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Variability and association parameters unriddle the genetic architecture of yield and yield attributes in rice [*Oryza sativa* (L.)] genotypes

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Abstract
The experiment was conducted to assess the variation prevailing in forty rice genotypes and also to study the relationship between the yield and its contributing traits. Nine traits including days to fifty percent flowering, plant height, tiller count and panicle number plant^{-1}, panicle length, grains per panicle, spikelet fertility, 1000 grain weight and grain yield per plant were observed. High PCV and GCV was noticed in plant height, tiller count/plant, number of panicles/plant, number of grains/panicle, spikelet fertility and thousand grain weight. The difference between PCV and GCV was low, indicating that the genotype contributes more to the expression of the trait. All the traits exhibited high GAM and moderate to high heritability, indicating that the yield components under study are the culmination of additive gene action. This will aid in an effective selection process. Correlation studies showed that days to 50% flowering had a significant positive relationship with grain yield/plant. Path analysis, while computing the direct and indirect effect revealed that days to 50% flowering and 1000 grain weight had positive direct effect towards grain yield per plant. Thus, these traits can be used in indirect selection for grain yield per plant.

Keywords: PCV, GCV, heritability, GAM, correlation, path analysis

Introduction

Rice (*Oryza sativa* L. 2n:2x:24) is the seed of the grass species *Oryza sativa* or *Oryza glaberrima*. The genus *Oryza* belongs to the tribe *Oryza* in the family Poaceae. As a cereal grain, it is the most widely consumed staple food for a large parts of the world's human population, especially in Asia (Fitzgerald *et al*., 2009) [8]. Rice is the oldest domesticated crop in the world. In China, preserved rice was found and it belongs to B.C 3000. It is the third agricultural commodity with highest worldwide production, after sugarcane and maize. South East Asia is the primary centre of origin of the cultivated rice. An enormous amount of rice germplasms is found in India. Rice cultivation covers 9% of total earth's arable land. In India, 43.8 Mha of paddy is under cultivation, yielding about 165.8 Mt of straw and 118.43 Mt of grain (Kaur *et al*., 2022) [12]. Rice is the major source of nutrition with 80% carbohydrates, 7-8% protein, 3% fat and 3% fiber (Juliano *et al*., 1986) [11]. Brown rice constitutes 71.1% of carbohydrates and 7.3% protein which can contribute to replace white rice by brown rice and has with a lower risk of diabetes (Sun *et al*., 2010) [27].

Greater the genetic diversity in the germplasm, the more would be the breeding potential and scope for improvement. The development of one or more varieties depends on the final selection of superior plants by the plant breeder, who uses several techniques to create the genetic variation and to select from that variation. Estimation of co-efficient of variation help to assess the variability in a population. Heritable variation can be effectively used with greater degree of accuracy when it is studied in conjunction with genetic advance. In any selection programme, it may not be always possible to select on the basis of yield above for evolving superior yielding genotypes because yield is a complex character and it is collectively influenced by many component characters. The interrelationships between yield and yield contributing characters are estimated by correlation co-efficient analysis. Such association studies provide information on nature of extent and direction of selection. Further the partitioning of correlation co-efficient into direct and indirect effects of the yield components on yield, will also throw more light on selection programme. Hence the current investigation was carried out to study the variability among 40 different rice genotypes which helps in the selection and improvement of the drop to further generations.

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Materials and Methods

Experimental Design: The present study was executed during Kharif 2018 at Plant Breeding Farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University. Forty different rice genotypes were used in the study as listed in table 1.

Table 1: List of different genotypes with origin

S. No	Genotypes	Origin
1	NDRK 11-21	Narendra Dev University of Agriculture and Technology, Kumarganj, Faizabad, Uttar Pradesh
2	NDRK 11-22	
3	NDRK 11-24	
4	CR2860-S-B-189-1-1-1	Central Rice Research Institute, Cuttack
5	CR3882-7-1-6-2-2-1	
6	CR3879-3-1-6-1-3-1	
7	CR 2839-1-S-10-B2-B-43-2B	
8	CR3884-244-8-5-11-1-4	
9	CR3884-244-8-5-6-1-1	
10	CR2838-1-S-2B-9-1	
11	CR3903-161-1-3-2	
12	CR3899-134-2-6-4	
13	CR3881-4-1-6-3-4-1	
14	CR3909-192-1-7-1	
15	TR 09027	International Rice Research Institute, Manila, Philippines
16	TR13069	
17	TR 09030	
18	PAU 3835-12-1-1-1	Punjab Agricultural University, Punjab
19	PAU 71114-3480-1-1-1-0	
20	PAU 3835-36-6-3-3-4	
21	CSR 7-1	Central Soil Salinity Research Institute, Karnal, Haryana
22	CSR-2748-4441-22	
23	CSR-2748-4441-111	
24	CSRC(S)47-7-B-B-1-1	
25	CSR-2748-4441-104	
26	CSR-2748-4441-193	
27	CSR2711-171	
28	CSR-2748-4441-133	
29	CSR-2748-197	
30	PUSA 44	Indian Agricultural Research Institute, Pusa, New Delhi
31	KS-12	National Agricultural Research Centre, Islamabad
32	KR 15003	Directorate of Rice Development, Patna
33	KR15006	
34	KR 15014	
35	KR 15005	
36	RAU 1396-14	Rajendra Agricultural University, Patna
37	JK-95	Jawaharlal Nehru Krishi Vishwavidyalaya, Jabalpur
38	CSAR 1610	Chandra Sekar Azad University, Kanpur
39	RP-320-4-3-2-1	Directorate of Rice Research Hyderabad
40	RP-5683-101-30-2-3-1	

Nursery was raised using seeds of all forty genotypes during May to June 2018 in beds. One seedling per hill was transplanted after twenty-five days in main field in 3m long rows, at a distance of 20 cm between rows and 15 cm within rows. The suggested agronomic techniques and plant protection measures were implemented.

Observations recorded: Yield attributes such as Days to 50% flowering, plant height, tiller count and panicle numbers per plant, panicle length, grains per panicle, spikelet fertility, 1000 grain weight and grain yield per plant were noted in five randomly selected plants representing each genotype and the mean values were computed.

Biometrical analysis: Experimental design used was Randomized Block Design with three replications. Every trait was analyzed using ANOVA (Analysis of Variance) as put forward by Panse and Sukhatme (1967) [20]. ANOVA splits the variation into the variation caused by genotypes, replication and also environment. Unit analyses such as range, average, variance and standard error was calculated. Variability parameters such as Phenotypic and Genotypic Co-efficient of Variation was worked out and categorized as suggested by Burton (1952) [4] and Sivasubramanian and Madhavamenon (1973) [26] respectively. Heritability in broad sense was calculated as said by Lush (1940) [15]. Genetic advance as percent of mean was assessed as given by Johnson *et al*. (1955a) [9]. Both were classified following the suggestion of Johnson *et al*. (1955a) [9]. Heritability together with GAM is helpful for predicting genetic gain under selection. The formula used in variability analysis are listed in Table 2. The examination of correlation and path coefficients involved applying the methodologies advocated by Johnson *et al*. (1955b) [10] and Dewey and Lu (1959) [6] respectively. Analysis was carried out using the software INDOSTAT version 8.1.

Table 2: List of formulae used for variability parameter analysis

Parameters	Formula	References
Average	Sum of all observations /Number of observations	
Genotypic variation	(GMS- EMS) / r	Johnson *et al*., (1955a) [9]
Environmental variation	EMS	
Phenotypic variation	Genotypic variation + Environmental variation	
PCV	(Phenotypic variation/ Mean) *100	Burton (1952) [4]
GCV	(Genotypic variation/ Mean) *100	
Heritability	(Genotypic variation /Phenotypic variation) *100	Lush (1940) [15]
Genetic Advance	(Genotypic variance/ Phenotypic Standard deviation) *K	Johnson *et al*., (1955a) [9]
GAM	(Genetic Advance/ Mean) *100	

GMS = Genotypic mean square; EMS = Error mean square; These two values from ANOVA table; r = replications; K = Selection differential, 2.06 at 5% selection intensity; GAM- Genetic Advance as % of Mean

Results and Discussion

The results of analysis of variance are presented in Table 3. Significant variations among the genotypes were observed in all yield attributes examined.

Table 3: Analysis of variance for 9 traits in forty rice genotypes

Source	df	Mean Sum of Squares								
		DFF	PH	TC/P	NP/P	PL	NG/Pa	SF	TGW	GY/P
Rep	2	94.52	6.56	9.13	4.9	3.56	30.80	19.49	9.96	2.18
Gen	39	1003.55**	1416.07**	49.21**	36.18**	29.31**	3483.77**	780.40**	84.17**	72.40**
Error	78	89.84	5.66	5.20	3.28	2.56	16.33	8.52	30.16	1.20

Rep- Replication; Gen - Genotype **Significant at 1% level; *Significant at 5% level

Traits- DFF- Days to 50% flowering; PH- Plant Height; TC/P- Tiller count per plant; NP/P- Number of Panicles per plant; PL- Panicle Length; NG/Pa- Number of Grains per panicle; SF- Spikelet Fertility; GY/P= Grain Yield per plant
Unit analyses such as mean, range, maximum and minimum values for each trait was computed and showcased in table 4. Genetic variation analysis using first and second order statistics would aid in identifying the best performing progenies, avoiding the impact of the environment (Shanmuganathan, 2010) [22].

Table 4: Mean, Range and Variability parameters for 9 yield attributes in forty rice genotypes

Traits	General Mean	Max	Min	CV (%)		h²(bs) %	GAM (%)
				Phenotypic	Genotypic		
DFF	100.30	130.64	64.66	19.80	17.40	77	31.49
PH (cm)	97.61	151.68	66.00	22.35	22.21	98	45.48
TC/P	17.76	25.33	11.00	25.09	21.56	73	38.15
NP/P	13.20	18.66	7.33	28.60	25.09	76	45.33
PL (cm)	25.61	120.40	34.30	12.44	12.09	94	24.19
NG/Pa	115.37	184.00	61.33	29.67	29.47	98	60.27
SF (%)	70.06	94.50	19.53	23.27	22.89	96	46.39
TGW (g)	20.72	40.15	9.45	33.41	20.47	37	25.78
GY/P (g)	28.26	39.00	17.54	17.67	17.24	95	34.64

Max – Maximum; Min- Minimum; h² (bs)- Heritability in broad sense; GAM- Genetic Advance as percent of mean

Traits- DFF- Days to 50% flowering; PH- Plant Height; TC/P- Tiller count per plant; NP/P- Number of Panicles per plant; PL- Panicle Length; NG/Pa- Number of Grains per panicle; SF- Spikelet Fertility; GY/P= Grain Yield per plant
The variability parameters are given in Table 4. As classified by Sivasubramanian and Madhavamenon (1973) [26], high PCV and GCV was remarked in the traits such as plant height, tiller count/plant, number of panicles/plant, number of grains/panicle, spikelet fertility and 1000 grain weight. Similar results were divulged by Shinde *et al*., (2022) [24] for plant height, Akshay *et al*., (2022) [1], Aravind *et al*., (2022) [2], Devi *et al*., (2020) [5] and Venkanna *et al*., (2022) [28] for number of grains/panicle, Parimala *et al*., (2020) [21], Venkanna *et al*., (2022) [28] and Murali *et al*., (2023) [17] for 1000 grain weight. Moderate PCV and GCV was noticed in days to 50% flowering, panicle length, grain yield/plant. These results were in consonance with the outcome of Devi *et al*., (2020) [5] for plant height; Nithya *et al*., (2020) [19] for tiller number; Faysal *et al*., (2022) [7] for grain yield per plant;

Singh *et al*., (2020) [25] for panicle length. Traits with high PCV and GCV showed the prevalence of more diversity (Sharma *et al*., 2021) [23]. Minimum difference between PCV and GCV states that the influence of environment on the expression of genes responsible for these traits is low. Heritability estimates the extent of transmission of traits from preceding to succeeding generation. High heritability was executed by all the traits studied except 1000 grain weight, which exhibited moderate heritability. This was similar to the results of Bhargavi *et al*., (2021) [3]. High GAM was manifested by all the yield attributes studied. This was in accordance with Lakshmi *et al*., (2021) [14] for tiller count and grain yield/plant, Akshay *et al*., (2022) [1], Faysal *et al*., (2022) [7] for 1000 grain weight; Murali *et al*., (2023) [17] for days to 50% flowering and plant height; Venkanna *et al*., (2022) [28] for number of grains/panicle, 1000 grain weight and yield. Heritability coupled with genetic advance furnish the extent of genetic gain under selection. Thus, all the traits showed moderate to high heritability paired with high GAM,

which provides light to the fact that the yield attributes studied are the result of additive gene action, which will help in efficient selection process (Monika *et al*., 2021) [16].

Table 5: Genotypic correlation among the nine yield attributes

Traits	DFF	PH	TC/P	NP/P	PL	NG/Pa	SF	TGW	GY/P
DFF	1.00	-0.259	0.008	0.006	-0.096	-0.262	-0.098	0.210	0.403**
PH		1.000	0.232	0.250	0.344**	0.339*	-0.014	-0.007	-0.079
TC/P			1.000	0.928**	0.236	-0.072	-0.029	0.226	0.218
NP/P				1.000	0.224	-0.157	-0.041	0.002	-0.207
PL					1.000	0.125	-0.463**	-0.200	-0.207
NG/Pa						1.000	0.127	-0.206	-0.109
SF							1.000	0.128	0.224
TGW								1.00	0.266
GY/P									1.000

DFF- Days to 50% flowering; PH- Plant Height; TC/P- Tiller count per plant; NP/P- Number of Panicles per plant;
PL- Panicle Length; NG/Pa- Number of Grains per panicle; SF- Spikelet Fertility; GY/P= Grain Yield per plant
**Significant at 1% level *Significant at 5% level G - Genotypic correlation P - Phenotypic correlation

Yield is a polygenic trait, which gets altered by the effect of other traits. Studying the association between the yield and its contributing traits would help in the indirect selection, which will simultaneously help in the improvement of both yield attribute and subsequently, the yield. Genotypic association between the nine yield parameters is given in the table 5. Significant positive correlation of yield was noticed with days to 50% flowering. It was alike with results of Lakshmi *et al*., (2021) [14]. Tillers per plant and spikelet fertility showed positive correlation with yield. These traits can be used for indirect selection of genotypes for yield. Similar results were produced by Kumar *et al*., (2023) [13] for tiller count. Significant positive correlation was noticed between number of tillers and number of panicles per plant, plant height with panicle length and number of grains per panicle. Significant negative correlation was found between panicle length and spikelet fertility. The traits, plant height, number of panicles per plant, panicle length, number of grains per plant showed negative correlation with yield. These results were similar to Aravind *et al*., (2022) [2]; Nath and Kole (2021) [18]. This shows that these traits are to be given less attention while selection for yield.

Table 6: Direct and indirect effects of yield attributing traits on grain yield per plant in rice genotypes

Traits	DFF	PH	TC/P	NP/P	PL	NG/Pa	SF	TGW	GY/P
DFF	0.365	0.024	-0.005	0.005	0.001	-0.044	-0.018	0.070	0.403**
PH	-0.094	-0.093	-0.153	0.230	-0.020	0.057	-0.002	-0.002	-0.079
TC/P	0.002	-0.022	-0.661	0.853	-0.014	-0.012	-0.005	0.076	0.218
NP/P	0.002	-0.023	-0.614	0.920	-0.013	-0.026	-0.007	0.001	-0.207
PL	-0.034	-0.032	-0.156	0.206	-0.057	0.021	-0.086	-0.067	-0.207
NG/Pa	-0.095	-0.032	0.047	-0.144	-0.007	0.168	0.024	-0.069	-0.109
SF	-0.035	0.001	0.0192	-0.038	0.027	0.021	0.186	0.043	0.224
TGW	0.076	0.001	-0.150	0.002	0.012	-0.035	0.024	0.335	0.266

Residual effect = 0.10

DFF- Days to 50% flowering; PH- Plant Height; TC/P- Tiller count per plant; NP/P- Number of Panicles per plant; PL- Panicle Length; NG/Pa- Number of Grains per panicle; SF- Spikelet Fertility; GY/P= Grain Yield per plant
The impact of other traits is divided into direct and indirect effects on one another by path analysis. Effect of yield-related

attributes, both direct and indirect, on grain yield per plant in rice genotypes is tabulated above (Table 6). The traits days to 50% flowering, number of panicles per plant and 1000 grain weight had maximum positive direct effect towards grain yield per plant. Number of grains per panicle and spikelet fertility had low positive direct effect on single plant yield. Likely results were stated by Kumar *et al*., (2023) [13] Plant height and panicle length had negligible direct effect on grain yield/ plant. Number of tillers per plant had high negative direct effect. The traits which have positive direct effect have significant role in increasing the single plant yield. Traits with high negative direct effect should be taken into careful consideration, while selecting for yield. High positive indirect effect of tiller count per plant on yield through number of panicles per plant, plant height on yield through number of panicles per plant, panicle length on yield through number of panicles per plant was also noticed. These traits have positive contribution to increase the yield indirectly by influencing other related yield attributes. High negative indirect effect of number of panicles per plant on yield through number of tillers per plant was noticed. Other yield attributes show negligible indirect effect, which cannot be used in selection. Residual effect (0.10) shows that the 90% of the variation contributing traits have been explored.

Conclusion
Thus, the present investigation was carried out to find out the extent of variation prevailing among the genotypes studied. High PCV and high GCV along with minimum difference between them, revealed the maximum contribution of genotype for phenotype observed. Heritability and GAM showed that the gene action is additive and the selection would be effective. Association between the yield attributes and yield was worked out, which would help in the simultaneous selection of these attributes for yield. The analysis disclosed that the traits days to 50% flowering and 1000 grain weight, would be effective when selecting for yield.

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