

Genetic divergence among rice landraces of Goa

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ABSTRACT

Twenty four genotypes of rice comprising landraces of Goa and improved cultivars were studied for genetic diversity on the basis of yield and its attributing characters. Based on D² analysis, the 24 rice genotypes were grouped into 6 clusters. Cluster I consisted maximum of 13 genotypes followed by Cluster III with six genotypes. The grouping of most of the landraces of Goa and few improved cultivars of rice into one cluster (III) indicates genetic relatedness among these genotypes. Cluster II had two genotypes, while the remaining clusters viz., Cluster IV, Cluster V and Cluster VI were represented by single genotypes each viz., Shidde, Saalsi and Kolyo respectively. Among different traits, days to 50% per cent flowering (38.77 %), 1000 grain weight (19.93), grain breadth (17.75) and plant height (14.86) had maximum contribution towards the total divergence.

Key words: rice, landrace, Goa, genetic diversity, D² analysis

Rice is one of the most important food crops and a primary food source for more than one third of world's population (Singh and Singh, 2008). In India, rice is being cultivated in more than 42 m ha and is the major food crop for more than 70% of the population. In Goa, rice is the principal food crop. It is cultivated in an area of 47,000 ha comprising about 29% of the total cropped area in the State with average productivity of 3.5 t/ha. Rice is cultivated traditionally in Goa, and had a rich diversity of native cultivars / landraces distributed in various regions of the State. These landraces are being maintained by the local farmers to meet their specific needs and are part and parcel of their traditional crop management system. They are highly adapted to the regions, having special uses with varying levels of resistance to biotic and abiotic stresses. For instance, based on the traditional knowledge gathered from the contributing farmers, during the survey work, it is learnt that landraces viz., Korgut, Asgo and Shidde cultivated in coastal saline soils and are tolerant to soil salinity. Landraces viz., Kendal and Kochri are suitable for cultivation in sandy soils, Kolyo in upland and Panyo are known to tolerate flooding. With the introduction of high-yielding rice

varieties, many of these landraces are slowly on the verge of extinction. To avoid further loss and preserve the existing diversity among the landraces, collection, conservation, evaluation and characterization of such invaluable genetic resources of rice is essential.

Characterization and quantification of genetic diversity has long been a major goal in evolutionary biology and plant breeding. Information on genetic diversity within and among closely related crop germplasm is essential for rational use of genetic resources (Arunachalam, 1981; Kwon *et al.*, 2002). Parents selected on the basis of such study would help in obtaining higher amount of heterotic expression in F₁s and broad spectrum of variability in subsequent segregating generations (Vivekanandan and Subramanian, 1993). Keeping in view of the above, the present effort has been made to collect, conserve and characterize 24 rice genotypes including landraces and improved cultivars for various quantitative characters and to study the genetic diversity among them so as to utilize them in the hybridization programme for development of new lines with improved grain yield and tolerance to biotic and abiotic stress conditions.

MATERIALS AND METHODS

The experimental material consisted of 24 rice genotypes comprising 10 improved cultivars and 14 landraces. Landraces were collected from different regions of Goa from farmers' field from 2009 to 2011 and improved cultivars obtained from different rice breeding Institutes of India (Table 1). All these genotypes were grown at ICAR Research Complex for Goa during 2011 wet season to evaluate them for yield and its contributing characters. The experiment was laid out in randomized block design with three replications. Each plot consisted of 8 rows of 3 m length with row to row and plant to plant spacing maintained at 20cm and 15cm, respectively. Recommended package of practices was followed to raise the crop. Ten competitive plants were selected at random from each genotype in each replication. Observations were

Table 1. Landraces and improved cultivars of rice used in the present study

S. No.	Genotypes	Source/Site of collection
Landraces of Goa		
1	Belo	Asapur, North Goa
2	Damgo	Anconem, North Goa
3	Mudgo	Anconem, North Goa
4	Kala Belo	Asapur, North Goa
5	Walayo	Torxem, North Goa
6	Kendal	Neura, North Goa
7	Korgut	Chorao Island, North Goa
8	Shidde	Amona, North Goa
9	Red Kochri	Sangolda, North Goa
10	White Kochri	Sangolda, North Goa
11	Saalsi	Gadongrim, South Goa
12	Kolyo	Kotigao, South Goa
13	Panyo	Gadongrim, South Goa
14	Asgo	Loutulim, South Goa
Improved cultivars		
15	Jaya	ZARS, Mandya, Karnataka
16	Naveen	CRRI, Cuttack, Odisha
17	Pusa - 44	CRRI, Cuttack, Odisha
18	Jyothi	RARS, Pattambi, Kerala
19	Akshayadhan	DRR, Hyderabad, AP
20	Chandan	CRRI, Cuttack, Odisha
21	Swarna (<i>Sub-1</i>)	CRRI, Cuttack, Odisha
22	Karjat - 3	RARS, Karjat, Maharashtra
23	Karjat - 7	RARS, Karjat, Maharashtra
24	TRC-2005-1	ICAR Tripura Centre, Tripura

recorded on 12 important yield and its contributing characters *viz.*, days to 50% flowering, plant height, number of tillers per hill, productive tillers per hill, panicle length, total grains per panicle, per cent fertility, 1000 grain weight, grain length, grain breadth, length to breadth ratio, grain yield and harvest index. The genetic distance between the genotypes was worked out using Mahalanobis D² analysis (1936) and grouping of varieties into clusters was done following the Tochers method as detailed by Rao (1952).

RESULTS AND DISCUSSION

Analysis of variance showed significant differences among the genotypes for all the 12 traits studied indicating high variability among the 24 genotypes. Based on D² analysis, the 24 rice genotypes were grouped into 6 clusters (Table 2). Cluster I consisted maximum of 13 genotypes followed by cluster III with six genotypes. Cluster II had two genotypes, while the remaining clusters *viz.*, cluster IV, cluster V and cluster VI were represented by single genotypes each *viz.*, Shidde, Saalsi and Kolyo respectively. The grouping of most of the landraces of Goa and improved cultivars into one cluster indicates genetic relatedness between these genotypes. Close resemblance with respect to days to maturity, productive tillers, panicle length, per cent fertility and for grain breadth among these genotypes might have grouped them into a single cluster. This can be further explained by free flow of genes between these accessions. Similar is the case with cluster III where in all the improved cultivars clustered together. Clustering pattern also showed the random distribution of genotypes into different clusters,

Table 2. Clustering pattern of 24 rice genotypes based on D² statistics

Clusters	No. of Genotypes	Name of the genotypes
I	13	Jaya, Naveen, Chandan, Karjat-3, Belo, Walayo, Kendal, Damgo, Kala Belo, Mudgo, Korgut, Asgo, Panyo
II	2	Red Kochri, White Kochri
III	6	Jyothi, Karjat-7, Pusa-44, TRC-2005-1, Akshayadhan, Swarna (<i>sub-1</i>)
IV	1	Shidde
V	1	Saalsi
VI	1	Kolyo

indicating that geographical diversity and genetic diversity are not related. Similar findings on non correspondence of genetic diversity with geographical diversity were earlier reported by Shanmugasundaram *et al.* (2000) in released rice varieties and Nayak *et al.* (2004) in aromatic rice germplasm.

The inter cluster distance is higher than intra cluster distance indicating wide genetic diversity among the genotypes. The highest inter-cluster distance was observed between the cluster II and IV, followed by cluster II and III, cluster IV and VI and cluster V and II indicating high diversity among these clusters (Table 3). The lowest inter-cluster distance was observed between the cluster V and VI indicating that these genotypes included in them are closely related. Subudhi *et al.*, (2008) and Mohanty *et al.* opined that crossing between highly divergent genotypes would produce a broad spectrum of variability enabling further selection

Table 3. Intra (diagonal) and inter cluster average D² and D (parenthesis) in 24 rice genotypes

Group I	II	III	IV	V	VI	
I	160.22 (12.65)	1439.07 (37.93)	434.33 (20.84)	387.43 (19.68)	340.35 (18.44)	524.96 (22.91)
II		34.51 (5.87)	1901.47 (43.60)	2714.11 (52.09)	1005.89 (31.71)	953.36 (30.87)
III			310.89 (17.63)	877.03 (29.61)	825.37 (28.72)	732.31 (27.06)
IV				(0.00)	785.41 (28.02)	1195.22 (34.57)
V					(0.00)	266.47 (16.32)
VI						(0.00)

and improvement. The highest intra cluster distance was observed in cluster III followed by cluster I and cluster II. Selection within such clusters might be executed based on maximum mean value for the desirable characters.

Highest cluster mean for ear bearing tillers was reported in Cluster II, while, highest cluster means for grains panicle⁻¹, grain length, L/B ratio, grain yield ha⁻¹ and harvest index was reported in cluster III (Table 4). Cluster IV recorded highest cluster mean for plant height, panicle length, 1000 grain weight and for grain

Table 4. Cluster mean for different quantitative characters in 24 rice genotypes

Clusters	DFF	PHT(cm)	EBT hill ⁻¹	PL(cm)	Grains panicle ⁻¹	Percent fertility	1000 gr wt (g)	GL (mm)	GB (mm)	L/B	GY (t ha ⁻¹)	HI
I	94.82	150.48	10.48	25.16	119.09	83.08	26.64	6.04	2.70	2.24	5.27	0.31
II	55.67**	109.40	10.90*	20.75	68.20**	83.97	28.20	5.95	2.59	2.09	1.20	0.24
III	100.56	109.39**	9.58**	24.24	136.18*	82.99	22.63	6.29*	2.30**	2.73*	6.43*	0.35*
IV	108.67*	188.20*	10.00	29.97*	99.33	79.67**	30.10*	6.27	2.99*	2.10	3.72	0.23
V	85.00	151.27	10.80	28.85	125.40	88.24*	18.73	4.69**	2.79	1.82**	4.68	0.27
VI	89.00	119.60	12.60	19.73**	67.73	79.91	15.57**	5.13	2.83	2.10	1.12**	0.13**
Mean	92.92	137.10	10.37	24.69	116.42	83.07	25.12	6.01	2.61	2.32	4.96	0.30
CV (%)	1.33	4.77	13.86	5.29	16.83	5.15	3.91	2.69	2.49	2.78	12.17	11.25
SEM±	0.71	3.78	0.83	0.75	11.31	2.47	0.57	0.09	0.04	0.04	0.35	0.02

*, ** represent maximum and minimum values, respectively for different characters

DFF=Days to 50% flowering, PHT=Plant height, EBT=Ear bearing tillers, PL=Panicle length, GL=Grain length, GB=Grain breadth, GY=Grain yield, HI=Harvest Index

breadth. Highest cluster mean for per cent fertility was reported in Cluster V. Genotypes of cluster III had recorded the highest grain yield ($t\ ha^{-1}$) while the genotypes of the cluster VI recorded the lowest grain yield. The promising genotypes with high mean values for different traits from divergent clusters can be used in hybridization programme depending upon the objective of the breeding programme to derive superior transgressive segregants (Mishra *et al.*, 2003; Chaturvedi and Maurya, 2005).

Thus in the present study, the genotypes from cluster I *viz.*, Korgut and Asgo, local landraces are very popular among the farmers in the coastal saline soils. However, these landraces tend to grow tall up to 150-160 cm and lodge at the time of harvest with yield potential of hardly $1.5-2.0\ t\ ha^{-1}$. Hence, crossing these landraces with the improved cultivars in cluster III *eg.* Pusa-44 having high mean yield ($7.2\ t\ ha^{-1}$) and semi dwarf plant type (100 cm) would produce transgressive segregants combining high grain yield, semi tall plants (non-lodging) and tolerant to salinity. Further, Shidde, another salt tolerant landrace, from cluster IV, possessed many desirable traits like long panicles (29.97 cm), high 1000 grain weight (30.10 g) and grain breadth (2.99 mm). Bold grain traits in the rice grains of this landrace is preferred by the local farmers as these are more suited to parboiled rice, a common rice eaten mostly in Goa, Kerala and in coastal belt of Karnataka.

The contribution of different characters to that of total divergence was estimated based on ranking system (Table 5). In this study, days to 50% per cent flowering contributed maximum to the total divergence (38.77%) followed by 1000 grain weight (19.93), grain breadth (17.75) and plant height (14.86). These traits together contributed to 91.31 per cent towards total divergence. Bisht *et al.*, (2007) while working on genetic diversity of paddy landraces of Uttarakhand Himalaya and Subudhi *et al.*, (2008) in promising rice lowland rice varieties of eastern India also reported the high contribution of these characters towards the total divergence. Thus, it is suggested to consider these traits while selecting parents for further breeding programme in this particular set of germplasm.

In this study, 24 rice genotypes were grouped into six clusters based on the 12 quantitative characters. Three genotypes *viz.*, Shidde, Saalsi and Kolyo formed single genotype clusters revealing their uniqueness.

Table 5. Relative contribution of 12 quantitative characters towards total divergence

Characters	Time ranked first	Contribution (%)
Days to fifty per cent flowering	107	38.77
Plant height	41	14.86
Productive tillers hill ⁻¹	1	0.36
Panicle length	7	2.54
Grains panicle ⁻¹	0	0.00
Per cent fertility	1	0.36
1000 grain weight	55	19.93
Grain length	3	1.09
Grain breadth	49	17.75
Length breadth ratio	3	1.09
Harvest Index	5	1.81
Grain yield ($t\ ha^{-1}$)	4	1.45

Four characters *viz.*, days to 50 % flowering, plant height, 1000 grain weight and grain breadth contributed maximum to the total divergence in our study. Goan rice landraces, so far not utilized in the breeding programs, have potential for use in future rice improvement programmes aiming at development of rice varieties with high yield, better grain quality and multiple stress tolerance.

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