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Genetic diversity and association studies in Rice (*Oryza sativa* L.)

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Abstract

Understanding of genetic divergence and traits association among 108 rice genotypes, nine morphological traits were studied. Based on their D^2 values the genotypes were grouped into 14 clusters and the maximum of 37 genotypes grouped under cluster 1. The highest intra and inter cluster distance was observed in cluster X and between cluster XII and XIV respectively. The trait grain length recorded maximum contribution to the divergence followed by plant height. Selection based on these traits would be more effective in creation of divergent population. Moderate Phenotypic and genotypic coefficient of variation, high heritability and high genetic advance as percentage of mean were observed for all the traits studied. The traits, number of productive tillers per plant, number of grains per panicle and thousand grain weight had shown significant positive correlation with yield and also recorded high direct effect on yield. Hence the selection based on these traits may helpful in planning efficient breeding programs.

Keywords: Rice, genotypes, diversity, variability, association analysis

Introduction

Oryza sativa L. ($2n = 24$) is one of the cultivated rice in Asia provides food for more than one third of the world's population. About one-fifth of the total land area is covered under cereals (Chakravarthi and Naravaneni, 2006) [4] and 90% of the world's rice is grown in Asia (Bandumala, 2017) [1]. Among Asian countries, India stands second in rice production after China producing 119 million tonnes per annum (USDA world crop production summary 2020-21). The demand of food grains to feed growing population is increasing every year, and hence to achieve sustainable production in rice, advanced breeding methods and biotechnological tools are required. A Number of rice varieties were developed by the continuous cultivation and selection process over the years, though landraces usage in plant breeding programmes is very limited and so utilisation of these diverse genotypes in breeding events may useful in improving the productivity.

The efficiency of selection in the divergent population largely depends on the range of genetic variability present in a population. The phenotypic variation observed in the genotypes is the result of interaction between genotypic and environmental factors (GXE) and genetic factor alone heritable. The association of traits provides information about the direct and indirect relationship of yield components to the yield through correlation and path analysis by which direction of selection is made. The current study was carried out to estimate genetic diversity, variability, correlation and path coefficient analysis among rice genotypes for selection of divergent genotypes and identification of traits rewarding yield improvement in rice.

Materials and methods

The experimental material comprised of 108 rice genotypes collected from AC&RI, Killikulam, NIPGR, New Delhi, TRRI, Tamilnadu and Regional Research Station, Pattambi. The seeds were sown in nursery beds and transplanted to the main field on 25 DAS during Kharif 2019 at AC and RI, Killikulam. The crop was maintained under the standard management practices throughout the entire crop period. The biometric observations were recorded for the following nine quantitative characters *viz.*, days to fifty percent flowering, plant height (cm), number of productive tillers per plant, panicle length (cm), number of grains per panicle, thousand grain weight (g), single plant yield (g), grain length (mm) and grain breadth (mm). The statistical analysis was done by using INDOSTAT software. The variability parameters such as PCV and GCV, heritability and genetic advance as percentage of mean categorized by the methods given by Burton (1952) [3], Lush (1940) [7] and Johnson *et al.*, (1955) [6] respectively. For diversity studies, grouping of genotypes was done by using Tocher's method (Rao 1952) [10].

Results and discussion

i) Genetic diversity studies

The analysis of variance (ANOVA) showed significant differences for all the nine biometric traits observed (Table 1). The study material comprised of 108 rice genotypes were classified into 14 major groups based on Mahalanobis D² values (Table 2). The maximum of 37 genotypes included in Cluster I followed by the clusters III, IV, X and VIII included 26, 18, 11 and 7 genotypes respectively and it implies the genotypes included in these clusters showed lesser divergence within cluster. The other clusters had single genotypes each (mono-genotypic). The average intra and inter cluster distance driven from D² values is shown in Table 3. The highest intra cluster distance observed in cluster X (45.72) followed by cluster IV (33.23) and VIII (32.48) indicating maximum divergence among the genotypes in the clusters. The maximum inter cluster distance was observed between clusters XII and XIV (84.52) followed by clusters VII and XIV (72.77). It implied that the selection of genotypes from these clusters in crossing programs would provide high heterotic and transgressive segregants.

Cluster mean values for nine different traits presented in Table 4. Clusters XIII (Patani) and IX (White sanam) showed highest mean values for single plant yield (78.90 g and 63.85 g), cluster XII (Kuruvaikalanjium) recorded high mean values for grain length (8.55 mm) and cluster VII (Bharathi) recorded high mean value for panicle length (28.45 cm) and grain length (8.85 mm). Thus selection made from these clusters may be useful in yield improvement programs. The contribution of each character to the total divergence was assessed and depicted in Table 4. Among the characters studied grain length (25.56%), plant height (21.77%), days to 50% flowering (17.26) and number of grains per panicle (13.03%) recorded maximum contribution to the divergence (Figure 1). Similar findings were reported by Banumathy *et al.*, 2010^[2] except for grain length

ii) Genetic variability studies

Phenotypic and genotypic coefficient of variation computed and phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation for all the traits which is consistent with the results of Vishwanath *et al.*, 2016^[13]. Moderate PCV and GCV were found for all the nine biometric traits ranges from 12.10 to 18.84 and 12.06 to 18.06 respectively (Table 5) (Figure 2) and it revealed that the presence of sufficient variation among the genotypes for the nine biometric traits studied.

All the traits studied showed high genetic advance as percentage of mean ranged from 23.82% to 36.86% together with high heritability ranges between 91.98% to 99.38% (Table 5) (Figure 3). It indicates that these characters attribute additive gene action and direct selection is a way to improvement of these characters.

iii) Association studies

Correlation and path analysis was done to identify the direct and indirect association of traits to the yield. The traits, number of productive tillers per plant, number of grains per panicle and thousand grain weight (g) were recorded positive and significant correlation with yield (Table 6) and also shown positive direct effect on single plant yield (Table 7) (Figure 4). Similar results revealed by Hossain *et al.*, 2018^[5] for number of grains per panicle and Rajendra Singh *et al.*, 2018^[9] and Sonu kumar *et al.*, 2018^[11] for test weight (g).

The association among other yield components also studied and it revealed significant positive correlation between days to fifty percent flowering with plant height and number of grains per panicle; panicle length with number of grains per panicle, grain length and grain breadth; number of grains per panicle with grain length; grain length with grain breadth at genotypic level (Table 6).

Table 1: ANOVA for nine quantitative traits in rice

Source of variation	Df	Mean sum squares								
		DFF	PH	NPT	PL	NGP	TGW	GL	GB	SPY
Replication	1	1.1898	20.9352	4.4481	2.6108	196.3519	6.2729	0.0366	0.005	0.5648
Genotypes	107	219.984**	992.114**	18.594**	20.129**	1929.743**	17.463**	1.628**	0.272**	182.302**

* ** indicates level of significance at 0.05 and 0.01 respectively

DFF - Days to fifty percent flowering, PH - Plant height, NPT- Number of productive tillers per plant, PL - Panicle length, NGP – Number of grains per panicle, TGW - Thousand grain weight, GL - Grain length, GB - Grain breadth, SPY - Single plant yield

Table 2: Grouping of rice genotypes into different clusters through D² analysis

Cluster Number	Number of genotypes	Name of the genotypes
I	37	Kallondaikar, Poongar, Karnellu, Kattisamba, Navara 6263, Vattan 5052, Jaisreeram, Vasanaisamba, Chitteni 5525, Chuvanna chitteni 7135, Chitteni 7256, ARYAN 6333, Norungan, ARYAN 1203, Chenthodi, ARYAN 5532, Navara 5571, ARYAN 917, Noothipattu, Kotara samba, ARYAN 1023, Shabahidhan, Thamarai, Shadabaha, Ohenellu 6305, Chinapunchan, Veethiruppu, Mattai, Thuyamalli, Kayamma, C039, ARYAN 1102, Chemban 986, Chandaikar, Navara black, Varakunanellu, Jaya
II	1	Company Thavalaikannan
III	26	Anjali, Chiruchitteni 882, Kullakar, Karuvalli, TN1, IR64, Abiyan, Virendra, Thondi, Maranellu, Adukan, Kattanoor, Srilanka, Rajalakshmi, Navara 957, Pusa basmati, Dhalahaera, White ponni, Salem senna, Kaivara samba, Aman, Karukot, Kodaikannan, Swarnamalli, Annada, Kichalisamba
IV	18	Kunju kunju 1811, Kunju kunju 6974, Kunju kunju 7168, Chembavu 4331, Mulampunchan, Chembavu 5599, Chitteni 5520, Chomala 826, Chenkayamma 5523, Chitteni 1123, Oheru chitteni, Purple puttu, Karsamba, Meikuruvai, Surakuruvai, Chennellu 4735, Molikarumbu, Navara 957
V	1	Kalinga
VI	1	Mallikar
VII	1	Bharathi
VIII	7	Chittiraikar, Kuliyaichan, Varaprabha, Kalakeri, Kalyani, Chennellu 5590, Sivappumalli
IX	1	White sanam

X	11	Bommi, Gowni, Mapillai samba, Kerala gandasala, Illupaiipoosamba, Seeraga samba, Swarna masuri, Palkudavazhai, Krishnahemavathy, Karutha navara, Uma
XI	1	Tetep
XII	1	Kuruvaikalanjium
XIII	1	Pattani
XIV	1	Kothamalli samba

Table 3: Intra and Inter cluster distances among 14 clusters

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
I	27.63	32.94	38.35	42.96	35.28	32.78	44.22	36.43	33.4	45.56	44.83	52.09	37.88	47.4
II		0.0	51.23	30.12	50.10	39.00	52.79	43.29	26.50	50.01	61.51	69.77	41.95	38.13
III			31.12	51.11	35.45	40.88	38.50	42.58	48.00	43.59	41.96	38.80	52.27	63.45
IV				33.23	55.12	46.09	49.63	46.90	42.40	51.04	68.50	69.38	55.81	50.80
V					0.00	23.56	34.46	34.85	47.70	53.15	37.33	34.60	56.45	68.96
VI						0.00	41.37	29.00	45.33	53.95	44.63	51.97	52.21	53.69
VII							0.00	39.17	59.94	52.35	62.49	48.26	69.22	72.77
VIII								32.48	50.86	55.28	55.03	54.21	54.14	54.50
IX									0.00	46.93	48.08	59.24	31.90	50.22
X										45.72	55.25	58.78	51.07	62.88
XI											0.00	36.69	48.16	67.67
XII												0.00	66.38	84.52
XIII													0.00	41.72
XIV														0.00

Table 4: Cluster mean values and contribution of traits to the total divergence

Clusters	DFP	PH	NPT	PL	NGP	TGW	GL	GB	SPY
I	80.01	141.61	18.20	23.68	159.07	24.87	6.41	2.85	59.31
II	90.00	164.85	15.00	24.45	147.00	26.85	5.60	2.65	53.35
III	87.46	118.85	16.87	25.44	185.04	23.11	7.59	2.99	58.80
IV	101.06	161.89	13.50	24.14	168.06	24.20	6.57	2.89	50.54
V	72.50	130.00	17.50	24.50	138.50	21.90	7.50	2.60	43.95
VI	76.00	136.10	13.00	23.85	139.50	20.10	6.55	2.95	34.60
VII	86.50	157.60	13.50	28.45	154.50	26.95	8.85	3.15	51.15
VIII	80.36	146.11	16.07	19.91	148.29	23.19	7.26	3.26	47.87
IX	88.50	142.85	22.00	23.70	158.00	20.85	5.45	2.10	63.85
X	91.36	133.88	16.05	27.54	220.68	24.74	6.86	2.86	63.65
XI	73.50	78.05	18.50	25.55	162.50	21.45	6.15	2.50	56.95
XII	87.00	89.05	19.50	21.65	147.50	21.00	8.55	2.40	59.85
XIII	75.00	132.90	19.00	18.70	201.00	23.60	5.15	2.80	78.90
XIV	86.00	138.05	14.50	22.10	160.50	29.80	4.50	3.70	63.65
Contribution %	17.26	21.77	0.02	2.39	13.03	0.21	25.56	12.08	7.68

DFP - Days to fifty percent flowering, PH - Plant height, NPT- Number of productive tillers per plant, PL - Panicle length, NGP - Number of grains per panicle, TGW - Thousand grain weight, GL - Grain length, GB - Grain breadth, SPY - Single plant yield

Table 5: Estimation of variability parameters for nine quantitative traits

Traits	Mean	Coefficient of variation		Heritability in broad sense (%) (h^2)	Genetic advance as percentage of mean (%) (GAM)
		Phenotypic (PCV)	Genotypic (GCV)		
DFP	86.63	12.10	12.06	99.30	24.75
PH	138.05	16.12	16.07	99.34	33.00
NPT	16.63	18.84	18.06	91.98	35.69
PL	24.33	13.08	12.93	97.72	26.34
NGP	172.17	18.07	17.98	99.03	36.86
TGW	24.11	12.48	12.01	92.64	23.82
GL	6.83	13.20	13.16	99.38	27.03
GB	2.91	12.69	12.64	99.27	25.95
SPY	57.17	16.71	16.61	98.79	34.01

DFP - Days to fifty percent flowering, PH - Plant height, NPT- Number of productive tillers per plant, PL - Panicle length, NGP - Number of grains per panicle, TGW - Thousand grain weight, GL - Grain length, GB - Grain breadth, SPY - Single plant yield

Table 6: Genotypic and Phenotypic correlation coefficient matrix for nine quantitative traits

Traits	Correlation coefficient (r)	PH	NPT	PL	NGP	TGW	GL	GB	SPY
DFF	G	0.262**	-0.391**	0.096	0.211*	-0.022	0.155	-0.001	-0.158
	P	0.259**	-0.374**	0.094	0.209*	-0.023	0.156	-0.001	-0.156
PH	G		-0.188	0.04	-0.074	0.15	-0.126	0.071	-0.143
	P		-0.178	0.04	-0.074	0.142	-0.125	0.07	-0.141
NPT	G			-0.12	-0.163	-0.073	-0.174	-0.224*	0.564**
	P			-0.115	-0.158	-0.056	-0.171	-0.214*	0.542**
PL	G				0.475**	0.077	0.242*	0.280**	0.177
	P				0.465**	0.072	0.236*	0.276**	0.174
NGP	G					0.016	0.233*	0.153	0.480**
	P					0.015	0.231*	0.154	0.476**
TGW	G						-0.204*	0.148	0.288**
	P						-0.198*	0.144	0.275**
GL	G							0.218*	-0.098
	P							0.217*	-0.096
GB	G								-0.091
	P								-0.089

*, ** indicates level of significance at 0.05 and 0.01 respectively

DFF - Days to fifty percent flowering, PH - Plant height, NPT- Number of productive tillers per plant, PL - Panicle length, NGP – Number of grains per panicle, TGW - Thousand grain weight, GL - Grain length, GB - Grain breadth, SPY - Single plant yield

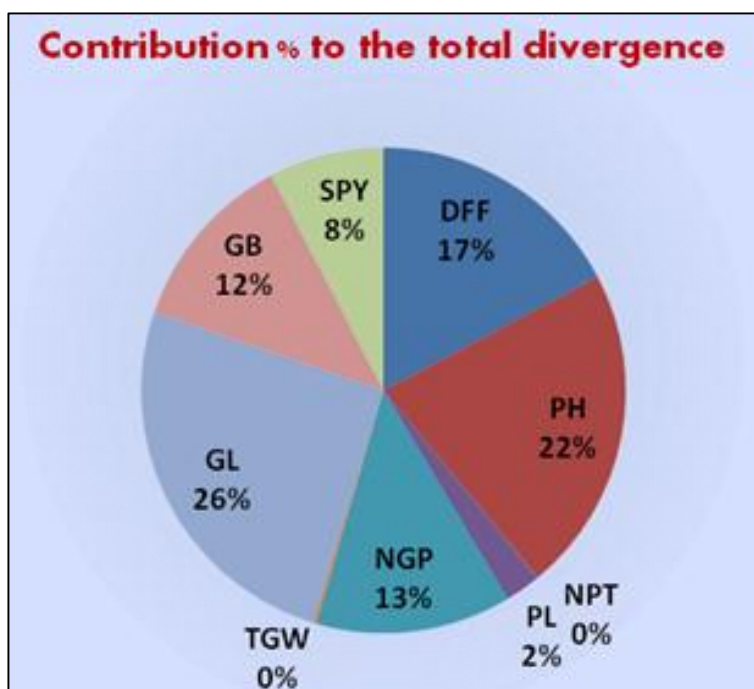
Table 7: Path matrix for nine quantitative traits

Traits	DFF	PH	NPT	PL	NGP	TGW	GL	GB	SPY
DFF	-0.011	-0.005	-0.256	-0.003	0.130	-0.007	-0.006	0	-0.158
PH	-0.003	-0.019	-0.123	-0.001	-0.046	0.050	0.005	-0.005	-0.143
NPT	0.004	0.004	0.655	0.004	-0.100	-0.024	0.006	0.016	0.564**
PL	-0.001	-0.001	-0.079	-0.032	0.293	0.026	-0.009	-0.020	0.178
NGP	-0.002	0.001	-0.107	-0.015	0.617	0.005	-0.009	-0.011	0.480**
TGW	0.001	-0.003	-0.048	-0.003	0.010	0.334	0.008	-0.010	0.288**
GL	-0.002	0.002	-0.114	-0.008	0.144	-0.068	-0.037	-0.015	-0.098
GB	0.000	-0.001	-0.147	-0.009	0.095	0.050	-0.008	-0.071	-0.092

Diagonal value represents direct effects

*, ** indicates level of significance at 0.05 and 0.01 respectively

DFF - Days to fifty percent flowering, PH - Plant height, NPT- Number of productive tillers per plant, PL - Panicle length, NGP – Number of grains per panicle, TGW - Thousand grain weight, GL - Grain length, GB - Grain breadth, SPY - Single plant yield

**Fig 1:** The relative contribution of nine quantitative traits to the total divergence

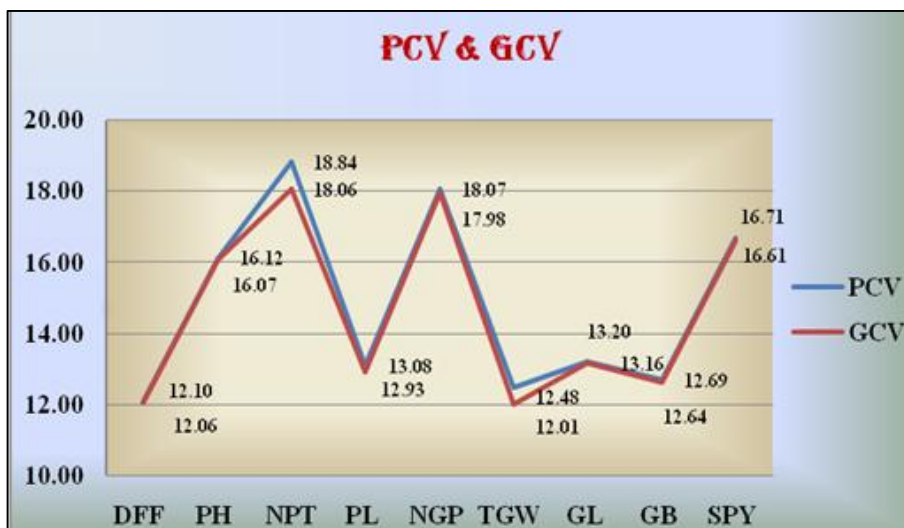


Fig 2: Phenotypic and Genotypic coefficient of variation for nine quantitative traits

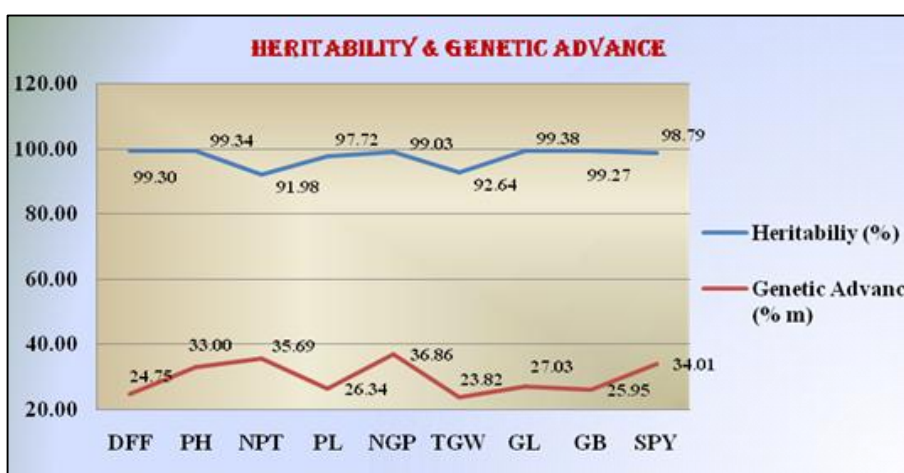


Fig 3: Heritability and Genetic advance as percentage of mean for nine quantitative traits

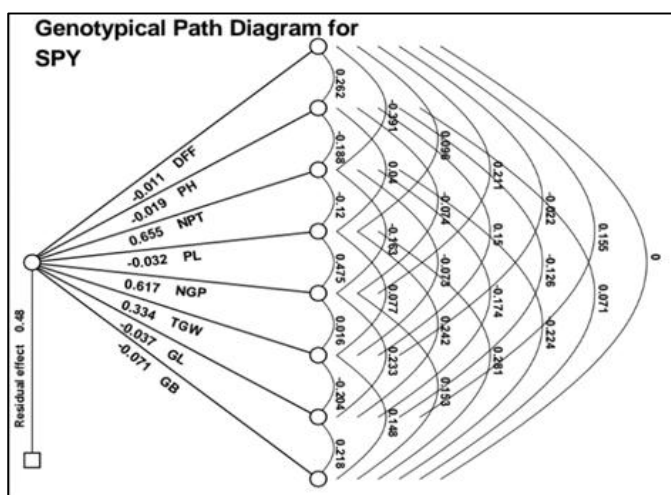


Fig 4: Path diagram for nine yield components

Conclusion

The extent of variability observed in a population is may be of diverse nature of genotypes or by the environmental effects on phenotypes. The cross made between the genotypes Kuruvaikalanjium (cluster XII) X Kothamallisamba (cluster XIV) and Kuruvaikalanjium (cluster XII) X Bharathi (cluster VII) gives more divergent population due to their high inter cluster distance and also these genotypes had high cluster

mean values for different traits may it provide high level of heterosis. The direct selection of genotypes from the clusters IX, X and cluster XIV for the traits viz., number of productive tillers per plant, number of grains per panicle and thousand grain weight could be useful for breeders in yield enhancement programs in rice.

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