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Research Article

Genetic variability and relatedness among yield characters in rice landraces and improved varieties

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Abstract

Sixty-nine cultivars of rice were examined for fourteen biometrical characteristics to study the degree of genetic divergence, heritability and genetic gain as a percentage of mean, character relationship and path coefficient analysis. Yield per plant reported the highest estimate of PCV and GCV followed by the total effective tillers per plant, hundred seed weight, number of filled seeds per panicle and flag leaf length indicating that these traits may be given importance while exercising selection. Plant height, panicle length, total tillers, total effective tillers per plant, flag leaf length, grain length, grain L/B ratio, the number of filled seeds per plant, hundred seed weight and yield per plant exhibited remarkable genetic gain and high heritability, implying a predominance of additive gene action. Hence, genetic advancement through simple selection would be more beneficial. Among the yield traits examined, days to 50% flowering, total tillers per plant, the number of effective tillers per plant, flag leaf breadth, the number of filled seeds per panicle, and hundred-seed weight recorded a positive significant correlation with direct effects on yield per plant asserting that these traits were the most efficient and promising selection criteria.

Keywords: Rice, PCV, GCV, heritability, genetic gain, correlation and direct effects

INTRODUCTION

Rice (*Oryza sativa* L.) is one of the world's most significant food crops and is the mainstay of the population throughout Asia, Africa and Latin America. Over 90% of the world's rice is cultivated and consumed in Asia, so considered the "rice bowl of the world". Since it is the staple food for 60% of the world's population and three quarters of the world's impoverished, rice is at the forefront of the global struggle against hunger and poverty (Dubey *et al.,* 2022). Rice is cultivated on 45.76 million hectares in India, with a total production of 124.36 million metric tonnes and an average yield of 2.71 tonnes per hectare (INDIASTAT 2020-2021). Tamil Nadu holds an area of 2.03 million hectares under rice cultivation with an output of 6.88 million metric tonnes and productivity of 3.38 tonnes per hectare (INDIASTAT 2020-2021). Landraces with novel traits are valuable genetic resources and they harness "adaptability genes" for certain ecological conditions. Incorporating adaptation genes from landraces might assure the region's optimal grain output. Any crop breeding programme has to estimate genetic gain to appraise its strengths and shortcomings and plan future breeding initiatives. It is vital to understand the variability of distinct features to accelerate genetic gain (Kumar *et al.,* 2021).

In order to commence a repeatable breeding programme and ascertain the level of variability in landraces

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it is essential to study the genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance as rice exhibit a wide array of genetic variability (Rahman *et al.,* 2021). The inherited component of variability is calculated using the genotypic coefficient of variation (Burton *et al.,* 1952). Heritability is a trustworthy measure providing information on the transmissibility of qualities from one generation to the subsequent. In the estimation of gain under selection towards the identification of superior genotypes, genetic advance implies its importance by describing the degree of improvement of characteristics under selection pressure. Character association aids in the selection for character improvement by revealing the degree of correlation amongst the quantitative attributes (Roy and Kumaresan, 2019). Since rice grain yield is a challenging phenomenon that is greatly impacted by a multitude of constituents, in order to develop an effective selection strategy, the correlation coefficient test is used to determine the degree of the reciprocal link between various agronomic parameters as well as the emphasizing positive or negative relationship among yield and its constituents (Ahamed *et al.,* 2021). To understand the cause-and-effect relationship, it is crucial to partition the correlation coefficient by employing path analysis. This aids in conceptualizing the relative significance of component traits and explicit the implication of various characters in a single genotype for increasing seed yield.

Considering the aforementioned particulars, this investigation was carried out for the improvement of yield and its components by examining the genetic variability, correlation and path analysis which enables the identification of superior genotypes for effective utilization in future breeding programmes.

MATERIALS AND METHODS

An experiment was carried out in the Breeding experimental farm, Agricultural College and Research Institute, Madurai during Summer, 2022 using rice landraces and genetically superior varieties collected from Agricultural Research Stations in various parts of Tamil Nadu and RARS, Marteru, Andhra Pradesh as given in **Table 1**. The trial was laid out in a Randomized Block Design (RBD) with two replications wherein the 69 genotypes were raised in three rows of 3 m length with a spacing of 20 cm x 15 cm by adhering to the standard package of practices. Five plants selected randomly from each entry were evaluated for fourteen biometrical characteristics, including plant height (cm), the total tillers per plant, the total effective tillers per plant, panicle length (cm), flag leaf length (cm), flag leaf breadth (cm), the number of filled seeds per panicle, grain length (mm), grain breadth (mm), length breadth ratio, hundred-seed weight (g) and yield per plant (g), while days to 50 per cent flowering and days to maturity were recorded on a plot basis. Using the method stated by Burton (1952), the genotypic and phenotypic coefficient of variation (GCV and PCV) were calculated. The multitude of variations was categorized as suggested by Sivasubramanian and Madhavamenon (1973). Broad sense heritability was calculated as per the method suggested by Lush (1940) and by deploying the method developed by Johnson (1955) the genetic advance was evaluated. The recorded biometrical data were subjected to analysis using TNAUSTAT (Manivannan, 2014), a statistical package where ANOVA was computed based on the mean performance of 69 rice cultivars for fourteen biometric characteristics. The correlation coefficient was calculated by leveraging Falconer (1989) recommended equations and the relationship between yield and its component characteristics as well as between characters was estimated by applying the formula provided by Dewey and Lu (1959) for path analysis.

RESULTS AND DISCUSSION

ANOVA revealed the existence of remarkable variation for nine out of fourteen characters studied which suggest that genotypes under study possess different genetic heritage as presented in **Table 2**. The PCV estimates for the characters considered were marginally higher than the comparable GCV estimates, suggesting that the characters were less driven by the environment similar to the finding reported by Bhargavi *et al.* (2021) **(Table 3**). Thus, phenotypic selection might be beneficial in the improvement of traits under consideration. Days to maturity recorded the lowest PCV and GCV illustrating that there was meagre variation in these parameters and the results were in concordance with Aswin *et al.* (2021) and Emi *et al.* (2021). Moderate PCV and GCV were noticed for the plant height and length of the panicle similar to the findings of Bhargava *et al.* (2021) and Prasannakumari *et al.* (2020); grain L/B ratio in corroboration with the results of Roy *et al.* (2021) and Aswin *et al.* (2021) and for grain length reported by Priyanka and Gauraha (2020). Effective tillers per plant, hundred seed weight and yield per plant recorded the highest PCV and GCV, indicating the presence of more variation which is in accordance with Bharath *et al.* (2018) and Htwe *et al.* (2019) for productive tillers per plant. Similar results were reported by Bhargava *et al.* (2021) and Yashwanth *et al.* (2021) for hundred seed weight and yield per plant. High GCV and PCV for flag leaf length and filled seed per panicle as that of the present study was reported by Ahamed *et al.* (2021), Bordoloi *et al.* (2021) for the respective traits. High PCV and moderate GCV were recorded by total tillers per plant which is akin to the findings of Singh *et al.* (2020) and also for grain breadth as that of Jan *et al.* (2020). Moderate PCV and low GCV were recorded for days to 50% flowering and flag leaf breadth similar to the report of Chuchert *et al.* (2018).

Out of fourteen characters studied, twelve characters exhibited high heritability which varied from 99.793

Table 1. List of cultivars used in the study

S. No.	Landraces / Varieties	S. No.	Landraces/Varieties
1	*Norungan*	36	IC 214151
2	*Sivappu Kavuni*	37	IC 377474
3	*Kothamalli Samba*	38	IC 387752
4	*Arubatham Kuruvai*	39	IC 379076
5	*Navarai*	40	IC 300329
6	*Seeraga Samba*	41	VGD 1
7	*Karunguruvai*	42	CO47
8	*Kuliyadichan*	43	CO 50
9	*Chinnar*	44	CO 51
10	*Poongar*	45	CO 52
11	*Mattaikar*	46	CO 54
12	*Sivappu chithiraikar*	47	TRY 4
13	*Chithiraikar*	48	TRY 3
14	*Kallurudaikar*	49	TRY 2
15	*Mappilai samba*	50	TRY 1
16	*Kichidi samba*	51	TKM 9
17	*Kullakkar*	52	TKM 12
18	*Nootripathu*	53	TKM 13
19	*Milagu samba*	54	TKM 14
20	*Thuyamalli*	55	ASD 17
21	*Rakthasali*	56	ASD 19
22	CBMAS 14065	57	ADT 38
23	APO	58	ADT 39
24	ANNA R-4	59	ADT 40
25	*Kumkumshali*	60	ADT 42
26	*Manipuri Black*	61	ADT 45
27	IC 465229	62	ADT 46
28	IC 435320	63	ADT 48
29	IC 300250	64	ADT 50
30	IC 463894	65	ADT 51
31	IC 458822X	66	ADT 53
32	IC 378252	67	ADT 55
33	IC 377396	68	ADT 56
34	IC 514196	69	ADT 57
35	IC 599520		

(hundred seed weight) to 62.553 (productive tillers) indicating that these traits may be improved upon selection. The results are in accordance with Manivelan *et al.* (2022) for days to 50% flowering, plant height, panicle length, hundred seed weight, grain length, grain L/B ratio; Yaseen *et al.* (2020) for effective tillers per plant; Keerthiraj and Biju (2020) for flag leaf length and flag leaf width and Syed Sajid Ali *et al.* (2021) for total tillers per plant, hundred-seed weight and yield per plant. Moderate heritability was observed for flag leaf breadth and grain breadth supporting the findings of Priyanka and Gauraha (2020). The high genetic advance was observed for eleven out of fourteen parameters studied and it ranged from 62.971(yield per plant) to 20.410 (grain breadth) while moderate genetic advance was noticed for days to 50% flowering and days to maturity. These findings were consistent with the reports of Manivelan *et al.* (2022) for the number of productive tillers per plant, hundred seed weight and grain breadth; Khalid *et al.* (2020) for plant height, panicle length, the number of tillers/plants, filled seeds per panicle, yield per plant, days to 50% flowering and days to maturity and

Table 2. Analysis of variance for fourteen biometrical characters

CHARACTER	MEAN SUM OF SQUARES		
	Replication	Treatment	Error
Plant height	0.251	454.291*	9.9340
Days to 50% flowering	12.181	146.244*	6.387
Days to maturity	0.464	187.833*	4.331
Panicle length	0.040	26.153*	1.484
Total tillers/plant	2.838	18.062*	5.202
Effective tillers/Plant	8.132	14.665*	3.378
Flag leaf length	9.749	89.088*	4.195
Flag leaf breadth	0.007	0.0284	0.011
Filled seeds per panicle	88.48	1013.599*	69.251
Grain length	0.002	1.291*	0.015
Grain breadth	0.190	0.534	0.229
Grain L/B ratio	0.003	0.373*	0.026
Hundred seed weight	0.001	0.629*	0.001
Yield per plant	23.001	143.270*	18.544

*Significant at 5 % level

Table 3. Genetic parameters for fourteen characters in rice

Characters	Mean	Range		PCV (%)	GCV (%)	h^2 %	GAM
		Maximum	Minimum				
Plant height	94.44	54.58	135.20	16.133	15.784	95.718	31.810
Days to 50% flowering	83.27	45.50	106.50	10.491	10.043	91.631	19.803
Days to maturity	119.87	63.50	138.00	8.177	7.991	95.492	16.086
Panicle length (cm)	23.78	13.13	32.94	15.630	14.767	89.264	28.742
Total tillers/plant	14.39	9.20	24.90	22.804	18.771	67.754	31.829
Effective tillers/plant	11.08	6.70	18.40	27.097	21.431	62.553	34.917
Flag leaf length (cm)	27.76	12.21	57.91	24.604	23.472	91.007	46.126
Flag leaf breadth (cm)	1.32	1.12	1.73	10.724	7.001	42.617	9.415
Filled seeds per panicle	94.87	46.20	195.90	24.526	22.904	87.209	44.062
Grain length (mm)	6.25	4.22	8.16	12.921	12.772	97.699	26.005
Grain breadth (mm)	2.49	1.58	5.66	24.848	15.690	39.872	20.410
Grain L/B ratio	2.59	1.48	3.78	17.258	16.084	86.865	30.881
Hundred seed weight (g)	2.21	1.29	3.60	25.454	25.428	99.793	52.327
Yield per plant (g)	22.68	9.02	45.82	39.659	34.818	77.079	62.971

Singh *et al.* (2020) for grain breadth and grain L/B ratio. Flag leaf breadth recorded the low genetic advance and this observation was in concordance with the report of Chuchert *et al.* (2018).

Since direct selection was deemed to be less successful for complex attribute yield, it is important to note that selection focused on a single feature might directly or indirectly affect the performance of another characteristic. Thus, association studies were used for evaluating the specifics of relationship between yield and other related variables which further aids in the indirect selection of those traits for yield improvement. The correlation coefficient for the traits under study was presented in **Table 4** and depicted in **Fig. 1**. In this study, yield per plant showed a positive significant correlation with days to 50% flowering, total tillers, the number of effective tillers, flag leaf breadth, filled seeds per panicle, grain length, grain L/B ratio and hundred seed weight. These results were in agreement with the findings of Bhargava *et al.* (2021) for effective tillers per plant; Nath and Kole (2021) for days to 50% flowering and hundred-seed weight and

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Table 4. Genotypic correlation coefficients among 14 biometric traits in 69 rice genotypes

	PH	DFF	DM	PL	TT	NET	FLL	FLB	NFS	GL	GB	Grain L/B	HSW	YPP
PH	1.00	-0.22**	-0.082	0.364**	-0.152	-0.185*	0.512**	0.293**	0.118	0.601**	-0.307**	0.065	0.245**	0.106
DFF		1.00	0.829**	-0.006	0.395**	0.375**	-0.093	-0.067	0.069	-0.114	0.096	0.068	0.076	0.364**
DM			1.00	0.036	0.269**	0.205*	0.067	0.166	0.061	-0.136	0.127	0.016	-0.016	0.166
PL				1.00	-0.133	-0.134	0.320**	-0.081	0.095	0.019	-0.090	-0.005	0.259**	0.054
TT					1.00	0.959**	-0.263**	0.216*	0.200*	-0.031	0.023	-0.093	-0.126	0.445**
NET						1.00	-0.312**	0.193*	0.210*	-0.043	0.028	-0.119	-0.123	0.445**
FLL							1.00	0.103	0.042	0.011	-0.041	0.011	0.090	-0.09
FLB								1.00	-0.100	0.043	-0.188*	0.037	0.042	0.252**
NFS									1.00	0.334**	0.449**	-0.212*	0.497**	0.343**
GL										1.00	-0.682**	-0.119	0.522**	0.295**
GB											1.00	-0.052	-0.120	-0.123
Grain L/B												1.00	-0.162	0.418**
HSW													1.00	0.564**
YPP														1.00

PH – Plant height ; DFF – Days to 50 per cent flowering ; DM – Days to maturity; PL – Panicle length ; TT– Total tillers per plant; NET – Number of effective tillers per plant; FLL- Flag leaf length ; FLB- Flag leaf breadth ; NFS – Number of filled seeds per panicle; GL- Grain length ; GB- Grain breadth; Grain L/B – ratio between grain length and grain breadth; HGW – Hundred grain weight ; YPP – Yield per plant

** & *Significant at 1 and 5 % level, respectively

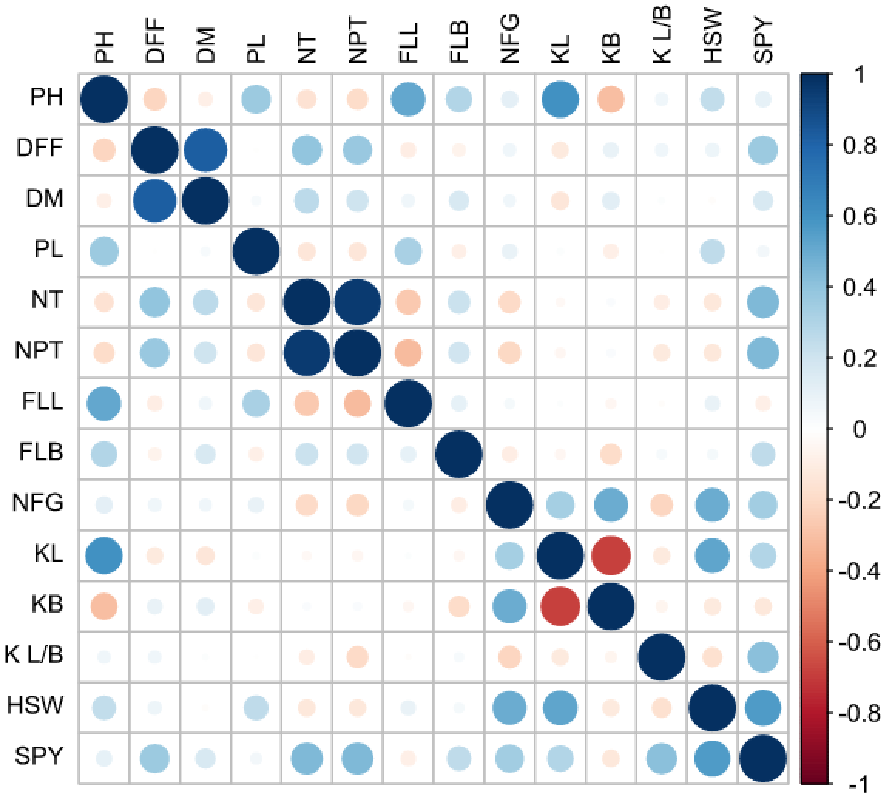

Fig. 1. Correlogram depicting the genotypic correlation among the biometrical traits in 69 rice genotypes

Table 5. Direct and indirect effects partitioned by path analysis in rice genotypes

	PH	DFF	DM	PL	TT	NET	FLL	FLB	NFS	GL	GB	Grain L/B	HSW	Correlation co-efficient for YPP
PH	**-0.015**	-0.033	0.008	-0.020	-0.018	-0.076	0.014	0.034	0.038	0.008	-0.028	0.023	0.172	0.106
DFF	0.003	**0.152**	-0.079	0.001	0.046	0.155	-0.003	-0.008	0.040	0.005	0.005	-0.007	0.053	0.364**
DM	0.001	0.126	**-0.096**	-0.002	0.032	0.085	0.002	0.019	0.009	0.004	0.006	-0.009	-0.012	0.166
PL	-0.006	-0.001	-0.003	**-0.056**	-0.016	-0.055	0.009	-0.009	-0.003	0.007	-0.001	0.007	0.182	0.054
TT	0.002	0.060	-0.026	0.007	**0.118**	0.395	-0.007	0.025	-0.054	0.014	0.001	-0.002	-0.089	0.445**
NET	0.003	0.057	-0.020	0.008	0.113	**0.412**	-0.009	0.022	-0.069	0.015	0.002	-0.002	-0.086	0.445**
FLL	-0.008	-0.014	-0.006	-0.018	-0.031	-0.129	**0.028**	0.012	0.007	0.003	-0.001	0.003	0.063	-0.090
FLB	-0.004	-0.010	-0.016	0.005	0.025	0.079	0.003	**0.115**	0.021	-0.007	-0.002	0.014	0.029	0.252**
NFS	-0.001	0.010	-0.001	0.001	-0.011	-0.049	0.000	0.004	**0.585**	-0.015	0.005	0.004	-0.114	0.418**
GL	-0.002	0.011	-0.006	-0.005	0.024	0.087	0.001	-0.012	-0.124	**0.070**	-0.015	-0.033	0.349	0.343**
GB	-0.009	-0.017	0.013	-0.001	-0.004	-0.018	0.001	0.005	-0.070	0.023	**-0.046**	0.051	0.367	0.295**
Grain L/B	0.005	0.015	-0.012	0.005	0.003	0.012	-0.001	-0.022	-0.031	0.032	0.031	**-0.075**	-0.084	-0.123
HSW	-0.004	0.012	0.002	-0.015	-0.015	-0.051	0.003	0.005	-0.095	0.035	-0.024	0.009	**0.702**	0.564**

Residual effect: 0.04260

PH – Plant height ; DFF – Days to 50 per cent flowering ; DM – Days to maturity; PL – Panicle length ; TT– Total tillers per plant; NET – Number of effective tillers per plant; FLL- Flag leaf length ; FLB- Flag leaf breadth ; NFS – Number of filled seeds per panicle; GL- Grain length ; GB- Grain breadth; Grain L/B – ratio between grain length and grain breadth; HGW – Hundred grain weight ; YPP – Yield per plant

Dey *et al.* (2019) for filled grains per panicle.Besides, dealing with intercorrelation, plant height was reported to show a significant positive correlation with panicle length, flag leaf length, flag leaf breadth, grain length, and hundred seed weight. The results were in concordance with the findings submitted by Roy and Kumaresan (2019) for panicle length; Syed Sajid Ali *et al.* (2021) for flag leaf length and flag leaf breadth; Nirubana *et al.* (2019) for hundred seed weight, Seneega *et al.*(2019) for grain length and Manivelan *et al.* (2022) for grain breadth. Days to 50% flowering displayed a positive significant correlation with days to maturity, the number of tillers and effective tillers per plant in accordance with Singh *et al.* (2022) for days to maturity, Kiruthikadevi *et al.* (2020) and Amegan *et al.* (2020) for the number of tillers per plant and Singh *et al.* (2020) and Roy *et al.* (2021) for the number of effective tillers per plant. Days to maturity recorded significant positive relation with the number of tillers and the number of effective tillers per plant corroborating with evidence publicized by Amegan *et al.* (2020) for both the number of tillers and effective tillers per plant. Flag leaf length and hundred seed weight were found to have a positive significant correlation with panicle length. The number of tillers and the number of effective tillers per plant were intercorrelated to each other and were correlated positively and significantly with flag leaf breadth and the number of filled seed per panicle identical to the reports produced by Emi *et al.* (2021) and Kiruthikadevi *et al.* (2020) for the number of filled grains per panicle. The number of filled grains per panicle reported a positive significant correlation with grain length, grain breadth and hundred seed weight similar to the findings by Prasannakumari *et al.* (2020. A significant positive correlation was noticed between grain length and hundred seed weight similar to the documentation by Manivelan *et al.* (2022) and Seneega *et al.* (2019).

In order to elucidate the interaction between yield and its attributed qualities, path analysis was used for the assessment of explicit and implicit influences as correlation analysis may not foreshadow the salience of the yield-contributing features when ascertaining the relationship between the characteristics. The direct and indirect effects partitioned by path analysis for fourteen biometric traits were presented in **Table 5**. A high positive direct effect indicated relative significance revealed by hundred seed weight (0.702), filled seeds per panicle (0.585), effective tillers (0.412), and days to 50 per cent flowering (0.152), total tillers (0.118) and flag leaf breadth (0.115) reported a low positive impact on yield per plant similar to the findings by Fathima *et al.* (2021) and Nirubana *et al.* (2019) for hundred seed weight. As these characters featured high positive effects, implies yield improvement can be achieved through the deliberate selection of these features. The low indirect effect on yield per plant was revealed by days to maturity *via* days to 50 per cent flowering. The high indirect positive effect was shown on yield per plant by effective tillers *via* total tillers per plant and days to 50 per cent flowering akin to the reports publicized by Fathima *et al.* (2021) for total tillers per plant. Hundred seed weight was known to show a positive indirect effect on yield per plant *via* plant height, panicle length, grain length, grain breadth and negative effect through filled seeds per panicle. These outcomes were in corroboration with the insights documented by Nirubana *et al.* (2019) for filled seeds per panicle and plant height.

From the above discussion, it may be concluded that for traits productive tillers, flag leaf length, filled seeds per panicle, hundred seed weight, yield per plant with high GCV and PCV and direct selection may result in genetic advancement. Plant height, panicle length, the total tillers, total productive tillers per plant, flag leaf length, grain length, grain L/B ratio, filled seeds per panicle, hundred seed weight and yield per plant all show substantial genetic advance as percentage of mean and high heritability, indicating a preponderance of additive gene action in their genetic regulation. Therefore, simple selection would indeed be efficient in enhancing these characteristics. Days to 50% flowering, the total tillers, effective tillers, flag leaf breadth, the filled seeds per panicle and hundred seed weight were shown to have significant positive correlation coefficients with direct impacts in response to yield per plant among the yield traits examined which may be given due consideration while exercising selection.

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