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Studies on genetic variability, correlation and path analysis in rice (*Oryza sativa* L.) under natural saline condition

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Abstract

The present investigation on genetic diversity was carried out with 25 rice genotypes including saline tolerant check variety, TRY 1 and TRY (R) 3 during navarai 2018. 25 rice genotypes were used to evaluate their response in saline condition for 12 biometrical traits viz., days to first flowering, plant height, number of productive tillers per plant, number of grains per panicle, 100 grain weight, grain length, grain breadth, grain L/B ratio, kernel length, kernel breadth, kernel L/B ratio and grain yield per plant. The characters namely, grain length and grain yield per plant were the two major contributors for genetic diversity. The traits viz., grain yield per plant and number of productive tillers per plant recorded high GCV and PCV. High heritability along with genetic advance as per cent of mean was observed for all the traits viz., days to first flowering, plant height, number of productive tillers per plant, number of grains per panicle, 100 grain weight, grain length, grain breadth, grain L/B ratio, kernel length, kernel breadth, kernel L/B ratio and grain yield per plant indicate that these traits controlled by additive gene action. Since the genetic advance as per cent of mean is also high, the expected progress under selection could be obtained in the early generation itself. The correlation co-efficient revealed that number of productive tillers and number of grains per panicle had positive significant association with grain yield per plant at both genotypic and phenotypic level. The cause and effect of relationship indicated high positive direct effect on grain yield per plant through number of productive tillers per plant, number of grains per panicle and grain breadth. Hence, the foresaid traits deserved greater importance in breeding programme to develop high yielding new plant type rice cultivars under saline condition.

Keywords: Variability, saline condition, correlation, path analysis

Introduction

Rice (*Oryza sativa* L.2n=2x=24) is the most important cereal cultivated widely in many parts of the world. The genus *Oryza* belongs to the tribe Oryzeae in the family poaceae. Genus *Oryza* included 24 species of which 22 species are wild and only two species *viz.*, *O. sativa*, *O. glaberrima* are cultivated. Salt stress is a major problem in vast areas of the world, and in Asia alone, more than 12 million hectare of rice land are currently affected. Salinity stress is the serious threat to sustainable rice production for growing demand. The first towards genetic improvement mainly depends on the amount of genetic variability present in the population. Information on the nature and degree of genetic divergence would help the plant breeder in choosing the right type of parents for future breeding programme to develop hybrids.

Development of high yielding varieties requires the existence of genetic variability and genetic variability of agronomic traits is the key component of breeding programmes for broadnening the gene pool (North, 2013) ^[9]. Selection will be effective when there is a significant amount of variability among the breeding materials (Sumanth *et al.*, 2017) ^[14]. The knowledge about the variability parameters such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h²) and genetic advance as percent of mean (GA as per cent of mean) of breeding material is the prime need for successful breeding programme. The path co-efficient of analysis would be quite useful as it permits the separation of direct effects from indirect effects through other traits (Dewey and Lu, 1959) ^[6]. Therefore, the objective of the present study was to assess and evaluate genetic variability, correlation and path analysis of 25 rice genotypes.

Materials and Methods

The experimental material for this genetic divergence study comprised of 25 rice genotypes collected from various places were utilized for study.

The details of the materials are presented in table 1. The experiment was carried out at the Experimental Farm of Plant Breeding Department ($11^{\circ}24^{\circ}N$ latitude and $79^{\circ}44^{\circ}E$ longitude 5.79m MSL), Tamilnadu, India during Navarai, 2018 (December - January). Seeds of the 25 rice genotypes were sown in raised nursery bed under saline soil with electrical conductivity (EC) of 2.1 dsm⁻¹ and pH 8.5. In each genotype, one seedling per hill was transplanted in the main

field after 25 days with the spacing of 20 cm between rows and 15cm between plants in 3m long rows. The experiment was carried out in randomized block design with three replications. Recommended agronomic practices and need based plant protection measures were taken up to maintain healthy crop stand. Standard statistical procedures were used for the correlation and path coefficient analysis suggested by Wright (1921)^[17] and elaborated by Dewey and Lu (1959)^[6].

Table	1:	List	of	rice	genotypes	selected
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Genotype Code	Genotype Names	Origin
G1	Jgl 1798	Krishi Vigyan Kendra, Nellore, Andhra Pradesh
G2	Ir 20	International Rice Research Institute, Philippines.
G3	Adt 43	Tamil Nadu Rice Research Institute (TRRI), Aduthurai, Tamil Nadu, India
G4	Trupthi	Krishi Vigyan Kendra, Nellore, Andhra Pradesh.
G5	Adt 45	Tamil Nadu Rice Research Institute (TRRI), Aduthurai, Tamil Nadu, India
G6	Adt(r) 49	Tamil Nadu Rice Research Institute (TRRI), Aduthurai, Tamil Nadu, India
G7	Nlr 34449	Krishi Vigyan Kendra, Nellore, Andhra Pradesh.
G8	Adt(r) 50	Tamil Nadu Rice Research Institute (TRRI), Aduthurai, Tamil Nadu, India
G9	Tkm 9	Rice Research Station, Thirurkuppam.
G10	Co 43	Tamil Nadu Agricultural University, Coimbatore.
G11	Sonam	Krishi Vigyan Kendra, Nellore, Andhra Pradesh.
G12	Adt 39	Tamil Nadu Rice Research Institute (TRRI), Aduthurai, Tamil Nadu, India
G13	Co(r) 51	Tamil Nadu Agricultural University, Coimbatore.
G14	Adt 46	Tamil Nadu Rice Research Institute (TRRI), Aduthurai, Tamil Nadu, India
G15	Bpt 5204	Agricultural College, Bapatla, Andhra Pradesh, India.
G16	Adt 37	Tamil Nadu Rice Research Institute (TRRI), Aduthurai, Tamil Nadu, India
G17	Akshaya	Banaras Hindu University, Varanasi
G18	Try 1	Agriculture College & Research Institute (TNAU), Trichy
G19	Adt 36	Tamil Nadu Rice Research Institute (TRRI), Aduthurai, Tamil Nadu, India
G20	Swarna sub 1	Krishi Vigyan Kendra, Nellore, Andhra Pradesh.
G21	White ponni	Tamil Nadu Agricultural University & RI, Coimbatore.
G22	Asd 16	Regional Research Station, Ambasamudram, TN, India.
G23	Try(r) 3	Agriculture College & Research Institute (TNAU), Trichy
G24	C0(r) 50	Tamil Nadu Agricultural University, Coimbatore
G25	Adt 41	Tamil Nadu Rice Research Institute (TRRI), Aduthurai, Tamil Nadu, India

Results and Discussion

Variability available in a population is an asset to a plant breeder in any crop improvement programme. Knowledge of genetic diversity in respect of yield and its associated characters is very valuable in breeding programme since it helps to choose the best yield determining attributes. Yield and its component characters are highly influenced by the environment. It is thus difficult to conclude whether the observed variability is heritable or not. Therefore, it becomes essential to partition the observed variability into its heritable and non-heritable components. Such variability in a population can be measured by phenotypic and genotypic coefficient of variation.

High GCV estimates were recorded for the characters, grain yield per plant and number of productive tillers per plant (Table 2). This is in conformity with the findings of Ashok kumar Tuwar *et al.* (2012) ^[1]. Moderate GCV estimates were recorded for the characters *viz.*, hundred grain weight, grain

L/B ratio, kernel L/B ratio, number of grains per panicle, days to first flowering, plant height, grain breadth, kernel breadth, grain length and kernel length indicating their greater role of contribution to the variability among the genotypes. Similar observations were made by Islam *et al.* (2016) ^[7] and Vinod Kumar *et al.* (2018) ^[16].

A high estimate of GCV and PCV was recorded by grain yield per plant and number of productive tillers per plant. Similar findings were made by Chanbeni *et al.* (2012). A comparison of GCV and PCV estimates for all the characters studied possessed a low value. Thus estimates indicated, the characters studied were less susceptible to the environmental conditions and therefore selection for such traits will be rewarding as the genetic factors play the greater role in determining the variability for these characters. The results obtained by Karuppaiyan *et al.* (2013) ^[8] in rice agreed with the results of present investigation.

S No	Character	Coefficient	of variation
5. NO.	Character	Genotypic (%)	Phenotypic (%)
1	Days to first flowering	17.23	17.41
2	Plant height	15.80	16.00
3	Number of productive tillers per plant	21.27	22.20
4	Number of grains per panicle	18.16	18.20
5	100 grain weight	19.48	19.53
6	Grain length	13.75	13.76
7	Grain breadth	15.80	15.83
8	Grain l/b ratio	19.48	19.51
9	Kernel length	10.26	10.27
10	Kernel breadth	17.10	17.11
11	Kernel l/b ratio	19.11	19.13
12	Grain yield per plant	25.94	26.43

Table 2: Magnitude of	genotypic and	phenotypic var	iability for various	characters of 25 rice genotypes
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Fable 3: Estimates of Heritability and Genetic advance	s per cent of mean for various Characters of 25 rice Genotypes
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S. No.	Character	Heritability (%) (h ²)	GA as % of mean
1	Days to first flowering	97.95	35.12
2	Plant height	97.54	32.15
3	Number of productive tillers per plant	91.80	41.99
4	Number of grains per panicle	99.64	37.36
5	100 grain weight	99.48	40.02
6	Grain length	99.98	28.34
7	Grain breadth	99.56	32.48
8	Grain l/b ratio	99.67	40.06
9	Kernel length	99.89	21.13
10	Kernel breadth	99.87	35.21
11	Kernel l/b ratio	99.82	39.33
12	Grain yield per plant	96.26	52.42

High heritability and genetic advance as per cent of mean was observed for all the characters such as days to first flowering, plant height, number of productive tillers per plant, number of grains per panicle, 100 grain weight, grain length, grain breadth, grain L/B ratio, kernel length, kernel breadth, kernel L/B ratio and grain yield per plant (Table 3). These characters were mostly controlled by additive gene action, hence it could be inferred that direct selection based on phenotypic observations may be effective for crop improvement of these traits. Similar findings were also reported by Ashok Kumar Tuwar *et al.* (2012)^[1].

The ultimate aim of any crop improvement programme is

yield improvement. Since yield is a complex trait, knowledge of association of different yield components with yield and inter correlations among themselves are important. A study of phenotypic correlation is adequate while correlation coefficients are based on the heritable part of the values (genotypic correlation) provide a dependable basis for selection. Estimation of phenotypic and genotypic correlations between the response variable (yield) and the predictor (yield components) and among the yield components themselves, may provide information for the breeding programme when selection is based on two or more characters simultaneously.

Table 4: Genotypic and	phenotypic correlation	among various characters	s of 25 rice genotypes
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Characters		Days to first flowering	Plant Height	Number of productive tillers per plant	Number of grains per panicle	100 grain weight	Grain length	Grain breadth	Grain L/B ratio	Kernel length	Kernel breadth	Kernel L/B ratio	Grain yield per plant
Days to	G	1.000	0.274	0.221	0.282	-0.020	0.179	0.444	-0.230	0.240	0.402*	-0.228	0.312
first flowering	Р	1.000	0.265	0.208	0.279	-0.021	0.177	0.439*	-0.226	0.238	0.397*	-0.224	0.299
Plant	G		1.000	-0.181	-0.064	-0.098	-0.277	0.409*	-0.483*	-0.222	0.399*	-0.437*	-0.104
height	Р		1.000	-0.170	-0.063	-0.097	-0.274	0.402*	-0.475*	-0.220	0.393*	-0.431*	-0.098
Number of	G			1.000	0.934**	-0.192	0.103	-0.071	0.118	0.071	-0.071	0.099	0.966**
productive tillers per plant	Р			1.000	0.893**	-0.182	0.099	-0.071	0.115	0.069	-0.068	0.094	0.911**
Number of	G				1.000	-0.084	0.136	0.114	-0.008	0.101	0.110	-0.049	0.973**
grains per panicle	Р				1.000	-0.900**	0.128	0.136	-0.008	0.100	0.109	-0.048	0.956**
100 grain	G					1.000	0.123	0.011	0.042	-0.063	-0.045	-0.009	-0.148
weight	Р					1.000	0.122	0.011	0.041	-0.064	-0.044	-0.009	-0.142
Grain	G						1.000	0.057	0.661**	0.892**	-0.141	0.631**	0.088
length	Р						1.000	0.057	0.660**	0.892**	-0.141	0.630**	0.087
Grain	G							1.000	-0.701**	0.182	0.955**	-0.700**	0.078
breadth	Р							1.000	-0.701**	0.181	0.953**	-0.698**	0.078

Grain L/B	G				1.000	0.505**	-0.806**	0.988**	-0.008
ratio	Р				1.000	0.504**	-0.805**	0.986**	-0.009
Kernel	G					1.000	0.071	0.500**	0.046
length	Р					1.000	0.071	0.500**	0.045
Kernel	G						1.000	-0.813**	0.061
breadth	Р						1.000	-0.814**	0.059
Kernel L/B	G							1.000	-0.028
ratio	Р							1.000	-0.027
Grain yield	G								1.000
per plant	Р								1.000

In this study, grain yield per plant expressed significant positive correlation with number of productive tillers per plant and number of grains per panicle at both genotypic and phenotypic level (Table 4). This positive association of these yield attributing characters with grain yield per plant was also reported by Augustina et al. (2013)^[2]. From the foregoing discussion, it may be seen that number of productive tillers per plant and number of grains per panicle can be appropriately used as selection criteria for the improvement of grain yield per plant in rice.

Days to first flowering expressed the positive significant association with kernel breadth at both genotypic and phenotypic levels. Plant height showed positive significant association with grain breadth and kernel breadth at both genotypic and phenotypic level. Similar findings were observed by Rupika Sharma et al. (2012)^[1].

Number of productive tillers per plant had positive significant association with number of grains per panicle and grain yield per plant at both genotypic and phenotypic level. Similar results were observed by Rajamadhan et al. (2011) [10]. Trait like, number of grains per panicle had positive significant association with grain yield per plant at both genotypic and phenotypic level. 100 grain weight had non-significant association with grain yield per plant. Grain length had positive significant association with grain L/B ratio, kernel length and kernel L/B ratio at both genotypic and phenotypic level. Grain breadth had significant positive association with kernel breadth at both genotypic and phenotypic level. Grain L/B ratio had positive significant association with kernel L/B ratio and kernel length at both genotypic and phenotypic levels. Kernel length had positive significant association with kernel L/B ratio at both genotypic and phenotypic level. Kernel breadth had negative significant association with kernel L/B ratio at both genotypic and phenotypic level. Kernel L/B ratio had non-significant negative association with grain yield per plant at both genotypic and phenotypic level.

Table 5: Path co-efficient analysis depicting the direct, indirect effects and genotypic correlations of various characters on grain yield per plant in 25 rice genotypes

Characters	Days to first flowering	Plant height	Number of productive tillers per plant	Number of grains per panicle	100 grain weight	Grain length	Grain breadth	Grain L/B ratio	Kernel length	Kernel breadth	Kernel L/B ratio	Grain yield per plant
Days to first flowering	0.0868	-0.0282	0.0674	0.1946	0.0008	-0.0650	0.3154	0.0027	0.0089	-0.2200	-0.0510	0.312
Plant height	0.0238	-0.1029	-0.0553	-0.0438	0.0020	0.1008	0.2905	0.0058	-0.0083	-0.2185	-0.098	-0.104
Number of productive tillers per plant	0.0191	0.0186	0.3051	0.6450	0.0039	-0.0374	-0.0506	-0.0014	0.0028	0.0388	0.0221	0.966
Number of grains per panicle	0.0244	0.0065	0.2850	0.6906	0.0017	-0.0495	0.0814	0.0000	0.0037	-0.0601	-0.0109	0.973
100 grain weight	-0.0017	0.0100	-0.0586	-0.0598	-0.0206	-0.0446	0.0075	-0.0009	-0.0023	0.0246	-0.0019	-0.148
Grain length	0.0155	0.0285	0.0314	0.0940	-0.0025	-0.3638	0.0403	-0.0079	0.0334	0.0772	0.1416	0.088
Grain breadth	0.0385	-0.0421	-0.0217	0.0789	-0.0002	-0.0206	0.7103	0.0084	0.0068	-0.5228	-0.1571	0.078
Grain L/B ratio	-0.0199	0.0496	0.0360	-0.0053	-0.0008	-0.2403	-0.4976	-0.0121	0.0189	0.4415	0.2217	-0.008
Kernel length	0.0208	0.0228	0.0215	0.0698	0.0016	-0.3246	0.1290	-0.0061	0.0375	-0.0389	0.1123	0.046
Kernel breadth	0.0348	-0.0410	-0.0216	0.0759	0.0009	0.0516	0.6781	0.0097	0.0026	-0.5476	-0.1826	0.061
Kernel L/B ratio	-0.0197	0.0449	0.0301	-0.0335	0.0001	-0.2295	-0.4972	-0.0119	0.0187	0.4455	0.2244	-0.028
Residual effect =	0.2356		Direct effects-D	iagonal bold y	alues							

Indirect effects-Unbold values

Direct effects-Diagonal bold values

In the present investigation, the estimated residual was 0.2356. The traits via., number of productive tillers per plant, number of grains per panicle, grain breadth had recorded high positive direct effect on grain yield per plant. Similar observations were reported by Siva Rami Reddy and Anbuselvam, (2012) ^[13]. The trait, kernel L/B ratio had moderate positive direct effect on grain yield per plant (Table 5). The characters via., days to first flowering, plant height, 100 grain weight, grain length, kernel length, kernel breadth, kernel L/B ratio, grain L/B ratio was found to be positively and negatively negligible values on grain yield per plant. Similar results were reported by Bhadru *et al.* (2011)^[3].

In addition to its direct effect, indirect effect of days to first flowering on grain yield per plant through grain breadth had moderate positive indirect effect. Plant height had moderate positive indirect effect on grain yield per plant via. grain breadth. Number of productive tillers per plant had high positive indirect effect on grain yield per plant via., grain length. Number of grain per panicle had moderate positive indirect effect on grain yield per plant via., number of productive tillers per plant. 100 grain weight had low positive indirect effect on grain yield per plant via., kernel breadth. Similar results obtained by Saravanan and Sabesan (2010)^[12]. Among the grain quality traits grain length had low positive

indirect effect *via.*, kernel L/B ratio. Grain breadth had low positive indirect effect *via.*, days to first flowering and number of grains per panicle. Grain L/B ratio had high positive indirect effect *via.*, kernel breadth and moderate positive indirect effect *via.*, kernel L/B ratio on grain yield per plant. Kernel length had low positive indirect effect *via.*, kernel L/B ratio and grain breadth on grain yield per plant. Kernel breadth had high positive indirect effect *via.*, grain breadth. Kernel L/B ratio had high positive indirect effect *via.*, grain breadth. Kernel L/B ratio had high positive indirect effect *via.*, kernel breadth. Similar findings were made by Damodar Reddy (2012) ^[5].

From the above discussion, it is inferred that the pattern of path coefficient observed in the present study is in agreement with the correlation obtained. In general, grain breadth followed by number of grains per panicle exerted maximum positive direct effect towards grain yield per plant. The high positive direct effect of the grain breadth towards grain yield per plant was nullified by the indirect negative direct effects of the kernel breadth. But, the high positive direct effect of the number of grains per panicle towards grain yield per plant was attributed by the contribution of number of productive tillers per plant. Hence, it may be declared that selection and manipulation of number of grains per panicle would simultaneously improve grain yield per plant.

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