ASSESSEMENT OF GENETIC PARAMETERS AND DETERMINATION OF YIELD COMPONENTS IN RICE (*ORYZA SATIVA* L.) UNDER NATURAL SALINE CONDITION

P. Karthikeyan, M. Venkatesan, R. Eswaran and G. Suganya

Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University,
Annamalai Nagar–608002, Tamilnadu, India.

Abstract

The study was carried out in an effort to assess the extent of genetic divergence, variability, character association and path-coefficient analysis in 40 genotypes of rice for 8 characters *viz.,* days to first flower, plant height, number of tillers per plant, number of panicles per plant, panicle length, number of grains per panicle, thousand grain weight and grain yield per plant. The analysis of variance indicated considerable amount of variability in all genotypes. Based on D^2 analysis six clusters were formed indicating that there were no association between eco-geographical distribution of genotypes and genetic divergence. Based on the inter and intra cluster distances, the genotypes belonging to clusters II, IV, V and VI could be used for hybridization programme. The characters namely grain yield per plant, number of panicles per plant, number of tillers per plant and number of grains per panicle recorded high PCV and GCV. High heritability coupled with high genetic advance as percent of mean was observed for number of grains per panicle, plan height, thousand grain weight, number of tillers per plant, grain yield per plant and number of panicle per plant. The genetic correlation revealed that grain yield per plant had strong positive and significant association with number of panicles per plant, number of tillers per plant, number of grains per panicle and thousand grain weight. Path coefficient analysis indicated that maximum direct effect on grain yield per plant was through number of panicles per plant, number of grains per panicle and thousand grain weight.

Key words : Genetic divergence, variability, correlation, path analysis.

Introduction

Rice (*Orzya sativa* L. 2n=2x=24) is the world's largest food crop, providing the calorific needs of millions of people daily and cultivated in many parts of the world. The genus Oryza belonging to the family Poaceae. Globally, rice is cultivated on 154 million hectares with annual production of around, 600 million tonnes and average productivity of 3.9 tons/ha. Rice is differentially affected by salinity at different stages. Rice is moderately susceptible to salinity, since most rice plants are severely injured at an EC 8-10 dS/m and yield reduction is estimated at 30-50 percent (Babu *et al.,* 2005). Variation among crop species is the gift of nature. Genetic variability is a prerequisite for response to selection in respect of any biological population, it would be appropriate to consider variability inconsonance with genetic diversity. The increase in productivity is mainly depending on exploitation of genetic resources already present in the ecosystem.

The success of any plant breeding programme largely depends on the diversity exist among the genotypes (Allard, 1960). Only 15% of the genetic diversity has been utilized so far. The "morphism" was used by Huxley (1955) for genetic diversity implying "genetic polymorphism" which means the coexistence of distant genetic forms in population. Thus, the variability could be estimated by studying the existence of genetic divergence among the rice genotypes under natural saline condition before embarking upon hybridization and selection.

Materials and Methods

The material for the present investigation consisted of 40 rice genotypes. The experiment was conducted at the Plant Breeding Farm (11º24' N latitude and 79º 44' E longitude, +5.79MSL), Faculty of Agriculture, Annamalai University, Annamalai nagar, Tamil Nadu, India during the year 2016-17. The experiment was laid out in a Randomized Block Design with three replications, using

20 x 20 cm spacing. These genotypes were grown in natural saline soil with electrical conductivity(EC) of 3.83 dS/m. All there commended agronomical practices and plant protection measures were followed to ensure normal crop. Observations were recorded on ten randomly selected plants for all characters. The analysis of variance was performed as per the standard statistical procedures (Singh and Chaudhary, 1985). The Mahalanobis D^2 distance was calculated to estimate the genetic divergence (Mahalanobis, 1936). The genotypes were grouped into different clusters on the basis of D^2 values, as suggested by (Rao, 1952). The intra and inter cluster distance was calculated as per Singh and Chaudhary (1985). Genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), was estimated, broad senseheritability (h^2) and geneticadvance as per cent of mean by Singh and Chaudhary (1985). The genotypic and phenotypic correlation co-efficient were worked out following Aljibouri *et al.,* (1958). The direct and indirect effect of yield attributing traits were calculated through path co-

suggesting that the genotypes selected for the present study were genetically divergent. This indicates that there is ample scope for selection of promising varieties from the present genepool for yield and its components. Significant variability due to genotypes for all the characters was also confirmed by Nayak *et al.,* (2004) and Sabesan *et al.,*(2009). Here the 40 genotypes were grouped into 6 clusters (Table 2). The clustering pattern of the genotypes indicated that there was little parallelism between geographical origin and genetic diversity. Similar results were reported by many workers (Nayak *et al.,* 2004). Cluster I encompasses the largest number of 20 genotypes followed by clusters III with eight genotypes and clusters IV had six genotypes. Cluster V comprise of three genotypes, clusters II had two genotypes and cluster VI is monogenotypic cluster.

The intra and inter cluster distances of various characters are tabulated in table 3. The intra cluster distance varied from 0.00 (cluster VI) to 13.01 (cluster V). Inter cluster distance was maximum between II and VI (16.31) followed by clusters I and VI (16.17) and

Table 1: Analysis of variance for eight characters in rice genotypes.

Source	Df	Days to first flower (days)	Plant height (cm)	No. of tillers per plant	No. of panicles per plant	Panicle length (cm)	No. of grains per panicle	Thousand grain weight (g)	Grain yield per plant (g)
		MSS							
Replication	2	47.18	28.33	4.11	6.58	1.38	1.31	1.26	26.94
Genotype	39	77.04**	506.59**	54.70**	38.81**	16.73**	2190.41**	26.50**	312.89**
Error	78	8.44	10.93	2.82	2.91	1.62	46.01	0.57	16.27

**significant at 1 per cent level.

Table 2: Distribution of rice genotypes in different clusters based on D^2 analysis.

Cluster No.	Number of genotypes	List of the genotypes
I	20	ADT 36, ADT 37, ADT 39, ADT 41, ADT 42, ADT 43, ADT 45, ADT 46, ADT 47, ADT 48, ADT 49, ADT 50, CO 49, CO 50, IR 64, IR 72, ASD 16, TRY 2, GAYATHRI
II	2	VIJAY MASOORI, JAI SHRIRAM
III	8	TRY 3, TKM 9, PMK 3, AD 06207, TPS 5, ANNA 4, MDU 4, MTU 1010
IV	6	NLR 34449, RNR 1446, BPT 5204, MTU 1001, JAI JAILU, SWARNA
V	3	TN 1, UMA, ASD 19
VI	1	PY 3

efficient analysis as suggested by Wright (1921) and elaborated by Dewey and Lu (1959).

Results and Discussion

Genetic Divergence

The analysis of variance for different characters are presented in table 1. It revealed presence of significant differences among all the genotypes for all eight characters under study at 5 per cent level of significant

Table 3: Intra (bold) and inter cluster (unbold) distances of various characters in rice.

Cluster No.	I	II	III	IV	V	VI
I	10.66	10.54	12.74	12.04	11.94	16.17
II		4.13	14.53	9.29	12.13	16.31
III			12.56	14.92	12.58	15.98
IV				10.45	12.08	15.33
V					13.01	15.41
VI						0.00

cluster III and VI (15.98) suggesting wider distance to get more variability and high heterotic effect. This clearly indicates that the genotypes included in these clusters are having broad spectrum of genetic diversity. Minimum inter cluster distance existed between cluster 11 and IV (9.29) followed by I and II (10.54) and I and V (11.94) reflecting minimum diversity among the genotypes within the respective cluster. This is in conformity with the findings of Venkatesan (2004). The genotypes included in cluster I originated from different origin indicating that there was no parallelism between clustering pattern and geographic distribution of genotypes Nayak *et al.,* (2004). The kind of diversity belonging to same geographic origin might be due to difference inadoption, selection criteria, selection pressure in environmental conditions (Maurya

and Singh, (1977), Shanmugasundaram *et al.,* (2000), Sandeep *et al.,* (2013).

Variability Studies

Variability available in a population is an asset to a plant breeder in any crop improvement programme (table 4). A high estimate of PCV and GCV recorded for grain yield per plant (35.68 & 33.04), number of panicles per plant (31.64 & 28.32), number of tillers per plant (28.28 & 26.58) and number of grains per panicle (21.23 & 20.53) and this is similar with the findings of Augustina *et al.,* 2013. A narrow difference between PCV and GCV values suggestive of the fact that the characters studied indicated that these traits are less susceptible to the environment condition and therefore selection for such traits will be rewarding as the genetic factors play the greater role in determining the variability for these characters.

High heritability and genetic advance as percent of mean was recorded for all the characters. Characters suchas number of grains per panicle (93.97 & 41.04), plant height (93.78 & 30.13), thousand grain weight (93.53 & 30.31), number of tillers per plant (88.29 & 51.35), grain yield per plant (85.77 & 63.13) and number of panicles per plant (80.58 &

Table 4: Magnitude of variability, heritability and genetic advance as per cent of mean.

Characters	Coefficient of variation		Heritability (%)	Genetic advance as per cent of mean
	Phenotypic (%)	Genotypic (%)		
Days to first flower (days)	8.75	7.44	73.07	13.17
Plant height (cm)	15.61	15.10	93.78	30.13
Number of tillers per plant	28.28	26.58	88.29	51.35
Number of panicles per plant	31.64	28.32	80.58	52.44
Panicle length (cm)	11.55	10.04	75.44	17.87
Number of grains per panicle	21.23	20.53	93.97	41.04
Thousand grain weight (g)	15.71	15.25	93.58	30.31
Grain yield per plant (g)	35.68	33.04	85.77	63.13

Table 5: Phenotypic and genotypic correlation coefficients among yield attributing characters in rice genotypes.

Characters		Days to first flower (days)	Plant height (cm)	No. of tillers per plant	No. of panicles per plant	Panicle length (cm)	No. of grains per panicle	Thousand grain weight (g)	Grain yield per plant (g)
Days to first flower (days)	P	1.00	0.16	0.06	0.15	0.03	0.14	0.02	0.28
	G	1.00	0.19	0.15	0.23	-0.03	0.17	0.07	0.34**
Plant height (cm)	P		1.00	0.09	0.08	0.25	0.00	0.07	0.07
	G		1.00	0.09	0.09	0.31	-0.00	0.07	0.08
Number of tillers per plant	P			1.00	0.94**	0.04	-0.13	-0.05	0.61**
	G			1.00	0.98**	0.05	-0.15	-0.05	0.62**
No. of panicles per plant	P				1.00	0.07	-0.15	0.00	0.69**
	G				1.00	0.07	-0.15	-0.00	0.65**
Panicle length (cm)	P					1.00	-0.04	0.02	0.05
	G					1.00	-0.05	0.05	0.05
No. of grains per panicle	P						1.00	-0.27	0.34*
	G						1.00	-0.27	0.45**
Thousand grain weight (g)	P							1.00	0.37*
	G							1.00	0.36*
Grain yield per plant (g)	P								1.00
	G								1.00

*significant at 5 per cent level, **significant at 1 per cent level. P- Phenotypic correlation coefficient, G- Genotypic correlation coefficient.

Table 6: Path coefficients analysis showing direct and indirect effects of yield attributing characters in rice genotypes.

Characters	Days to first flower (days)	Plant height (cm)	No. of tillers per plant	No. of panicles per plant	Panicle length (cm)	No. of grains per panicle	Thousand grain weight (g)	Grain yield per plant (g)
Days to first flower (days)	0.041	-0.007	-0.023	0.191	-0.000	0.123	0.037	0.367
Plant height (cm)	0.005	-0.038	-0.018	0.092	0.009	-0.000	0.034	0.098
Number of tillers per plant	0.003	-0.002	-0.160	0.879	0.000	-0.073	-0.018	0.633
No. of panicles per plant	0.008	-0.006	-0.151	0.918	0.003	-0.089	-0.000	0.659
Panicle length (cm)	-0.003	-0.013	-0.004	0.054	0.024	-0.021	0.020	0.051
No. of grains per panicle	0.006	0.000	0.018	-0.124	-0.000	0.637	-0.115	0.431
Thousand grain weight(g)	0.004	-0.004	0.007	-0.001	0.000	-0.158	0.478	0.341

Residual effect = 0.1784341   Direct effect - diagonal bold values   Indirect effect - un bold values

52.44) expressed both high heritability and high genetic advance as per cent of mean. 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 improvement of these traits. Days to first flower and panicle length was accompanied by moderate estimate of genetic advance as percent of mean and high estimation of heritability, which indicated preponderance of non-additive gene action hence selection cannot be rewarding which was also agreed by Berhanu *et al.,* (2013) and Aishwarya Singh Rajput *et al., (*2014).

Correlation Studies

The genotypic correlation coefficient was higher in magnitude than the corresponding phenotypic correlation coefficient in general for most of the characters (Table 5). This is possibly due to the linkage or modifying effect of the gene and environment in genetic association between characters. There were strong positive and significant phenotypic and genotypic correlation between grain yield per plant and number of panicles per plant (0.69 & 0.65) followed by number of tillers per plant (0.61 & 0.62), number of grains per panicle (0.34 & 0.45) and thousand grain weight (0.37 & 0.36). This positive association of these yield contributing characters with grain yield per plant was also reported by Kannan and Sarvanan, (2013).

Path Coefficient Analysis

Path analysis furnishes a method of partitioning the correlation coefficients into direct and indirect effects and measures the relative importance of the casual factors involved. Here the residual effect was 0.1784341. The maximum direct effect of number of panicles per plant (0.918) was noted over grain yield per plant, followed by number of grains per panicle (0.637) and thousand grain weight (0.478). Almost similar results were reported by Ramesh Babu and Raghava Reddy (2006). In addition to its direct effect, indirect effect of number of tillers per

plant via number of panicles per plant was high (0.879) and positive on grain yield per plant (0.633). The indirect effect of thousand grain weight was positive via days to first flower (0.004), number of tillers per plant (0.007) and panicle length (0.000). The character days to first flower, panicle length, number of tillers per plant and plant height exhibited variable performance for direct and indirect effect and more similarly for correlation coefficient. Hence, selection of such characters could be postponed to later generations until there is favorable and constant association of genes controlling the characters.

The superior genotypes of cluster II may be crossed with any superior genotypes cluster VI to produce good segregants with more suitable traits for higher yield. The narrow difference between PCV and GCV values is suggestive of the fact that phenotypic variation was determined by large by genotype with negligible influence of extraneous factors and therefore selection for such traits will be rewarding. For association analysis, direct yield contributing characters, namely, number of panicles per plant, number of grains per panicle and thousand grain weight showing positive association with grain yield per plant reflected that these characters can be enhanced simultaneously to improve grain yield per plant.

References

Rajput, A.S., G. Suresh Babu and M. Bhatti (2014). Genetic diversity of irrigated medium duration of rice genotypes suited for eastern plain zone of U.P. *Journal of Agricultural and Veterinary Science,* **7(3):** 42-45.

Aljibouri, H.A., P.A. Miller and H.F. Robinson (1958). Genotypic and environmental variance and covariance in upland cotton cross of inter specific origin. *Argon. J.,* **50:** 633-636.

Allard, R.W. (1960). Principles of plant breeding. John Wiley and Sons Inc., New York.

Augustina, U.A., B.P. Iwunor and O.R. Ijeoma (2013). Heritability and character correlation among some rice genotypes for

yield and yield components. *J. Plant breed. Genet.*, **1(2):** 73-84.

Babu, S., J. Malarmathi, A. Sheeba, P. Yogameenakshi and P. Rangasamy (2005). Stability in performance of salt tolerant rice hybrids. *Oryza*, **42:** 222-224.

Berhanu, D.B., S. Rakhia, G.K. Naveen, P.J. Kundur and H.E. Shashidhar (2013). Estimation of genetic variability and correlation studies for grain zinc concentrations and yield related traits in selected rice (*Oryza sativa* L.) genotypes. *Asian J. Exp. Biol. Sci.,* **4(3):** 391-397.

Burton,G.W. (1952). Quantitative inheritance in grasses. Proc. 6th Interaction. *Grassland Cong.*

Dewey, D.R. and K.H. Lu (1959). A correlation and Path coefficient analysis of component of crested wheat grass seed production. *Agron. J.,* **51:** 515-518.

Huxley, J. (1955). Morphism and Evaluation, Heritiability, **9:**1-5.

Kannan, K. and K. Saravanan (2013). Studies on Genetic Divergence for Yield and Yield contributing traits in some improved genotypes of rice (*Oryza sativa* L.). M.Sc. (Ag.) Thesis, Annamalai Univ., Annamalainagar, India.

Mahalanobis, P.C. (1936). On the generalized distance in statistics. Poc. Nat. *Inst. Sci. (India)*, **2:** 49-55.

Maurya, D.M. and D.P. Singh (1977). Genetic divergence in rice. *Indian J. Genet.,* **37(3):** 395-402.

Nayak, A.R., D. Chaudhary and J.N. Reddy (2004). Genetic divergence in scented rice. *Oryza*, **41:** 79-82.

Ramesh Babu, P. and P. Raghava Reddy (2006). Correlation and path analysis between yield and yield components in twenty one F_1 non basmathi rice crosses. Second Natl. Plant Breed. Cong. TNAU, Coimbatore., 1-3 March, p 70-71.

Rao, C.R. (1952). Advanced Statistical Methods in Biometrical Research. *John Wiley and Sons, Inc.,* New York.

Sabesan, T., K. Saravanan and A. Anandan (2009). Genetic divergence analysis for certain yield and quality traits in rice (*Oryza sativa L.)* grown in irrigated saline low land of Annamalai nagar, South India. *Central European J. Agric.*, **10(4):** 405-410.

Soni, S.K., V.K. Yadav, N. Pratap, V.P. Bhadana and T. Ram (2013). Selection criteria, yield relationship with components traits and grouping of tropical japonica, indica lines and derived hybrids of rice (*Oryza sativa L.). SAARC J. Agric.*, **11(2):** 17-32.

Shanmugasundaram, P., J. Souframanien and S. Sadasivam (2000). Genetic divergence among rice varieties released from paddy breeding station, Coimbatore, India. *Oriza*, **37(3):** 225-228.

Venkatesan, M. (2004). Studies on genetics of certain economic characters in rice (*Oryza sativa* L.). Ph.D. Thesis, Annamalai Univ., Annamalainagar, India.

Wright, S. (1921). Correlation and association. *J. Agric. Res*., **20:** 550-587.

Singh, R.K and B.D. Chaudhary (1985). Biometrical Methodsin Quantitative Genetic Analysis (3rd Ed). Kalyani Publishers, New Delhi-Lu.