

Genetic Divergence in Lowland Rice (*Oryza sativa* L.) Genotypes of Nagaland

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Abstract

The nature and magnitude of genetic divergence were assessed in 32 local lowland rice genotypes of Nagaland along with three improved genotypes. Based on the relative magnitude of D^2 values, 35 genotypes were grouped into eight clusters. The coefficient of variation for different characters indicated that panicle weight (42.40%), effective tillers per plant (35.08%) and yield per plant (27.02%) contributed maximum towards divergence. The genotypes belonging to cluster VII could be utilized as diverse parent in hybridization program with the genotypes of clusters II and VIII respectively, to achieve greater variability in the segregating generations.

Key words : Genetic divergence, Rice.

In any crop improvement program, germplasm is the valuable source of base population and provides the scope for selection for wider adaptability. However, to understand the useable variability, grouping or classification of genetic stocks based on minimum divergence or resemblance between them is quite imperative. The nature and magnitude of genetic divergence helps the plant breeder in choosing the right type of parents for higher amount of heterotic expression in F_1 and broad spectrum of variability in subsequent segregation generations (1). Information available on genetic diversity in local rice (*Oryza sativa* L.) genotypes of Nagaland is limited. Therefore, the

present study was carried out to analyze the genetic diversity in local rice genotypes to select the potential parents for breeding program.

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Methods

The present investigation was conducted on the experimental farm of ICAR Research Complex for NEH Region (Jharnapani) during 2003. Thirty-two

Table 1. Clustering pattern of 35 genotypes of rice on the basis of genetic divergence.

Cluster no.	No. of genotypes	Genotypes included
I	18	Kuki Chaushi, Tevuru (white), Keituo-ulha, Nyapie, Rhineinya, Khezharhi, Ngobanya, Mekrilha (Kapel-u), Thevuru (Kezha-u), Chamben (N. S. Kumelo-u), Tsorenya, Rosholha, Khenou, Kemony Kehnau (white), Kekhnie-LHE-Kenelo-u, Thevurie Tieca, Petkoti, & Aboru
II	3	Ranjit, Bahadur and Piolee
III	6	Wonder rice, Kewhi Vuru, Rulonya, Tsorenya, Kemony Kehnau (white), and Malong
IV	2	Ngoba and Mehuru
V	2	Thevuru (Kelo-u) and Teke
VI	2	Krumiavinya, and N. S. Keniese-u
VII	1	Mekrilha
VIII	1	Mekninya Khol

Table 2. Average intra and inter-cluster distance.

Cluster no.	I	II	III	IV	V	VI	VII	VIII
I	118.20	404.87	16.58	129.11	340.17	143.91	277.57	501.20
II		61.31	463.61	294.17	366.84	461.04	776.63	276.61
III			88.94	203.04	189.54	216.16	257.46	421.36
IV				65.01	343.34	164.57	197.94	532.99
V					98.79	465.28	520.02	196.67
VI						137.33	280.86	671.63
VII							0.00	935.52
VIII								0.00

local genotypes of rice of Nagaland namely Mekrilha, Ngoba, Mekninya Khol, Thevuru (Kelou), Kuki Chaushi, Wonder rice, Krumiavinya, Tevuru (white), Keituo-ulha, Nyapie, N. S. Keniese-u, Kewhi Vuru, Rulonya, Rhineinya, Khezharhi, Ngobanya, Mekrilha (Kepei-u), Thevuru (Kezha-u), Chamben (N. S. Kumelo-u), Kencnya Kumui (Red), Tsorenya, Rosholha, Khenou, Nyuceimo, Kemony Kehnau (white), Kekhnie-LHE-Kenelo-u, Thevurie Tieca, Petkoti, Malong, Teke, Aboru, Mehuru along with three improved genotypes Ranjit, Bahadur and Poilee were grown in randomized complete block design with three replications in plots of 2m × 1m size at spacing of 20 cm between rows and 15 cm between plants in a row. All the recommended agronomic practices were followed for raising a good crop. Observations were recorded on five plants sampled randomly in each replication for days to 50% flowering, 50% flowering to maturity, effective tillers per plant, plant height, panicle weight, panicle length, grains per panicle, grain filling percent, length-breadth ratio, 1000 grains

weight and yield per plant. The genetic divergence among genotypes was computed by means of Mahalanobis D² technique (2) and genotypes were grouped into different clusters following Tocher's method of cluster formation (3). The relative contribution of characters towards divergence was estimated according to Sharma (4).

Results and Discussion

The analysis of variance revealed significant differences among the genotypes for all the characters indicating high genetic variability present in the population. Based on the relative magnitude of D² values, 35 genotypes were grouped into eight clusters (Table 1). Cluster I had maximum number of 18 genotypes while clusters VII and VIII had the minimum 1 genotype each. Interestingly the three improved genotypes Ranjit, Bahadur and Poilee belonged to the same cluster i.e. cluster II. The pattern of distribution of genotypes in different clusters indi-

Table 3. Cluster wise mean values of 11 characters in rice.

Cluster no.	No. of cultivars	Days to 50% flowering	50% flowering to maturity	Effective tillers/plant	Plant height	Panicle weight	Panicle length	Grains per panicle	Grain filling percent	Length-breadth ratio	1000 grains weight	Yield per plant
I	18	109.61	27.92	5.45	137.70	4.04	27.90	110.22	71.90	2.75	26.66	10.90
II	3	84.00	25.55	8.53	102.89	4.08	25.00	98.22	79.17	2.34	22.80	22.16
III	6	106.11	33.61	4.64	142.11	6.94	26.83	117.11	77.30	2.54	28.69	11.94
IV	2	108.83	26.00	9.01	133.83	3.78	25.33	105.82	80.33	3.00	27.04	12.77
V	2	90.50	33.00	4.30	138.83	8.49	26.66	127.16	84.72	3.08	32.60	15.24
VI	2	107.67	32.66	5.10	136.50	2.17	25.33	139.83	76.92	2.61	22.76	14.43
VII	1	117.33	35.67	9.07	187.33	5.47	29.00	154.00	61.87	3.09	33.51	10.50
VIII	1	86.00	20.33	4.07	149.00	8.30	29.67	159.33	79.35	2.27	32.59	17.53
CV %		12.30	17.79	35.08	16.40	42.40	6.49	17.91	9.02	11.80	15.14	27.02

cated that genetic diversity was not related to ecosystem differentiation. Many genotypes of close geographic proximity fell in different clusters and vice-versa. Clustering of genotypes from different ecosystem into one cluster could be attributed to the possibility of free exchange of breeding material. This was in agreement with the findings of Rahaman et al. (5) and Datt and Mani (6).

The estimates of intra- and inter- cluster distances are presented in Table 2. The intra- cluster distance ranged from 0.00 (clusters VII and VIII) to 137.33 (cluster VI). The inter-cluster distance was observed to be highest between clusters VII and VIII (935.52) followed by clusters II and VII (776.63) indicating greater diversity between these clusters. Hence the genotypes of cluster VII could be utilized as diverse parent in hybridization program with the genotypes of clusters II and VIII respectively, to achieve greater variability in the segregating generations. Inter-cluster distance was minimum between clusters I and IV (129.11) followed by clusters I and VI (143.91) indicating genotypes belonging to these clusters are relatively closer. Such analysis was meant to avoid selection of parents from genetically closer clusters which may in turn result narrow genetic base and inbreeding depression.

Comparison of cluster means (Table 3) revealed that cluster VII gave exceptionally high values for six characters namely days to 50% flowering, 50% flowering to maturity, effective tillers per plant, plant height, L/B ratio and 1,000-grain weight. Cluster mean for panicle weight and grain filling percent was high-

est for cluster V, panicle length and grains per panicle for cluster VIII and yield per plant for cluster II. The coefficient of variation for different characters indicated that panicle weight (42.40%), effective tillers per plant (35.08%) and yield per plant (27.02%) contributed maximum towards divergence. This was in agreement with the findings of Roy and Das (7) for effective tillers per plant and Roy and Das (7), Datt and Mani (6) and Sobita Devi et al. (8) for yield per plant.

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