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Research Article

Genetic variability, cause and effect analysis for yield components and phosphorous content in rice (*Oryza sativa* L.) genotypes

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Abstract
Thirty rice genotypes were evaluated for ten morphological traits along with phosphorous content in shoot and grains to examine the nature and magnitude of variability, character association and path coefficient. Among all traits, single plant yield exhibited the highest estimate of PCV and GCV followed by shoot phosphorous content, number of productive tillers per plant, number of tillers per plant, number of filled grains per panicle and hundred grain weight indicated that choice of these traits would be valuable. High heritability jointly with high genetic advance as percent of mean were observed for hundred grain weight, days to 50 per cent flowering, number of filled grains per panicle, plant height, single plant yield, shoot phosphorous content, number of productive tillers per plant, number of tillers per plant and grain phosphorous content indicated that these characters were governed by additive gene action. Hence genetic improvement through selection for these traits may be more helpful. Shoot P content showed negative non-significant association and grain P content had non-significant positive connection with grain yield. Reduced shoot P content is related to increased P use efficiency for grain production. Hence these traits may be useful for developing genotypes tolerant to phosphorous deficiency. Path coefficient analysis revealed that the highest direct effect on grain yield per plant was exerted by number of productive tillers per plant followed by plant height, grain P content, days to 50% flowering, hundred grain weight and shoot P content showing its more accountability for higher grain yield.

Key words
Rice, variability, character association, path coefficient analysis and phosphorous content

Introduction

Rice is life. Rice is considered as the most important human nourishment crop in the world for direct feeding a larger number of population. It contributes about 42 and 45 per cent of the total food grain and total cereal production of our country. Although the present trend of rice production is on par with the country's requirement, it has been estimated that India's rice production and productivity needs to be enhanced significantly to feed the ever-growing population. The biotic and abiotic stresses are major factors affecting the rice production and productivity. Among the abiotic stresses, drought, salinity and nutrient deficiency are the most important. Among the nutrients, phosphorous (P) is one of the important nutrients required for growth and development of rice plant, but uptake from soil can be difficult and an important factor in achieving optimal yields in agriculture (Smit *et al.,* 2009). Phosphorus deficiency has been identified as one of the major problematic factor in rice production because it forms complexes with Fe^{3+} and Al^{3+} ions and becomes unavailable to the plants (Bieleski, 1973; Holford and Mattingly, 1976; Shen *et al.*, 2011). Phosphorous deficiency causes rice plants to become stunted, reduced yield and delayed flowering and maturity. Addition of phosphate fertilizers may solve this problems but increasing of fertilizer cost will be a serious problems for poor farmers. Improving P efficiency of crops would be an important contribution to sustainability of agroecosystems (Richardson *et al.,* 2011). To solve this crisis, development of phosphorous efficient genotypes which can thrive well in low P soil is one of the solutions for profitable rice farming. Hence it is necessary to study the variability present in the available genotypes for yield attributes and phosphorous related traits. With this view, this investigation was chiefly aimed at assessing the variability, correlation and path analysis for yield components and phosphorus content in rice genotypes for identifying high yielding along with phosphorous efficient genotypes for future breeding programme.

Materials and Methods

The experiment was conducted with 30 genotypes with different maturity duration (early, medium and long) including two phosphorous deficient tolerant lines (IR 64 *Pup* 1 and Samba Mahsuri *Pup* 1) at Agricultural College and Research Institute, Madurai during 2017. Experiment was laid out in randomized block design (RBD) with two replications and the genotypes were raised in three rows of 3 m length at spacing of 25x15 cm with recommended agronomic practices. Mean performance of 30 rice genotypes for 10 quantitative traits were presented in Table 1.

The following quantitative characters were observed *viz.*, days to 50 per cent flowering (DFF), plant height (PH), number of tillers per plant (NT), number of productive tillers per plant (PT), panicle length (PL), number of filled grains per panicle (NFG), hundred grain weight (HGW), shoot P content (SP), grain P content (GP) and single plant yield (SPY). Phosphorous content in shoot and grain samples was estimated separately using the Vanado-molybdate method using spectrophotometer analysis (Piper, 1966). Data on morphological traits were recorded on randomly selected five plants of each genotype for each replication for the selected traits.

The collected morphological data were subjected to statistical analysis using GENRES software package. Analysis of variance was estimated following methods of Panse and Sukhatme (1957). Phenotypic and genotypic coefficients of variation were estimated as per Burton (1952), heritability as described by Lush (1940), the genetic advance as per cent of mean was estimated using the formula suggested by Johnson *et al*. (1955). The correlation coefficient was worked out using the formulae suggested by Falconer (1964) and path analysis by Dewey and Lu (1959).

Results and Discussion

Analysis of variance indicated the presence of highly significant variation for all the ten characters studied. This suggested that there is an inherent genetic difference among the genotypes (Table 2). Similar discovery for various traits were reported by Ratnakar *et al.* (2017). The estimates of phenotypic variance (Vp), genotypic variance (Vg), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2b), genetic advance (GA) and genetic advance as per cent of mean (GAM) for different characters are presented in Table 3. The highest phenotypic variance (1006.60) and genotypic variance (959.41) was found for number of filled grains per panicle and the lowest magnitude was observed for shoot phosphorous content (0.002). Comparatively higher PCV was observed than GCV for all the characters which indicates the influence of the environment to some degrees in the phenotypic expression of the characters. Similar conclusions were earlier reported by (Saha *et al.*, 2019). Highest PCV and GCV were observed for single plant yield (33.53% and 32.17%) followed by shoot phosphorous content (32.33% and 29.16%), number of productive tillers per plant (31.21% and 24.81%), number of tillers per plant (28.40% and 22.88%), number of filled grains per panicle (24.24% and 23.67%) and hundred grain weight (21.98% and 21.93%) (Table 3 and Fig. 1). Saha *et al.* (2019) also observed the higher magnitude of PCV and GCV for number of filled grains per panicle. Selection of these traits would be effective for yield improvement. Moderate PCV and GCV were recorded for plant height (18.76% and 18.30%) followed by grain phosphorous content (18.49% and 15.45%) and days to fifty per cent flowering (11.88% and 11.83%). These results are in conformity with the findings of Kishore *et al.*, (2015) for days to fifty per cent flowering.

Broad sense heritability ranged from 63.17% (number of productive tillers per plant) to 99.54% (hundred grain weight) (Table 3 and Fig. 2). High estimates of heritability were observed for all the traits and these characters are less influenced by the environment and helps in effective selection of superior genotype based on the phenotypic performance. Similar results for hundred seed weight and number of productive tillers per plant were earlier recorded by Sumanth *et al.*, (2017). Genetic advance was found to be the highest for number of filled grains per panicle (62.29) followed by plant height (39.34) and days to 50 per cent flowering (22.16) and the lowest for shoot phosphorous content (0.07) among the traits. These traits are in comparable with Kishore *et al.*, (2015) who observed higher genetic advance for number of filled grains per panicle and days to 50 per cent flowering. The genetic advance as percentage of mean was the highest for the single plant yield (63.57) and the lowest for panicle length (17.27).

High heritability together with high genetic advance as percentage of mean was observed for the traits *viz.*, hundred grain weight, days to 50 per cent flowering, number of filled grains per panicle, plant height, single plant yield, shoot phosphorous content, number of productive tillers per plant, number of tillers per plant and grain phosphorous content indicated that the characters were generally governed by additive gene action. Hence genetic improvement through selection for these traits may be more valuable. Shet *et al.*, (2018) also reported high heritability accompanied with high genetic advance as per cent of mean for grain phosphorus content, shoot phosphorous content, plant height, days to 50 per cent flowering and grain yield per plant.

Relationship among yield and its contributing traits were studied in the route of correlation analysis and it helps the plant breeders to focus on yield improvement in the desired direction. Genotypic correlation coefficient of 30 rice genotypes is presented in Table 4. Among the ten morphological traits, days to 50 per cent flowering (r = 0.469), plant height (r = 0.426), number of tillers per plant (r = 0.545), number of productive tillers per plant (r = 0.568), panicle length (r = 0.417) and number of filled grains per panicle (r = 0.462) were positively and significantly linked with single plant yield. Hence, it might be inferred that these traits could be measured as most important yield contributing traits in rice. This is in agreement with the findings of Singh *et al.*, (2014) for days to 50 per cent flowering and total number of tillers per plant. Phosphorous content in shoot and grain did not show significant direct association with grain yield per plant. Shoot P content showed negative non significant (r = -0.308) relationship and grain phosphorous content found non-significant positive connection with grain yield (r = 0.075). Similar conclusion was also reported by Shet *et al.* (2018) for leaf P content and grain P content. Rose *et al.* (2010) also suggested that there was no significant association between grain yield and P concentrations in stem and leaf. Negative correlation between P concentration and and accumulation in straw and grain yield was reported by Wang *et al*. (2017). A low straw P concentration related with enhanced P translocation from straw to grain allowed concurrent improvement of PUEg (phosphorous use efficiency for grain production) and grain yield by reducing application of P fertilizer.

In terms of inter correlation, days to 50% per cent flowering had positive significant correlation with panicle length and number of filled grains per panicle and plant height had significant positive association with panicle length. The same result is in conformity with Patil and Sahu (2009). Number of tillers per plant had positive significant relationship with number of productive tillers per plant and panicle length was positively associated with number of filled grains per panicle. Shoot P content showed negative significant association with grain P content. Wang *et al.* (2017) reported that there was no correlation between the P concentrations in grain and straw.

Path coefficient analysis was undertaken to study the direct and indirect effects of the different traits on yield. The direct and indirect effects of ten characters on grain yield are presented in Table 5. Path analysis revealed that number of productive tillers per plant (1.032) had the highest positive direct effect on grain yield per plant followed by plant height (0.582), grain P content (0.531), days to 50% flowering (0.466), hundred grain weight (0.312) and shoot P content (0.204) had moderate direct effect. Hence, direct selection for these traits would be rewarding for yield improvement, which will also reduce the undesirable effect of the component traits studied. High positive direct effect of plant height and days to 50% flowering on grain yield were also reported earlier by Singh *et al*. (2019). Regarding the indirect effect of component traits on grain yield, number of productive tillers per plant had high indirect effect through number of tillers per plant (0.972). The plant height had high indirect effect through panicle length (0.341).

On the basis of above findings, it can be concluded that the characters, days to 50 per cent flowering, plant height, number of tillers per plant, number of productive tillers per plant, panicle length and number of filled grains per panicle were positively and significantly linked with single plant yield indicating the useful of these traits for improving upon grain yield in rice. Path coefficient analysis revealed that the highest direct effect on grain yield per plant was exerted by number of productive tillers per plant followed by plant height, grain P content, days to 50% flowering, hundred grain weight and shoot P content showing its more accountability for higher grain yield. Grain P concentration is relatively stable and conserved in comparison with straw P concentration. A low straw P concentration is related to improved phosphorous use efficiency and grain yield because translocation of P from straw to grain is achieved. Therefore, it may be possible to improve phosphorous deficiency tolerance along with yield by selecting the genotypes based on the above characters.

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Table 1. Mean performance of 30 rice genotypes for 10 quantitative traits

S.No	Genotypes	DFF	PH	NT	NPT	PL	NFG	HGW	SP	GP	SPY
1	ADT 37	84.00**	95.17*	12.67	7.67	20.19	123.50	2.04	**0.254****	0.309	13.19
2	ADT 39	90.00	95.50*	11.50	10.67	23.25	135.34	1.84	0.082	0.381	15.62
3	ADT 43	82.50**	93.50**	**23.67****	**20.17****	22.62	115.33	1.75	0.105	0.330	22.99
4	ADT 47	89.50	137.58	14.34	13.00	25.99	170.00**	2.00	0.125	0.374	32.84**
5	ADT (R) 48	**69.50****	84.80**	13.17	10.50	20.64	76.50	2.02	0.177	0.363	14.92
6	ADT 49	89.00*	99.50	16.17	13.34	22.02	165.84**	1.25	0.155	0.351	13.84
7	Anna (R) 4	87.50**	100.63	17.34	12.84	27.03*	128.17	2.54**	0.131	0.331	15.19
8	APO	90.00	119.17	15.34	9.50	26.22	150.83**	2.30**	0.082	0.326	19.65
9	ASD 16	86.00**	96.62*	20.50*	15.84	22.09	129.33	2.42**	0.098	**0.392***	26.83**
10	CO 43	106.00	106.30	16.67	11.83	24.44	**190.50****	1.89	0.134	0.266	22.28
11	CO 51	87.00**	100.87	15.34	12.84	22.27	135.33	2.34**	0.104	0.343	23.25
12	CO 52	96.50	108.84	21.33*	17.67*	27.00*	164.67**	1.53	0.100	0.359	23.20
13	CR 1009 *Sub* 1	**127.50**	121.17	23.50**	18.84**	26.10	149.17*	2.17	0.102	0.289	**38.15****
14	Improved Pusa Basmati 1	91.00	106.30	12.50	10.67	**28.75****	126.50	2.35**	0.102	0.307	17.65
15	Improved samba mahsuri	102.50	101.99	13.34	11.17	23.37	156.50**	1.40	0.169	0.316	18.82
16	IR 20	99.50	105.25	12.50	9.67	28.37**	120.67	1.84	0.152	0.379	18.78
17	IR 36	89.00*	99.85	12.00	10.00	22.93	122.17	2.15	0.123	0.381	15.53
18	IR 50	91.00	86.83**	15.17	11.34	20.54	91.67	2.04	0.208**	0.271	10.22
19	PMK (R) 3	79.50**	118.00	16.67	13.67	22.00	147.00*	**2.92****	0.157	0.362	21.60
20	IR 64	88.50*	96.89*	16.50	13.50	24.70	112.67	2.54**	0.195*	0.255	15.55
21	MDU 5	82.50**	83.33**	19.00	17.00	**19.29**	**59.67**	2.15	0.196*	**0.163**	15.14
22	MDU 6	86.50**	103.00	18.67	17.34*	24.10	114.17	2.42**	0.145	0.177	25.80**
23	PMK 1	92.00	153.45	13.50	11.67	27.17*	153.50**	2.75**	0.150	0.373	28.97**
24	PMK 2	86.00**	**157.10**	8.17	6.67	24.57	118.84	2.85**	0.174	0.345	23.94*
25	RMD (R) 1	75.50**	98.87	9.67	8.17	21.48	70.33	2.55**	**0.054**	0.350	**9.59**
26	TKM (R) 12	94.00	150.50	**8.00**	**5.83**	25.95	115.67	1.95	0.178	0.308	11.05
27	TKM 13	93.00	110.17	15.50	12.67	22.69	181.67**	1.35	0.173	0.330	19.28
28	UPLRI 5	105.50	106.52	15.84	11.50	26.87	138.00	2.49**	0.154	0.309	23.75*
29	IR 64 *Pup* 1	94.00	94.14**	16.17	13.00	25.07	103.67	2.67**	0.198*	0.341	21.09
30	Samba Mahsuri *Pup* 1	106.50	**78.00****	11.67	10.17	21.02	158.50**	**1.22**	0.159	0.366	17.65
	Mean	91.38	106.99	15.21	12.28	23.95	130.85	2.12	0.144	0.325	19.87
	SE	1.98	3.62	0.72	0.63	0.47	5.72	0.09	0.008	0.010	1.19
	SEd	1.07	4.43	2.55	2.32	1.46	6.86	0.03	0.020	0.033	1.88
	CD (0.05)	2.19	9.07	5.23	4.76	2.99	14.04	0.06	0.041	0.067	3.85
	CD (0.01)	2.96	12.22	7.05	6.41	4.03	18.93	0.08	0.055	0.091	5.19
	Minimum	69.50	78.00	8.00	5.83	19.29	59.67	1.22	0.054	0.163	9.59
	Maximum	127.50	157.10	23.67	20.17	28.75	190.50	2.92	0.254	0.392	38.15
	Range	58.00	79.10	15.67	14.34	9.47	130.84	1.71	0.200	0.230	28.57

DFF – Days to 50 per cent flowering (days); PH – Plant height (cm); NT – Number of tillers per plant; NPT – Number of productive tillers per plant; PL – Panicle length (cm); NFG – Number of filled grains per panicle; HGW – Hundred grain weight (g); SP – Shoot P content (mg/g shoot weight); GP - Grain P content (mg/g grain weight); SPY – Single plant yield (g)

Table 2. Analysis of variance for 10 quantitative characters in rice

Characters	Mean sum of squares		
	Replications (df=1)	**Treatments (df=29)**	**Error (df=29)**
Days to 50% flowering	2.02	234.92**	1.15
Plant height (cm)	2.30	786.63**	19.67
Number of tillers per plant	19.21	30.77**	6.55
Number of productive tillers per plant	12.46	24.01**	5.42
Panicle length (cm)	0.11	13.30**	2.14
Number of filled grains per panicle	0.96	1966.01**	47.19
Hundred grain weight (g)	0.005	0.43**	0.001
Shoot P content (mg/g)	0.016	0.004**	0.004
Grain P content (mg/g)	0.001	0.006**	0.001
Single plant yield (g)	9.82	85.34**	3.55

*Significant at 5% level **Significant at 1% level

Table 3. Genetic parameters for 10 quantitative traits of 30 genotypes in rice

Characters	Vp	Vg	PCV%	GCV%	h^2%	GA	GAM
Days to 50 per cent flowering	118.03	116.88	11.88	11.83	99.02	22.16	24.25
Plant height (cm)	403.15	383.47	18.76	18.30	95.12	39.34	36.77
Number of tillers per plant	18.66	12.11	28.40	22.88	64.90	5.78	37.97
Number of productive tillers per plant	14.72	9.29	31.21	24.81	**63.17**	4.99	40.62
Panicle length (cm)	7.72	5.58	**11.60**	**9.86**	72.24	4.13	**17.27**
Number of filled grains per panicle	**1006.60**	**959.41**	24.24	23.67	95.31	**62.29**	47.61
Hundred grain weight (g)	0.218	0.219	21.98	21.93	**99.54**	0.96	45.08
Shoot P content (mg/g)	**0.002**	**0.002**	32.33	29.16	81.35	**0.07**	54.19
Grain P content (mg/g)	0.004	0.003	18.49	15.45	69.76	0.09	26.58
Single plant yield (g)	44.44	40.89	**33.54**	**32.17**	92.01	12.64	**63.57**

Vp - Phenotypic variance; Vg -Genotypic variance; PCV - Phenotypic coefficient of variation; GCV - Genotypic coefficient of variation; h^2 – Heritability; GA - Genetic advance; GAM - Genetic advance as per cent of mean

Table 4. Genotypic correlation coefficient among 10 morphological characters in 30 rice genotypes

Characters	DFF	PH	NT	NPT	PL	NFG	HGW	SP	GP	SPY
DFF	1	0.143	0.246	0.172	0.476**	0.537**	-0.290	-0.063	-0.096	0.469**
PH		1	-0.340	-0.331	0.586**	0.316	0.336	-0.098	0.194	0.426*
NT			1	0.942**	-0.033	0.153	-0.066	-0.236	-0.375*	0.545**
NPT				1	-0.089	0.096	-0.097	-0.262	-0.388*	0.568**
PL					1	0.368*	0.229	-0.391*	0.210	0.417*
NFG						1	-0.391*	-0.206	0.342	0.462*
HGW							1	-0.043	-0.089	0.195
SP								1	-0.421*	-0.308
GP									1	0.075

*Significant at 5% level, **Significant at 1% level

Table 5. Path analysis direct (diagonal) and indirect effects of ten characters on grain yield in rice

	DFF	PH	NT	NPT	PL	NFG	HGW	SP	GP	Correlation coefficient
DFF	**0.4660**	0.0831	-0.0190	0.1772	-0.0726	-0.0113	-0.0904	-0.0128	-0.0508	0.469**
PH	0.0664	**0.5829**	0.0263	-0.3418	-0.0894	-0.0066	0.1048	-0.0200	0.1030	0.426*
NT	0.1145	-0.1983	**-0.0772**	0.9727	0.0050	-0.0032	-0.0206	-0.0480	-0.1994	0.545**
NPT	0.0800	-0.1930	-0.0728	**1.0325**	0.0135	-0.0020	-0.0303	-0.0534	-0.2066	0.568**
PL	0.2218	0.3415	0.0025	-0.0916	**-0.1526**	-0.0077	0.0714	-0.0798	0.1115	0.417*
NFG	0.2501	0.1842	-0.0118	0.0986	-0.0561	**-0.0211**	-0.1221	-0.0420	0.1820	0.462*
HGW	-0.1350	0.1957	0.0051	-0.1003	-0.0349	0.0082	**0.3122**	-0.0088	-0.0470	0.195
SP	-0.0292	-0.0573	0.0182	-0.2701	0.0597	0.0043	-0.0134	**0.2041**	-0.2238	-0.308
GP	-0.0445	0.1129	0.0289	-0.4011	-0.0320	-0.0072	-0.0276	-0.0858	**0.5318**	0.075

Residual effect = 0.15 ****Significant at 1% level** ***Significant at 5% level**

Fig.1. Phenotypic and genotypic coefficients of variation for ten characters of 30 genotypes in rice

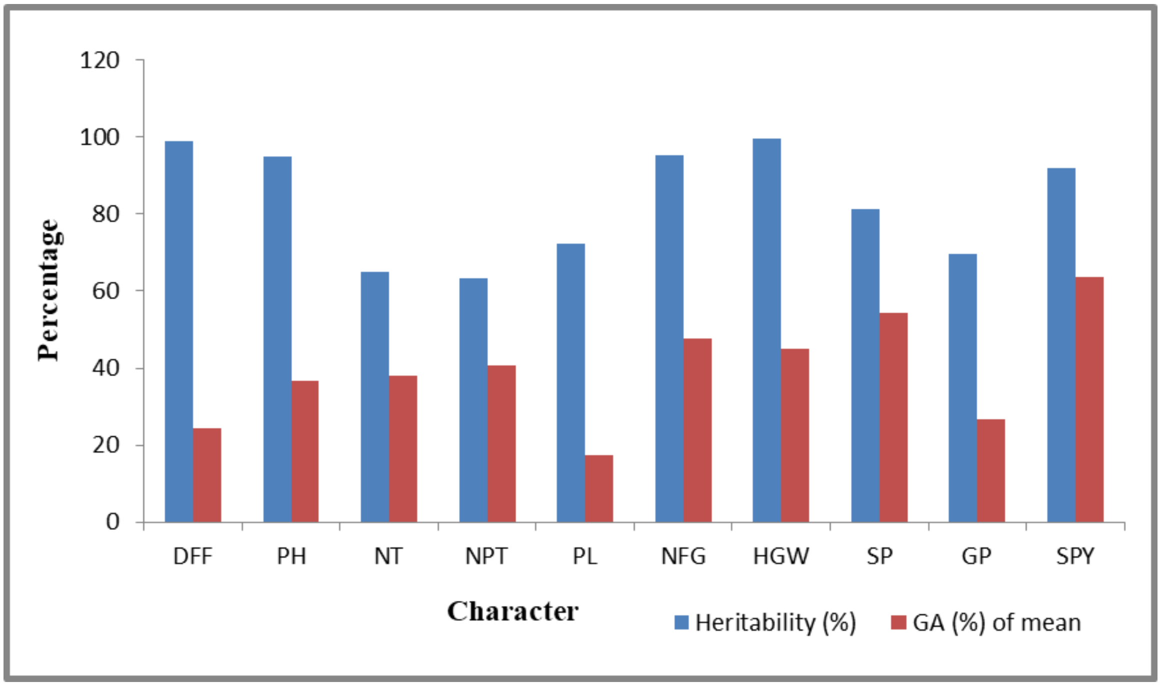

Fig.2. Heritability and genetic advance as per cent of mean for ten characters of 30 genotypes in rice