Study on Genetic Diversity and Character Associations in Traditional and Indigenous Rice (Oryza Sativa L.) Genotypes Under Rainfed

Abstract

The nature and magnitude of genetic divergence was estimated in thirty rice landraces using Mahalanobis D^2 statistics considering twenty quantitative characters. ANOVA exhibits the prescence of considerable amount of variability among the genotypes. High genotypic coefficient of variation (GCV) was observed for number of secondary branches coupled with high phenotypic coefficient of variation (PCV) in biological yield per plant. High heritability coupled with high genetic advance as percentage was showed by number of grains per panicle. Considerable amount of diversity was revealed by Mahalanobis D^2 analysis. The 30 landraces were grouped into 9 clusters. In the present study the highest inter cluster distance observed between cluster V and cluster VII (3913.55) followed by cluster I and cluster VII (3144.26) suggesting that the genotypes in these clusters may be used as parent for future hybridization programme. The maximum intra cluster distance of showed by cluster IV (544.43) followed by cluster III (512.44) which showed maximum divergence. Traits like; days to heading, Number of secondary branches and grain length were major contributors to genetic divergence.

Key words: Rice landraces, genetic divergence, GCV, PCV, D^2 analysis, heritability and genetic advance.

Introduction

Rice (*Oryza sativa* L.) is a self-pollinated, short-day, annual, monocotyledonous crop of family Poaceae (Graminae) with chromosome number 2*n* = 24. Rice is considered as an energising and reviving food (Rasane *et al.,* 2015). It is the most staple and cereal component that sustains the two-third of world population (Sen *et al.* 2020). The protein fat proportion in food reduces with the degree of increase in polishing (Nawaz *et al.* 2018). The endosperm contains various protein fractions consist of 5-8% prolamin, 15% albumin plus globulin, and the rest of glutelin (Uraipong *et al.* 2016). When it comes to the amino acid profile, reveals a high aspartic acid and glutamic content, with lysine being the limiting amino acid (Carcea *et al.* 2021). Brown rice contains polyunsaturated fatty acids can help prevent osteoarthritis, cancer and autoimmune disorders. Brown rice is higher in dietary fibre, vitamins and minerals specifically the B group such as Thiamine (B1), Ribofavin (B2), Niacin (B3), Pantothenic acid (B5), Pyridoxine (B6) and Biotin (B7) (Mohidem *et al.,* 2022).

Rice landraces have been developed through artificial selection imposed by farmers during the long-term domestication process. Although the global rice diversity is well characterized, few studies have conducted an in-depth analysis of genetic diversity on a local scale. India being the centre of rice diversity, has a wealth of traditional landrace varieties. Important issues concerning crop genetic diversity and its relationship with local cultures can only be answered by rigorously studying rice germplasm collected from geographically isolated regions (Roy *et al.,* 2014). The landraces are valuable as they possess a huge treasure of genetic material which may prove valuable in future crop development and improvement programs (Sinha and Mishra., 2013). Landraces possess significant genetic potential for enhancing desirable traits, making them valuable for agricultural improvement. Unlike high-yielding varieties that have limited variability due to long-term selection, landraces maintained by farmers exhibit tremendous genetic diversity.

For a better breeding program, the major thrust area lies in identifying desirable parents for hybridization for which knowledge about germplasm diversity and genetic relationship among breeding materials serves as valuable aid (Kumar *et al.,* 2017). Genetic divergence is an efficient tool for an effective choice of parents for hybridization programme. The parents involved in the development of varieties should be divergent. The germplasm provides immense scope for wide variability (Banumathy *et al.,* 2010). Cross combinations involving divergent parents provide an opportunity for bringing together gene constellations of diverse nature and also promising segregant derivatives which result due to complementary interaction of divergent genes in parents are expected (Kumar *et al.,* 2017). Therefore, characterization of genetic diversity on existing landraces of rice reveals important traits of interest that can be utilized in rice improvement programmes (Guru *et al.,* 2017).

Materials and Methods

The present study comprised of 30 rice landraces laid in randomized block design (RBD) with three replications conducted at the Field Experiment Centre of Department of Genetics and Plant Breeding, Allahabad School of Agriculture, U.P., during *kharif,* 2022. Recommended package of practices was followed accordingly. Observations were recorded for ten randomly selected plants from each replication for Plant Height (cm), Number of Tillers Per Plant, Number of Productive Tillers Per Plant, Flag Leaf Length (cm), Flag Leaf Width (cm), Flag Leaf Area, Panicle Length (cm), Number of primary branches, Number of secondary branches, Number of Spikelets Per Panicle, Number of Grains Per Panicle, Grain Length (mm), Grain Breadth (mm), Test Weight (g) and Days to Heading, Days to Fifty percent Flowering, Days to maturity were recorded on plot basis. The data was subjected to Mahalanobis D^2 statistics to measure genetic divergence as suggested by Rao (1952).

Results and discussions

Analysis of variance showed significant differences for all the characters studied among thirty genotypes. A range of high GCV and PCV were recorded for biological yield per plant, grain yield per plant, and number of secondary branches. High heritability was expressed by days to heading, followed by days to fifty percent flowering, days to maturity, grain length, number of secondary branches, number of grains per panicle, number of primary branches, test weigh, flag leaf length, grain breadth, flag leaf area, number of spikelets per panicle, grain yield per plant, plant height, number of tillers per plant, biological yield per plant. High genetic advance as percentage mean was recorded for number of secondary branches, grain yield per plant, biological yield per plant, number of grains per panicle, test weight, number of tillers per plant, number of spikelets per panicle, flag leaf area, number of primary branches, grain length, number of productive tillers per plant, days to heading, flag leaf length, days to fifty percent flowering, harvest index, days to maturity, plant height, grain breadth, and flag leaf width. The perusal of results was depicted in Table 1.

Table 1 GCV, PCV, h2 (bs) % and Gen. Adv as % of Mean

Sl No	Characters	GCV	PCV	h2 (bs) %	Gen. Adv as % of Mean
1	Days to heading	17.52	17.58	99.30	35.96
2	Days to Fifty percent Flowering	16.39	16.46	99.20	33.63
3	Days to maturity	14.32	14.40	98.90	29.34
4	Plant Height (cm)	16.70	19.69	71.95	29.18
5	Number of Tillers Per Plant	29.54	34.98	71.34	51.41
6	Number of Productive Tillers Per Plant	25.68	36.73	48.88	36.99
7	Flag Leaf Length (cm)	18.61	20	84.81	35.30
8	Flag Leaf Width (cm)	14.11	15.01	88.42	27.34
9	Flag Leaf Area	25.06	27.01	86.08	47.89
10	Panicle length (cm)	8.29	14.35	33.43	9.88
11	Number of primary branches	20.48	21.40	91.63	40.39
12	Number of secondary branches	38.00	38.27	98.57	77.71
13	Number of Spikelets Per Panicle	26.11	28.55	83.64	49.19
14	Number of Grains Per Panicle	27.08	27.97	93.72	54.01
15	Grain Length (mm)	18.47	18.59	98.75	37.81
16	Grain Breadth (mm)	14.81	15.84	87.41	28.53
17	Test Weight (g)	26.91	28.15	91.40	53.01
18	Harvest Index	19.75	26.15	57.06	30.73
19	Biological Yield Per Plant (g)	34.91	41.75	69.91	60.13
20	Grain Yield Per Plant (g)	34.01	39.04	75.88	61.03

GCV = Genotypic coefficient of variation

PCV = Phenotypic coefficient of variation

h2 (bs) % = Heritability in broad sense

Gen. Adv as % of Mean = Genetic advance as percentage mean

Based on D^2 values, 30 rice landraces were grouped into into 9 clusters following Tocher's method. The cluster I, II, III, IV and V were poly genotypic with 11,5, 5, 3, and 2 genotypes respectively (Table 2). Whereas cluster VI, VII, VIII, and IX were mono genotypic (1 genotypes each). The values of average intra and inter cluster distance (D^2) revealed that the maximum intra cluster distance of showed by cluster IV (544.43) followed by cluster III (512.44), cluster II (488.58), cluster I (451.04) and cluster V (438.61). There is no inter cluster distance recorded for Clusters VI, VII, VIII, and IX.

Table 2: Clustering of 30 genotypes by Tocher method

Sl N0	Cluster	No. of Genotypes	Genotypes
1	I	11	Kalamallifool, Poongar, Njavara, Mahamaya, Zinco rice MS, Triveni, C.G zinc Rice 1, Bhadi, Dular, C G MAdhuraj, and Basmathi 370
2	II	5	TarnBhogsel 1, Parimala sale, Green rice, Kala jeera and, Kliro
3	III	5	Red rice, F R 13 A, Numali, Black Rice, and Kogli sale
4	IV	3	C G Devbhog, Tyaa pin, and IGKV Maheshwari
5	V	2	Shyamala and Purnima
6	VI	1	Assam black
7	VII	1	Anamika
8	VIII	1	Madhu scale
9	IX	1	Sheetal

The highest inter cluster distance was observed between cluster V and cluster VII (3913.55), followed by cluster I and cluster VII (3476.76), cluster VII and cluster VIII (3144.26), cluster II and cluster V (2720.65), cluster IV and cluster VIII (2263.77), cluster IV and cluster VII (2242.04), cluster VI and cluster VII (2172.61), and cluster V and cluster IX (2068.86). The lowest inter cluster distance was observed between cluster III and cluster IX (722.34) followed by cluster VIII and cluster IX (727.21), cluster VI and cluster IX (729.43), and cluster VI and cluster VIII (748.71). The average intra and inter cluster D^2 values were depicted in Table 3.

Table 3: Average intra and inter cluster D^2 values of rice landraces

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8	Cluster 9
Cluster I	**451.04**	**1954.13**	**1315.77**	**999.46**	**818.99**	**853.03**	**3476.76**	**1093.74**	**1394.00**
Cluster II		**488.58**	**856.15**	**1534.75**	**2720.65**	**1411.96**	**1617.72**	**1882.83**	**858.65**
Cluster III			**512.44**	**1355.53**	**1463.06**	**831.57**	**1539.73**	**1153.05**	**722.34**
Cluster IV				**544.43**	**1745.19**	**1173.45**	**2242.04**	**2263.77**	**1514.27**
Cluster V					**438.61**	**1024.09**	**3913.55**	**1056.62**	**2068.86**
Cluster VI						**0.00**	**2172.61**	**748.71**	**729.43**
Cluster VII							**0.00**	**3144.26**	**1453.63**
Cluster VIII								**0.00**	**727.21**
Cluster IX									**0.00**

It is evident from divergence analysis that the highest inter cluster distance was between cluster V and VII, followed by cluster I and VII. Indicates wide diversity between them. Genotypes from these clusters could be used as parents in hybridization programme for the identification of best recombinants in further segregating generations. Best recombinants may be selected for the development of improved rice cultivars. The minimum inter-cluster distance was found between cluster III and IX followed by cluster VIII and IX indicating that the genotypes belonging to these clusters were genetically similar and selection of parents from these clusters should be avoided to maintain relatively broad genetic base.

The per cent contribution of 20 biometrical traits of 30 rice landraces towards genetic divergence was estimated and given in Table 4. The character first flowering (19.5%) had maximum contribution towards genetic divergence followed by number of secondary branches(13.9%), grain length (13.8%), days to maturity (11.5%), spikelets per panicle (11.2%), days to fifty percent flowering (7.6%), number of grains per panicle (4.6%), leaf width

(3.4%), test weight (2.7%), leaf length (2.2%), number of primary branches(2.2%), leaf area (1.9%), seed width (1.3%), harvest index (1.1%), yield per plant (0.9%), plant height (0.7%), number of tillers per plant (0.6%), panicle length (0.4%), productive tillers per plant (0.3%) and biological yield per plant (0.3%).

Table 4: Per cent contribution of 20 biometrical traits of 30 rice landraces towards genetic divergence

Charachers	Contribution (%)	Times Ranked First
Days to heading	19.5	85
Days to Fifty percent Flowering	7.6	33
Days to maturity	11.5	50
Plant Height (cm)	0.7	3
Number of Tillers Per Plant	0.6	3
Number of Productive Tillers Per Plant	0.3	1
Flag Leaf Length (cm)	2.2	10
Flag Leaf Width (cm)	3.4	15
Flag Leaf Area	1.9	8
Panicle length (cm)	0.4	2
Number of primary branches	2.2	10
Number of secondary branches	13.9	60
Number of Spikelets Per Panicle	11.2	49
Number of Grains Per Panicle	4.6	20
Grain Length (mm)	13.8	60
Grain Breadth (mm)	1.3	6
Test Weight (g)	2.7	12
Harvest Index	1.1	5
Biological Yield Per Plant (g)	0.2	1
Grain Yield Per Plant (g)	0.9	4

Crosses between divergent parents usually produce greater heterotic effect than closely related ones. The results revealed that the contribution of trait days to heading was maximum for genetic divergence, followed by number of secondary branches, grain length, days to maturity, spikelets per panicle, and days to fifty percent flowering. Higher inter-cluster distance was observed between cluster V and cluster VII followed by cluster V and VII. Higher intra cluster distance was observed between genotypes of cluster IV

Conclusion

The investigation reported significant morphological variation, particularly in seed coat color and seed shape, among 30 rice landraces. Analysis of variance revealed significant differences in all studied traits, with Kliro standing out as superior for grain yield per plant. Traits such as biological yield per plant, grain yield per plant, secondary branches, productive tillers, spikelets per panicle, test weight, grains per panicle, primary branches, and leaf area exhibited high genetic and phenotypic variability. These traits were considered essential for selection, with PCV surpassing GCV, suggesting less environmental influence. High heritability and genetic advance were observed for most traits, indicating their suitability for direct selection, except for productive tillers, harvest index, and panicle length. Selection based on positive correlations between biological yield, tiller numbers, productive tillers, harvest index, grain length, and fertile grains per panicle could lead to high-yield and quality offspring. Path analysis highlighted the importance of biological yield, harvest index, grains per panicle, and productive tillers for grain yield enhancement. The results revealed that the contribution of trait days to heading was maximum for genetic divergence, followed by number of secondary branches, grain length, days to maturity, spikelets per panicle, and days to fifty percent flowering. Higher inter-cluster distance was observed between cluster V and cluster VII followed by cluster V and VII. Higher intra cluster distance was observed between genotypes of cluster IV.

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