

VARIABILITY, HERITABILITY GENETIC ADVANCE AND GENETIC DIVERSITY ANALYSIS FOR ECONOMIC TRAITS IN RICE (*Oryza sativa*) GENOTYPES

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ABSTRACT

The present investigation consists of forty rice genotypes and the experiment was conducted during 2016 in Randomized Block Design with three replications. The data were recorded for eight economic traits to study genetic variability, heritability, genetic advance and diversity analysis. Analysis of variance among forty genotypes showed significant differences for all traits studied. Highest genotypic co-efficient of variation (GCV) and phenotypic co-efficient variation (PCV) was observed for grain yield per plant followed by number of panicles per plant. Indicating that these characters could be used as selection parameters for crop improvement. Highest heritability were observed for all the traits studied. High genetic advance as percent of mean were observed for grain yield per plant and followed by thousand grain weight, indicating predominance of additive gene effects and possibilities of effective reselection for the improvement of these traits. In clustering pattern grouped in to six clusters revealed that considerable diversity existed in and both clusters. Therefor keeping in view of yield potential and other characteristics, it is suggested that hybridization might be carried out among distantly related parents to clusters II, IV, V and VI could be suitable for grain yield and other characteristics in hybridization programme to achieve desired sergeants.

Keywords: Variability, heritability, genetic advance and diversity.

INTRODUCTION

Breeding programmes for improvement of crops involving a large population needs prediction of genetic advance, which is facilitated by obtaining phenotypic and genotypic coefficients of variation in the absence of which field evaluation of every genotype would be physically less feasible. Hence there is iced to study variability. Variability for different traits in the source population is a prerequisite for crop improvement since all attempts of breeding and selection would be futile unless major portion of variability is heritable. Mather (1949) indicated

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that the success of crop improvement programme depends on the definition and assembly of the required genetic variations and selection for yield through highly heritable characters, excluding the environmental components. Therefore in view of the aforesaid facts, an investigation was carried out with 102 rice genotypes to explore the genetic variability by determining the magnitude of genetic coefficient of variation, heritability and genetic advance for ratoon grain yield and its contributing traits.

MATERIALS AND METHODS

The present investigation was conducted at the Plant Breeding Farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalai Nagar, Tamil Nadu, India during the year 2015-16. Seeds of forty rice genotypes collected from various places were utilized for the study. The details of the materials are presented in Table 1.

Seeds of the forty genotypes were sown in raised nursery beds during January, 2018. The 25-days old seedlings were transplanted to the main field. These genotypes were grown in saline soil with electrical conductivity (EC) of 3.83 dsm^{-1} . The experiments were conducted at the experimental Farm of Plant Breeding ($11^{\circ}24'$ N latitude and $79^{\circ}44'$ E longitude, + 5.79 m MSL), Annamalai University, Tamil Nadu, India. The experiment was laid out in a Randomized Block Design with three replications, using 20×20 cm spacing.

Observations recorded on 40 rice genotypes for eight 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 were subjected to statistical analysis and the results are presented below.

Observations were recorded and the data was subjected to statistical analysis. Statistical analysis for the above characters were done following Rao (1952) for clustering pattern, Burton (1952) for Co-efficient of variation, Lush (1949) for heritability and genetic advance.

RESULT AND DISCUSSION

The present investigation was carried out with 40 rice genotypes collected from different eco-geographical regions of India. Observations were recorded on various quantitative and qualitative characters as per the standard evaluation system descriptor. The data recorded were subjected to various statistical analysis namely variability, heritability, genetic advances as percent of mean.

The analysis of variance for different characters are presented in Table 2. The treatment *i.e* mean sum of square due to genotypes showed significant differences for all eight characters under study at 5 per cent level of significant 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 gene pool for yield and its components.

Employing Mahalanobis generalized distance, the divergence in 40 genotypes of rice were estimated for yield characters under natural saline condition. The results are furnished in Table 3.

Table 1. List of genotypes used in study

S. No.	Name of genotype	ORIGIN	S. No.	Name of genotype	ORIGIN
1	ADT36	TRRI, TN, India	21	TKM9	RRS, Tirur, India
2	ADT37	TRRI, TN, India	22	PMK3	ARS, Paramkudi, India
3	ADT39	TRRI, TN, India	23	AD 06207	TRRI, Aduthurai, T.N, India
4	ADT41	TRRI, TN, India	24	TPS5	ARS, Thirupathisaram, India
5	ADT42	TRRI, TN, India	25	ANNA 4	ARS, Paramkudi, India
6	ADT43	TRRI, TN, India	26	MDU4	Agricultural College, Madurai, India
7	ADT45	TRRI, TN, India	27	NLR 34449	A.N.G.R.A.U Research station, A.P, India
8	ADT46	TRRI, TN, India	28	RNR 1446	A.N.G.R.A.U Research station, A.P, India
9	ADT47	TRRI, TN, India	29	BPT 5204	Agricultural college, Bapatla, India
10	ADT48	TRRI, TN, India	30	MTU 1001	ARS, Maruteru, A.P, India
11	ADT49	TRRI, TN, India	31	MTU 1010	ARS, Maruteru, A.P, India
12	ADT51	TRRI, TN, India	32	Vijay masoori	Land race, Telangana, India
13	CO 49	AC & RI, Coimbatore, India	33	Jaijailu	Land race, Telangana, India
14	CO 51	AC & RI, Coimbatore, India	34	Jai shriram	Land race, Telangana, India
15	CO 50	AC & RI, Coimbatore, India	35	Swarna	CRRI, Cuttack, India
16	IR64	IRRI, Philippines	36	TNI	Directorate of Rice Research Institute, Hyderabad
17	IR72	IRRI, Philippines	37	Gayathri	CRRI, Cuttack, India
18	ASD 16	RRS, Ambasamudram, T.N, India	38	UMA	Rice Research Station, Monocompu, Kerala

19	TRY 2	Agricultural college and research institute, Trichy, T.N, India.	39	PY3	KVK, Pondicherry, India
20	TRY 3	Agricultural college and research institute, Trichy, T.N, India.	40	ASD 19	RRS, Ambasamudram, T.N, India

Forty genotypes of rice were grouped into six clusters using clustering technique based on the relative magnitude of D values. The compositions of different clusters are presented in Table 11. Cluster I comprised of twenty genotypes, followed by cluster III comprise of eight genotypes, cluster IV had six genotypes, cluster V had three genotypes, cluster II comprise of two genotypes and cluster VI is monogenotypic in nature.

The intra and inter cluster distances among the eight clusters were determined and are presented in Table 4. The intra cluster distance ranged from 0.00 to 13.03. The cluster VI showed minimum intra cluster distance (0.00) since it contained a single genotype and maximum intra cluster distance was exhibited by cluster V (13.03) followed by cluster III (12.61).

The inter cluster distance varied from 9.27 to 16.34. Highest inter cluster distance was observed between clusters II and VI (16.34). This was followed by clusters I and VI (16.14), clusters III and VI (15.95) and clusters V and VI (15.47). Lowest inter cluster distance was recorded between clusters II and IV (9.27), followed by clusters I and II (10.52) and clusters I and V (11.92).

The cluster mean values for eight characters were studied. They are presented in Table 5. Concised accounts of results are given below character wise.

Days to first flower: Among the six clusters, the cluster V took minimum number of days to first flower (59.71 days). This was followed by cluster I (63.13 days), cluster VI (64.26 days) and cluster III (65.10 days). However the cluster II recorded a maximum of 70.76 days. Two clusters registered (I and V) registered lower values than the general mean of 64.05 days.

Plant height: The cluster I (82.42 cm) recorded minimum cluster value while the cluster VI (123.46 cm) showed high mean value for plant height. Three clusters exhibited lower values than the general mean of 84.92 cm.

Number of tillers per plant: The maximum and minimum cluster mean value for number of tillers per plant was observed in cluster V (19.86) and cluster VI (13.53) respectively. Four clusters namely clusters II, III, IV and V exhibited higher values than the general mean of 15.73 for this trait.

Number of panicles per plant: For number of panicle per plant the cluster mean performance was varied from 10.93 to 14.97. The highest and least cluster mean value for number of panicles per plant was recorded in cluster V (14.97) and cluster VI (10.93) respectively. Among the six clusters, cluster II, III, IV and V registered higher values than the general mean of 12.20 for this character.

The contribution of characters towards the total genetic divergence is important in deciding the characters for selection. The relative contribution of individual character towards the expression of genetic diversity estimated over character wise D^2 value is presented in Table 6. Grain yield per plant (49.61 per cent), thousand grain weight (19.35 per cent) and number of grains per panicle (17.05 per cent) were the top three major contributors towards the total genetic divergence among the genotypes.

Plant height (6.02 per cent) and panicle length (3.71 per cent) were moderate contributing factors to genetic diversity. Number of tillers per plant (1.79 per cent), days to first flower (1.28 per cent) and number of panicles per plant (1.15 per cent) contributed least towards genetic diversity.

Variability was measured by estimation of mean, coefficient of variation such as phenotypic coefficient of variation, genotypic coefficient of variation, heritability (broad sense) and genetic advance. Environment plays an important role in the expression of phenotype and genotype facts which are inferred from phenotypic observations.

The estimate of PCV and GCV was studied for all eight characters and are furnished in Table 6. Heritability and genetic advance as per cent of mean was studied for eight characters and presented in Table 6.

The phenotypic coefficient of variation ranged from 8.73 to 35.70 per cent for days to flower and grain yield per plant respectively. Higher magnitude of phenotypic coefficient of variation (PCV) was recorded for grain yield per plant (35.70 per cent) followed by number of panicle per plant (31.62 per cent), number of tillers per plant (28.26 per cent) and number grains per panicle (21.22 per cent). Moderate PCV was observed for panicle length (11.53 per cent), plant height

(15.63 per cent) and thousand grain weight (15.74 per cent). Low PCV was observed for days to first flower (8.73 per cent).

The genotypic coefficient of variation (GCV) is lower than phenotypic coefficient of variation (PCV) for all the traits studied. A wide range of genotypic coefficient of variation (GCV) was observed for traits ranging from 7.46 to 33.07 per cent for days to first flower and grain yield per plant respectively.

High GCV was observed in grain yield per plant (33.07 per cent), number of panicles per plant (28.37 per cent), number of tillers per plant (26.55 per cent) and number of grains per panicle (20.57 per cent) while moderate estimates of GCV was recorded for panicle length (10.01 per cent), plant height (15.13 per cent) and thousand grain weight (15.22 per cent). Low GCV was observed for days to first flower (7.46 per cent).

A perusal of data it is evident that the heritability (broad sense) and genetic advance as per cent of mean was estimated for eight characters of rice genotypes and are presented in the Table 6.

Heritability (h^2)

Heritability is a measure of the extent of phenotypic variation caused by the action of genes. The heritability values ranged from 73.09 to 93.95 per cent days to first flower and number of grains per panicles respectively. High heritability was observed for traits viz; number of grains per panicle (93.95 per cent), plant height (93.76 per cent), thousand grain weight (93.53 per cent), number of tillers per plant (88.27 per cent), grain yield per plant (85.79 per cent), number of panicles per plant (80.53 per cent), panicle length (75.41 per cent) and days to first flower (73.09 per cent).

A perusal of genetic advance as per cent of mean for all the eight characters under study was varied from 13.14 to 63.10 per cent for days to first flower and grain yield per plant respectively. High genetic advance as per cent of mean was observed for grain yield per plant (63.10 per cent), number of panicles per plant (52.45 per cent), number of tillers per plant (51.39 per cent) number of grains per panicle (41.08 per cent), thousand grain weight (30.33 per cent) and plant height (30.19 per cent). Panicle length (17.91 per cent) and days to first flower (13.14 per cent) showed moderate estimate of genetic advance as per cent of mean.

The present study was undertaken to identify genetic diversity, variability, correlation and path analysis among the 40 rice genotypes collected from various sources. Mahalanobis D^2 statistic is a potential tool for estimating genetic diversity as has been emphasized by many workers (Murthy and Arunachalam, 1966; Arunachalam, 1981; Karthikeyan, 2002; Sabesan, 2005).

The analysis of variance revealed presence of significant differences among all the genotypes for eight characters studied and indicated considerable amount of variability in the genotypes. Significant variability due to genotypes for all the characters was also confirmed by Nayak *et al.* (2004), Rajasekaran (2006) and Sabesan *et al.* (2009).

Genetic divergence as measured by Mahalanobis (1936) in terms of generalized distance (D^2) has been one of the important statistical tools to estimate the genetic distance between any two genotypes. It provides rational basis for selection of parents for hybridization programme. Crosses among divergent parents are likely to yield desirable combinations. Therefore, a crossing programme should be initiated between the genotypes belonging to different clusters. In the present investigation the 40 genotypes were grouped into 6 clusters. 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). The genotype of clusters II and VI is most diverse may be selected as donor parent in formulating breeding programme which could be utilized for getting desirable segregants and high heterotic response. This is in conformity with the findings of Karthikeyan (2002), Venkatesan (2004).

The clustering pattern of genotypes revealed that the genotypes from different centres or states were clubbed together or genotypes originated from same centre or states were distributed in different cluster. 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 distribution of genotypes also indicated that the genotypes from Telangana and Andhra Pradesh were distributed in different clusters. Therefore the kind of diversity belonging to same geographic origin might be due to difference in adoption, selection criteria, selection pressure in environmental conditions (Maurya and Singh, 1977; Shanmugasundaram, 2000; Sandeep *et al.*, 2013).

The mean performance of cluster IV, the largest cluster had desirable mean value higher than the general mean for six characters viz., plant height, number of tillers per plant, number of panicles per plant, number of grains per panicle, thousand grain weight and grain yield per plant and also

cluster V is the largest cluster had mean value higher than the general mean for six clusters viz., number of tillers per plant, number of panicles per plant, thousand grain weight and grain yield per plant. For days to first flower and plant height are less than the general mean.

In all the combinations of inter cluster distances each character is recorded on the basis of inter cluster distances. Percentage contribution of each character is calculated on the basis of these ranks. Grain yield per plant (49.61 per cent), thousand grain weight (19.35 per cent) and number of grains per panicle (17.05 per cent) were the major contributors towards the total genetic divergence among the genotypes tested. Similar findings were made by Sabesan *et al.* (2009) and Arivoli *et al.* (2009) for number of grains per panicle and grain yield per plant, Senguttuvel *et al.* (2013).

Other characters like plant height (6.02 per cent), panicle length (3.71 per cent), number of tillers per plant (1.79 per cent) and days to first flower (1.28 per cent) were also contributed in differentiating genotypes morphologically, number of panicles per plant (1.15 per cent) had the minimum contribution to the total divergence. The major traits contributing to total divergence may be utilized as parents in selecting genetically diverse parents.

Manonmani and Khan (2004) stated that merely the presence of high amount of genetic diversity in a population may not be adequate to effect crop improvement over best existing cultivars. Singh *et al.* (1987) opined that while considering the genetic diversity among the parents to be included in hybridization programme, their yield potential should not be ignored.

It is necessary to carefully analyze the selection of a particular cluster from which genotypes are to be chosen in crossing programme as well as selection of a particular genotype from a selected cluster. While selecting genotypes from distinct cluster for hybridization programme their per se performance of different traits should also be given due importance depending upon the traits to be combined.

The present investigation revealed that considerable diversity existed both in and between clusters. Therefore keeping in view of yield potential and other characteristics, it is suggested that the hybridization might be carried out among the distantly related parents belonging to clusters II, IV, V and VI could be suitable for grain yield and other character in hybridization programme to achieve desired segregants.

The analysis of variance for various characters, gave a clear picture of the existence of wide genetic variability among the genotypes chosen for the study, as indicated by the significant

differences at genotypic level. In the present investigation, phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV). High PCV estimates were recorded for the characters viz., grain yield per plant, number of panicles per plant, number of tillers per plant and number of grains per panicle indicating their greater role of contribution to the variability among the genotypes. Similar observations were observed by Agustina *et al.* 2013, Kulanthaivel and Sabesan, 2014 for grain yield per plant. Moderate PCV estimates were registered for the traits namely thousand grain weight, plant height and panicle length. This is in conformity with the findings of Chanbeni *et al.* 2012. Low PCV estimates were recorded for the trait days to first flower.

A high estimate of PCV and GCV recorded for grain yield per plant, number of panicles per plant, number of tillers per plant and number of grains per panicle and this is agreement with the findings of Agustina *et al.*, 2013. A moderate estimate of PCV and GCV was recorded by thousand grain weight, plant height and panicle length. This is in uniformity with the findings of Chanbeni *et al.*, 2012 and Pratap *et al.*, 2012 for days to first flower, plant height and panicle length.

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. Such recommendations are also made by Karuppaiyan *et al.* (2013).

A quantitative estimate of that portion of variability which is due to genetic effect termed as heritability provides information of the relative practicability of selection and to determine the extent to which the character will respond to selection pressure. However, heritability and genetic advance when calculated together would prove more useful in predicting the resultant effect of selection on phenotypic expression, without genetic advance the estimates of heritability will not be of practical value and emphasized the concurrent use of genetic advance along with heritability (Jonson *et al.*, 1955).

High heritability was recorded for all the characters. Characters such as number of grains per panicle, plant height, thousand grain weight, number of tillers per plant, grain yield per plant and number of panicles per plant 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. Similar findings were also reported by Kulanthaivel and Sabesan (2014).

Days to first flower and panicle length was accompanied by moderate estimate of genetic advance as per of mean and high estimate of heritability, which indicated preponderance of non-additive gene action hence selection cannot be rewarded which was also agreed by Berhanu *et al.* 2013 and Aishwarya Singh Rajput *et al.* 2014.



Table 2. Analysis of variance for eight characters in rice genotypes

S. No.	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							
1	Replication	2	47.12	28.37	4.14	6.54	1.31	1.30	1.29	26.91
2	Genotypes	39	77.02**	506.66**	54.71**	38.86**	16.76**	2190.58**	26.34**	312.97**
3	Error	78	8.41	10.99	2.32	2.89	1.64	46.05	0.59	16.37

**Significant at 1 per cent level



Table 3. Distribution of rice genotypes in different clusters based on D² analysis

Cluster No.	Number of Genotypes	List of the genotypes
I	20	ADT 36, ADT37, ADT 39, ADT41, ADT 42, ADT 43, ADT 45, ADT 46, ADT 47, ADT 48, ADT 49, ADT 50, Co 49, Co 51, Co 50, IR 64, IR 72, ASD 16, TRY2, GAYATHRI
II	2	Vijay Masoori, Jai Shriram
III	8	TRY 3, TKM 9, PMK 3, AD O6207, TPS 5, ANNA 4, MDU4, MTU 1010
IV	6	NLR 34449, RNR 1446, BPT 5204, MTU 1001, Jaijailu, Swarna
V	3	TN 1, UMA, ASD 19
VI	1	PY3

Table 4. Average intra (bold) and inter cluster D and D² (unbold) values in rice.

Cluster No.		I	II	III	IV	V	VI
I	D	(10.70)	(10.52)	(12.72)	(12.01)	(11.92)	(16.14)
	D ²	114.53	110.79	161.92	144.31	142.15	260.68
II	D		(4.16)	(14.55)	(9.27)	(12.12)	(16.34)
	D ²		17.37	211.78	85.99	147.11	267.17
III	D			(12.61)	(14.98)	(12.52)	(15.95)
	D ²			159.103	224.41	156.92	254.44
IV	D				(10.49)	(12.02)	(15.32)
	D ²				110.07	144.51	234.77
V	D					(13.03)	(15.47)
	D ²					169.83	239.60
VI	D						(0.00)
	D ²						0.00

Parenthesis – D values

Table 5. Cluster means of rice genotypes for different traits

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Days to First Flower (days)	63.13	70.76	65.10	65.60	59.71	64.26
Plant height (cm)	82.42	85.27	87.27	83.86	84.43	123.46
Number of tillers per plant	14.31	18.60	16.35	16.98	19.86	13.53
Number of panicles per plant	11.30	14.00	12.80	12.62	14.97	10.93
Panicle Length (cm)	22.73	21.51	22.31	22.15	21.62	22.64
Number of grains per panicle	129.50	161.66	101.96	157.91	125.77	144.20
Thousand grain weight (g)	18.29	15.64	20.72	19.88	21.39	23.18
Grain yield per plant (g)	26.56	35.54	26.74	39.16	38.28	36.37



Table 6. Variability, heritability, genetic advance as percent of mean and character contribution for various traits in rice

Characters	PCV (%)	GCV (%)	Heritability (%)	Advance as percent of mean	Character contribution (%)
Days to first flower (Days)	8.73	7.46	73.09	13.14	1.28
Plant Height (cm)	15.63	15.13	93.76	30.19	6.02
Number of tillers per plant	28.26	26.55	88.27	51.39	1.79
Number of panicles per plant	31.62	28.37	80.53	52.45	1.15
Panicle length (cm)	11.53	10.01	75.41	17.91	3.71
Number of grains per panicle	21.22	20.57	93.95	41.08	17.05
Thousand grain weight (g)	15.74	15.22	93.53	30.33	19.35
Grain yield per plant (g)	35.70	33.07	88.79	63.10	49.61

REFERENCES

1. Aishwarya Singh Rajput, G. Suresh Babu and Mahendra Bhatti. 2014. Genetic Diversity of irrigated medium duration of rice genotypes suited for eastern plain zone of UP. *Journal of Agricultural and Veterinary Science*, 7(3): 42-45.
2. Arivoli, V., K.Saravanan and M. Prakash. 2009. A study on D² analysis in rice. *Intl. J. Pl. Set*, 4(1): 157-160.
3. Arunachalam, V. (1981). Genetic divergence in plant breeding. *Indian J. Genet.*, 14: 226-236.
4. Augustina, U.A., Bokoch P. Iwunor, Okechukwu R. Ijeoma. 2013. Heritability and character correlation among some rice genotypes for yield and yield components. *J. Plant breed. Genet.*, 1(2): 73-84.
5. Berhanu D.B., S. Rakhia, G.K. Naveen, P.J. Kundur, 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.
6. Burton, G.W. 1952. Quantitative inheritance in grasses. Proc. 6th Interaction. *Grassland Cong.*
7. Chanbeni Y. Ovung, G.M. Lai and Prashant Kumar Rai. 2012. Studies on genetic diversity in Rice (*Oryza sativa* L.). *Journal of Agricultural Technology*, 8(3): 1059-1065.
8. Jonson, H.W., H.F. Robinson and R.E. Comstock. 1955. Genotypic and phenotypic correlation in soybean and their implications in selection. *Agron. J.*, 74: 477-483.
9. Karthikeyan, T. 2002. Studies on genetic divergence and genotype environment interaction in rice. *M.Sc. (Ag.) Thesis, Annamalai Univ., Annamalainagar, India.*
10. Karuppaiyan, R., Chandra Kapoor and R. Gopi. 2013. Variability, heritability and genetic divergence in lowland rice genotypes under the mid-hills of Sikkim. *Oryza*, 50(1): 81-84.

11. Kulanthaivel, M. and T. Sabesan. 2014. Studies on Genetic Divergence in rice (*Oryza sativa* L.). *M.Sc. (Ag.) Thesis, Annamalai Univ., Annamalainagar, India.*
12. Lush, J.L. 1949. Heritability of Quantitative characters in Farm Animals. *Hereditatis Lund. (Suppl): 356-387.*
13. Manalanobis, P.C. 1936. On the generalized distance in statistics. *Poc. Nat. Inst. Sci. (India), 2: 49-55.*
14. Manonmani, S. and A.K.F. Khan. 2004. Relationship between expression of heterosis and parental divergence in rice. *Madras Agric. J., 91: 202-205.*
15. Maurya, D.M. and D.P. Singh. (1977). Genetic divergence in rice. *Indian J. Genet., 37 (3): 395-402.*
16. Murthy, B.R. and V. Arunachalam. 1966. The nature of genetic divergence in relation to breeding system in crop plants. *Indian J. Genet., 26: 188-198.*
17. Nayak, A.R., D. Chaudhary and J.N. Reddy. 2004. Genetic divergence in scented rice. *Oryza, 41: 79-82.*
18. Pratap N., P.K. Singh, R. Shekhar, S.K. Soni and A.K. Mall. 2012. Genetic variability, character association and diversity analysis for economic traits in rice (*Oryza sativa* L.). *SAARCJ. Agri., 10(2): 83-94.*
19. Rajasekaran, A. 2006. Studies on genetic divergence of *indica* and *japonica* (*Oryza sativa* L.). *M.Sc. (Ag.) Thesis, Annamalai Univ., Annamalainagar, India.*
20. Rao, C.R., 1952. Advanced statistical method in biometrical research. *John Wiley and Sons Inc., New York.*
21. Sabesan, T. 2005. Studies on the genetics of quality traits in rice (*Oryza sativa* L.). *Ph.D Thesis, Annamalai Univ., Annamalainagar, India.*
22. 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 Annamalainagar, South India. *Central European J. Agric, 10(4): 405-410.*

23. Sandeep Kumar Soni, 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.). *SAARCJ. Agri.*, 11(2): 17-32.
24. Senguttuvel, P., K. Thiyagarajan, C. Vijayalakshmi, S. Geetha, J.R. Kannan Bapu, and B.C. Viraktamath. 2013. Genetic divergence of *Indica* rice genotypes in saline and non-saline environmental conditions. *African Journal of Agric. Res.*, 8(48): 6234-6240.
25. 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.
26. Singh R.K. and Chaudhary, B.D. 1985. Biometrical methods in quantitative, genetic analysis, Kalyani Publishers, New Delhi, India, P.303.
27. Singh, R.S., R.P. Singh, D.M. Mourya and O.P. Verma. 1987. Genetic divergence among low land rice cultivars. *Indian J., Genet.*, 47: 11-14.
28. Surek, H and Beser, N. 2003. Correlation and path co-efficient analysis for some yield-related traits in rice (*Oryza sativa*) under terrace conditions. *Truk, J, Agric. For* 27: 77-83
29. Venkatesan, M. 2004. Studies on genetics of certain economic characters in rice (*Oryza sativa* L). *Ph.D Thesis, Annamalai Univ., Annamalainagar, India.*