

Original Research Article

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Genetic Diversity Analysis with Morphological Traits on Rice (*Oryza sativa* L.) for Cold Tolerance Breeding

Shyam Chandra Ghosh^{ID}* and Tapash Dasgupta

School of Agriculture and Rural Development, Faculty Centre for Integrated Rural Development and Management, Ramakrishna Mission Vivekananda Educational and Research Institute (RKMVERI), Narendrapur, Kolkata – 700103, India

*Corresponding author

ABSTRACT

Genetic diversity is one of the most important studies which provide general genetic component and background to understand the genetic architecture of the genotypes with respect to genetic relation and inheritance pattern and on the other hand help in pre-breeding work for the selection of appropriate genotype in the breeding programme. Looking to the breeding strategies, an experiment has been conducted during 2019-20 at the agricultural experimental farm (AEF), Narendrapur of IRDM Faculty Centre, RKMVERI, with 53 rice genotypes along with the reported cold tolerance rice varieties for nine quantitative morphological traits *i.e.* plant height, tiller per plant, panicle per plant, grain per panicle, panicle weight, panicle length, grain per panicle, grain length, grain breadth and test weight have been evaluated during the experiment with two replication and analyzed the data with the program GENES with the help, Mohalanobis D^2 and Tocher's methods. After analysis, found that the genotypes were in 13 genotypic groups and maximum genotypes (25) were IR36, Maharaja, ADT43, Kshitish, IRBB60, Shyamla, BD11, R71, Hanahikaree, Ajaya, Radha, GB 2, K. Masuri, Sabita, IR72, CU48, MTU10, Lalat, Miniket, Dular, IRAT177, Sasarang, K335, Ketaki and DTCM1 found in cluster –I, genotypes (8), Hinohikari, Kinuhikari, Mirikikuin, SR5, K475, Setetaree, Haenchizen, Koshihari in cluster II, genotypes (6) J. Assam (w), K. Jeera, J. Assam, C. Moni, J. Bao and Jeera in cluster – III, 2 genotypes in cluster IV (Bhalum1 and Bhalum5), V (Gourab and Mukdashree), VI (Lemont and R.-Bhagbati), and VII (Barhashal and Cypress) each and one genotypes in cluster VIII (Koshar), IX (Basmati), X (Prasad), XI (Khasa), XII (Taruri Basmati) and XIII (IR 64) in each. Therefore, looking to the genetic grouping/cluster and distance, crossing programme may be adopted for the better improvement of genotype with respect to cold tolerance and sensitivity response as well as genetic distance and group of the genotypes or respective genotype.

Keywords

Cluster, Cold Tolerance, Diversity, Genotypes, Morphological, *Oryza sativa* L

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Introduction

Rice (*Oryza sativa* L.) is the main staple food crop of Asia where it is consumed by more than half of the world's population. It is mainly grown in large areas in Asia, Latin America and Africa that are characterized by a semi-tropical climate with alternating rainy and dry seasons (Rao *et al.*, 2016). Rice accessions are a rich reservoir of useful genes that rice breeder can harness for rice improvement programme. Genetic diversity is the pre-requisite for any crop improvement programme because it helps in the development of superior recombinants (Manonmani and Fazlullah Khan, 2003), through selection of parents having wider variability for different characters. Since, the last few centuries, rice has faced loss in diversity due to replacement of native varieties with high yielding varieties. Genetic divergence analysis evaluates the genetical distance among the selected genotypes and shows the relative contribution of specific traits towards the total divergence (Nayak *et al.*, 2004). A higher heterosis could be achieved from crosses between genetically distant parents (Falconer, 1960).

Cold stress in rice leads to poor germination and stunted growth of seedlings, delays flowering, lengthens the growth cycle, reduces tillering, increases plant mortality and causes significant yield loss in rice production. Our local landraces can contribute resistant/tolerant genes in developing the improved varieties but fact is that due to vertical selection of the high yielding varieties and cultivated by most of the farmers in the modern cultivation practices; people are losing the genetic diversity along with the sources of genetic diversity or stress tolerance trait in the genetic resources. During intensive cultivation along with cropping pattern changes the cultivation practices but practically, we are facing some problem during cultivation and failing the crop yield due to different biotic and abiotic stress and uncertainty in the cultivation practices; we are including different new and newer varieties but growers don't know more about the varieties as aware about the traditional varieties. Looking to the same, we need to know better about

the genetic divergence about the varieties those are to be used in the breeding program with better option on selection of crop improvement/breeding programme.

Variability highlights and measures how each component contributes to total phenotypic variation. The objective of this study is to characterize diverse different genotypes collected from hill and mountain environments of the country having cold tolerance using agro-morphological data and efficient use of these diverse genotypes looking to the breeding strategies genetic divergence for the better understanding about the collected rice collections/genotypes with respect to cold tolerance breeding.

Materials and Methods

Study the genetic divergence among the collected rice collection/genotypes an experiment was designed with RCBD with rice genotypes (Table-1) and were grown following the standard cultivation package and practices with two replications at the Agricultural Experimental Farm (AEF), Narendrapur, IRDM Faculty Centre, during *Rabi*, 2019-20.

Rice genotypes were collected from different institute and farmer's field from different parts of India during 2018-19. Before sowing all the genotypes have been treated at 50^oC for 7 days in the seed dryer and germinated at 28^oC and pre-germinated seed were sown in the wet seed bed followed by transplanting in main field at 30 days old seedling with 15 x 20 cm spacing under irrigated ecology. Agro-morphological observations were recorded at the time of harvesting and post harvest.

Due to Covid-19 pandemic situations, only nine agro-morphological trait observations have been recorded following SES, IRRI (2002) from 5 plants for each replication. The collected replicated mean data and replicated mean values were analysis with the GENE program for ANOVA, Genetic Divergence and Genetic distance with respect to

Mohalanobis (1936) D^2 statistics for genetic distance and followed by clustering with Tocher's method as described by Rao (1950).

Results and Discussion

The recorded replicated mean data were analyzed for agro-morphological nine traits for all the fifty three genotypes and all the genotypes revealed significant variance for all the traits (Table-2).

All the recorded traits have been shown the level of significance for fifty three genotypes as studied in the experiment.

Genetics parameters *i.e.* phenotypic coefficient of variance (PCV), genotypic coefficient of variance (GCV), heritability (%) and genetics advance (GA) were estimated (Table- 3) for the nine traits *i.e.* plant height, no. of tiller per plant, no. of panicle per plant, panicle weight, panicle length, no of floret per panicle, grain length, grain breadth and 1000 grain weight. Per se performance highest were noticed for plant height with respect to PCV, GCV, h^2 and GA followed by others. Highest heritability noticed in 1000 grains weight (86.30%), followed by plant height (78.65%), grain length (78.5%), panicle weight (76.07%), panicle length (75.64%), grain breadth (68.64%), floret per panicle (64.63%), tiller per plant (58.83%) and panicle no. per plant (47.7%). Heritability is the indicator which indicates inheritability of the trait in the next generation and help in understanding the influence of environmental variance as well as different variance components *i.e.* phenotypic coefficient of variance (PCV), genotypic coefficient of variance (GCV) and environmental variance (ECV). Per se genetics advance persisted highest in plant height (37.33) followed by 1000 grains weight (13.73), panicle length (6.93), tiller per plant (5.81), no of panicle per plant (3.83), grain length(3.2), panicle weight(3.13), floret per panicle(2.71) and grain breadth(2.09). Genetic advance (GA), directly direct for improvement of the trait with selection process of the respective trait persisted with higher GA. Glaszmann *et al.*, (1990) and Jayasudha and Sharma

(2010) and Kumar *et al.*, (2017) also reported the similar results.

Magnitude of relative D^2 values clustered the genotypes into thirteen genotypic groups to all the 53 genotypes with respect to their nine agro-morphological traits (table 3). Cluster I, was found to be the most diverse group among thirteen clusters along with 25 genotypes followed by 25 genotypes *i.e.* IR36, Maharaja, ADT43, Kshitish, IRBB60, Shyamla, BD11, R71, Hanahikaree, Ajaya, Radha, GB3, K. Masuri, Sabita, IR72, CU48, MTU10, Lalat, Miniket, Dular, IRAT177, Sasarang, K335, Ketaki and DTCM1 were found to be in cluster –I, 8 genotypes *i.e.* Hinohikari, Kinuhikari, Mirikikuin, SR5, K475, Setetaree, Haenchizen, Koshihari, in cluster II, 6 genotypes *i.e.* J. Assam (w), K. Jeera, J. Assam, C. Moni, J. Bao and Jeera in cluster – III, 2 genotypes in cluster IV(Bhalum1 and Bhalum5), V (Gourab and Mukdashree), VI (Lemont and R.-Bhagbati), and VII(Barhashal and Cypress) each and one genotypes in cluster VIII(Koshar), IX(Basmoti), X (Prasad), XI (Khasa), XII (Taruri Basmoti) and XIII (IR 64). Therefore, creation of variability or transfer of the targeted trait or incorporating the trait by breeding from among the divers cluster is advisable for the improvement accelerating the breeding programme in right direction for better outcome from the crosses and progenies to be developed.

The cluster means of different traits present in the table 4, which is the indicator for the cluster and trait relationship with respect to scope of improvement of the trait with selection or hybridization. Plant height ranges from 77.08 (cluster-II) to 125.04 (cluster-VII) whereas, remains other 11 clusters in-between these two clusters. Tiller per plant ranges from 7.00 to 21.34 whereas, remaining others 11 clusters between these two clusters. Panicle per plant ranges from 6.92 to 19.17 whereas, other 11 clusters remains between these two clusters. Panicle weight ranges from 2.22 to 8.59 whereas, others 11 clusters remains between these two clusters. Panicle length ranges from 15.67 to 26.13 whereas, others 11 clusters remains between these two clusters.

Floret per axis ranges from 7.10 to 12.67 whereas, others 11 clusters remains between these two clusters. Grain length ranges from 4.48 to 12.67 whereas, others 11 clusters remains between these two clusters. Grain breadth ranges from 5.42 to 10.42 whereas, others 11 clusters remains between these two clusters. Test weight ranges from 12.75 to 30.85 whereas, others 11 clusters remains between

these two clusters. Therefore, as per requirement or objective of the trait improvement parentage to be selected for the breeding programme from the clusters as depicted under this pre-breeding as under taken for the respective trait. Sarawgi and Srivastav (1996) and Pradha and Ray (1990) also reported the similar results.

Table.1 Rice genotypes under study

Sl. No.	Varieties	Sl. No.	Varieties	Sl. No.	Varieties	Sl. No.	Varieties	Sl. No.	Varieties
1	ADT 43	12	GB 3	23	Jindi Bao	34	Koshar	45	Radha
2	Ajaya	13	Gourab	24	Joha	35	Koshihikaree	46	Rajendra Bhagabati
3	Barhashal	14	Haenuniki	25	Joha (w)	36	Lalat	47	Sabita
4	Bhalum 1	15	Hanahiechizen	26	K 335	37	Lemont	48	Sasarang
5	Bhalum 3	16	Hinohikari	27	K 475	38	Maharaja	49	Setetaree
6	Bina Dhan 11	17	IR 36(CS)	28	Kali Jeera	39	Miniket	50	Shyamla
7	Chowan Moni	18	IR 64(NC)	29	Karma Masuri	40	Mirikikuin	51	SR 5
8	CU 48(CT)	19	IR 72	30	Ketaki	41	MTU 1010	52	Taruri Basmati
9	Cypress	20	IRAT 177	31	Khasa	42	Muktashri	53	Tetap
10	DTCM 1	21	IRBB 60	32	Khitish	43	Prasad		
11	Dular	22	Zeera	33	Kinuhikari	44	R 71		

Table.2 ANOVA of nine traits for 53 genotypes

Source of Variance	df	Mean Sum of Squares								
		Plant Height (cm)	No. of Tiller/ Plant	No. of Panicle/ Plant	Panicle Weight (g)	Panicle Length (cm)	No. Floret or Axis/ Panicle	Grain Length (mm)	Grain Breadth (mm)	1000 Grains Weight (g)
Replication	1	2372.095	42.996	26.841	4.192	2.123	1.014	3.409	2.151	58.639
Treatment	51	519.471*	21.963**	14.499**	3.816**	18.923**	3.956**	3.752**	2.097**	56.995*
Error	51	110.896	9.042	7.584	0.913	4.610	1.399	0.806	0.658	7.807

Significant at $p < 0.01$

Table.3 Estimates of variability, heritability and genetic advance for agro -morphological traits

Characters	Mean	Range		PCV (%)	GCV (%)	Heritability in (broad sense) (h ²) (%)	Genetic Advance (GA)
		Max.	Min.				
Plant Height(cm)	118.22	172.83	64.67	259.735	204.288	78.65	37.33
No. of Tiller/ Plant	14.15	22.67	5.33	10.981	6.460	58.83	5.81
No. of Panicle/Plant	12.38	21.00	5.33	7.250	3.458	47.70	3.83
Panicle Weight(g)	5.29	12.41	2.04	1.908	1.451	76.07	3.13
Panicle Length(cm)	27.80	38.75	13.00	9.461	7.156	75.64	6.93
No. Floret or Axis/ Panicle	11.40	18.50	6.00	1.978	1.278	64.63	2.71
Grain Length(mm)	9.72	16.42	5.00	1.876	1.473	78.50	3.20
Grain Breadth(mm)	10.37	17.33	5.33	1.049	0.720	68.64	2.09
1000 Grains Weight(g)	27.82	49.48	9.92	28.497	24.594	86.30	13.73

Table.4 Genetic Divergence of Genotypes on nine morphological traits

Group	Genotypes	No. of Genotypes	Total Entries (%)
I	IR 36, Maharaja, ADT 43, Kshitish, IRBB 60, BB 11, R 71, Hanahichizen, Ajaya, Radha, GB 3, K. Masuri, Sabita, IR 72, CU 48, MTU 1010, Lalat, Miniket, Dular, IRAT 177, Sasarang, K 335, Ketaki, DTCM 1	25	47
II	Hinohikaree, Kinuhikari, Mirikkiquuin, SR 5, K 475, Setetari, Haenhikari, Koshihikari,	8	15
III	Joha(w), K. Jeera, Joha, C. Moni, Jeera, J. Bao	6	11
IV	Bhalum 1, Bhalum 3	2	4
V	Gourab, Mukdashri	2	4
VI	Lemont, Rajendra Bhagaboti	2	4
VII	Barhashal, Cypress	2	4
VIII	Koshar	1	2
IX	Basmati	1	2
X	Prasad	1	2
XI	Khasa	1	2
XII	Taruri Basmati	1	2
XIII	IR 64	1	2

Table.5 Mean values of different characters rice genotypes (53) in thirteen cluster

Cluster	Plant Height (cm)	No. of Tiller Per Plant	No. of Panicle Per Plant	Panicle Weight (g)	Panicle Length (cm)	No. Floret per Panicle	Grain Length(mm)	Grain Breadth (mm)	1000 Grains Weight (g)
Cluster I	91.95	10.93	10.03	4.34	22.25	9.45	8.16	8.11	22.05
Cluster II	77.08	10.09	9.44	3.87	17.10	7.10	6.42	9.52	27.23
Cluster III	112.65	13.03	9.28	2.92	23.75	9.89	6.07	6.97	12.75
Cluster IV	110.21	7.00	6.92	8.59	23.67	12.67	9.54	10.42	30.40
Cluster V	121.59	14.92	14.42	4.03	24.86	9.92	9.17	8.18	26.40
Cluster VI	106.67	8.92	8.50	6.08	26.13	9.42	9.29	8.84	30.85
Cluster VII	125.04	8.60	8.45	4.95	19.73	9.40	7.90	8.76	23.71
Cluster VIII	98.75	14.00	7.00	4.42	15.67	7.67	6.00	7.92	23.96
Cluster IX	108.83	21.33	14.67	3.38	21.67	7.67	8.00	8.17	20.68
Cluster X	76.25	16.00	13.17	2.22	19.34	8.17	6.50	8.59	19.00
Cluster XI	112.33	19.00	15.84	2.75	21.75	8.00	4.84	5.42	16.53
Cluster XII	118.17	12.67	12.34	6.66	25.47	10.34	11.17	7.75	22.62
Cluster XIII	93.33	21.34	19.17	5.37	22.25	7.84	9.34	8.33	27.44

Table.6 Percent contribution of each character towards total genetic divergence in genotypes (53)

Source	Times Rank 1st.	Contribution (%)
Plant Height(cm)	125.04	125.04
No. of Tiller Per Plant	21.34	21.34
No. of Panicle Per Plant	19.17	19.17
Panicle Weight(g)	8.59	8.59
Panicle Length(cm)	26.13	26.13
No. Floret or Axis Per Panicle	12.67	12.67
Grain Length(mm)	11.17	11.17
Grain Breadth(mm)	10.42	10.42
1000 Grains Weight(g)	30.85	30.85

With respect to contribution of the trait has been noticed highest in plant height followed by test weight, panicle length, tiller per plant, panicle per plant, floret per panicle, grain length, grain breadth and panicle weight. Therefore, the improvement of the trait is influence as per the trait contribution which is the indicator pre-breeding to improve the respective trait in the breeding program which gives the pre-view for with respect to group and variety of the trait to be considered under breeding program.

Genetics components like genotypic co-efficient of variance (GCV), phenotypic co-efficient of variance (PCV), Heritability (%) and Genetic Advance give an idea regarding the genotype with respect to their trait expression in generation after generation and indication on selection of proper breeding tools and techniques for their trait improvement.

Under the experiment, plant height and test weight might be good with respect to selection response in

the breeding cycle. Cluster analysis were grouped the genotypes in thirteen clusters and cluster I found to be most diverse with twenty fine genotypes and on the other hand inter-cluster breeding would be helpful for better heterosis and intra cluster would be better for selection in improvement. Breeding for improvement with respect to the cold response of the genotype to be elected based on their genetics distance or cluster for better outcome from the breeding program *i.e.* varieties Bhalum-3, Bhalum 1 from cluster III to be crossed with Kshitish or Satabdi, whose were sensitive as well as popular varieties of West Bengal for winter season. The potential response to natural selection, relation between the genetics architecture of the trait of past and selection and understanding the response to environment these all are the factor for the performance of the genotypes and their traits.

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References

- Falconer, D. S. 1960. *Introduction to Quantitative Genetics*. The Ronald Press, New York.
- Glaszmann, J. C., Kaw, R. N. and Khush, G. S. (1990) Genetic divergence among cold-tolerant rices (*Oryza sativa* L.). *Euphytica* 45, 95-104.
- Jayasudha, S. and Sharma, D. 2010. Genetic parameters of variability, correlation and path-coefficient for grain yield and physiological traits in rice (*Oryza sativa* L.) under shallow lowland situation. *Electronic Journal of Plant Breeding*, 1(5): 1332-1338.
- Kumar, R. P., Radha Krishna, K. V., Bhawe, M. H. V. and Subba Rao, L. V. 2017. Genetic variability, heritability and genetic advance in boro rice (*Oryza sativa* L.) germplasm. *International Journal of Current Microbiology Applied and Sciences*, 6(4): 1261-1266.
- Mahalanobis, P. C. 1936. On the generalized distance in statistics. *Proc. Nat. Inst. Sci. India*, pp. 12-49.
- Manonmani, S. and Fazlullah Khan. 2003. Analysis of genetic diversity for selection of parents in rice. *Oryza*, 40: 54-56.
- Nayak, A. R., Chaudhury, D. and Reddy, J. N. 2004. Genetic divergence in scented rice. *Oryza*, 41: 79-82.
- Pradha, K and Ray, A. 1990. Genetics Divergence in Rice, *Oryza*, 27:415-418.
- Rao, C. R., 1950. *Advances Statistical Methods in Biometrical Research*, John Wiley and Sons, New York.
- Rao, M., Grithlahre, S., Bisen, P., Singh, N. K., Dar, M. H., Singh, U. S. and Singh, P. K. 2016. Genetics of marker assisted backcross progenies of the cross HUR-105 X Swarna-SUB1. *International Journal of Agriculture, Environment & Biotechnology*, 9: 499-505.
- Sarawgi, A. K. and Srivastav, M. N., 1996. Genetics divergence in rice irrigated and rainfed condition. *Adv. Plant Sci.*, 9(2):93-100.

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