

Genetic Divergence Studies for Yield and its Components in Rice

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Abstract

The nature and magnitude of genetic divergence were estimated in 118 rice genotypes using Mahalanobis D² statistics by considering 11 quantitative characters. ANOVA revealed the presence of significant differences among all the characters under study, indicating the greater diversity among the genotypes. High estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for grain yield per plot, followed by number of filled grains per panicle and 1000 grain weight. High heritability coupled with high genetic advance was recorded for number of tillers per plant, number of productive tillers per plant, plant height, panicle length, number of filled grains per plant, grain yield per plant, yield per plot and harvest index. Mahalanobis D² analysis revealed considerable amount of diversity in the material. The genotypes were grouped into twelve clusters, cluster III was the largest comprising of 42 genotypes and the higher amount of divergence was observed between clusters IV and XII (3298579) followed by clusters I and XII (2735295) suggesting that the genotypes constituted in these clusters may be used as parents for future hybridization programme. The genotypes falling in cluster V (26469.49) had the maximum divergence, which was closely followed by cluster IV (17711.43). Traits like yield per plot, number of filled grains per panicle and plant height were major contributors towards genetic diversity.

Introduction

Rice is the world's largest food crop, providing the daily caloric needs of more than half of the global population. Globally, rice is cultivated on 154 million hectares with annual production of around 600 million tones and average productivity of 3.9 tons/ha. More than 90% of the rice is produced and consumed in Asian countries. The other continents in which rice is grown are Africa (7.78% of the global area), South America (6.4%) and North America (1.4%) (Viraktamath, 2007). Rice plays a pivotal role in Indian economy being the staple food for two third of the population.

Rice crop has vast amount of diversity at different levels with eleven genera, 24 species and a number of genotypes or accessions within each sub-species. Of the 11 genera viz., *Chikusiochloa*, *Hygroryza*, *Leersia*, *Luziola*, *Prosochloa*, *Rhynchoryza*, *Zizania*, *Zizaniopsis*, *Parteresian*, *Potamophila* and *Oryzae*; *Oryza* is the only one with cultivated species (Ram *et al.*, 2013). Genus *Oryza* has two cultivated and 22 wild species. Of the two distinct types of domesticated rice, *O. sativa* (2n=24 AA,

Asian rice) is grown worldwide with a high concentration in Asia while *O. glaberrima* (2n=24 AA, African rice) is cultivated on a limited scale in West Africa (Vaughan *et al.*, 2003). As genetic variability is a prerequisite for any crop improvement programme, the large spectrum genetic variability present in the gene pool comprising of indigenous and exotic germplasm offers better scope for selection. It is the choice of the germplasm, which virtually determines the success and nature of end product and a wrong choice would result in the wastage of resources. Information on the nature and degree of genetic divergence would help the plant breeders in choosing the right parents for breeding programme (Vivekanandan and Subramanian, 1993).

Efficient and economic crop improvement scheme refers to the collection of superior alleles into a single population. The grain yield is the primary trait targeted for improvement of rice productivity in both favourable and unfavourable environments from its present level. Grain yield is a complex character, which depends on its main



components viz, number of panicles per plant, panicle length, number of grains per panicle and 1000 grain weight. These components are further dependent for their expression on several morphological and developmental traits, which are interrelated with each other and therefore, the parents selected for the breeding programmes aimed at increased seed yield should possess wide range of genetic variation for the above said morphological and developmental character.

Genetic diversity can be evaluated with morphological traits, seed protein, isozymes and DNA markers. Conventionally, it is estimated by the D^2 analysis, Metroglyph and Principal Component Analysis (PCA) using morphological traits. The D^2 technique (Mahalanobis, 1936) based on multivariate analysis had been found to be a potent tool in quantifying the degree of divergence in germplasm. This analysis provides a measurement of relative contribution of different components on diversity both at intra and inter-cluster level and genotypes drawn from widely divergent clusters are likely to produce heterotic combinations and wide variability in segregating generation. Recognizing the importance of variability in plant breeding experiments, the present research work was taken up with the objective of assessing the genetic diversity in rice germplasm comprising of various groups such as land races from north east, tropical *japonica* and introgression lines from wild species.

Material and Methods

The plant material consisted of 118 rice genotypes comprising of land races from north eastern part of India, tropical *japonica* accessions and introgression lines from wild species as test entries. Varieties such as Jaya, IR 64, MTU 1010, MTU 1081 and NLR 34449 were used as checks. The investigation was undertaken at ICAR-Indian Institute of Rice Research (ICAR-IIRR), Ramachandrapuram farm, ICRISAT Campus, Patancheru, Hyderabad, during *Kharif* 2014. The experimental material was laid out in Augmented Block Design (ABD) wherein test entries were sown only once while checks were replicated. The layout design was generated using on line 'Design Resources Server' of ICAR-Indian Agricultural Statistical Research Institute (IASRI) website (www.iasri.res.in) by filling in the number of test treatments (118), control treatments (checks-5) and number of blocks (5).

Twenty five days old seedlings of each genotype sown in raised dry bed nursery in lines were transplanted in 3 rows of 6 m length by adopting a spacing of 15 cm between plants and 20 cm between rows. Recommended agronomic practices and plant protection measures for raising a healthy crop were taken up from time to time during the

crop growth period. Data was collected on eleven yield component characters viz., number of tillers per plant (TN), number of productive tillers per plant (PTN), plant height (PH), days to 50% flowering (DFF), days to maturity (DM), panicle length (PL), number of filled grains per panicle (GN), 1000 grain weight (TW), grain yield per plant (SPY), yield per plot (Y) and harvest index (HI). The mean values were considered for statistical analysis. The data was subjected to statistical analyses following Gomez and Gomez (1984) using windostat version 9.2 statistical programme. The genetic parameters were computed following Singh and Chaudhury (1985) and estimation of genetic divergence and clustering of genotypes was done using Tocher's method.

Results and discussion

Analysis of variance for the experiment for 11 yield component characters revealed that the mean sum of squares were highly significant for all the characters indicating the greater diversity among the rice genotypes (Table 1).

Genetic parameters

A perusal of genetic parameters revealed that phenotypic and genotypic coefficients of variation were high for characters like number of tillers per plant, number of productive tillers per plant, number of filled grains per plant, harvest index, 1000 grain weight and yield per plot. The values of genotypic and phenotypic coefficients of variation were low for days to 50% flowering, panicle length and days to maturity. High heritability coupled with high genetic advance as per cent of mean was observed for characters like plant height, number of tillers per plant, number of productive tillers per plant, number of filled grains per panicle, harvest index, plot yield, 1000-grain weight and grain yield per plant. This indicated that these traits were controlled by additive type of gene action in the inheritance of these characters. These characters can be further improved by following simple selection procedure. The high estimates of heritability coupled with low genetic advance as per cent of mean for days to 50% flowering and days to maturity indicated the presence of non-additive gene effects, in addition to influence of environment to some extent. (Table 2).

Genetic divergence

The genetic divergence was high and 123 genotypes were grouped into 12 clusters (Fig. 1 and 2). Out of 12 clusters, cluster III was the largest comprising of 42 genotypes followed by clusters I with 24 genotypes, cluster II with 21 genotypes, cluster V with 16 genotypes, cluster IV with 13 genotypes and clusters VI, VII, VIII, IX, X, XI and XII

with one genotype each. The clusters VI, VII, VIII, IX, X, XI and XII were represented by single genotype indicating high degree of heterogeneity among the genotypes.

Inter and intra-cluster distances among the clusters generated are presented in Table 3. The higher amount of divergence was observed between clusters IV and XII (3298579) followed by clusters I and XII (2735295), clusters III and XII (2178405.50) and cluster VIII and cluster XII (1754711), while it was low between clusters VIII and IX (5235.73) (Table 4). Maximum intra cluster distance was observed in cluster V (26469.492), followed by cluster IV (17711.43), cluster III (12829.94), cluster II (10504.917), and cluster I (8634.53). Solitary clusters (VI, VII, VIII, IX, X, XI and XII) showed zero intra cluster distances. Based on the inter cluster distances, hybridization between the genotypes of clusters IV and XII, clusters I and XII, clusters III and XII, clusters VIII and XII is suggested to generate promising segregants for grain yield would produce encouraging results.

The intra cluster distance varied from 8634.53 (cluster I) to 26469.49 (cluster V). This reveals the presence of more diversity among the genotypes within the clusters. Therefore due emphasis should be given on the constituents of clusters V and IV for selection of parents for hybridization programme. Hence, selection within these clusters may be exercised based on the highest areas for the desirable traits, which would be made use of in improvement through intervarietal hybridization (Joshi *et al.* 2008).

The clusters VI, VIII, X, XI and XII recorded high mean values for the yield components like number of days to fifty per cent flowering, plant height, panicle length, days to maturity and number of tillers per plant, number of productive tillers per plant, number of filled grains per panicle, 1000 grain weight and harvest index and they were also divergent from each other (Table 4). Hence, crosses between genotypes selected from these clusters may be used to generate rice genotypes with good grain yield. None of the clusters contained genotypes with all the desirable traits which could be directly selected and utilized. All the minimum and maximum cluster mean values were distributed in relatively distant clusters. Similar results were also reported by Bose and Pradhan (2005).

Contribution towards Genetic divergence

Table 5 shows the number of times each of the ten characters appeared in first rank and its respective per cent contribution towards genetic divergence. The results

showed that the contribution of yield per plot was highest towards genetic divergence (89.47%) ranking first by 6713 times followed by number of filled grains per panicle (7.24%) by 543 times, plant height (3.15%) by 236 times, harvest index (0.07 %) by 5 times, days to 50% flowering 0.04% by 3 times, days to maturity (0.03%) by 2 times and 1000 grain weight (0.01%) by 1 time. The results were in conformity with Ramya and Senthil Kumar (2008) and Vennila *et al.* (2011).

The experimental material comprised of genotypes that were classified into land races, tropical *japonica* accessions, introgression lines from wild species and elite cultivars. Interestingly, clustering of these genotypes did not follow any segregation pattern based on origin or geography or specific groups to which they were classified. Genotypes from all groups were present in different clusters except solitary clusters.

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Table 1. Analysis of variance for eleven quantitative traits among rice genotypes

	Block (Ignoring treatments)	Treatment (eliminating blocks)	Checks	Checks+ Varieties vs. varieties	Error
d.f	4	122	4	118	116
No. of tillers/ Plant	38.36 ***	7.11***	17.63 ***	6.75 ***	1.01
No. of productive tillers/plant	31.50 ***	6.38 ***	12.55 ***	6.17***	1.38
Plant height (cm)	5736.57 ***	731.12 ***	401.98 ***	742.27 ***	43.89
Days to 50% flowering	159.70 ***	37.21 **	13.94	38.00 **	10.36
Days to maturity	199.41 **	49.78	97.54 *	48.16	31.71
Panicle length (cm)	24.14 **	9.32 *	8.40	9.35*	4.36
Filled grains /Panicle	1216.30 **	2018.38 ***	1629.11 ***	2031.58 ***	184.18
Grain yield/plant(g)	83.526***	26.25 **	48.66**	25.49 **	6.58
1000 grain weight (g)	98.25 ** *	38.10 ***	112.09 ***	35.59 ***	4.62
Plot yield(g/m ²)	311718.300***	99129.83 ***	79755.10 *	99786.60***	21363.85
Harvest index (%)	207.65 **	85.13 **	114.52 *	84.13 **	27.54

* Significant at 5 per cent level; ** Significant at 1 per cent level

Table 2. Estimates of variability, heritability and genetic advance among rice genotypes.

Characters	Genotypic variance	Phenotypic variance	GCV%	PCV%	h ² (bs)%	GA as % of Mean (5%)
No. of tillers/ plant	5.77	6.78	20.72	22.47	85.05	39.37
No. of prod. tillers/plant	4.72	6.10	20.64	23.47	77.33	37.39
Plant height (cm)	587.25	631.14	19.21	19.91	93.05	38.17
Days to 50% flowering	26.19	36.56	5.13	6.07	71.65	8.96
Days to maturity	19.79	51.50	3.37	5.44	38.43	4.30
Panicle length (cm)	4.57	8.93	8.52	11.91	51.17	12.56
Filled grains /panicle	1598.17	1782.36	29.07	30.70	89.67	56.71
Grain yield/plant (g)	18.12	24.70	16.03	18.72	73.37	28.29
1000 grain weight (g)	28.92	33.54	24.32	26.19	86.22	46.52
Plot yield (g)	71823.05	93186.91	41.34	47.09	77.07	74.77
Harvest index (%)	50.34	77.89	22.64	28.17	64.63	37.50

Table 3. Intra (diagonal) and inter cluster average distance (D²) in Rice genotypes (Tocher method)

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X	Cluster XI	Cluster XII
Cluster I	8634.53	198724.39	43328.93	38818.68	570346.44	905601.06	312887.16	114916.31	120287.81	926786.00	318634.09	2735295.00
Cluster II		10504.92	77977.02	369684.59	114741.64	269688.66	20807.18	19615.20	21387.63	284582.94	33247.18	1487060.50
Cluster III			12829.94	130426.16	336662.66	602067.75	150602.56	30255.82	32321.10	615259.00	150809.36	2178405.50
Cluster IV				17711.44	838445.00	1243093.75	522047.78	249795.27	255928.28	1263673.00	521416.88	3298579.00
Cluster V					26469.49	60339.10	55863.10	187307.63	180776.64	59913.95	56351.46	844903.63
Cluster VI						0.00	159217.02	392153.28	388247.88	9638.51	182835.00	497607.47
Cluster VII							0.00	55574.84	61191.06	177934.59	23278.08	1208647.13
Cluster VIII								0.00	5235.73	403653.56	56937.70	1754710.63
Cluster IX									0.00	389957.63	49418.19	1748580.25
Cluster X										0.00	172690.64	494238.53
Cluster XI											0.00	1236637.50
Cluster XII												0.00

Table 4. Cluster means for 11 quantitative traits (Tocher method)

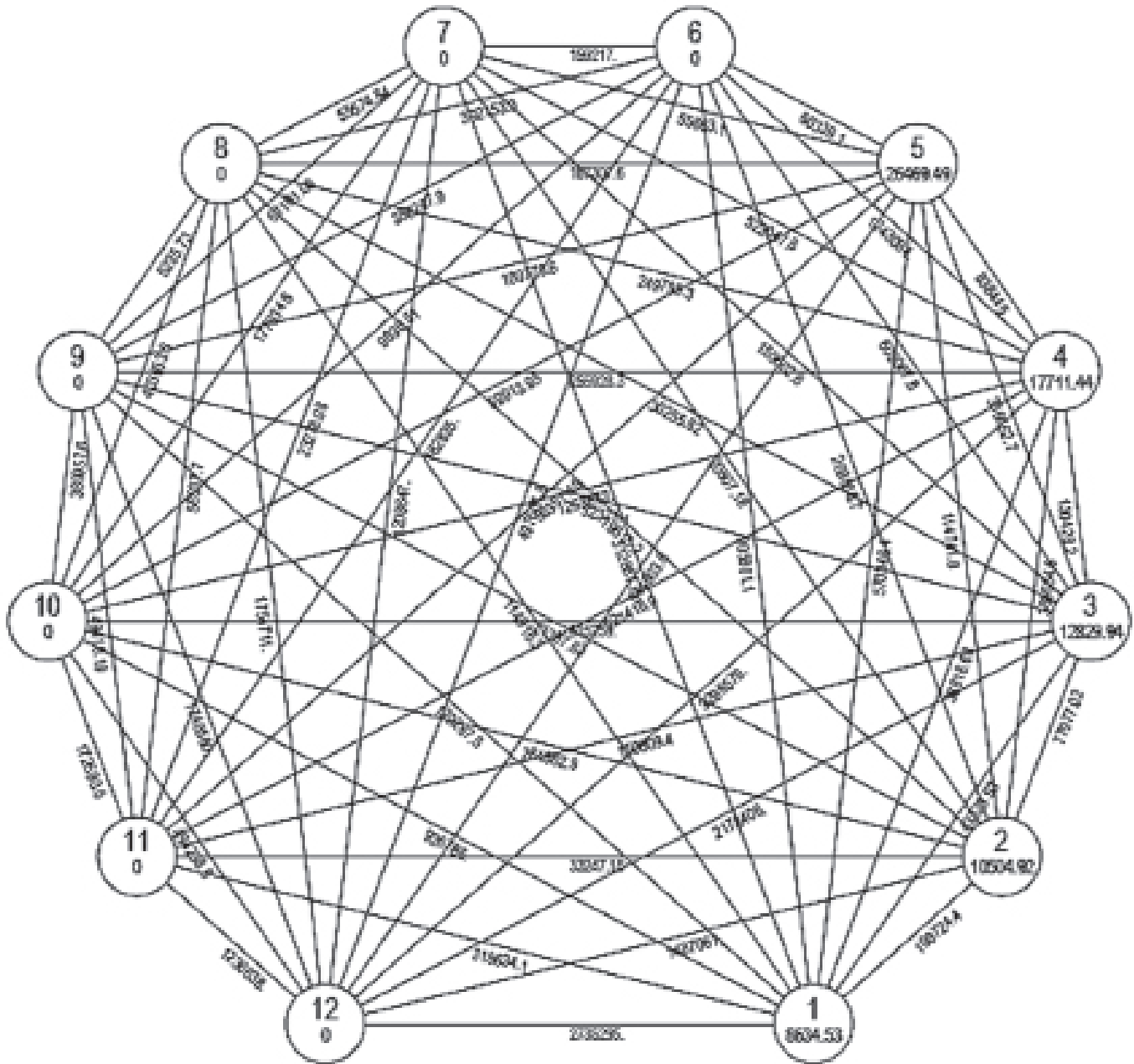
	TN	PTN	PH (cm)	DFF	DM	PL (cm)	GN	GY (g)	TW (g)	PY (g/m ²)	HI (%)
Cluster I	11.73	10.41	116.86	99.33	130.38	24.44	112.85	21.87	20.48	396.95	23.31
Cluster II	12.13	11.17	119.85	102.54	135.34	25.71	120.58	26.39	21.07	832.12	32.80
Cluster III	11.56	10.69	129.69	99.21	130.29	24.88	143.37	26.73	22.29	575.11	31.52
Cluster IV	11.39	10.15	125.27	99.10	131.18	24.86	124.26	27.06	23.56	235.10	31.85
Cluster V	11.73	10.58	124.66	97.22	133.25	24.67	183.41	32.30	23.11	1137.47	39.58
Cluster VI	15.59	13.63	98.06	93.36	136.04	25.53	123.26	25.94	15.39	1345.94	40.60
Cluster VII	11.99	11.43	137.38	99.56	130.24	25.93	93.39	34.78	29.57	950.73	55.44
Cluster VIII	7.79	6.03	169.18	93.56	138.24	24.93	139.72	27.80	21.17	724.29	25.86
Cluster IX	8.03	6.75	123.38	104.76	134.44	27.53	193.72	20.23	23.38	727.82	25.36
Cluster X	10.23	8.95	106.98	104.76	140.44	29.93	219.39	30.76	19.88	1351.32	35.50
Cluster XI	5.95	5.91	167.22	103.56	136.64	30.49	238.72	23.87	28.27	940.92	25.34
Cluster XII	12.99	12.03	152.78	89.56	131.24	23.33	146.05	37.18	27.57	1048.62	42.96



Table 5. Relative contribution of different characters towards genetic diversity in rice genotypes

Character	Times ranked first	Contribution (%)
Number of tillers / plant	0.01	0.00
Number of prod. tillers/plant	0.01	0.00
Plant height (cm)	236	3.15
Days to 50% flowering	3	0.04
Days to maturity	2	0.03
Panicle length (cm)	0.01	0.00
Filled grains/ panicle	543	7.24
Grain yield/ plant (g)	0.01	0.00
1000 grain weight (g)	1	0.01
Plot yield (g)	6713	89.47
Harvest index (%)	5	0.07

Tocher Method



Mahalanobis Euclidean Distance (Not to the Scale)

Fig. 2. Statistical distance among 123 genotypes of rice (Not to the scale)