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Genetic variability and frequency distribution studies for yield in *OsPSTOL1* gene introgressed segregating populations of rice (*Oryza sativa* L.)

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Abstract
During *rabi* 2019, a field experiment was conducted with F_3 populations of two crosses *viz.,* Anna(R) 4 × IR 64 *Pup1* and Anna(R) 4 × Samba Mahsuri *Pup1* raised in non replicated trial at at Agricultural College and Research Institute, Killikulam and the observation was recorded for eight biometrical traits. High magnitude of variation in the experimental material of the study is reflected by high values of mean and range for all the characters studied. The results indicated that, high phenotypic coefficient of variation was observed as compared to genotypic coefficient of variation, suggesting the environmental influence on the expression of traits and heritability is high for most of the characters. The F_3 populations of Anna(R) 4 × IR 64 *Pup1* exhibited moderate PCV and GCV for single plant yield, number of productive tillers per plant, number of filled grains per panicle, number of tillers per plant and Anna(R) 4 × Samba Mahsuri *Pup1* exhibited high PCV and GCV for single plant yield indicated that high variability among the lines. The F_3 populations of Anna(R) 4 × IR 64 *Pup1* showed high heritability coupled with high genetic advance as per cent of mean for number of tillers per plant, number of productive tillers per plant, number of filled grains per panicle and single plant yield and Anna(R) 4 × Samba Mahsuri *Pup1* for number of productive tillers, panicle length, number of tillers per plant, hundred seed weight, days to fifty per cent flowering, and single plant yield which showed that these characters were controlled by additive gene effects and phenotypic selection for these characters were likely to be effective.

Keywords: Rice, Genotypic coefficient of variation (GCV), Phenotypic coefficient of variation (PCV), heritability and genetic advance

Introduction
Rice (*Oryza sativa* L.,) is the second most important widely grown cereal crop and it is the staple food for more than half of the world's population. The world population is predicted to reach nine billion by the year 2050, but already by the year 2035, an estimate of 116 Mt of milled rice will be needed worldwide to meet the increasing in demand (Amegan *et al.,* 2020) [1]. In India, rice is grown in 44.10 million hectares in diverse ecological conditions with an annual production of 105.5 million tonnes and productivity of 2391 kg/ha (Patel *et al.*, 2018) [22]. Rapidly increasing demand due to ever increasing Indian population has forced us to search for another quantum jump in rice production. The projection of India's rice production target for 2020 A.D is 120 million tones which can be achieved only by increasing the rice production by over 2.0 million tones /year in the coming decade (Rukmini devi *et al.*, 2020) [20] and the increase in food demand may inversely affect, which cause shrinkage of rice cultivable area. Therefore, increasing the crop productivity becomes the main concern in sustaining the rice cultivation.

The extent of biotic and abiotic stresses possesses a great threat for getting higher yield of crop production. Among the abiotic stresses, nutrient deficiency a major stress influencing the yield reduction in rice. Phosphorus (P) is an important macro nutrient essential for plant growth and development. Phosphorus deficiency constitutes a major complexity leads to reduced tillering, rate of assimilate production per leaf area and rate of leaf expansion (Radin and Eidenbock, 1984) [24]. Application of fertilizers may solve the problem but it is very expensive and can cause environmental and health problems and therefore, the development of phosphorous deficient tolerant cultivars is one of the most effective and eco-friendly solutions (Nirubana *et al.*, 2019) [20]. However, a major quantitative trait (QTL), *Phosphorus uptake* (Pup1) has been located on rice chromosome 12 found to be associated with the phosphorus deficiency tolerance (Wissuwa *et al.*, 1998) [30].

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Crop improvement for particular trait has been achieved through effective use of segregating population and fixing desirable combinations (Khandappagol *et al.,* 2019) [14]. For any crop improvement programme, knowledge on genetic variability, gene action, heritability of yield and its contributing traits are the basic requirements to breed ideal plant type varieties. Therefore, the assessment of variability for yield and yield contributing characters is a pre-requisite to plan for an appropriate breeding strategy (Balat *et al.*, 2018) [4]. Estimates of genetic variability parameters, heritability for yield and related traits provide immense value in the selection of superior segregants. Heritability estimates provide the transmission of information of characters from parents to progeny (Abhilash *et al.*, 2018) [2]. Therefore, the present study has been undertaken to determine the estimates of variability, heritability and genetic advance as per cent of mean for grain yield and its component traits of phosphorous deficiency tolerance in F_3 segregating generation of selected two crosses to identify the useful segregants for further breeding programme.

Materials and Methods
The present investigation was carried out during *rabi,* 2019 in the experiment field of Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Killikulam. The experimental material received from Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Madurai, consisted of F_3 progenies of two crosses *viz.,* Anna(R) 4 × IR 64 *Pup1* and Anna(R) 4 × Samba Mahsuri *Pup1* which were developed involving Anna (R) 4 is a drought tolerant variety but susceptible to phosphorous starvation tolerance. IR 64 *Pup* 1 and Samba Mahsuri *Pup* 1 are the lines tolerant to phosphorous deficiency carrying *OsPSTOL*1 gene. In this study cross 1 (C_1) indicates Anna(R) 4 × IR 64 *Pup1* and cross 2 (C_2) indicates Anna(R) 4 × Samba Mahsuri *Pup1*. The seeds of the segregating populations of the two crosses *viz.,* Eighty seven genotypes of C_1 and ninety genotypes of C_2, were raised during *rabi* 2019 (Oct-Jan) in a non replicated plots. All the seeds of C_1 and C_2 of F_3 population were sown in the raised bed nursery along with their parents. 21 days old seedlings were transplanted to main field with the spacing of 20 cm between rows and 10 cm between plants. The recommended agronomic practices and crop protection measures were followed throughout the crop growth period to obtain a good harvest. The observations were recorded on ten randomly selected plants for parents and 250 plants of each cross combination in F_3 for the following eight biometrical traits *viz.,* days to 50 per cent flowering, plant height (cm), number of tillers per plant, number of productive tillers per plant, Panicle length (cm), number of filled grains per panicle, hundred grain weight (g), single plant yield (g). The mean data for each character was subjected to statistical analysis. Standard statistical procedures were used for the analysis of mean, variance, genotypic and phenotypic coefficient of variation (Burton, 1952) [6], heritability (Lush, 1940) and genetic advance (Johnson *et al,* 1955) [13]. Skewness, the third degree statistics and Kurtosis, the fourth degree statistics were estimated as per Snedecor and Cochran (1974) [29] to understand the nature of distribution of eight quantitative traits in F_3 population.

Result and Discussion
The estimates of phenotypic and genotypic coefficient of variation are necessary to interpret the role of environment influence on different traits. Knowledge on the nature and magnitude of phenotypic and genotypic variability present in any crop plays an important role in formulating successful breeding programmes (Mohana Sundaram *et al.*, 2019) [18]. The estimates of PCV was higher than their corresponding GCV for all the traits studied, denoting environmental factors influencing their expressions to some degree or other. Narrow difference between PCV and GCV suggested their relative resistance to environmental alteration. (Saha *et al.,* 2019) [28]. The estimates of phenotypic variance, genotypic variance, phenotypic coefficient of variation, genotypic coefficient of variation, heritability, genetic advance and genetic advance as per cent of mean for eight quantitative traits of the two crosses are presented in (Table 1 and Table 2).

In C_1, number of filled grains per panicle, hundred seed weight and single plant yield showed negative skewness under this study, indicating duplicate gene effects, while other characters exhibited positive skewness, suggesting complementary gene action. Days to 50% flowering, number of productive tillers per plant, panicle length, number of filled grains per panicle and single plant yield showed negative kurtosis, indicating gene interactions, while other traits showed an absence of gene interaction. Govinthraj *et al.*, (2018) reported the panicle length and number of filled grains per panicle showed positive kurtosis in rice. Anna(R) 4 × IR 64 *Pup1* exhibited the highest phenotypic variance (206.07) and genotypic variance (183.57) was found for the number of filled grains per panicle indicating the magnitude of environmental influence and the lowest magnitude was observed for hundred seed weight (0.05). The moderate estimates of phenotypic and genotypic coefficient of variation (10-20%) were recorded in Anna(R) 4 × IR 64 *Pup1* for single plant yield (19.82% and 19.33%) followed by number of productive tillers per plant (18.63% and 17.99%), number of filled grains per panicle (17.86% and 16.86%), number of tillers per plant (15.35% and 14.76%). This indicated that these traits could be improved for breeding high yielding rice varieties through selection and hybridization. Divya *et al.* (2018) [8] also observed moderate magnitude of PCV and GCV for number of productive tillers per plant, number of filled grains per panicle and single plant yield.

The low estimates (10%) of PCV and GCV were recorded in Anna(R) 4 × IR 64 *Pup1* for days to fifty per cent flowering (5.27% and 5.02%), plant height (5.06% and 4.96%), panicle length (9.66% and 8.99%), hundred seed weight (9.50% and 9.04%). Lower genotypic and phenotypic coefficient of variation obtained indicate the presence of narrow genetic base for these traits and hence for their improvement, their genetic base must be widened. Similar findings were reported by Abhilash *et al.,* (2018) [2] for *viz.,* days to fifty per cent flowering, plant height and spikelet fertility percentage Patel *et al.*, 2018 [22] observed low PCV and GCV for days to 50% flowering, plant height, panicle length, 100 grain weight, kernel length, kernel breadth, kernel L/B ratio. Low PCV and GCV estimates were reported by Prasad *et al.* (2017) [21] and Mallimar *et al.* (2015) for characters like plant height, days to fifty per cent flowering and hundred seed weight.

The co-efficient of variation indicates only the extent of variability existing for various characters, but does not give any information regarding heritable proportion of it. Hence, the amount of heritability permits greater effectiveness of selection by separating out the environmental influence from the total variability and to indicate accuracy with which a genotype can be identified phenotypically. In the present study, the broad sense heritability ranged from 86.60%

(panicle length) to 96.08% (plant height) (Table 1 and Fig 1). High estimates of heritability in broad sense were recorded for almost all the characters studied *viz*., plant height (96.08%), single plant yield (95.03%), number of productive tillers per plant (93.17%), days to 50% flowering (90.66%), hundred seed weight (90.48%), number of filled grains per panicle (89.08%), panicle length (86.60%). Similar results for all the traits were recorded by Kumar *et al*., (2018). Genetic advance as per cent of mean was found to be the highest for single plant yield (38.82) followed by number of productive tillers per plant (35.77), number of filled grains per panicle (32.78) and lowest for days to 50% flowering (9.84%). Similar results observed by Dhavaleshvar *et al.,* (2019) [7] for single plant yield and Ghimire and Mahat (2019) [9] for number of filled grains per panicle and also lowest for days to 50% flowering.

In C$_1$, high heritability coupled with high genetic advance was observed for the traits *viz*., single plant yield, number of filled grains per panicle, number of productive tillers per plant and number of tillers per plant indicated that these characters were generally governed by additive gene action and simple selection would be effective for genetic improvement. This result was in agreement with the earlier studies of Rashid *et al.* (2017) [25] for single plant yield and number of filled grains per panicle, and Girma *et al.* (2018) [10] for number of productive tillers per plant and number of tillers per plant. Similarly high heritability with moderate genetic advances estimates were recorded for plant height, panicle length and hundred seed weight. Similar results observed by Behera *et al.*, (2018) [5] for panicle length suggesting the role of both additive and non-additive gene effects in their inheritance, therefore, adoption of breeding procedures which could exploit both the gene actions would be effective approach.

In C$_2$, number of productive tillers per plant and number of filled grains per panicle showed negative skewness under this study, indicating duplicate gene action. Contradictory results have been previously reported by Govintharaj *et al.* (2018). Number of tillers per plant and number of productive tillers per plant showed negative kurtosis, indicating absence of gene interactions, while other traits showed presence of gene interactions. Khandappagol *et al.*, (2018) reported number of tillers per plant had negative kurtosis in rice. The Platykurtic and positive skewed distribution recorded for single plant yield, panicle length and hundred grain weight indicated that, these traits are governed by large number of segregating genes having decreasing effect displaying dominant and dominant based complementary epistasis in inheritance. Similar findings was observed by Khandappagol *et al.*, (2019) [14]. Anna(R) 4 × Samba Mahsuri *Pup1* exhibited the highest phenotypic variance (84.94%) and genotypic variance (83.34%) was found for days to 50% flowering and the lowest magnitude was observed for hundred seed weight (0.08) (Table 2 and Fig 2). The High estimates of PCV and GCV were observed for single plant yield (28.26% and 27.80%) which showed the major influence of genetic control and less variable due to environmental factor. Similar conclusions were reported by Nirubana *et al*, (2019) [20] for single plant yield. The moderate estimates of phenotypic and genotypic variation (10-20%) were recorded for hundred seed weight

(15.47% and 15.01%), number of productive tillers per plant (15.14% and 14.30%), number of tillers per plant (13.50% and 12.76%), panicle length (13.18% and 12.57%), number of filled grains per panicle (11.82% and 10.40%), days to 50% flowering (11.28% and 11.17%). The existence of moderate variability of these traits, which could be exploited for improvement of the traits through selection in advanced generation. The low estimates (10%) of PCV and GCV were recorded on plant height (5.02% and 4.91%) and similar conclusion were earlier reported by Hefena *et al*. (2016) [11], Badri *et al*. (2016) [3], Sala and Shanthi *et al*. (2016) [27]. Lower genotypic and phenotypic coefficient of variation obtained indicate the presence of narrow genetic base for these traits and hence for the improvement, their genetic base must be widened.

Heritability estimates are useful in selection of genotypes based on phenotypic performance and genetic advance as per cent of mean provides information on expected genetic gain resulting from selection of superior individuals. So considering heritability values along with genetic advance would be more reliable and helpful in predicting the gain under selection than heritability estimate alone. In the present study, broad sense heritability ranged from 77.36% (number of filled grains per panicle) and 98.11% (days to 50% flowering) (Table 2 and Fig 2). High estimates of heritability in broad sense were recorded for all the characters *viz*., days to 50% flowering (968.11%), single plant yield (96.81%), plant height (95.75%), hundred seed weight (94.08%), panicle length (91.00%), number of tillers per plant (89.33%), number of productive tillers per plant (89.25%), and number of filled grains per panicle (77.34%). It revealed that these characters are less influenced by environment and there could be greater correspondence between phenotypic and breeding values. These results are in accordance with the earlier report of Iqbal *et al*. (2018) [12] for number of number of filled grains per panicle. Genetic advance as per cent of mean was found to be the highest for single plant yield (56.36%) followed by hundred seed weight (29.99%), number of productive tillers per plant (27.84%), number of tillers per plant (24.85%), panicle length (24.71%) and days to 50% flowering (22.80%) and lowest for plant height (9.91%). High values of genetic advance as per cent of mean indicates that these characters are governed by additive genes and selection of such traits will be beneficial. Similar results were reported earlier by Behera *et al*. (2018) [5] for days to 50% flowering, panicle length and single plant yield.

In C$_2$, high heritability coupled with high genetic advance was observed for the traits *viz*., single plant yield, number of tillers per plant, hundred seed weight, days to 50% flowering, panicle length, number of productive tillers per plant and number of tillers per plant indicated that these characters were generally governed by additive gene action. Similarly high heritability with moderate genetic advances estimates were recorded for plant height and number of filled grains per panicle. Similar results observed by Ghimire and Mahat (2019) [9] for plant height suggesting additive gene effects and direct selection for these traits would be more effective for desired genetic improvement.

Table 1: Estimates of genetic variability parameters for eight quantitative characters in F$_3$ progenies of cross Anna(R) 4 × IR 64 *Pup1* in rice.

Character	Mean	σ2p	σ2e	σ2g	GCV(%)	PCV(%)	h²%	GA	GAM(%)	Skewness	Kurtosis
DFF (days)	78.52	17.14	1.6	15.54	5.02	5.27	90.66	7.73	9.84	1.38	5.13
PH (cm)	104.75	28.12	1.1	27.02	4.96	5.06	96.08	10.49	10.02	0.22	-0.45
NTPP	28.08	18.59	1.4	17.19	14.76	15.35	92.47	8.21	29.24	0.09	-0.15

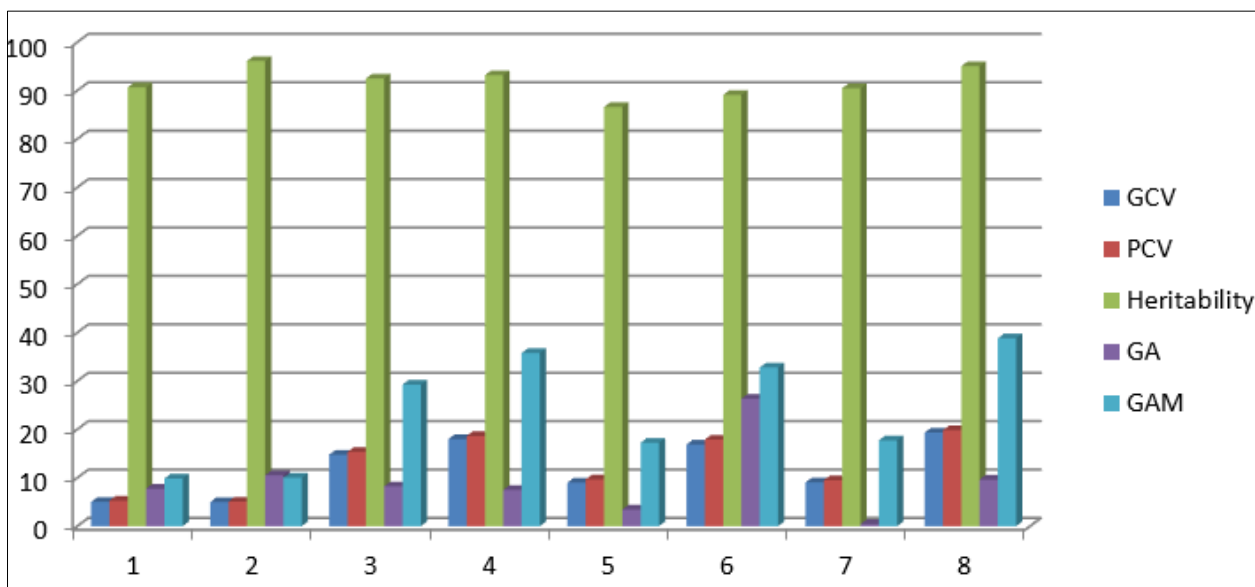| NPTP | 20.93 | 15.23 | 1.04 | 14.19 | 17.99 | 18.63 | 93.17 | 7.49 | 35.77 | 0.67 | 0.39 |
PL (cm)	19.98	3.73	0.5	3.23	8.99	9.66	86.6	3.447	17.24	0.46	0.49
NFGPP	80.34	206.07	22.5	183.57	16.86	17.86	89.08	26.34	32.78	-0.32	0.31
100SW(gm)	2.41	0.05	0.005	0.04	9.04	9.5	90.48	0.42	17.72	-0.32	-0.38
SPY (gm)	24.78	24.16	1.2	22.96	19.33	19.82	95.03	9.62	38.822	-0.42	0.37

Fig 1: Genetic variablity parameters of Anna(R) 4 × IR 64 *Pup1* F₃ progenies in rice

Table 2: Estimates of genetic variability parameters for eight quantitative characters in F₃ generation of Anna(R) 4 × Samba Mahsuri *Pup1* in rice

| Character	Mean	σ2p	σ2e	σ2g	GCV(%)	PCV(%)	h²%	GA	GAM(%)	Skewness	Kurtosis
DFF (days)	81.59	84.94	1.60	83.34	11.17	11.28	98.11	18.62	22.80	1.12	0.07
PH (cm)	101.40	25.93	1.10	24.83	4.916	5.024	95.75	10.04	9.910	0.49	0.97
NTPP	26.89	13.13	1.40	11.73	12.76	13.50	89.33	6.669	24.85	0.10	-0.27
NPTP	20.61	9.682	1.04	8.642	14.30	15.14	89.25	5.721	27.84	-0.25	-0.05
PL (cm)	17.93	5.55	0.50	5.05	12.57	13.18	91.00	4.420	24.71	0.45	0.34
NFGPP	84.55	99.39	22.50	76.89	10.39	11.82	77.36	15.88	18.83	-0.04	0.25
100SW(gm)	1.885	0.08	0.01	0.079	15.01	15.47	94.08	0.563	29.99	0.73	0.72
SPY (gm)	21.54	37.68	1.20	36.48	27.80	28.26	96.81	12.24	56.36	0.69	0.20
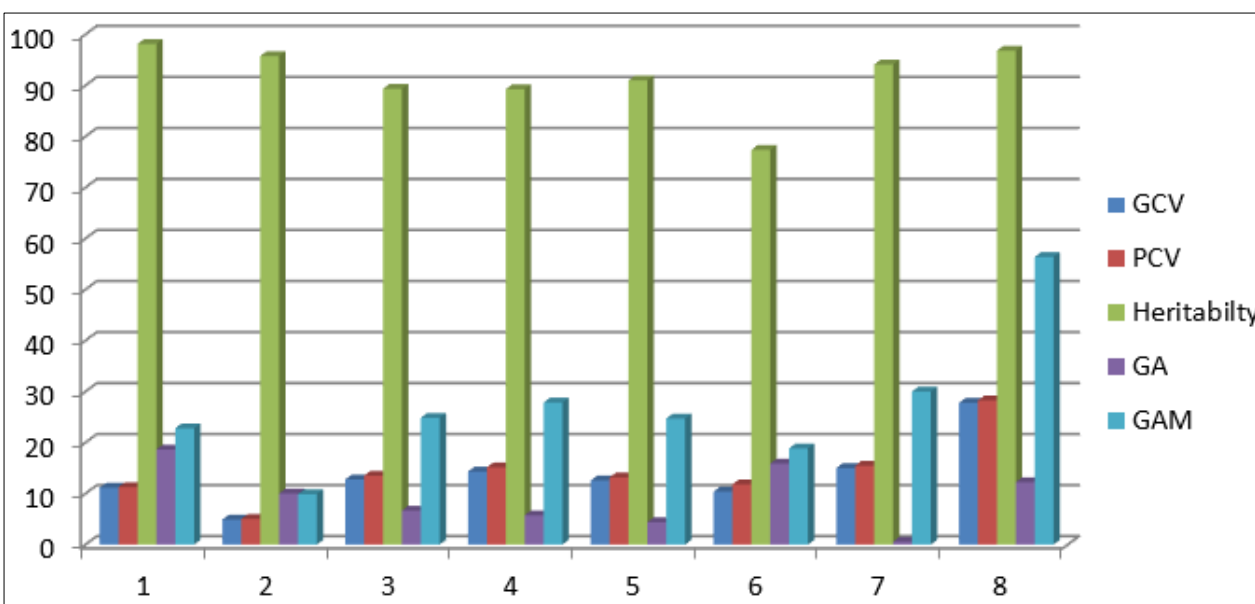
Fig 2: Genetic variability parameters of Anna(R) 4 × Samba Mahsuri *Pup1* F₃ progenies in rice.

Fig 3: Field View of F$_3$ population of two crosses. Rabi, 2019

Conclusion

There is a wide scope for yield improvement by adopting suitable breeding methods and selection procedure, since high PCV and GCV prevailed for grain yield in both the crosses studied. The present study revealed that characters having high GCV, PCV, heritability, coupled with high genetic advance as percent of mean that indicating presence of additive gene effects in its inheritance and such character could be improved by selection. Whereas low heritability and low genetic advance also indicates greater role of non additive gene action in their inheritance suggesting heterosis breeding could be useful for improving these traits. Considering the results of heritability and genetic advance of the two crosses studied, the traits *viz.*, single plant yield, number of productive tillers per plant, number of tillers per plant had high heritability coupled with high genetic advance, hence simple selection procedure like pedigree selection can be used for the improvement of this trait.

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