

Genetic diversity analysis in some upland rice (*Oryza sativa* L.) landraces of Nagaland using grain quality and yield attributing traits

H. LALRINDIKI¹, KIGWE SEYIE¹, H.P. CHATURVEDI^{1*} AND HARENDRA VERMA²

¹Department of Genetics and Plant Breeding, School of Agricultural Sciences, Nagaland University, Medziphema-797106 Nagaland, India

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ABSTRACT

An experiment was laid out to evaluate the genetic diversity in upland races of rice grown in Nagaland using a randomized complete block design with two replications during Kharif, 2020 at the research farm of ICAR, Nagaland centre. Observations were recorded for 11 yield contributing traits and 11-grain quality parameters. Diversity analysis among 50 upland landraces of rice of Nagaland revealed that maximum inter cluster distance was observed between cluster III and V indicating large genetic differences among genotypes of these two clusters with wide diversity which will serve as desirable parent in breeding programmes to exploit heterosis. Diversity analysis revealed that grain yield per plant was highest in the genotype belonging to cluster V while amylose content was highest in the genotype belonging to cluster VII. Diversity analysis also revealed that among the yield parameters test weight and grain yield per plant were the major contributing trait towards genetic diversity whereas among grain quality traits amylase content and gel consistency contributed the most towards genetic diversity, hence, these traits should be given importance during choosing parents for hybridization and selection in the segregating populations.

Keywords: Rice, quality, yield, cluster, genetic diversity

INTRODUCTION

Rice is one of the world's most important staple cereal crops and is cultivated in at least 114 countries under diverse environmental conditions (Anis *et al.*, 2016). It forms an important food source for over 3.5 billion people, contributing more than 20% of total dietary calories (Khush, 2013). About 90% of rice is produced and consumed in Asia. Northeast India is one of the primary centres of origin of rice representing a rich source of genetic diversity and reservoir of valuable genes. A major part of Assam, Arunachal Pradesh, Manipur, Mizoram, Meghalaya, Nagaland, Tripura and West Bengal are endowed with non-basmati rice cultivars which are cultivated casually as way of life (Punyo and Chaturvedi, 2020), with almost no bend towards their commercial exploitation. Nagaland has the richest pockets of rice germplasm in valleys as well as in hilly areas. The upland landraces of rice exhibit large variations in morphology, thus signifying the vast genetic diversity among the cultivars. Genetic divergence for agronomic traits is the key component of breeding programmes for broadening the gene pool of rice. The genetic diversity among rice genotypes have been

reported by Chaturvedi and Maurya (2005). In any crop, germplasm is a valuable source of base population and provides the scope for wider variability. However, to understand the useable variability, grouping or classification of genetic stocks based on minimum divergence or resemblance between them is quite imperative (Zhimomi, and Chaturvedi, 2019). Therefore present study was undertaken to study the genetic diversity among 50 upland landraces of rice grown in Nagaland.

MATERIALS AND METHODS

The experimental material for the present investigation comprised of pure seeds of 50 upland rice landraces received from ICAR Research Centre for NEH region, and evaluated for grain quality and yield contributing traits at the research farm of ICAR, Nagaland centre using Bhalum-1 and Bhalum-3 as check (Table 1) during kharif 2020. Observations were recorded on Days to 50% flowering (50% F), Days to 80% maturity (80% M), Amylose content (AC), Decorticated grain length (DGL), Decorticated grain length to breadth ratio (DGL: B), Decorticated grain width (DGW), Gel consistency (GC), Grain length (GL), Grain

* Corresponding Author Email: hpchaturvedi68@gmail.com, ²ICAR Research Complex for NEH Region, Nagaland Centre, Medziphema-797106, Nagaland, India

length to breadth ratio (GL:B), Grain length after cooking (GLAC), Gelatinization temperature (GT), Grain width (GW), Grain width after cooking (GWAC), Grain yield per plant (GYPP), Number of filled grains per plant (NOFG), Number of panicles per plant (NOP), Number of tillers per plant (NOT), Number of unfilled grains per plant (NOUG), Plant height (PH), Panicle length (PL), Total number of grains per plant (TNGPP) and Test weight (TW). Amylose content (AC) was determined by the method as described by Juliano (1971). Gelatinization temperature (GT) was assessed indirectly as the

alkali spreading value (ASV) of hulled kernels, as per the modified procedure of Little *et al.* (1958). Similarly, gel consistency (GC) was measured by the procedure of Cagampang *et al.* (1973). Physical grain quality parameters were measured using a vernier caliper. Analysis of variance was done by using the standard statistical procedure. The genetic divergence among genotypes was computed by means of Mahalanobis D^2 technique (Mahalanobis, 1936) and the genotypes were grouped into different clusters following Tocher's method (Rao, 1952).

Table 1: List of upland races of rice under investigation

Sl. No	Genotypes	Place of collection	Sl. No	Genotypes	Place of collection
1	Mapok	Longjang village (Mokokchung)	26	Tei Yoh	Hukpang, Longleng Dist.
2	Mepongchuket Masu	Khensa village, (Mokokchung)	27	Nukjan Shola	Tangha, Longleng Dist.
3	Angja	Tangha village, (Longleng)	28	Mapok Tsuk	Longkhum, Mokokchung Dist.
4	Chali Yoh	Tangha village, (Longleng)	29	Khemaru	Longkhum, Mokokchung Dist.
5	Motso Tsuk	Wokha town, (Wokha)	30	Arunachal	Kilomi, Zunheboto Dist.
6	Yimso Tsuk	Mopongchuket, Mokokchung Dist.	31	Dulong	Hukpang, Longleng Dist.
7	Doiha	Tangha, Longleng Dist.	32	Lamjet	Hukpang, Longleng Dist.
8	Tsuksemla	Dibuia, Mokokchung Dist.	33	Yamchinga	Hukpang, Longleng Dist.
9	Amiisu	Kiding, Tuensang Dist.	34	Vam	Tangha, Longleng Dist.
10	Samaro	Sanis, Wokha Dist.	35	Yamuk	Hukpang, Longleng Dist.
11	Aor Chang	Ungma, Mokokchung Dist.	36	Maso Tsuk	Dibuia, Mokokchung Dist.
12	Aphagi	Sumisettsu, Zunheboto Dist.	37	Manen Tsuk	Longjang, Mokokchung Dist.
13	Chamnya Yoh	Dungkhao, Longleng Dist.	38	Bhalum-1	Check Variety
14	Hyung Yoh	Hukpang, Longleng Dist.	39	Neikedou lha tsia	Kohima, Kohima Dist.
15	Toiya	Hukpang, Longleng Dist.	40	Moya Tsuk	Longkhum, Mokokchung Dist.
16	Hahnyak	Nyang, Longleng Dist.	41	Maibo	Tangha, Longleng Dist.
17	Shupho	Nyang, Longleng Dist.	42	China Tsone	Noklak, Noklak Dist.
18	Yunghah	Tangha, Longleng Dist.	43	Laza	Longjang, Mokokchung Dist.
19	Samro Yoh	Tangha, Longleng Dist.	44	KD 5-2-8	Longkhum, Mokokchung Dist.
20	Nangza Tsuk	Wokha, Wokha Dist.	45	Malanken	Wokha, Wokha Dist.
21	Vepsu Tsuk	Wokha, Wokha Dist.	46	Maro Etyo	Wokha, Wokha Dist.
22	Engcha Yoh	Dungkhao, Longleng Dist.	47	Meitak	Kohima, Kohima Dist.
23	Nukneyi	Nyang, Longleng Dist.	48	Eshie	New Chungliiyimti, Mokokchung Dist.
24	Pfutsero Ru	Pfutsero, Phek Dist.	49	Sopa	Wokha, Wokha Dist.
25	Mati Pasi	Kohima, Kohima Dist.	50	Bhalum 3	High yielding check variety

RESULTS AND DISCUSSION

In the present study 50 genotypes were characterized by 11 yield and 11 quality parameters.

Diversity analysis

Analysis of genetic divergence through D^2 statistics revealed the existence and extent of

diversity among the group of genotypes, diversity between pairs of populations can be measured and denoted in the unit and a relative contribution of each character to the total divergence can be measured. D^2 analysis further permits tracing out the inter-variety variability. Quantification of genetic diversity existing within and between groups of genotypes is important and useful in the selection of diverse parents obtaining useful recombinants.

Table 2: Distribution of 50 genotypes of upland rice into various clusters by Tocher's method

Cluster	Number	Name of the genotypes
I	27	Chali Yoh, Doiha, Yimso Tsuk, Toiya, Vepvu Tsuk, Tei Yoh, Samro Yoh, Samaro, Motso tsuk, Duolong, Khemaru, Mepongchuket Masu, Mapok, Tsuksempla, Moya Tsuk, Malanken, Meitak, Chamnya Yoh, Mati Pati, Bhalum-1, Neikedo Iha Tsia, Shuphok, Hahnyak, Engcha Yoh, Hyung Yoh, Maro Epyo, Manen Tsuk.
II	15	Mapok tsuk, Arunachal, Amiisu, Eshie, China Tsone, Lamjet, Nukneyi, Maso Tsuk, KD 5-2-8, Laza, Aor Chang, Yamchinga, Bhalum-3, Nukjan Shola, Yamuk.
III	1	Nangza Tsuk
IV	1	Maibo
V	3	Aphagi, Sopa, Vam
VI	1	Angja
VII	1	Pfutsero Ru
VIII	1	Yunghah

Analysis of variance revealed significant differences for all the characters studied. Based on D^2 values of 11 yield attributing traits and 11-grain quality traits, 50 genotypes of upland races of rice were grouped into 8 clusters (Table 2, Fig. 1) following Tocher's method (Rao, 1952). Cluster I had maximum genotypes comprising 27 genotypes followed by cluster II comprising 15

genotypes, cluster V comprising 3 genotypes, and Cluster III, IV, VI, VII and VIII comprising 1 genotype each. The genetic heterogeneity among the 50 genotypes from different parts of Nagaland is not a direct consequence of their distribution as indicated by the random clustering pattern.

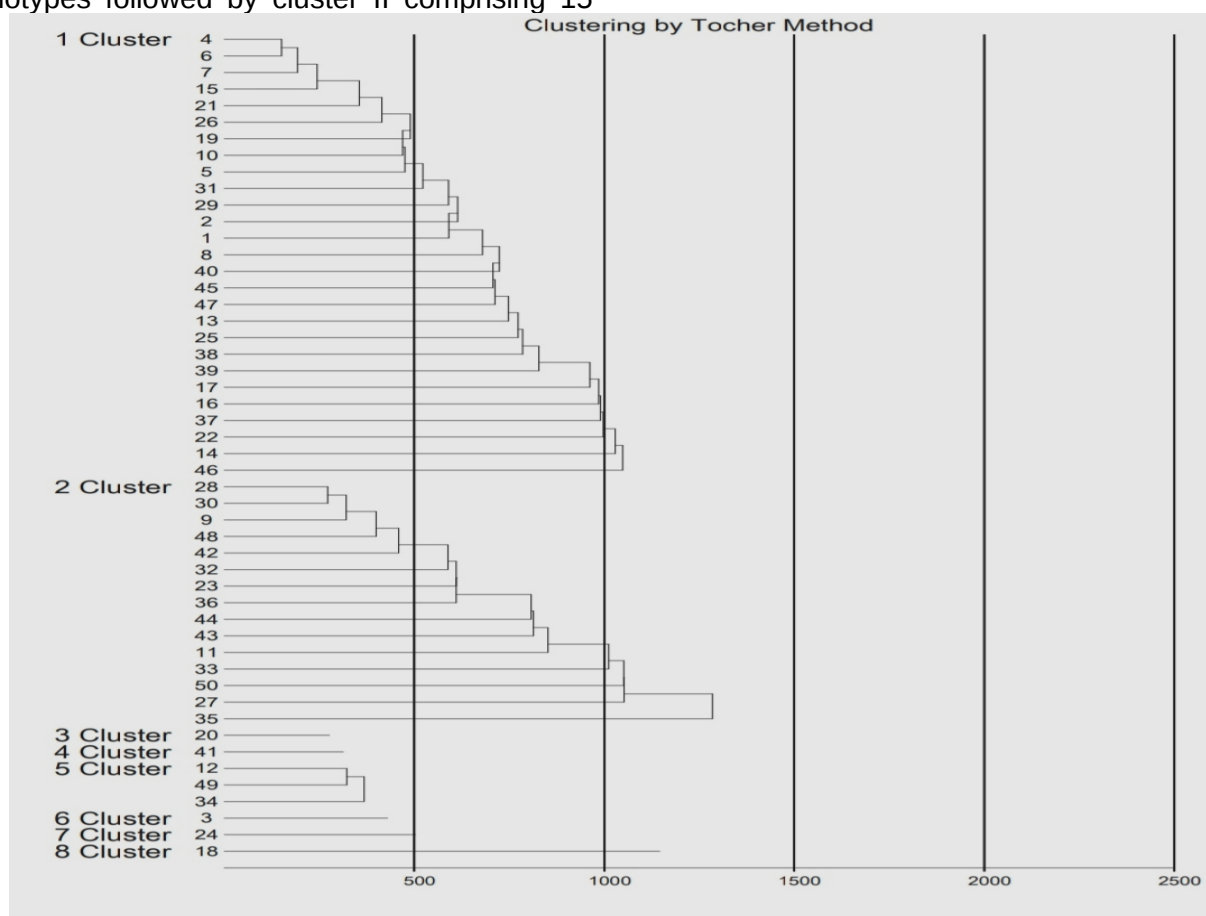


Fig. 1: Dendrogram of genotypes depicting cluster patterns

Table 3: Average inter and intra-cluster distances of 50 cultivars of upland rice

Clusters	I	II	III	IV	V	VI	VII	VIII
I	29.08							
II	41.65	31.23						
III	36.21	53.88	0.00					
IV	33.98	47.28	21.11	0.00				
V	50.29	43.65	69.63	62.76	21.82			
VI	38.23	47.56	24.85	20.74	63.78	0.00		
VII	34.77	40.99	36.45	36.18	57.85	37.65	0.00	
VIII	46.45	55.74	55.78	59.83	66.87	56.67	40.73	0.00

Inter and intra cluster distances

Greater heterogeneity among the groups is denoted by maximum inter-cluster distance whereas a closer association is denoted by minimum inter-cluster distance (Singh *et al.*, 1987). Genotypes belonging to different clusters separated by high estimated statistical distance could be used in breeding programme in order to obtain a significant variation among the segregating population (De *et al.*, 1992). Therefore, the genotypes present in the more distanced clusters will serve as a good source of divergent genes and these are desirable parent in breeding programmes to exploit heterosis as reported by Gill *et al.*, (1995), Chaturvedi and

Maurya (2005), Chaturvedi *et al.* (2011) and Chakraborty and Chaturvedi (2014).

In the present study (Table 3), maximum inter cluster distance was estimated between cluster III and cluster V (69.63) followed by cluster VIII and cluster V (66.87), cluster VI and cluster V (63.78), cluster V and IV (62.76), VIII and IV (59.83). Minimum inter cluster distance was estimated between cluster VI and cluster IV (20.74) followed by distance between cluster IV and cluster III (21.11), VI and III (24.85), IV and I (33.98), VII and I (34.77). Based on the cluster distance observed in the present study, crossing between genotypes from cluster V and III, VIII and V, VI and V would give rise to the highest heterotic crosses and wide spectrum of variation among the segregants.

Table 4: Cluster mean for 11 yield attributing traits in 50 upland rice genotypes of Nagaland

Clusters	50% F	80% M	PH	NOT	NOP	PL	TNGPP	NOFG	NOUG	TW	GYPP
I	88.26	109.15	101.36	3.67	3.09	25.31	121.80	81.85	40.50	4.29	196.54
II	87.83	114.17	105.40	4.60	3.97	26.76	107.90	82.93	24.97	3.92	230.03
III	85.50	109.50	113.00	6.00	5.50	26.95	195.50	135.50	60	10.52	117.00
IV	81.00	104.00	69.15	6.00	5.00	21.15	103.00	58.00	45	2.45	124.50
V	87.67	111.00	94.57	5.17	4.17	28.20	85.67	59.67	26	6.23	293.33
VI	76.50	118.50	106.50	6.00	5.00	27.20	92.00	41.00	51	1.30	107
VII	86.00	112.00	79.55	4.50	3.50	22.85	105.00	44.00	61	1.25	225
VIII	111.50	136.00	106.70	3.00	2.00	26.85	99.00	61.50	37.50	1.95	187.50

Cluster mean

From the analysis of 11 yield attributing traits and 11 grain quality traits, data on cluster means are summarised in Table 4 and Table 5 respectively. It revealed that different cluster exhibited marked differences in respect of all the characters. Cluster II exhibited genotypes having the highest mean values for GT and least mean value for NOUG while genotypes belonging to cluster III exhibited highest mean values for characters such as PH, NOT, NOP, TNGPP, NOFG and TW and lowest mean values for GT.

Cluster IV exhibited highest mean values for NOT and lowest mean values for 80% M, PH, PL and GWAC. Cluster V contains genotypes with highest mean values for PL, GW, DGW, GC and GYPP and lowest mean values for TNGPP, Grain shape, DGL: B and AC. Hence, genotypes belonging to cluster V may be utilized as a suitable source for yield improvement breeding programmes. Cluster VI accounts for highest mean values in NOT and lowest mean values for 50% F, NOG, GYPP, GL, GW, DGL, DGW, GLAC and GT. Cluster VII exhibited highest mean values for NOUG, GL, Grain shape, DGL.

Table 5: Cluster mean for 11 grain quality parameters in 50 upland rice genotypes of Nagaland

Clusters	GL	GW	Grain shape	DGL	DGW	DGL: B	GLAC	GWAC	AC	GT	GC
I	7.43	2.84	2.63	5.34	2.45	2.20	6.55	3.12	10.35	2.02	46.15
II	8.45	2.85	2.98	6.12	2.48	2.47	7.17	3.18	13.17	2.77	101.97
III	6.44	2.37	2.72	4.68	2.07	2.27	5.18	2.50	15.05	1.00	30.00
IV	6.20	2.19	2.83	4.47	1.99	2.26	4.84	2.25	17.89	1.00	46.50
V	7.63	3.75	2.04	5.33	3.07	1.74	6.78	3.59	7.85	1.50	108.50
VI	5.65	2.12	2.66	3.97	1.80	2.20	4.72	2.28	15.38	1.00	55.50
VII	9.08	2.88	3.15	6.34	2.47	2.56	7.61	3.75	28.43	1.50	44.50
VIII	8.46	2.84	2.98	6.28	2.51	2.51	8.11	3.94	12.98	1.50	28.00

DGL: B, AC and lowest mean values for TW. Whereas, cluster VIII exhibited highest mean values for 50% F, 80% M, GLAC and GWAC along with lowest mean values for characters such as NOT, NOP and GC.

The relative contribution of each trait towards divergence would reflect the pattern of divergence among the populations and is

presented in Table 6. The maximum contribution in genetic divergence was observed for gel consistency followed by amylase content, test weight and grain length. Hence gel consistency, amylase content, test weight and grain length should be given importance during choice of parents for hybridization and selection in the segregating populations.

Table 6: Contribution of individual character towards divergence

Sl. No	Character	Per cent contribution towards divergence	Sl. No	Character	Per cent contribution towards divergence
1	50% F	0.33	12	GL	6.78
2	80% M	2.20	13	GW	0.00
3	PH	1.55	14	Grain shape	0.16
4	NOT	0.00	15	DGL	1.55
5	NOP	0.00	16	DGW	0.82
6	PL	0.24	17	DGL:B	4.57
7	TNGPP	0.16	18	GLAC	2.45
8	NOFG	0.24	19	GWC	2.94
9	NOUG	0.16	20	AC	16.33
10	GYPP	2.61	21	GT	2.53
11	TW	8.65	22	GC	45.71

CONCLUSIONS

The magnitude of heterosis largely depends upon the degree of genetic diversity in the parental lines (Roy and Panwar, 1993). Maximum inter cluster distance was observed between cluster III and V indicating large genetic differences among genotypes of these two clusters with wide diversity which will serve as a good source of divergent genes and desirable parents in breeding programmes to exploit heterosis as reported by Gill *et al.*, (1995). Cluster V contains genotypes with highest mean

values for PL, GW, DGW, GC and GYPP. The study revealed that the genotypes belonging to cluster V may be utilized as a suitable source for yield improvement breeding programmes. The maximum contribution in genetic divergence was observed for gel consistency followed by amylase content, test weight and grain length. Hence gel consistency, amylase content, test weight and grain length should be given importance during choice of parents for hybridization and selection in the segregating populations.

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