. The direct effects reveals that an increase of these traits *viz.*, the number of filled grains per panicle, hundred-grain weight, and the number of productive tillers per plant would directly increase the yield of the plant.

Keywords: Rice, Phosphorus starvation tolerance, Genetic variability, Correlation, Path analysis.

INTRODUCTION

Rice (*Oryza sativa* L.) is a versatile and staple food crop that serves as a chief food source for over half of the global population. It plays an important role in safeguarding food security for the rural population (Timmer *et al.*, 2010). About 95 percent of global rice is produced and consumed in Asia. The current consumption rate of rice is 90 percent and the demand for rice is still increasing in Asia. It is projected that the demand for rice will rise by up to 650 million tonnes globally by 2050 (Chibuike *et al.*, 2019). Rice is one of

the most significant cereal crops on the globe, serving as the main source of energy and income for the majority of the World's human population. The total amount of food grains produced in the country is estimated to be 316.06 million tonnes in the second advance estimates for 2021–2022, an increase of 5.32 million tonnes from the production of foodgrains in 2020–2021. The amount of rice required to be produced globally in 2021–2022, which is 11.49 million tonnes more than the 116.44 million tonnes of average production over the previous five years, is 127.93 million tonnes. Abiotic stresses, *viz.*, water stress,

including deficit or drought and excess water or flood, salinity, phosphorus deficiency in soils, and heat, cause extensive losses to agricultural production in rainfed areas worldwide (Haefele *et al.*, 2014). The rainfed environments account for 40 percent of global rice production. These abiotic factors account for 50 percent of global yield losses (Arif *et al.*, 2019). Nutrients are the major and essential source, required at all growth stages, and an understanding of the soil's ability to provide the necessary nutrients is crucial for profitable crop production. Insufficient soil phosphorus stress is one of the major limitations on plant growth which affects the yield of many crops, including rice (Zhang *et al.*, 2014). Phosphorus deficiency is a major constraint in India, with approximately 60 percent of the rice-growing areas in South India suffering from this deficiency (Chitrammenal *et al.*, 2018). The lack of phosphorus could cause the rice to mature a week or two later than the usual period (Fageria, 1980). The phosphorus-related developmental factors *viz.*, accelerated root growth, enhanced flower development, improved seed germination, extended stem and stalk quality, improved harvest quality, uniform, and earlier harvest development, and higher resistance to plant diseases are considered of prior importance. Thus when phosphorus is depleted, cellular functions are remodeled, and phospholipids are converted into galactolipids and sulfolipids at a high rate. A red-light-induced activation of P uptake mediated by phytochrome-B13 and the availability of iron in acidic soil causes the primary root growth to stop, which affects the cell's proliferative potential at the meristem and root tip. Additionally, a decrease in tissue phosphorus content negatively impacts plant growth, which results in plant death. It is essential to screen genotypes under P-starved conditions, to perceive the importance of traits and their genetic basis, and the nature of heredity, to produce plants that are tolerant of low soil phosphorus. Rice requires phosphorus to survive and thrive and is highly prone to phosphorus starvation. Thus enhancing crop phosphorus efficiency through the introgression of the *OsPSTOL 1* gene from the donor Samba Mashuri to CR1009 Sub 1 would significantly contribute to the sustainability of agroecosystems (Richardson *et al.*, 2011). With this information, the present study was carried out to analyze the major yield contributing traits.

MATERIALS AND METHODS

The research work was carried out at the Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Madurai during the *Rabi* season of 2021–2022. The experimental materials include 12 backcross populations (C2-3-1, C2-3-2, C2-3-3, C2-4-1, C2-4-2, C28-7-1, C28-7-2, C28-7-3, C28-7-4, C28-1, C28-2 and C28-3) of BC₃F₂, generated from a cross between CR 1009 Sub 1 and Samba Mashuri Pup 1. CR

1009 sub 1, a short bold variety used as the recipient parent, and Samba Mashuri Pup 1 a fine grain variety as the donor parent, having the phosphorus starvation tolerant gene (*PSTOL 1*). Plants were raised in the field in four rows covering 3 meters in length with a spacing of 20 cm × 15 cm and recommended crop agronomic practices were followed to maintain a healthy stand. Ten plants agronomically superior and similar to the recipient parent from each population were selected and various biometrical observations *viz.*, days to 50% flowering, days to maturity, plant height, panicle length, the total number of tillers, productive tillers, spikelet fertility, hundred-grain weight, and single plant yield were recorded. The genetic variability analysis was carried out using a Microsoft Excel spreadsheet by Johanson *et al.* (1955). The association studies were analyzed using TNAU STAT statistical package as given by Manivannan (2014).

Formulae and Equations

1. Phenotypic and genotypic coefficients of variation were calculated as put forward by Burton (1952).

$$PCV(\%) = \frac{\sqrt{\text{Phenotypic variance}}}{\text{Grand mean}} \times 100$$

$$GCV(\%) = \frac{\sqrt{\text{Genotypic variance}}}{\text{Grand mean}} \times 100$$

The P.C.V. and G.C.V. are categorized as suggested by (Sivasubramanian and Madhavanenon, 1973).

Category	Percent of variation
Low	Less than 0-10 percent
Moderate	10-20 percent
High	> 20 percent

2. **Heritability.** The estimation of heritability helps the breeder in selection of elite genotypes from diverse populations. It is the ratio of the genotypic variance to the total or phenotypic variance. Heritability is calculated in the Broad sense [$h^2(\text{BS})$] was calculated as recommended by Lush (1940).

$$h^2(\text{B.S}) = \frac{\sqrt{\sigma_g^2}}{\sqrt{\sigma_p^2}} \times 100$$

3. **Genetic advance as percent of mean.** Genetic advance as percent of mean can be obtained by using the formula derived by Johnson *et al.* (1955).

$$\text{GA as a percent of mean} = \frac{\text{Genetic advance}}{\text{Grandmean}} \times 100$$

The range of genetic advance as percent of mean is classified as given by Johnson *et al.* (1955)

Category	GA Percent value
Low	< 10 percent
Moderate	10-20 percent
High	>20 percent

Genotypic correlation coefficient:

$$rg(xy) = \frac{COV(gxy)}{\sqrt{\sigma_{gx} \times \sigma_{gy}}}$$

Path coefficient analysis. The method of path coefficient analysis as suggested by Dewey and Lu was

used to assess the relative influence of yield components on yield both directly (direct effects) and indirectly (indirect effects) (1959). Based on the scale shown below, the direct and indirect effects derived from path analysis were categorized (Lenka and Misra 1973).

Range	Category
0.0 to 0.09	Negligible
0.10 to 0.19	Low
0.20 to 0.29	Moderate
0.30 to 0.99	High
More than 1.00	Very high

RESULTS AND DISCUSSION

Segregating generations are ideal for imposing selection because they exhibit significant segregation and recombination (Thirugnanakumar *et al.*, 2011). To accomplish efficient breeding programs, it is critical to determine the type and level of phenotypic and genotypic variation present in any crop (Sundaram *et al.*, 2019). The genetic variability components of variation were analyzed as discussed by Johanssen (1909). Heritability and genetic advance are taken into consideration as additional criteria for choosing superior genotypes in addition to genetic variability. The fundamental criteria for selection are yield variability and its related properties (Bhargava *et al.*, 2021).

Estimates of PCV and GCV. The estimates of PCV, GCV, heritability, and genetic advance as percent of means are listed in Table 1. High estimates of PCV and GCV were observed for plant height followed by single plant yield, number of productive tillers, the total number of tillers, and filled grains per panicle, indicating the influence of environment with a high degree of variation are described in Fig. 1. Similar results were reported by Pavithra *et al.* (2022); Lilly *et al.* (2018); Nirubana *et al.* (2019); Bharath *et al.* (2018); Bhargava *et al.* (2021); Yaseen *et al.* (2020);

Dhavaleshvar *et al.* (2019), respectively. Moderate PCV and GCV were observed for hundred-grain weight by Lingaiah *et al.* (2018). The other characters showed low PCV and GCV which exhibits a significant amount of genotype-environment interaction for all variables, as shown by the PCV values being bigger than the GCV values (Saha *et al.* (2019); Ahmed *et al.* (2021); Kumari *et al.* (2022)).

Heritability and genetic advance as percent of mean. According to Johnson *et al.* (1955), estimations of PCV and GCV alone are insufficient for selecting component qualities in improving yield. Thus, a combination of heritability and genetic gain estimates must be used for more trustworthy results. Burton proposed that "genetic variation paired with heritability estimates would provide a better notion of selection effectiveness." The parameters to consider for effective gain under selection and selecting superior varieties include heritability estimates and genetic progress (Ali *et al.*, 2002). Among the various characteristics tillering ability is one of the significant yield-determining features of rice. The results revealed that all the traits showed higher heritability, excluding spikelet fertility and hundred-grain weight. High heritability coupled with high genetic advance is observed for plant height, succeeded by single plant yield, filled grains per panicle, the total number of tillers, and the number of productive tillers, indicating the effective selection of these genotypes. Nirubana *et al.* (2019); Manivelan *et al.* (2022) showed comparable results for the traits *viz.*, plant height, total tiller count, and the number of productive tillers. Similar outcomes with single plant yield were reported by Elayaraj *et al.* (2022). Pavithra *et al.* (2022) showed similar results for the trait, filled grains per panicle, and the number of productive tillers per plant. The heritability and genetic advance estimates are described in Fig. 2.

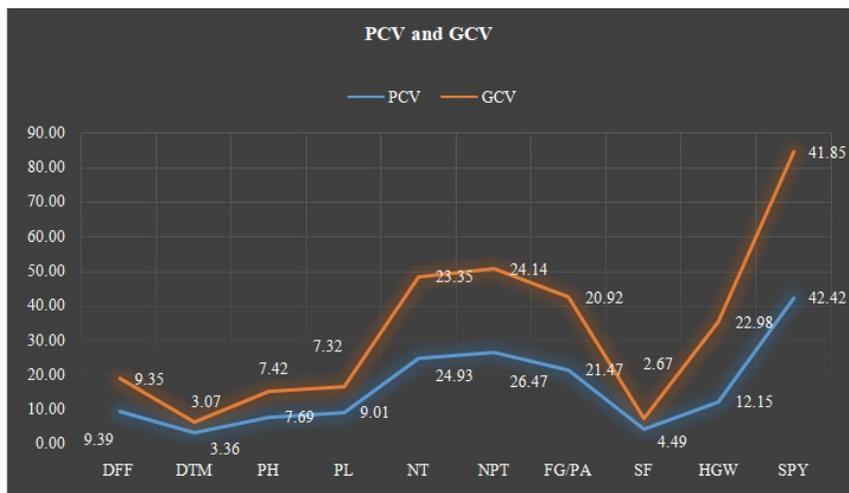


Fig. 1. Phenotypic and genotypic coefficient of variations for the 120 backcross inbred lines.

Table 1: Estimates of genetic variability for ten quantitative traits.

Characters	PCV (%)	GCV (%)	H ²	GAM
DFF	9.39	9.32	99.12	19.17
DTM	8.96	8.85	97.62	18.02
PH	79.97	79.95	99.95	164.65
PL	9.01	7.32	66.10	12.26
NT	24.93	23.35	87.71	45.05
PT	26.47	24.14	83.17	45.36
FPP	22.44	21.91	95.32	44.07
SF	4.49	2.67	35.25	3.26
HGW	12.15	11.61	28.82	7.21
SPY	42.42	41.85	97.35	85.07

Note: DFF- Days to 50 percent flowering; DTM – Days to maturity; PH – Plant height (cm); NT – Total number of tillers per plant; PT - Number of productive tillers per plant; FPP – Filled grains per panicle; SF – Spikelet fertility (%); HGW- Hundred-grain weight (g); SPY- Single plant yield (g)

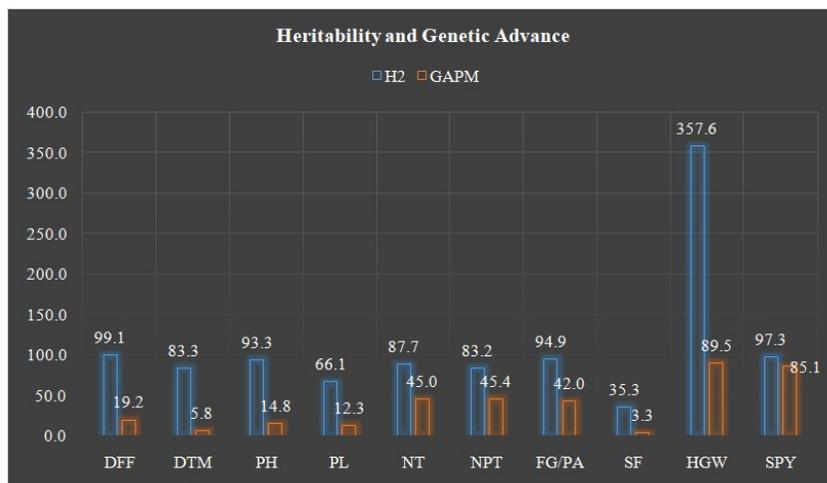


Fig. 2. Heritability and genetic advance as percent of mean for the 120 backcross inbred lines.

Estimates of correlation coefficients. Correlation analysis serves as an example of the existence and degree of interdependence among the component factors. It also identifies the attributes that can be chosen to genetically increase grain yield. Correlation analysis among the traits studied is presented in Table 2. The number of productive tillers per plant showed the highest direct correlation followed by the number of tillers per plant, filled grains per panicle, spikelet fertility, and plant height on single plant yield. The total number of tillers per plant had a significant and positive correlation with plant height. The spikelet fertility showed a strong and positive association existed

between plant height, panicle length, the total number of tillers per plant, the number of productive tillers per plant, and filled grains per panicle. The number of filled grains per panicle was significantly and strongly correlated with plant height, panicle length, the total number of tillers per plant, and the number of productive tillers per plant. Oladosu *et al.* (2018); Kumari *et al.* (2019) reported similar results for the number of tillers per plant having a positive and significant association. Abhilash *et al.* (2018); Bhargava *et al.* (2021); Ahmed *et al.*, (2021) results were in concordance with the number of productive tillers per plant.

Table 2: Correlation analysis for yield and the yield attributing traits.

	DFF	DTM	PH	PL	NT	PT	FPP	SF	HGW	SPY
DFF	1.000									
DTM	0.120	1.000								
PH	0.001	0.025	1.000							
PL	0.059	0.029	0.029	1.000						
NT	0.033	0.081	0.186*	0.039	1.000					
PT	0.034	0.067	0.192*	0.049	0.961**	1.000				
FPP	-0.005	0.028	0.153*	0.213*	0.533**	0.550**	1.000			
SF	-0.024	-0.003	0.126	0.192*	0.479**	0.496**	0.947**	1.000		
HGW	0.040	0.104	-0.093	0.136	0.036	0.080	0.128	0.115	1.000	
SPY	0.082	0.012	0.244**	0.067	0.712**	0.750**	0.596**	0.509**	0.189**	1.000

* Significant at 0.05 percent, **Significant at 0.01percent

Note: DFF- Days to 50 percent flowering; DTM – Days to maturity; PH – Plant height (cm); NT – Total number of tillers per plant; PT - Number of productive tillers per plant; FPP – Filled grains per panicle; SF – Spikelet fertility (%); HGW- Hundred-grain weight (g); SPY- Single plant yield (g)

Similar results for panicle length were reported by Panigraha *et al.* (2018); Bhargava *et al.* (2021); Bhadru *et al.* (2012). Ahmed *et al.* (2021) showed similar results for the number of filled grains per panicle. It was found that raising the proportion of productive and total tillers per plant was crucial for enhancing the capacity to produce more rice. Plant height, panicle length, the total number of tillers per plant, productive tillers per plant, and filled grains per plant all demonstrated a significant and positive association with single plant yield.

Estimates of Path analysis for the yield traits. The direct and indirect effects of the traits are listed in Table 3. Grain yield was regarded as the dependent variable for path coefficient analysis, while the other features were regarded as independent variables. Path analysis is used to assess whether the independent variables have a false correlation. Path analysis showed that multicollinearity-related inflation is smaller since the majority of values are less than unity (Gravois and Helms 1992).

Direct effect. The number of filled grains per panicle, hundred-grain weight, and the number of productive tillers per plant all had a higher direct impact on single plant yield. Hossain *et al.* (2020); Naik *et al.* (2021); Elayaraj *et al.* (2022); Upadhyay *et al.*, (2022) reported similar results. Direct selection of these traits could significantly increase the single plant yield. Plant height shows a high and moderate direct effect estimated to be a vital trait for a single plant's yield. A high and negative direct effect on single plant yield is observed for spikelet fertility. The adverse direct effects revealed that selecting these traits would not boost rice productivity, unlike the high direct positive effects.

Indirect effect. The number of tillers per plant, and spikelet fertility had a significant indirect impact on single plant yield through the number of productive tillers and filled grains per panicle. The height of the plant had a favorable indirect effect on plant yield through the number of productive tillers per plant. This was by Nandan *et al.* (2010).

Table 3: Path analysis for yield and yield attributing traits.

	DFP	DTM	PH	PL	NT	PT	FPP	SF	HGW	SPY
DFP	0.062	-0.008	0.0002	-0.002	-0.002	0.021	-0.003	0.009	0.005	0.082
DTM	0.007	-0.067	0.002	-0.001	-0.005	-0.043	0.018	0.001	0.013	0.012
PH	0.0001	-0.001	0.101	-0.001	-0.012	0.122	0.097	-0.050	-0.017	0.244**
PL	0.003	-0.002	0.003	-0.042	-0.002	0.031	0.135	-0.076	0.017	0.067
NT	0.002	-0.005	-0.19	-0.001	-0.066	0.610	0.340	-0.189	0.004	0.712**
PT	0.002	-0.004	0.019	-0.002	-0.063	0.635	0.350	-0.196	0.010	0.750**
FPP	-0.0004	-0.001	0.015	-0.009	-0.035	0.349	0.636	-0.375	0.016	0.596**
SF	-0.001	0.0003	0.012	-0.008	-0.031	0.315	0.603	-0.395	0.014	0.509**
HGW	0.002	-0.007	-0.009	-0.005	-0.002	0.051	0.081	-0.045	0.125	0.189**

* Significant at 0.05 percent, **Significant at 0.01percent

Note: DFP- Days to 50 percent flowering; DTM – Days to maturity; PH – Plant height (cm); NT – Total number of tillers per plant; PT - Number of productive tillers per plant; FPP – Filled grains per panicle; SF – Spikelet fertility (%); HGW- Hundred-grain weight (g); SPY- Single plant yield (g)
Residual effect – 0.61

CONCLUSIONS

Plant height had the highest PCV and GCV estimates, followed by single plant yield, number of productive tillers per plant, the total number of tillers per plant, and filled grains per panicle, demonstrating the influence of the environment with a high degree of variation. High heritability coupled with high genetic advance is observed for plant height, succeeded by single plant yield, filled grains per panicle, the total number of tillers per plant, and the number of productive tillers per plant. The number of productive tillers per plant showed the highest direct correlation followed by the number of tillers per plant, filled grains per panicle, spikelet fertility, plant height, and single plant yield. The number of filled grains per panicle, hundred-grain weight, and the number of productive tillers all had a higher direct impact on yield. On analysis through the variability, correlation, and path studies it is revealed that the traits *viz.*, the number of productive tillers per plant, the total number of tillers per plant, and the number of filled grains per panicle are the key traits

considered in choosing elite genotypes to increase the single plant yield.

FUTURE SCOPE

The variability studies show that the major contributing traits of having high heritability coupled with high genetic advance are useful for increasing plant yield. As a result, cultivars with high yield and tolerance to phosphorus deficiency must be screened for developing P-efficient cultivars, as well as these traits are to be considered for increased yield.

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Conflict of interest: None.

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