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Exploration and agro-morphological evaluation of rice (*Oryza sativa* L.) land races grown under the upland ecosystem of Tripura

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Abstract

In the present study, 60 (Sixty) nos. of rice land races were collected from the upland province of Tripura through an extensive exploration programme. Subsequently experiment was carried out in ICAR Research Complex for North Eastern Hilly Region, Tripura Centre, Lembucherra, West Tripura to determine the agro-morphic characterisation of the collected landraces and also to assess their variability based on 14 (fourteen) qualitative and 12 (twelve) quantitative descriptors. The experiment was conducted in two subsequent *Kharif* seasons during the year 2015 and 2016 using Randomised Complete Block Design (RCBD) with two replications. Qualitative and quantitative characters under the study showed considerable polymorphism among the landraces. Environmental influence was meager on expression of characters as evidenced by narrow gap between genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV) for most of the quantitative traits. High magnitude of GCV, PCV as well as heritability coupled with moderate to high genetic advance were found for grain yield per plant (gm.), nos. of filled grain per panicle, nos. of spikelet per panicle and 100 seed weight (gm.), which implies effectiveness of those traits for selection of superior genotype. Cluster analysis based on Mahalanobis D^2 values grouped the land races into 6 nos. of groups. Significant magnitude of intracluster and intercluster distances within and between the groups ascertained ample scope for utilisation of the landraces in recombinant and heterosis breeding programme. Landraces namely Garo Malati, Chikanswari Kabar, Turkey, Galong proved themselves as most promising parents for future breeding programme.

Keywords: Rice, landraces, variability, heritability, genetic advance, genetic diversity.

Introduction

Rice is one of the major and staple foods for more than half of the world's population. Approximately 90% of the world rice grown and consumed in Asia, where as 50% of the world's population depends on rice for food (Tenorio *et al.*, 2013) [14]. Considering the fact, rice improvement activities are getting more and more emphasis in present day plant breeding programme and it is the landrace, which virtually determine the success and nature of such endeavors. Rice landraces, because of their effectual evolution process & enormous in built genetic variability can grow in a wide range of ecosystem under varying topography and climatic conditions. Thus the development programme of superior rice population should involve the intelligent use of available genetic variability of indigenous land races to cater the need of various farming situations of rice.

In any systematic breeding programme, steps like creation of genetic variability, practicing selection and utilization of selected genotypes to evolve promising varieties are very important (Paikhomba *et al.*, 2014) [8], thus, before conduction of any crop improvement programme, the exploration of local or traditional land races and their agro morphological characterization is a critical requirement as it is the fundamental in order to provide information for plant breeding programmes. Tripura, being a state of North East India is endowed with a great diversity of rice landraces in her varied topographical eco system. Even though in a small quantity, a significant numbers of local rice landraces are still being cultivated in the hilly region of the state. But our information about them is incomplete and in the present day's socio-economic scenario, where, economical yield of a particular crop is the main concern, the marginal and poor farmers who are the main keeper of these traditional landraces are showing more interest in cultivation of high yielding varieties but not on the conservation of the broad genetic base and variability. Therefore, it has become imperative to collect and conserve those land races of rice. In the context of the above, present experiment was planned to explore the local land races of rice presently grown in the state of Tripura followed by their agro morphological characterization and diversity analysis.

Materials and methods

Exploration and collection

Extensive survey was conducted in the remote villages of Tripura to collect several local indigenous landraces of rice in the month of August to October 2014. During exploration preference was given to collect the upland local landraces of rice. In this exploration programme, 60 (Sixty) Nos. of local rice land races (Table.1) were collected from six nos. of districts of the state *viz.* West Tripura, Khowai, Gomati, North Tripura, South Tripura & Dhalai district (Fig. 1). 04 (Four) nos. of hill ranges namely Baramurah, Atharomurah, Longtrai & Jampui hill were explored in this programme. Though, in a very small quantity, the marginal and small farmers of different tribal communities are still practicing the cultivation of the local land races. It has been experienced that few rice land races are familiar with different names in different localities. Care has been taken to avoid such type of duplication, if ample similarities exist between those duplicate land races. Views of the source farmers were taken into consideration while recording any special remarks against a particular landrace, subject to further field verification. After proper cleaning and optimum drying, the collected seeds were stored in freezer for further utilization in field experiment.



Fig 1: Exploration track of land races in different regions of Tripura

Table 1: List of the Rice land races collected under the study and their collection sites

S. No	Name of the Land races	Collection site	Dist.*	Latitude/ Longitude	S. No	Name of the Land races	Collection site	Dist.*	Latitude/ Longitude
1	Kaporok	Thamsarai para.	N	24°1'N /92°1'E	16	Lebuka	Thamsarai para	N	24°1'N /92°1'E
2	Releng	Boithang bari	N	24°1'N /92°8'E	17	Aaduma	Aswini rojapara,	D	23°3'N /91°5'E
3	Beti	Boithang bari	N	24°1'N /92°8'E	18	Fazu Sen	Boithang bari	N	24°2'N /92°1'E
4	Maimi Uzra	Purba Jalaibari	G	23°3'N /91°3'E	19	Fazu Ngoi	Boithang bari	N	24°2'N /92°1'E
5	Kalikhasa	Ganganagar	N	24°2'N /92°1'E	20	Beti Kalai	Brahmacharra	K	23°4'N /91°3'E
6	Chinal	Uttar Gakul Nagar	W	23°4'N /91°1'E	21	Saanki ka Phool	Dalapati	D	23°3'N /91°5'E
7	American	Rajnagar	N	24°1'N /92°8'E	22	Bihar	Brahmacharra	K	23°4'N /91°3'E
8	Khasa Kasam	Kairai	W	23°5'N /91°2'E	23	Chikanswari Kabar	Harbang	W	23°5'N /91°3'E
9	Biroin	Rajnagar	N	24°2'N /92°1'E	24	Bangbu Jhum	Nunnacharra Range	K	23°4'N /91°4'E
10	Galong	Boithang bari	N	24°2'N /92°1'E	25	Lal Biroin	Kameswar	N	24°2'N /92°1'E
11	Fazu Vom	Boithang bari	N	24°2'N /92°1'E	26	Dhala Balam	Rajnagar	N	24°1'N /92°7'E
12	Garo Malati	Uttar Gakul Nagar	W	23°4'N /91°1'E	27	Goria	CharGaria Para	W	23°5'N /91°3'E
13	Maimi Usha	Purba Jalaibari	G	23°1'N /91°3'E	28	Bahadur	South Ganga Nagar	N	24°2'N /92°1'E
14	Maimi Red	Thamsarai para	N	24°1'N /92°1'E	29	Maimiwatoklok Mandoori	Brahmacharra	K	23°4'N /91°3'E
15	Suri	Aswini rojapara	D	23°3'N /91°5'E	30	MaimiHungar	Twisarangchak para	W	23°5'N /91°3'E

* Dist. -District, D-Dhalai, G- Gomati, K-Khowai, N- North Tripura, S-South Tripura, W-West Tripura

Table 1: (contd.) List of the Rice land races collected under the study and their collection sites.

S. No	Name of the Land races	Collection site	Dist.*	Latitude/ Longitude	S. No	Name of the Land races	Collection site	Dist.*	Latitude/ Longitude
31	Darka Sona	Thamsarai para	N	24°1'N /92°1'E	46	Makajaria	Rajnagar	N	24°1'N /92°7'E
32	Tarikol Kolte	Boithang bari	N	24°2'N /92°1'E	47	Jilong	Bilaiham para	W	23°4'N /91°1'E
33	Sada Biroin	Ganganagar	N	24°2'N /92°1'E	48	American Ration	Thamsarai para	N	24°1'N /92°1'E
34	Maimi Taukha	Purba Jalaibari	G	23°1'N /91°3'E	49	Kala Dhan	Bilaiham para	W	23°4'N /91°1'E
35	Saluma	Purba Jalaibari	G	23°1'N /91°3'E	50	Turkey	Dalapati	D	23°3'N /91°5'E
36	Tarkol	Noangang	N	24°1'N /92°1'E	51	Saanki Kachak	Dalapati	D	23°3'N /91°5'E
37	Madoop	Dalapati	D	23°3'N /91°5'E	52	Maimi Ukhlaol	Purba Jalaibari	G	23°1'N /91°3'E
38	Waibang	Bilaiham para	W	23°5'N /91°4'E	53	Maiwasha	Old Dalapati Para	D	23°3'N /91°5'E
39	Jhum Bini	Garjeecherra	G	23°2'N /91°3'E	54	Maimi Watolok	Dalapati,	D	23°3'N /91°5'E
40	Fazu Sen (White)	Athramura range	K	23°5'N /91°4'E	55	Santinmaw Wakhum	Killa	S	23°3'N /91°3'E
41	Bongbu	Noangang	N	24°1'N /92°1'E	56	Yang Dhan	Killa	S	23°3'N /91°3'E
42	Sadok	Noangang	N	24°1'N /92°1'E	57	Badaya	Killa	S	23°3'N /91°3'E
43	Kala Jira	Kameswar	N	24°2'N /92°1'E	58	Kanchali	Killa	S	23°3'N /91°3'E
44	Gaigash	Murasingh Para	G	23°4'N /91°4'E	59	Australian Biroin	Kameswar,	N	24°2'N /92°1'E
45	Vanbang	Killa	S	23°3'N /91°3'E	60	Assam Paisom	Rajnagar	N	24°1'N /92°7'E

* Dist. -District, D-Dhalai, G- Gomati, K-Khowai, N- North Tripura, S-South Tripura, W-West Tripura

Field experiment and Statistical analysis

The field experiment was conducted in the field of ICAR Research Complex for North Eastern Hilly Region, Tripura Centre, Lembucherra, West Tripura (23°90'E, 92°29'N) in the *Kharif* seasons during the year 2015 and 2016. The trials were set in Randomised Complete Block Design with 2(Two) replication. Seeds were directly sowed at a distance of 25 cm. (row-row) x 25 cm. (plant -plant). Fertilizers were applied @ 60:40:40 Kg N:P:K ha⁻¹. Inter culture operation, irrigation and other pest control measures were followed as and when necessary during the whole growing periods. Qualitative characters are considered as the most important characters to identify a particular plant variety (Sinha *et al.* 2013) [12] as they are mostly genetically controlled and less influenced by the environmental factors, again several agronomical and yield contributing quantitative characters also play a significant role in selection of desirable plant type for crop improvement programme. Thus for primary analysis on agro morphological characterization, observations were collected for 14 different qualitative characters and Standard Evaluation System for Rice, IRRI, 2002 was taken as reference for grouping of the land races against the qualitative characters in different scales. As far as the quantitative characters are concerned, pulled mean values of 12 nos. of yield contributing quantitative characters *viz.* plant Height (cm.), nos. of productive tiller per plant, panicle length (cm.), nos. of primary branch per panicle, root length (cm.), root- culm ratio, nos. of spike lets per panicle, nos. of filled grain per panicle, spikelet fertility (%), 100 Seed's weight (gm.), harvest index (%) and grain yield per plant (gm.) were recorded from 05 nos. of competitive plants preferably from the middle rows over the replications.

Estimation of Genotypic coefficient of variance and Phenotypic Coefficient of variability were done to splits the total variation into different components and also to provide the test of significance carried out with replicated data.

The mean data were also subjected to heritability and genetic advance analysis as per Johnson *et al* (1955) [4]. In order to arrange the landraces in various groups and subgroups and

also to find out the behavioral similarity of them, cluster analysis was performed using the Mahalanobis's (1928) [6] D² analysis. The statistical distance (D²) between the pair of landraces were obtained as the sum of squares of the difference between the pairs of uncorrelated values of any two land races. The whole statistical analysis was done using Windostat Version 8.6 from Indostat service, Hyderabad.

Results & discussions

Observation on Qualitative characters

Qualitative characters are considered as the most important traits to identify a particular plant variety as they are mostly genetically controlled and less dependent on the environmental responses. Though, the qualitative characters have shown less variability as a whole, significant polymorphism have been observed in Lemma and Palea colour, (45% of Straw colour, 25% Gold and gold furrows on straw background, 10% with Brown spots on straw, 7% with Brown furrows on straw, 5% each for Purple furrows on straw and Purple and lastly Reddish to light purple colour of Lemma and Palea against 3% of rice land races under experiment. Similar considerable variability was also found by Sinha *et al.*, 2013 [12]. Whole seed pictures of some landraces are given in figure 2. to reflect clear cut idea on the variability of lemma and palea colour. Leaf blade colour showed polymorphism as Green colour (75%) Green colour with Purple tips (15%), Dark green colour (5%), Light green colour (3%) and Purple blotch or purple mixed with green (2%) which is in agreement with the observation of Parikh, 2012[9]. Others qualitative characters with remarkable variability are Culm Inter node colour. Panicle types, Leaf blade pubescence. Least variability was found in the Awning character as 90% of the landraces under the study do not have awn, while 5% of total landraces accounted for both short and partly awned as well as long and partly awned characters. Most of the variability results in the qualitative characters are more or less in agreement with the studies of Tandekar *et al.*, (2014) [13]. Grouping of the land races against the different qualitative characters in different scales is presented in Table 2.

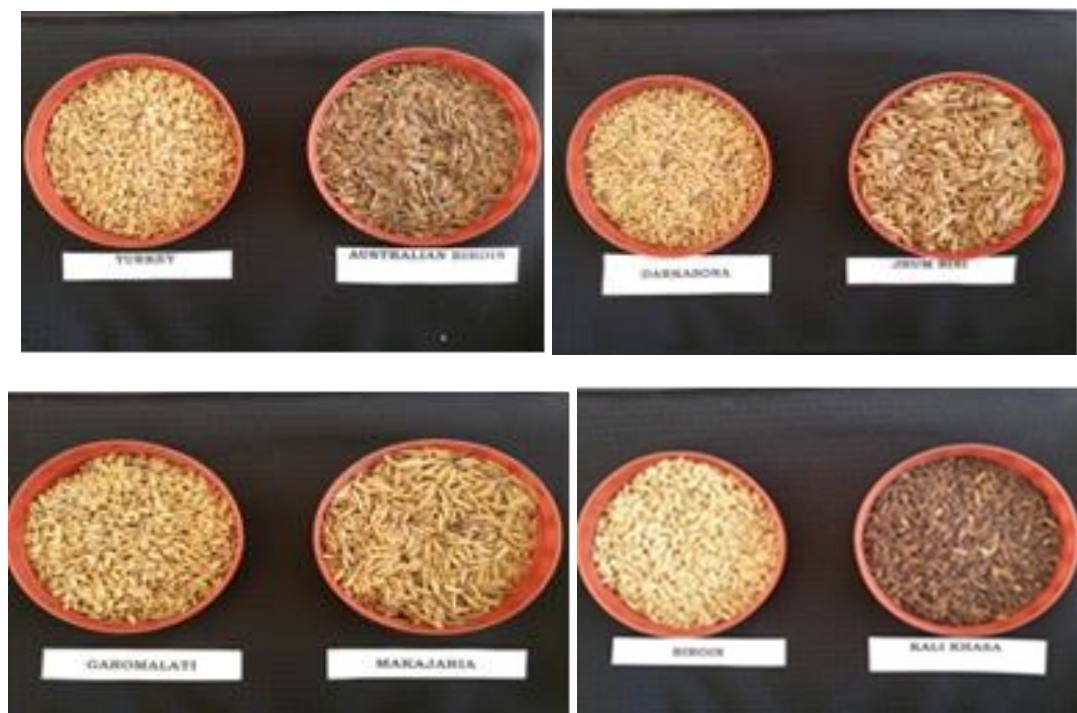


Fig 2: Variability in whole seeds of some land races found under the exploration programme.

Table 2: Grouping of the landraces based on Qualitative Traits with their Indicators and Scales used for evaluation.

Traits	Indicators and their scales*	Nos. of Landraces	Evaluation Phase
Seedling Vigour (Vg)	Vigorous (fast growing; have 1-2 tillers in majority of population)-3	15	Seedling stage
	Normal (plant at 4-leaf stage)- 5	30	
	Weak (plants somewhat stunted; 3- 4 leaves; thin population; no tiller formation.-7	15	
Leaf Blade Colour (LBC)	Light green-1	2	Stem elongation to Booting stage
	Green-2	45	
	Dark Green-3	3	
	Purple tips-4	9	
	Purple blotch (purple mixed with green)-6	1	
Leaf Angle (LA)	Erect-1	14	Stem elongation to Booting stage
	.Intermediate-3	29	
	Horizontal-5	17	
Flag Leaf Angle (FLA)	Erect-1	24	Stem elongation to Booting stage
	Intermediate-3	28	
	Horizontal-5	8	
Leaf Blade Pubescence (LBP)	Glabrous-1	1	Booting to Heading stage
	Intermediate-2	40	
	Pubescent-3	19	
Panicle Type (PnT)	Compact-1	25	Dough stage
	Intermediate-2	33	
	Open-3	2	
Panicle Axis (PnA)	Straight-1	18	Milk stage to Mature grain stage
	Droopy-2	42	
Panicle Exsertion (Exs)	Well exserted-1	40	Milk stage to Mature grain stage
	Moderately well exserted-3	18	
	Partly exserted-7	2	
Sterile Lemma Colour (SLmc)	Straw (yellow)-1	49	Mature Grain stage
	Gold-2	1	
	Red-3	3	
	Purple-4	7	
Ligule Color (LgC)	White-1	56	Stem elongation to booting stage
	Purple lines-2	4	
Ligule Shape (LS)	Acute to acuminate-1	48	Tillering to Stem elongation stage
	Cleft-2	11	
	Truncate-3	1	
Awning (An)	Absent-0	54	Milk stage to Mature grain stage
	Short and partly awned-1	3	
	Long and partly awned-7	3	

Table 2: (continuation) Grouping of the landraces based on Qualitative Traits with their Indicators and Scales used for evaluation.

Traits	Indicators and their scales*	Nos. of Landraces	Evaluation Phase
Awn Color (AnC)	Awnless-0	54	Heading stage
	Straw-1	3	
	Gold-2	1	
	Purple-5	2	
Culm Internode Color (CmlC)	Green-1	38	Milk stage to Mature grain stage
	Light gold-2	12	
	Purple lines-3	8	
	Purple-4	2	
Lemma and Palea Color (LmPC)	Straw-0	27	Mature grain stage
	Gold and gold furrows on straw background-1	15	
	Brown spots on straw-2	6	
	Brown furrows on straw-3	4	
	Reddish to light purple-5	2	
	Purple furrows on straw-7	3	
	Purple-8	3	

* As per Standard Evaluation System for Rice, IRRI, 2002

Observations on Quantitative characters**Analysis of Variance**

The analysis of variance (Table 3) showed that the difference among landraces for all the traits under study were highly significant. Significant difference has also been observed against the performance of the landraces over the years. This indicated that the genotypes were possessing inherent genetic variances among themselves with respect to the character studied. Similar result was reported by Bekele *et al.*, (2013) [2]

and Rashid *et al.*, (2017) [11].**Estimates of genetic parameters**

The magnitude of phenotypic and genotypic coefficient of variations (PCV and GCV) were higher for grain yield and several yield attributing traits under the study but the difference between the PCV and GCV for the studied characters were very low indicating low sensitivity to environment and consequently greater role of genetic factors

influencing the expression of these characters. Similar findings were also reported by Tuhina Khatun *et al.*, (2015)^[15] and Uday Kumar *et al.*, (2017)^[16]. The result revealed that high Genotypic coefficient of variability (GCV) accompanied by high Phenotypic coefficient of variability (PCV) were found for Grain yield per plant (gm.) followed by Nos. of filled grain per panicle & Nos. of spikelet per panicle. Moderate values of GCV and PCV were found for root length, root: culm ratio, harvest index. Whereas characters like spikelet fertility, plant height, panicle length showed low magnitude of GCV and PCV. The results are in agreement with Kole *et al.*, (2008)^[5] and Mazid *et al.*, (2013)^[7].

Heritability and Genetic advance

The relative contributions of differences in genetic and non-genetic factors to the total phenotypic variance in a population are generally estimated by the heritability analysis. In selective breeding, heritability estimates plays an important role. The most important function of the heritability in the genetic study of quantitative characters is its predictive role to indicate the reliability of the phenotypic value as a guide to breeding value (Al-Tabbal *et al.*, 2012)^[1].

In the present study, high estimates of heritability (H^2) were observed in almost all the yield contributing traits like 100 seed weight (94%), nos. of filled grain per panicle (88%), nos. of spikelet per panicle (87%), grain yield per plant (84%) and root length (80%). Although high heritability estimates have been found to be effective in the selection of superior landraces on the basis of the phenotypical expression, but

heritability estimates along with genetic advance is more useful in predicting the effects for selection of desirable type of landraces.

Improvement of characters in genotypic value for the new population compared with the base population under selection refers to Genetic advance (GA) (Wolie *et al.*, 2013)^[17]. In this study, Genetic advance as percent mean (GAM) at 5% level had a general range between 7.02 % for spikelet fertility and 87.44 % for grain yield per plant. Among the characters comparatively higher values of GAM were recorded for number of filled grains per panicle, number of spikelets per panicle, root: culm ratio and root length. It was moderate for 100 seed weight, harvest index and nos. of primary branches per panicle.

Heritability and the genetic advance are found to be very effective selection parameters when considered jointly. High heritability estimates along with the high genetic advance is more helpful in predicting gain under selection than heritability or genetic advance estimates alone. Thus, the heritability estimates will be reliable if accompanied by high genetic advance. High heritability coupled with moderate to high genetic advance have been observed in grain yield per plant (gm.), nos. of filled grain per panicle, nos. of spikelet per panicle and 100 seed weight (gm.) which implies predominance of additive gene action for those character. Thus selection of land races based on those characters would be effective. Similar results were also reported by Dutta *et al.*, (2013)^[3]; Raffi *et al.*, (2014)^[10]. The estimates of GCV, PCV, Heritability & Genetic advance etc. are presented in Table 4.

Table 3: Analysis of variance of studied traits in 60 landraces under 02 successive *kharif* seasons of 2015 and 2016

Source of Variations	df	Mean Sum of Squares											
		PL HT	PR TLR	PN.LN	PRIBR /PNL	RT.LN.	R:C	SPKLT/ PN	FLD GRN/ PN	SPKLT FRT	100 SD WT	H.I.	GR Y/ PLT
Replicate	1	828.44 **	2.533 *	5.014	5.028 *	42.622 **	0.0005	510.737	160.753	37.067 *	0.003	20.050	39.349 **
Environments	1	642.88	0.697 **	64.387 **	12.051 **	61.772 **	0.029 **	437.751 *	388.876 *	5.642	0.311 **	171.754 **	30.702 **
Interactions	1	419.074 *	0.040	0.499	0.0005	4.965	0.0003	73.981	77.657	1.883	0.002	4.409	0.708
Overall Sum	3	630.133 **	1.090 *	23.300 *	5.693 **	36.453 **	0.009 **	340.823	209.095	14.864	0.105 **	65.404 *	23.586 **
Treatments	59	577.062 **	1.928 **	41.965 **	10.649 **	46.722 **	0.008 **	5294.398 **	4947.431 **	63.247 **	0.865 **	174.314 **	115.357 **
Error	177	84.068	0.393	6.744	1.108	2.643	0.0005	180.044	161.743	7.586	0.012	17.757	5.170

* Significant at 5% level, ** Significant at 1% level.

Table 4: Estimates of Genetic parameters for 12 nos. of quantitative traits under study

Character	Range		Grand Mean	Exp. Mean Next Gen.	CV	GCV	PCV	H^2	GA 5%	GA as percentage of mean 5%
	Min	Max								
PL HT.	86.66	148.58	113.55	131.18	8.075	9.77	12.68	0.59	17.63	15.52
PR TLR	3.16	6.08	4.3943	5.246	14.42	14.24	20.27	0.49	0.89	20.62
PN LN	17.66	31.99	24.49	29.09	10.60	12.11	16.09	0.56	4.6	18.77
PRI BR	5.16	11.99	7.91	10.54	13.3	19.51	23.61	0.68	2.62	33.20
RT LN	8.23	21.30	13.55	19.69	12.0	24.49	27.27	0.80	6.14	45.32
RT:CLM	0.07	0.26	0.15	0.237	14.70	28.13	31.74	0.78	0.08	51.35
SPKLT/PN	59.41	221.49	110.34	179.30	12.16	32.40	34.61	0.87	68.96	62.49
FLD GRN/ PN	53.08	209.58	97.73	164.61	13.01	35.39	37.70	0.88	66.87	68.42
SPKLT FRT	78.29	94.65	88.04	94.23	3.128	4.23	5.26	0.64	6.18	7.02
100 SD WT	1.15	3.11	2.48	3.41	4.46	18.58	19.11	0.94	0.92	37.23
HI	15.76	44.42	30.47	41.16	13.82	20.53	24.75	0.68	10.68	35.07
GR Y /PLT	5.20	30.35	11.34	21.26	20.04	46.26	50.41	0.84	9.92	87.44

PL HT - Plant Height (cm.), PR TLR-Nos. of Productive Tiller per plant, PN LN -Panicle length (cm.), PRI BR-Nos. of Primary branch per panicle, RT LN-Root length (cm.), RT:CLM-Root- Culm ratio, SPKLT/PN-Nos. of Spikelets per panicle, FLD GRN/ PN-Nos. of filled grain per panicle, SPKLT FRT-Spikelet fertility (%), 100 SD WT-100 Seed's weight (gm.), HI-Harvest Index (%), GR Y /PLT-Grain yield per plant (gm.)

Analysis of genetic divergence

60 nos. of rice landraces were grouped into 06 (six) nos. of clusters employing the Tocher's method with the standard that the intra-cluster average D^2 values should be less than the inter cluster D^2 values. The distribution pattern was at random with maximum number of 26 genotypes in Cluster-I. Cluster-

II found to be the second largest group with 12 nos. entries. Cluster -V & IV were consisted of 08 & 06 nos. of landrace members respectively, whereas, both Clusters-III & VI are having 04 nos. of members each. The distribution of landraces into 06 clusters is presented in Table 5.

Table 5: Clustering patterns of 60 nos. of rice land races under 6 nos. of clusters

Cluster	Nos. of landraces	Name of the land races
I	26	Fazu Sen, Bongbu, Tarikol Kolte, Badaya, Kala Dhan, Gaigash, Maimi Red, Beti Kalai, Maimi Taukha, Kaporok, Goria, Waibang, Dhala Balam, Saluma, Darka Sona, Vanbang, Sadok, Biroin, Lal Biroin, Sada Biroin, Maimi Uzra, Jhum Bini, Beti, Saanki Kachak, Chinal, Maimi Usha.
II	12	Lebuka, Maimi Watoklok Mandoori, American, American Ration, Madoop, Kanchali, Jilong, Maimi Ukhlaol, Makajaria, Saanki Ka Phool, Yang Dhan, Australian Biroin.
III	04	Garo Malati, Chikanswari Kabar, Turkey, Galong
IV	06	Aaduma, Bihar, Bahadur, Suri, Fazu Sen (White), Fazu Ngoi.
V	08	Fazu Vom, Santinmaw Wakhum, Bangbu Jhum, Maiwasha, Maimi Hungar, Releng, Tarkol, Maimi Watolok.
VI	04	Kalikhasa, Khasa Kasam, Assam Paisom, Kala Jira.

The average intra and inter cluster D^2 values within and between the groups were estimated and depicted in Table 6. Highest Intra cluster distance was found in Cluster-V (19.52) followed by Cluster-VI (16.78) and Cluster-IV (12.00), while the lowest intra cluster distance was observed in Cluster-I (8.38). High magnitude of intra cluster D^2 value of the clusters signified the existence of ample diversity among the members of the cluster. Thus, recombinant breeding may yield a fruitful result. Cluster-III with 04 nos. of members found to be the farthest group from cluster-VI with 06 nos. of members. The D^2 value as inter cluster distance between those clusters has

been observed as 80.51 followed by 78.55 between Cluster-V and Cluster-VI. Cluster-I and Cluster-V proved themselves as nearest groups with lowest inter cluster distance of 14.87. Further, Cluster -I and Cluster-II along with Cluster II and Cluster III also turned up as close neighbor groups with inter cluster distances of 15.57 and 18.56 respectively. The high values of inter cluster distance between Cluster-III and VI, Cluster-V and VI indicate significant amount of variability between the said groups, thus the members of those groups may be considered as good parents for heterosis breeding programme.

Table 6: Average Intra and Inter cluster D^2 values among 6 clusters in 60 (sixty) nos. of landraces of rice under the study.

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	8.38	15.57	33.57	21.29	14.87	55.96
Cluster II		10.38	37.69	18.56	27.26	34.20
Cluster III			8.19	54.26	37.43	80.51
Cluster IV				12.00	33.93	29.56
Cluster V					19.52	78.55
Cluster VI						16.78

But selecting parents groups simply on the measures of high values of inter cluster distance may not yield optimum until and unless they do have desirable characteristics. In most of the breeding programmes, where main objective is to enhance

the economic yield, it is always expected that the parents would have good yield contributing characters. The cluster mean values of different yield contributing characters are cited in Table 7.

Table 7: Cluster mean values of 6 clusters against different quantitative characters

Cluster	Quantitative characters											
	PL. HT.	PR TLR	PN LN	PRI BR	RT. LN	RT:CLM	SPKLT/PN	FLD GRN/ PN	SPK.FRT.	100 SD WT	H.I	GR Y /PLT
I	106.00	4.20	23.72	7.62	13.52	0.16	100.75	89.00	88.22	2.71	32.22	10.80
II	118.30	4.25	26.61	8.21	10.89	0.12	111.71	97.18	87.18	2.23	27.66	10.20
III	132.19	4.64	27.92	10.89	13.08	0.13	211.83	199.81	94.27	2.74	41.68	26.11
IV	114.55	4.89	23.90	6.85	18.12	0.21	84.97	75.14	88.43	2.07	22.72	7.84
V	109.42	3.96	24.31	8.27	14.94	0.18	111.39	94.95	84.26	2.94	31.64	12.07
VI	117.01	5.29	21.08	6.87	12.55	0.14	103.12	93.62	90.32	1.29	25.63	7.39

PL HT - Plant Height (cm.), PR TLR-Nos. of Productive Tiller per plant, PN LN -Panicle length (cm.), PRI BR-Nos. of Primary branch per panicle, RT LN-Root length (cm.), RT:CLM-Root- Culm ratio, SPKLT/PN-Nos. of Spike lets per panicle, FLD GRN/ PN-Nos. of filled grain per panicle, SPKLT FRT-Spikelet fertility (%), 100 SD WT-100 Seed's weight (gm.), HI-Harvest Index (%), GR Y /PLT-Grain yield per plant (gm.)

The data indicated a wide range of mean values between the characters. Plant height (cm.) showed wide range of variability in mean values with a highest range of 132.19 cm. in Cluster-III and lowest range of 106.0 cm. in Cluster-I. Indicators like Grain yield per plant, Harvest index, 100 seeds weight, Spikelet fertility, Nos. of filled grains per panicle etc. are generally considered as effective parameters towards selection of high yielding parents. Significantly, Cluster-III has highest mean values for grain yield per plant (gm.) [26.11], Harvest index (%) [41.68], spikelet fertility (%) [94.27], Nos. of filled grains per panicle [199.81] and Nos. of spike lets per panicle [211.83]. Certainly, the 04 nos. of landraces viz. Garo Malati, Chikanswari Kabar, Turkey, Galong of cluster III can be considered as promising parent in

future breeding programme. Again cluster-III is farthest neighbor of Cluster-VI and cluster VI is having highest mean value for Nos. of productive tillers per plant (5.29), which is another crucial yield contributing character. Thus, heterosis breeding programme between the members of those groups (III and VI) can be rewarding. The genotypes from the clusters with high mean values of different yield contributing characters may be directly used for adaptation or as parents in future hybridization programs as for a successful breeding program selection of genetically diverse parents is an important prerequisite to obtain better and desirable recombination. Relationship among the landraces is expressed as dendrogram based on D^2 values in Fig 3.

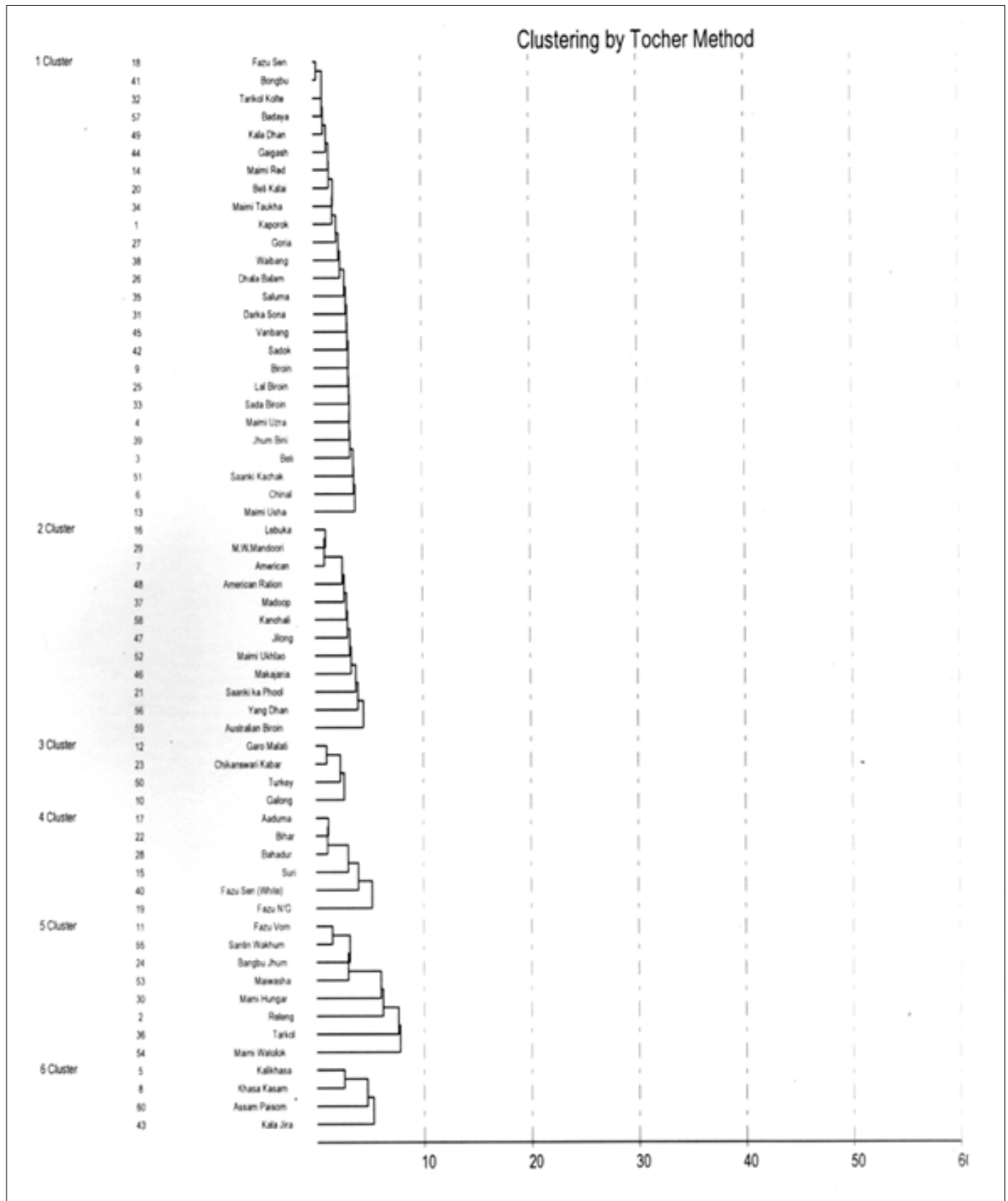


Fig 3: Dendrogram showing relationship among 60 land races of rice in six clusters based on Mahalanobis's D² values

Conclusion

The main purpose of the study was to collect and conserve the fast genetic eroded local rice landraces of Tripura at maximum possible extent. Side by side emphasis was also given on agro morphological characterisation and divergence analysis of the collected landraces. 60 nos. of landraces collected under the exploration programme have shown ample genetic variability in terms of different qualitative characters. Further, significant results on variability, heritability and

genetic advance have been found in many of the yield contributing quantitative characters under the study which indicated scope for improvement of rice grain yield through selection in this region. Grain yield per plant (gm.), nos. of filled grain per panicle, nos. of spikelet per panicle and 100 seed weight (gm.) can be considered to be effective traits towards selection of superior genotype for their high magnitude of heritability and genetic advance values. Under cluster analysis, none of the cluster have been found to be

solitary in nature along with all anticipated traits, thus direct selection of any genotype for instant uses in breeding programme could not be determined in this particular study. Therefore, hybridization between the selected genotypes from divergent clusters is essential to judiciously combine all the targeted traits. Garo Malati, Chikanswari Kabar, Turkey, Galong being the members of a single group, found to be most promising landraces under the study.

North Eastern region of India is always considered to be rich pocket of crop biodiversity. Though, in this study, extensive efforts have been rendered to collect maximum possible numbers of landraces from the farmers field of Tripura, still possibilities are there that a significant numbers of landraces remained unexplored. Therefore, more elaborate exploration programme are required to be conducted in future for comprehensive utilization of rice genetic resources under the upland ecosystem of the region.

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Conflict of interest

The authors express no conflict of interest.

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