

## Variability and Genetic Divergence Studies for Yield and Yield Component Traits in Rice (*Oryza sativa* L.) Genotypes in Hill Zone of Karnataka

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**Abstract** Variability and genetic diversity studies was conducted in 100 rice genotypes under hill zone condition. Variability studies reveal the presence of genetic variability in rice genotypes. Analysis of variance found to be significant for all the traits except for days to maturity. High phenotypic and genotypic co-efficient of variability observed for the traits panicle length and number of grains per panicle and also these two traits shows high heritability coupled with high genetic advance. Nature and magnitude of genetic diversity among rice genotypes was assessed in the present study by using mahalanobis  $D^2$  statistics. The 100 rice genotypes grouped in to eleven clusters out of which cluster IX has highest genotypes (20) in its cluster. Highest intra cluster distance was showed by the cluster VII (42.81) and highest inter cluster distance between the clusters IX and XI (66.87). The highest cluster mean was

shown by the cluster IV and contribution of each trait towards the diversity was more for the trait grain yield per plant. In the present study the genotypes viz. IET-25147, IET-25148, IET-25010 are found to be promising in breeding program to generate new genetic material.

**Keywords** Variability, Genetic advance, Genetic diversity.

### Introduction

Rice (*Oryza sativa* L. ) is the world's most important food crop and primary source of food for more than half of the world population. The genus *Oryza* contains two cultivated and 22 wild species which together constitute three gene pools. Rice crop is affected by numerous biotic and abiotic stresses at various stages of its life cycle. To deal with such losses, new resistant varieties are required. However, there is limited genetic diversity available in cultivated rice due to selection of desirable traits during the course of evolution. Thus, there is a need to explore the wild germplasm and landraces for desirable genes and transfer these into elite cultivars to raise rice yields and augment stress resistance. Genetic variability for quantitative traits is the key component of breeding program for broadening the gene

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**Table 1.** List of rice genotypes studied under present investigation with respective codes.

Code	Genotypes	Code	Genotypes	Code	Genotypes	Code	Genotypes	Code	Genotypes
G1	IET-24385	G22	IET-23561	G43	IET-24179	G64	IET-25004	G85	IET-25032
G2	IET-25025	G23	IET-24367	G44	IET-24189	G65	IET-25006	G86	IET-25033
G3	IET-24395	G24	IET-24450	G45	IET-23518	G66	IET-25007	G87	IET-25034
G4	IET-25021	G25	IET-25144	G46	IET-25045	G67	IET-25008	G88	IET-25035
G5	IET-23725	G26	IET-25145	G47	IET-24183	G68	IET-25009	G89	IET-25036
G6	IET-25019	G27	IET-25146	G48	IET-22952	G69	IET-25011	G90	IET-24521
G7	IET-24414	G28	IET-25147	G49	IET-24193	G70	IET-25013	G91	IET-25037
G8	IET-24261	G29	IET-25148	G50	IET-24197	G71	IET-25014	G92	IET-25038
G9	IET-24292	G30	IET-25149	G51	IET-25047	G72	IET-15015	G93	IET-25039
G10	IET-24418	G31	IET-25010	G52	IET-24188	G73	IET-25016	G94	IET-25040
G11	IET-24365	G32	IET-25150	G53	IET-24195	G74	IET-25018	G95	IET-25041
G12	IET-24297	G33	IET-25151	G54	IET-24192	G75	IET-25020	G96	IET-25042
G13	IET-24235	G34	IET-25005	G55	IET-24196	G76	IET-25021	G97	IET-25044
G14	IET-24443	G35	IET-25152	G56	IET-24997	G77	IET-25022	G98	IET-24491
G15	IET-25012	G36	IET-25153	G57	IET-24488	G78	IET-25023	G99	IET-25046
G16	IET-24480	G37	IET-25154	G58	IET-24998	G79	IET-25024	G100	IET-25048
G17	IET-24451	G38	IET-25155	G59	IET-24999	G80	IET-25026	CK 1	INTAN
G18	IET-24474	G39	IET-25156	G60	IET-25000	G81	IET-25028	CK 2	KPR-1
G19	IET-23930	G40	IET-25157	G61	IET-25001	G82	IET-25029	CK 3	TUNGA
G20	IET-23565	G41	IET-25158	G62	IET-25002	G83	IET-25030		
G21	IET-24471	G42	IET-22957	G63	IET-25003	G84	IET-25031		

pool of rice and other crops. High magnitude of variability in a population provides the opportunity for selection to evolve a variety having desirable characters. The genetic coefficient of variation together with heritability estimate would give the best picture of the amount of advance to be expected from the selection. The success of any plant breeding programs largely depends on the existence of diversity among the genotypes. This helps in the choice of parents for hybridization in yield improvement programs. Hence, estimation of genetic diversity for yields and its components among genotypes is important for planning the future crossing program. Hence, the present investigation was carried out in hill zone to study variability and genetic diversity (by using Mahalanobis  $D^2$  statistics) in rice genotypes.

### Materials and Methods

The experimental material consists of 100 AICRP rice genotypes along with three checks (Table 1). These genotypes were evaluated in an Augmented plot design during *khari*, 2015 at Agricultural Horticultural Research Station (AHRS), Ponnampet. The

experimental field consists of ten blocks where in each block consist ten genotypes and three checks repeated in all blocks, seedling of 25 day's old were transplanted with a spacing of 20 cm between row and 15 cm between plants. The observation recorded from all the genotypes for thirteen yield attributing traits viz., days to 50 % flowering, days to maturity, plant height, tillers per plant, number of productive tillers per plant, panicle length, number of spikelets per panicle, number of grains per panicle, percent spikelet fertility, test weight, grain yield per plant, straw yield per plant and harvest index were recorded in five randomly selected plant in all 100 hundred genotypes. The data of mean value for all the character were analyzed for their variance following augmented design outlined by Federer [1]. Mahalanobis [2]  $D^2$  statistic was used for assessing the genetic divergence between populations. Analysis of variance as well as  $D^2$  analysis was done by using the INDOSTAT software (9.2).

### Results and Discussion

The analysis of variance is presented in Table 2. The analysis of variance for thirteen yield and yield com-

**Table 2.** Analysis of variance for thirteen yield and yield component traits in 100 rice genotypes. \*\* Significance at 1% \* Significance at 5%.

Source of variation	df	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of tillers/plant	No. of productive tillers/plant	Panicle length (cm)	No. of spikelets/panicle
Blocks	9	0.03	0.53	12.54	0.01	0.02	0.10	27.26
Entries	102	162.16**	155.80*	204.58**	4.19**	3.82**	23.96**	55.86**
Checks	2	801.23**	1755.43**	623.25**	5.70**	2.18**	26.40**	2161.82**
Varieties	99	127.98**	100.45	122.36**	4.11**	3.83**	22.38**	486.30**
Checks vs Varieties	1	2267.86**	2435.57**	7507.41**	9.33**	6.19**	175.71**	4535.57**
ERROR	95	34.23	1231.76	32.43	0.30	0.12	2.03	36.16
Ci-Cj (CD @ 5%)	1	5.49	0.01	5.35	NS	0.32	1.33	5.65
Ci-VI (CD @ 5%)	1	14.88	0.02	14.49	0.57	0.88	3.62	15.30

**Table 2.** Continued.

Source of variation	df	No. of grains/panicle	Panicle fertility (%)	Test weight (g)	Grain yield /plant (g)	Straw yield /plant (g)	III
Blocks	9	44.16	4.79	9.56	0.01	0.06	0.00
Entries	102	444.69**	171.61**	18.10*	6.74**	5.00**	0.01**
Checks	2	1682.49**	158.09**	17.52	16.30**	3.45**	0.01**
Varieties	99	292.61**	141.09**	17.87*	5.38**	5.03**	0.01**
Checks vs Varieties	1	13024.87**	3220.21**	42.07*	122.36**	5.00**	0.06**
ERROR	95	8.37	5.27	8.97	0.77	0.08	0.00
Ci-Cj (CD @ 5%)	1	2.71	2.15	2.81	0.82	0.28	0.01
Ci-VI (CD @ 5%)	1	7.36	5.84	7.62	2.23	0.76	0.02

ponent characters were statistically tested and found to be significant for all the characters evaluated except days to maturity indicating presence of high variability among the genotypes. Thus, there is ample scope for selection of different quantitative characters for rice improvement. The genetic variability parameter viz., mean, range, standardized range, phenotypic co-efficient of variation (PCV), genotypic co-efficient of variation (GCV), heritability (broad sense) and genetic advance as per cent mean for all the thirteen characters are furnished in Table 3. In the present study, the phenotypic and genotypic coefficients of variability were recorded highest for the trait panicle length (22.93 and 21.66) this line with the observation recorded by Tuhina et al. [3] for this trait. The difference between phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) were low for all the traits except days to maturity and test weight. This indicates that these two traits are highly influenced by environment and selection for those traits is not so effective. The

trait days to maturity shows low heritability (27.85) coupled with low genetic advance (4.07) indicates that character is highly influenced by environmental effects and selection would be ineffective and the results were on par with the results of Ogunbayo et al. [4]. High heritability coupled with low genetic advance observed for the traits harvest index, test weight, days to 50% flowering which indicates the presence of non-additive gene action and high heritability is being exhibited due to favorable influence of environment rather than genotype and selection for that trait may not be rewarding and the same results were observed by Gangashetty et al. [5]. Further all other traits shows high heritability coupled with high genetic advance it indicate that most likely the heritability is due to additive gene effects and selection may be effective.

Knowledge about germplasm diversity and genetic relationships among breeding material could be an invaluable aid in crop improvement strategies.

**Table 3.** Estimates of mean, range, PCV, GCV, heritability and genetic advance for thirteen yield and yield component traits in rice genotypes. PCV (%) : Phenotypic coefficient of variation, GCV (%) : Genotypic coefficient of variation, GAM : Genetic advance as per cent mean,  $h^2$  : Heritability, SE : Standard error.

Sl. No.	Characters	Mean $\pm$ SE	Range		Coefficient of variation		$h^2$ Broad sense (%)	GAM (%)
			Minimum	Maximum	PCV (%)	GCV (%)		
1	Days to 50% flowering	106.02 $\pm$ 1.11	71	122	9.95	8.28	69.32	14.21
2	Days to maturity	137.14 $\pm$ 0.98	108	152	709	3.74	27.85	4.07
3	Plant height (cm)	78.54 $\pm$ 1.08	57.80	103.20	13.09	10.92	69.58	18.77
4	Number of tillers	10.01 $\pm$ 0.20	4.60	17.00	18.54	17.71	91.30	34.86
5	No. of productive tillers	9.35 $\pm$ 0.19	4.20	16.40	19.06	18.69	96.19	37.77
6	Panicle length (cm)	18.69 $\pm$ 0.47	11.10	24.30	22.93	21.66	89.20	42.15
7	No. of spikelets per panicle	96.63 $\pm$ 2.17	68.4	180.20	20.83	19.88	91.11	39.11
8	No. of grains per panicle	69.30 $\pm$ 1.66	31.20	128.00	22.36	21.97	96.55	44.47
9	Panicle fertility (%)	72.31 $\pm$ 1.18	35.45	98.05	14.94	14.60	9551	29.39
10	Test weight (1000 seed)	22.86 $\pm$ 0.45	15.29	25.81	16.47	11.05	45.00	15.27
11	Grain yield per plant (g)	10.69 $\pm$ 0.23	8.00	22.80	19.91	18.16	83.14	34.11
12	Straw yield per plant (g)	12.92 $\pm$ 0.22	9.20	25.00	15.80	15.63	97.86	31.86
13	Harvest index	0.45 $\pm$ 0.01	0.39	0.50	5.83	5.25	81.32	9.77

Genetic diversity determines the inherent potential of a cross for heterosis and frequency of desirable recombinants in advanced generations. For the same, genetic distance plays a vital role, as parental diversity in optimum magnitude is required to obtain superior genotypes in segregating population [6]. Hybridization program involving genetically diverse parents belonging to different clusters would provide an opportunity for bringing together gene constellations of diverse nature, promising hybrid derivatives resulted probably due to complementary interaction of divergent genes in parents. The use of Mahalanobis  $D^2$  statistics for estimating genetic di-

vergence has been emphasized by many workers [7, 8]. In this study 100 genotypes of rice were evaluated to assess the nature and magnitude of genetic diversity among the genotypes for further utilization in breeding programs.

Based on  $D^2$  value 100 genotypes were grouped into eleven clusters (Table 4) and among eleven cluster, cluster IX has highest genotypes (20) and cluster X and XI has lowest genotypes (4) in their cluster. The results obtained by Anandan et al. [8] shows similarity with present experimental results. The intra cluster distance varied from 2.55 in cluster XI

**Table 4.** Cluster-wise distribution of 100 rice genotypes. Codes indicate the genotypes of table 1.

Sl. No.	Cluster	No. of genotypes	Codes (Genotypes)
1.	I	10	G 8, G 9, G 10, G 37, G 44, G 58, G 59, G 60, G 87, G 94
2.	II	8	G 16, G 17, G 18, G 26, G 66, G 67, G 68, G 76, CK-1, CK-2, CK-3
3.	III	14	G 23, G 27, G 30, G 32, G 34, G 35, G 49, G 73, G 77, G 80, G 82, G 84, G 85, G 99
4.	IV	8	G 2, G 22, G 33, G 36, G 52, G 72, G 83, G 86
5.	V	8	G 24, G 38, G 45, G 50, G 74, G 88, G 95, G 100
6.	VI	4	G 4, G 7, G 54, G 57
7.	VII	12	G 1, G 3, G 5, G 6, G 12, G 13, G 51, G 53, G 55, G 56, G 62, G 63
8.	VIII	8	G 14, G 19, G 20, G 21, G 64, G 69, G 70, G 71
9.	IX	20	G 28, G 29, G 31, G 39, G 41, G 42, G 43, G 46, G 47, G 48, G 78, G 79, G 81, G 91, G 92, G 93, G 96, G 97, G 98
10.	X	4	G 11, G 40, G 61 G 90
11.	XI	4	G 15, G 25, G 65, G 75

**Table 5.** Average inter and intra cluster  $D^2$  values for thirteen yield and yield component traits in 100 rice genotypes. CI-clusters, Diagonal values indicates intra cluster distance. The values below diagonal values indicate inter cluster distances.

CI	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	<b>12.66</b>										
II	8.94	<b>3.95</b>									
III	12.91	10.41	<b>19.21</b>								
IV	15.52	10.98	15.89	<b>29.19</b>							
V	12.59	7.63	11.36	13.08	<b>7.41</b>						
VI	8.82	8.63	11.81	14.80	12.53	<b>7.27</b>					
VII	18.24	15.23	17.85	19.64	16.45	16.68	<b>42.81</b>				
VIII	17.37	12.79	19.05	18.12	13.08	17.42	22.83	<b>15.30</b>			
IX	47.19	31.70	46.33	38.69	31.12	48.54	48.32	35.62	<b>15.17</b>		
X	19.46	15.80	22.58	22.08	17.90	18.69	26.04	20.18	44.18	<b>37.22</b>	
XI	15.60	19.38	16.98	22.41	23.02	13.85	21.41	35.16	66.87	34.96	<b>2.55</b>

and to a highest distance of 42.81 in cluster VII (Table 5). This reveals the presence of less diverse genotypes within different clusters. The inter cluster  $D^2$  values also ranged widely with lowest value of 7.63 between cluster II and cluster V and highest value of 66.87 between cluster IX and cluster XI indicating greater diversity among the genotypes. Cluster IX with twenty genotypes and cluster XI with four genotype are the most divergent group with a highest inter-cluster distance (66.87) and these results are on par with the results of Lotan and Pradhan [9] as they obtained ten clusters for 35 deepwater rice genotypes and they had noted highest number of genotypes (11) in cluster I and lowest genotypes in cluster III, cluster V, cluster VI, cluster VIII, cluster IX, cluster X. It is desirable to select genotypes from these cluster showing higher inter cluster distance and also with high grain yield as parents in recombination breeding program for obtaining wide variability and desirable segregants.

Analysis of cluster means helps to identify clusters having different levels of variability for different characters, based on final ranks. It is possible to identify clusters having higher diversity for more number of characteristics and it also helps to identify clusters having less diversity for more number of characteristics. Utilization of low ranked clusters in breeding program is expected to yield desirable lines in advanced generation of selection. All the 100 genotypes were spread over eleven clusters and means were scored across the clusters for all the thirteen characters. The highest cluster mean was

given the I rank and next cluster possessing next best means were given II, III and so on up to XI rank for all the traits. However for days to 50% flowering and days to maturity is the lowest mean value given as I rank. Based on the overall score across thirteen traits, the lowest scoring cluster was given I rank. Accordingly, cluster IX with overall score of 57 across the thirteen characters received I rank followed by cluster I (60) and X (70). Presence of promising genotypes (eg. IET-25147, IET-25148, IET-25010) in these clusters can be extensively used for further breeding program to generate new genetic material. Among the thirteen quantitative characters studied the most important character contributing to the divergence was grain yield per plant. This was followed by days to 50% flowering and test weight. Similar results were also obtained by Praveen et al. [10].

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