CBCS
http://agrobiol.sggw.waw.pl/cbcs

Communications in Biometry and Crop Science
Vol. 1, No. 1, 2006, pp. 35–40

International Journal of the Faculty of Agriculture and Biology,
Warsaw Agricultural University, Poland

REGULAR ARTICLE

Genetic divergence in lowland rice of north eastern region of India

Pankaj K. Singh[1], Murli N. Mishra[2], Dipak K. Hore[3], Med R. Verma[1]

[1] ICAR Research Complex for NEH Region, Umroi Road, Umiam-793 103, Meghalaya, India.
[2] Department of Plant Breeding & Genetics, R.B.S. College, Bichpuri-283 105, Agra, U.P., India.
[3] National Bureau of Plant Genetic Resources, Regional Station, Barapani, Umroi Road, Umiam-793 103, Meghalaya, India.
* Corresponding author: P. K. Singh, E-mail: pksingh99@rediffmail.com

CITATION: Singh, P.K., Mishra, M.N., Hore, D.K., Verma, M.R. (2006). Genetic divergence in lowland rice of north eastern region of India. *Commun. Biometry Crop Sci.* 1 (1), 35-40.

Received: 1 March 2006, Accepted: 11 May 2006, Published online: 27 June 2006

ABSTRACT

Genetic divergence of 52 traditional lowland rice (*Oryza sativa* L.) genotypes from five states of North Eastern Region of India was investigated using Mahalanobis D^2 statistic. Based on 15 agro-morphological characters, these genotypes were grouped into six clusters. Out of 52 genotypes, 26 genotypes were grouped in cluster I; cluster VI comprised only one genotype. Genotypes from more than one state were grouped in one cluster, and genotypes from one state were grouped in more than one cluster. Geographical origin was not found to be a good parameter of genetic divergence. Clusters II, III, and IV exhibited high values for most of the characters. Plant height, followed by leaf angle and leaf area, highly contributed (32.43%) to the formation of clusters. Clusters II, IV, and V, which had maximum inter-cluster distances and high values of plant height, days to 50% flowering, panicle length, grain yield/plant, and milling percent, may be used for initiating a hybridization programme.

Key Words: *genetic variability; cluster analysis; genetic diversity; inter-cluster distance; crop diversity.*

INTRODUCTION

The northeast region of India lies between 21° 57' – 29° 28' north latitude and 89° 40' – 97° 25' east longitude; it covers a geographical area of $2.55 \cdot 10^5$ km^2. The region comprises eight states: Arunachal Pradesh, Assam, Manipur, Mizoram, Meghalaya, Sikkim, Nagaland and Tripura. High rainfall, high humidity, varied topography, and altitude make the region rich in biodiversity. The region is seen to be the richest resource of genetic variability in agricultural and horticultural crops. Nearly 90% (27 million) of the total population of the north-eastern region of India depends on agriculture. Rice is the principal food crop of this region;

it is extensively cultivated (72% of the total cultivated area) in upland, lowland, and deep-water conditions. The north-eastern region presents most diverse conditions for growing rice in terms of altitude, agro-climatic conditions, and rainfall (Hore, 2005). Diverse growing conditions have led to immense variability among rice cultivars. Initiation of a hybridization programme for improvement of rice requires knowledge of genetic diversity in order to get greatest likelihood of recovering promising segregants. Nevertheless, this beginning information (genetic variability) criterion cannot be successfully used for discrimination between parents without knowledge of genetic divergence (Ahmed and Borah, 1999). Selection of parents based on the extent of genetic diversity has been successfully used in different crops, e.g., by Moll et al. (1962), Joshi and Dhawan (1966), Murty and Arunachalam (1966), Bhatt (1970), and Kandamoorthy and Govindarasu (2005). The problem of selection might further be simplified if one could identify characters most suited for discrimination between parental lines. Hence, the present investigation was carried out to ascertain the value and magnitude of genetic diversity among a set of lowland rice genotypes.

MATERIAL AND METHODS

Fifty-two genetically diverse lowland genotypes, bred in five states of the North Eastern Region of India, were used for the present study. These genotypes were grown in acidic soil (pH = 4.3) with iron toxicity, during the *kharif* season of 2000 and 2001, at the experimental farm of NBPGR (National Bureau of Plant Genetic Resources) Regional Station, Barapani, Meghalaya, India. The seeds were sown in a nursery on 7th June in each year; 25-day old seedlings were transplanted to the field. The experiment was arranged in a randomized complete-block design with three replications, using 20 x 20 cm spacing, in four-row plots of 4 m length. The recommended agronomical practices and plant protection measures were followed to ensure a normal crop. Observations were recorded on five randomly selected plants in each replication from the two centre rows; the variables measured were days to 50% flowering, plant height, flag leaf area, flag leaf angle, number of effective tillers/plant, panicle length, number of branches/panicle, days to maturity, grains/panicle, panicle weight, seed length, seed breadth, 1000-seed weight, grain yield/plant, and milling percent. The data from the two years were pooled in the analysis. Mahalanobis D^2 analysis (Mahalanobis, 1936) was used to estimate genetic divergence among the 52 genotypes. Grouping of genotypes into clusters was carried out following Tocher's methods (Rao, 1952). Mean values of the variables, calculated based on measurements on plants from blocks and years for each genotype, were used in the cluster analysis.

RESULTS AND DISCUSSION

Via Tocher's methods, 52 genotypes were grouped into six clusters (Table 1). Cluster I comprised 26 genotypes, whereas cluster III comprised eight genotypes. Clusters IV and V included seven genotypes each, whereas cluster II had three genotypes. Cluster VI contained only one genotype that originated from Arunachal Pradesh. Genotypes from different states were grouped in the same cluster, as revealed by clusters I, II, IV and V. This suggested that geographical distribution did not necessarily determine genetic divergence; other researchers have also emphasized this (Singh, 1983; Ratho, 1984; Sarawgi and Srivastava, 1996; Rathore et al., 2001). The possible reason for grouping of genotypes of different states in one cluster could be the free exchange of germplasm among the breeders of different regions, or unidirectional selection practiced by breeder in tailoring the promising cultivars for different regions (Verma and Mehta, 1976). On the other hand, our study has also revealed the existence of genetic diversity within the same state, because genotypes from the same state were distributed across clusters. Among the selected genotypes, a rather small level of genetic divergence in yield was detected. Nevertheless, traits with high divergence can be

used for crop improvement. The objective of measuring genetic divergence is to identify the most divergent parents. Hence, we recommend selecting genotypes from distant clusters.

Table 1. Clustering pattern of 52 traditional lowland rice genotypes.

Clstr	No. of geno	Genotype	Origin and Number
I	26	IC-211599, NIC-202410, IC-211589, IC-211544, NIC-212429, NIC-201535, NIC-202436, IC-211477, IC-201590, IC-211524, IC-211578, NIC-202420, NIC-202428, IC-211517.	Arunachal Pradesh (14),
		NIC-202411, IC-211474, NIC-202435, IC-211550, NIC-202970, NIC-202433.	Assam (6),
		NIC-202416, NIC-202431, IC-211565, IC-201596.	Meghalaya (4),
		IC-211553, IC-211516.	Manipur (2)
II	3	IC-21123, IC-211460.	Arunachal Pradesh (2),
		IC-211575.	Meghalaya (1)
III	8	IC-211589, NIC-202450, NIC-202411, IC-211488, IC-211521.	Arunachal Pradesh (5),
		IC-211545, IC-211540, NIC-202439.	Assam (3),
IV	7	NIC-202430, NIC-202434, NIC-202417, NIC-202413.	Assam (4),
		NIC-202424.	Meghalaya (1),
		NIC-202415, NIC-202422.	Manipur (2)
V	7	IC-211485, NIC-202432, IC-211490, IC-211520.	Arunachal Pradesh (4),
		IC-211569, NIC-202425.	Tripura (2),
		NIC-202440.	Manipur (1)
VI	1	IC-211537	Arunachal Pradesh (1)

The maximum inter-cluster D^2 values were obtained between clusters II and IV (6.791) followed by clusters II and V (6.661) (Table 2). Parental lines selected from these three clusters may be used in a hybridization programme, since hybridization between divergent parents is likely to produce wide variability and transgressive segregations with high heterotic effects (Rama, 1992). Such recommendations were also made by Murty and Arunachalam (1966), Qian and He (1991), and Rao and Gomanthinayagam (1997). The smallest inter-cluster distance was observed between clusters V and I (4.219) followed by clusters II and VI (4.351). The lines belonging to these clusters were relatively closer to each other, in comparison to lines grouped in other clusters. Such analysis was meant to avoid selection of parents from genetically homogeneous clusters, and to maintain a relatively broad genetic base. The largest intra-cluster distance was recorded for cluster V (4.284) followed by clusters IV (4.198) and III (3.828); the lines included in clusters III, IV and V were relatively more diverse than those in the other clusters. Heterosis is generally attributed to genetic divergence among the parental lines involved in the crosses. Nevertheless, the genetic divergence for the maximum expression of the heterotic effect has a limit (Moll et al., 1965; Arunachalam and Bandyopadhya, 1984).

Comparison of means of various characters in different clusters revealed that clusters IV and V recorded the highest value for five characters each (Table 3). Cluster means for panicle length and grain length were the highest for cluster II. Plants of lines from cluster IV had the tallest plants, longest panicles, and largest number of grains/panicle; they also provided

high grain yield/plant. Cluster II showed lowest plant height, early flowering, longest grain minimum grain breadth, early maturity with good grain yield, and milling percentage. In this cluster, these characters were recorded for the genotype IC 21123. The single genotype (IC 211537) of cluster VI had short plant height, early flowering, low 1000-seed weight, and low grain yield. The lines belonging to clusters V, IV and II can be used in a hybridization programme to obtain recombinants with high values—like plant height, effective tiller per plant, panicle lengh, grain lengh, grains per panicle, panicle weight, 1000 seed weight, milling percentage, and yield per plant.

Table 2. Intra (bold) and inter cluster distances among clusters in paddy.

	Cluster					
Cluster	I	II	III	IV	V	VI
I	**3.556**	6.101	4.329	4.878	4.219	5.122
II		**3.197**	5.323	6.791	6.661	4.613
III			**3.828**	5.377	5.057	4.351
IV				**4.198**	4.971	5.587
V					**4.284**	5.725
VI						**0.000**

Table 3. Estimates of cluster means for the clusters groups among the 52 genotypes of rice based on pooled data over the two years 2000 and 2001.

	Mean														
Cluster	Plant height (cm)	Flag leaf area (cm^2)	Flag leaf angle	No. of effective tiller/ plant	Days to flowering	Panicle length (cm)	Days to maturity	No. of branch /panicle	Panicle weight (gm)	Grain/ panicle	Grain length (mm)	Grain breadth (mm)	1000 seed weight (gm)	Yield/ plant (gm)	Milling%
I	118.34	67.86	16.86	9.96	142.01	24.63	177.85	10.06	4.28	139.84	8.77	2.90	25.22	23.12	74.20
II	63.47	48.13	8.89	10.57	118.72	26.37	157.89	7.79	3.12	106.78	10.80	2.25	24.70	18.11	74.73
III	94.68	58.12	18.75	9.49	131.31	24.32	174.62	9.76	3.78	139.29	7.75	2.93	21.70	21.31	74.16
IV	130.22	75.63	71.91	12.45	134.76	25.94	170.61	9.36	4.16	146.53	7.69	2.69	21.45	23.04	76.23
V	120.67	79.16	20.24	8.58	153.12	24.98	196.33	9.44	4.53	126.37	7.95	2.79	27.24	17.27	75.15
VI	86.12	63.18	35.83	8.83	110.17	21.75	164.83	8.90	2.99	100.51	8.02	2.40	20.45	10.56	74.38
Contribution % to divergence	32.43	15.91	16.74	0.08	9.88	0.53	1.28	8.30	1.28	1.06	3.09	7.39	0.83	0.45	0.75

Contribution of individual characters towards divergence. In all the combinations of intercluster distances each character is ranked on the basis of intercluster distances. Rank 1 is given to the character having highest mean difference and rank p is given to the character having lowest mean difference, where p is the numbers of characters. Percentage contribution of each character is calculated on the basis of occurrence of these ranks. Plant height had the maximum contribution (32.43%) and number of effective tillers/plant had the minimum (0.08%) contribution to the total divergence. Flag leaf angle and flag leaf area were the

second most important characters; their contribution to the total divergence was 16.74% and 15.90%, respectively. Days to 50% flowering (9.88%), number of branch/panicle (8.30%), and grain breadth (7.39%) had moderate contribution, whereas number of effective tiller/plant, panicle length, 1000 seed weight, and yield/plant contributed up to 0.08%, 0.53%, 0.83% and 0.45%, respectively.

In summary, the results indicated that parental lines selected from clusters II, III and IV could be used in a hybridization programme, since hybridization between divergent parents is likely to produce wide variability and transgressive segregations. Crosses between unrelated lines tend to exhibit heterosis. Thus, diverse lines from different clusters should be chosen for crossing in a hybrid rice breeding programme.

ACKNOWLEDGEMENTS

Authors would like to thank three anonymous referees and the members of the Editorial Board of CBCS for their valuable comments, which helped bring the paper into the present form.

REFERENCES

Ahmed, T., Borah, P. (1999). Genetic diversity in glutinous rice germplasm of Assam. *Oryza* 36, 74–75.

Arunachalam, V., Bandyopadhyay, A. (1984). Limit to genetic divergence for occurrence of heterosis: Experimental evidence from crop plant. *Indian J. Genet.* 44, 548–554.

Bhatt, G.M. (1970). Multivariate analysis application in selection of parents for hybridization aiming at yield improvement in self-pollinated crops. *Aust. J. Agri. Res*. 21, 1–7.

Hore, D.K. (2005). Rice diversity collection and management in northeastern India. *Genet. Res. Crop Evol.* 52, 1129–1140.

Joshi, A.B., Dhawan, N.L. (1966). Genetic improvement in yield-with special reference to self-fertilization cops. *Indian J. Genet.* 26 A, 101–113.

Kandamoorthy, S., Govindarasu, R. (2005). Genetic diversity in extra early rice (*Oryza sativa* L.) under two cultural systems. *Indian J. Genet.* 65 (1), 43–44.

Mahalanobis, P.C. (1936). On the generalized distance in statistics. *Proceedings of National Institute of Sciences*, *India.* 2, 49–55.

Moll , R.H., Lonnquist, J.H., Johnson, E.C. (1965). The relation of heterosis and genetic divergence in maize. *Genetics* 52, 139–144.

Moll, R.W., Salpuana, W.S., Robinson, H.F. (1962). Heterosis and genetic diversity in various crosses of maize. *Crop Sci.* 2, 197–198.

Murty, B.R., Arunachalam, V. (1966). The nature of genetic diversity in relation to breeding system in crop plant. *Indian J. Genet.* 26, 188–198.

Qian, Y.W., He, K.M. (1991). Utilization of exotic rice germplasm resources in Guang-dong province. *Crop Genet. Resour.* 2, 36–37.

Rama, T. (1992). Heterosis and inbreeding depression in rice. *IRRI Newsletter*, Los Bonos 17 (5), 7.

Rao, C.R. (1952). *Advance Statistical Methods in Biometrical Research*. John Wiley & Sons, New York.

Rao, T.P., Gomathinayagam, P. (1997). Genetic diversity in semi dry rice under different environments. *Madras Agr. J.* 84, 314–317.

Ratho, S.N. (1984). Genetic divergence in scented varieties of rice. *Indian J.Agr. Sci.* 54, 699–701.

Rathor, A.G., Zargar, M.A., Sheikh, F.A. (2001). Genetic divergence in rice (*Oryza sativa* L.) under temperate conditions. *Indian J. Agr. Sci.*. 71(5), 344 –345.

Sarawgi, A.K., Srivastava, M.N. (1996). Genetic divergence in rice under irrigated condition. *Adv.Plant Sci.* 91, 93–100.

Singh, R.B. (1983). Studies on genetic variability in rice. *Madras Agr. J.* 70, 436–440.

Verma, V.S., Mehta, R.K. (1976). Genetic divergence in Lucerne. *J. Maharastra Agr. U.* 1, 23–28.