Briefing the Genetic Divergence of Quality Traits of Rice (Oryza sativa L.) Genotypes Cultivated in Upper Assam, India

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***Abstract*—A study has been conducted to estimate the essence and the extent of genetic divergence of 50 rice genotypes, on the basis of 19 agro-morphological traits following Mahalanobis' D^2 statistics. The genotypes were grouped based on D^2 values into eight cluster's following Tocher's method. Five multi-genotypic and three mono-genotypic clusters were found after grouping by Tocher's Method. The most divergent clusters were cluster IV and VIII (D^2= 24.81) followed by VII and VIII (D^2=21.98) and II and VIII (D^2= 20.62). Highest intra-cluster distance was observed in cluster VI followed by cluster V. Cluster I was the largest one containing 24 genotypes. Thus the genotypes belonging to the cluster II, IV, VII and VIII having highest cluster distance are suggested for incorporation in hybridization program because they are predicted to produce desired segregates.**

***Index Terms*—Genetic divergence, inter-cluster distance, intra-cluster distance, genotype**

I. INTRODUCTION

Rice (*Oryza sativa L.*) is the principal staple crop across North-East India, supporting the livelihoods of millions, especially resource-poor tribal farming communities. The region harbours a rich diversity of traditional rice landraces, adapted to unique ecological niches, ranging from floodplains to drought prevalent areas. Even though, the resource-poor farmers of this region face food insecurity due to lack of modern technology, unpredictable monsoons, climate–induced disasters, dependency on informal local seed system etc. In this context, the judicious selection and promotion of high yielding and genetically diverse rice varieties hold a transformative role in addressing the interlinked challenges of food insecurity, climate vulnerability and agricultural sustainability. Regional food security can be significantly enhanced through the adoption of high yielding varieties and incorporation of genetic diversity in varietal selection, which are well adapted to local climate and soil conditions. The success of any crop improvement initiative is contingent upon the effectiveness of germplasms. A sustainable breeding program hinges on a detailed comprehension of genetic divergence, particularly in relation to yield components and understanding the nature and extent of genetic variability (Ayenew *et al*., 2020). The D2 analysis, a form of multivariate analysis devised by Mahalanobis (Mahalanobis, P.C. 1936), is recognised as a powerful tool for measuring the extent of differences in germplasms by employing morphological traits. The aim of this study was to evaluate the genetic variability among rice genotypes collected from different pockets of North East India. This approach offers a pathway to improving livelihood. By cultivating varieties that offer better yield potential with minimal input costs, farmers can achieve higher returns on investment. Moreover, access to diverse crop options provides dietary diversity and economic security along with a reduction of crop failure risks, which is a critical factor in safeguarding the livelihood of marginal and tribal farmers in North East India. It also enhances local seed repositories and will build a sustainable and resilient agricultural system.

II. MATERIALS AND METHODS

The experimental material comprises of 50 genotypes collected from different rice growing pockets of North-East, India and was grown in randomized block design replicated five, during *kharif*, 2020-2021 and 2021-2022. Each plot consisted of three rows of 1.10 m length with inter and intra row distance of 20 cm and 15 cm respectively. The experimental field's soil composition consisted of alluvial sandy loam with a pH of 4.9. The average humidity throughout the season was documented at 79.80%, with a mean temperature of 24.1ºC. September experienced the highest temperature at 37ºC, while December recorded the lowest at 10.2ºC. Additionally, the average rainfall measured 2343 mm. (Anonymous, 2010). Nineteen quantitative characters namely height, productive tillers per plant, days to 50% flowering, leaf area index, flag leaf length, flag leaf width, total chlorophyll content (mg/g), grain length, grain width, length-breadth ratio, harvest index, length of the panicle, 1000 seeds weight, spikelet per panicle, percentage of grain filling, spikelet density, spikelet per plant, panicle per plant and grain yield were considered for evaluation. The assessment of agro-morphological traits adhered to the standard evaluation system for rice established by IRRI. 1996. The data underwent Mahalanobis's D2 analysis, and the genotypes were classified using Tocher's method as recommended by (Rao, 1952). All the statistical analyses were done in the computer software INDOSTAT 8.1.

III. RESULTS AND DISCUSSION

Analysis of variance, performed on various morpho-agronomic parameters, showed significant differences among the genotypes for all. This suggests a significant degree of genetic variation among them. Sowmiya and Venkatesan (2017), Behera *et al.* (2018), Shrestha *et al.* (2020), Kumar *et al.* (2020), and Shrestha *et al.* (2021) documented substantial diversity in agro-morphological traits among rice genotypes.

Table i: ANOVA of the experimented 19 characters of experimented 50 rice genotypes

Sl. No.	Characters	Mean sum squares		
		Replication (df=4)	Treatment (df=49)	Error (df=196)
1	HEIGHT	6.1	1523.1*	30
2	TILLER/PLANT	0.2	72.9*	2.1
3	DAYS TO FLOWERING	9.6	735.3*	10.5
4	LEAF AREA INDEX	123.2	2038.4*	64.2
5	FLAG-LEAF LENGTH	6	157.8*	10.6
6	FLAG-LEAF WIDTH	0	0.5*	0
7	TOTAL CHLOROPHYLL CONTENT	0	5.2*	0
8	GRAIN LENGTH	0.1	3.1*	0.2
9	GRAIN WIDTH	0	0.8*	0.1
10	L/B RATIO OF GRAIN	0.1	0.8*	0.1
11	HARVEST INDEX	43.8	679.0*	21.3
12	LENGTH PANICLE	5.4	73.2*	2.4
13	1000 SEEDS WEIGHT	0.6	142.4*	1.3
14	SPIKELET/PANICLE	76	36661.1*	124.3
15	PERCENTAGE OF GRAIN FILLING	28.8	187.9*	15.8
16	SPIKELET DENSITY	0.8	44.2*	0.4
17	SPIKELET/PLANT	182797.2	5072739.9*	60946.7
18	PANICLE/PLANT	2.6	78.0*	1.3
19	GRAIN YIELD	28465.7	729460.2*	14987.3

*Indicates 5% level of significance

Employing Tocher's method, the 50 rice genotypes were grouped into eight clusters, considering the relative magnitude of their D2 values. Cluster I was the largest one, consisting of twenty-four genotypes, followed by cluster II with thirteen genotypes. Clusters V and VI have five and three genotypes, respectively. Cluster VII comprised two genotypes, while clusters III, IV, and VIII each have only one genotype. Similar findings were also reported by Tuwar *et al*. (2013), Behera *et al.* (2018), and Singh *et al.* (2021).

Table ii: Cluster distribution of the genotypes

CLUSTER (No. of genotypes)	NAME OF THE GENOTYPES
CLUSTER I (24)	Gejepsali, Rongabora, Borjahingia, Vasmoti, Harmoni, Tilbora, Bordhan, Nania, Torawali, Nekera, Beoilahi, Nolsitiki, Bora, Kolapakhi, Gorundopakhi, Guwahatiabora, Adoliabao, Sowagmoni, Gorokhiasali, Malbhug, Sokuwa, Joha, Kolajoha, Mala.
CLUSTER II (13)	Solpuna, Sunmoni, Johabora, Rongajoha, Chutibora, Sorujahingia, Khoiron, Monlohi, Jahingia, Memlahi, Jaldubi, Moubora, Gumibora
CLUSTER III (1)	Bogijul
CLUSTER IV (1)	Laudubi
CLUSTER V (5)	Ahumsali, Bogisali, Monuharsali, Pakhoribora, Titaphuliabora,
CLUSTER VI (3)	Basdhan, Ijong, Konjoha
CLUSTER VII(2)	Katibora, Niokadam
CLUSTER VIII (1)	Ronjit

The inter-cluster distances showed significant divergence. The highest divergence was observed between cluster IV and cluster VIII (D2= 24.81), followed by cluster VII and VIII (D2= 21.98). It was followed by cluster II and cluster VIII (D^2= 20.62). It is noteworthy that cluster IV and cluster VIII were mono-genotypic and cluster VII consisted of only two genotypes. The largest intra-cluster distance was recorded for cluster VI (D^2= 11.39) followed by cluster V (D^2= 10.16). Comparison of means for various characters in different clusters revealed that the mono-genotypic cluster VIII recorded the highest mean value for six characters, viz. tillers per plant, flag-leaf width, harvest index, percentage of grain filling, panicle per plant, grain yield and the lowest mean value for height, 1000 seeds weight, spikelet per panicle, and spikelet density. Cluster III (another mono-genotypic cluster) had highest mean value for five characters namely height, days to 50% flowering, flag- leaf length, length-breadth ratio of grains and length of the panicle. Cluster V and cluster VII recorded the highest value for three characters each. Cluster means for leaf area index, total chlorophyll content and 1000 seeds weight were the highest for cluster V and grain length, spikelet per panicle and spikelet per plant were highest for cluster VII. Cluster IV (mono-genotypic) showed the highest mean value for grain width and spikelet density. The remaining three clusters viz. Cluster I, cluster II and cluster VI did not show the highest mean value for any character.

Table iii: Intra (bold) and inter-cluster distances

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	7.91	14.37	9.77	16.86	10.87	13.06	14.7	15.25
Cluster II		8.37	15.43	10.97	16.7	12.23	13.53	20.62
Cluster III			0	16.17	9.9	15.32	10.3	17.97
Cluster IV				0	18.29	16.17	12.85	24.81
Cluster V					10.16	17	15.03	19.32
Cluster VI						11.39	15.78	14.72
Cluster VII							7.72	21.98
Cluster VIII								0

Among the experimented 19 parameters, the most important character contributing to the divergence were total chlorophyll content (51.92%), followed by spikelet per panicle (24.49%) and 1000 seeds weight (7.18%). Four parameters viz. tillers per plant, flag leaf length, grain width and length breadth ratio had not shown any contribution towards divergence. The wide range of variations observed in all the characters may offer good scope in the selection of parents for fruitful future breeding programs. Similar findings were also documented by various researchers (Cheema, *et al.,* 2004; Thayumanavan *et al,* 2009; Ahmed *et al.* 2010). Bharadwaj *et al.* (2001) emphasized that the notable distinctions among the rice genotypes underscored the need for clustering to discern divergent groups. Similarly, Mehdi (1999) classified Sorghum genotypes into five distinct groups. This suggests that it would be prudent to classify the population based on the degree of divergence.

Parental lines chosen from the most divergent clusters, namely IV, V, and VIII, could be utilized in a hybridization program. Hybridization between such divergent parents is anticipated to yield extensive variability and transgressive segregations, potentially leading to high heterotic effects (Rama, T. 1992). Similar recommendations were also provided by Murty and Arunachalam (1966) and Rao and Gomanthinayagam (1997). Therefore, selecting parents for hybridization from two clusters with greater inter-cluster distance is recommended to attain maximum variability in the segregating generations (Bose and Pradhan, 2006). The relatively closer clusters were III and I, and III and V (D^2= 9.77 and 9.99 respectively) and hence were more or less homogenous. For attaining fruitful results, such homogenous clusters should keep away from breeding programmes. The largest intra-cluster distance was recorded for cluster VI and cluster V. Heterosis typically arises by using parental lines with high genetic divergence in crosses.

Table iv: Percentage contribution of characters towards divergence

Source	Times Ranked 1st	Contribution %
Plant height	20	1.63%
Tiller per plant	0	0.00%
Days to 50% flowering	30	2.45%
Leaf area index	17	1.39%
Flag leaf length	0	0.00%
Flag leaf width	53	4.33%
Chlorophyll content	636	51.92%
Grain Length	2	0.16%
Grain width	0	0.00%
Length breadth ratio	0	0.00%
Harvest Index	9	0.73%
Panicle length	7	0.57%
1000 Seeds weight	88	7.18%
Spikelet per panicle	300	24.49%
Percentage of grain filling	7	0.57%
Spikelet density	15	1.22%
Spikelet per plant	10	0.82%
Panicle per plant	28	2.29%
Grain yield	3	0.24%

Thus the genotypes included in clusters having highest intra-cluster distance were relatively more diverse than those in the other clusters and thus can help in achieving maximum genetic advance (Apsath Beevi, H and Venkatesan, M. 2015). Three clusters viz. Cluster III, cluster IV and cluster VIII showed zero intra-cluster distance because these clusters were mono-genotypic. From the cluster mean table, it was observed that the mean differences among the clusters were relatively low since most of the genotypes originated from similar climatic conditions. Such findings were also documented by

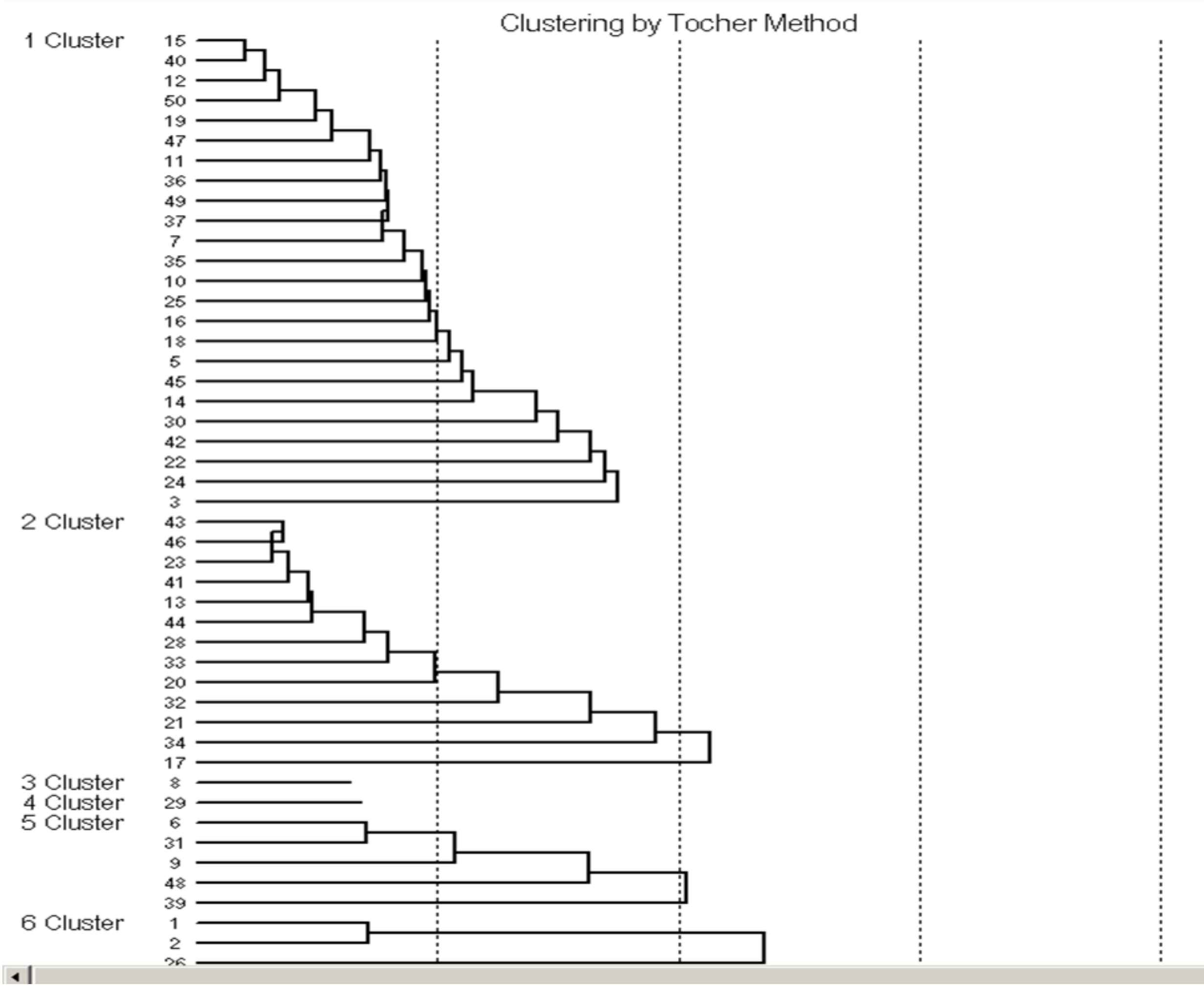
Ahmed *et al.*(2010), in Boro rice. Higher cluster values for all characters were not observed within any cluster. This suggests that none of the clusters comprised genotypes possessing all the desirable traits suitable for direct selection in future cultivation. In this context, recombination breeding involving genotypes from different clusters could be utilized. The results were found in agreement with Amegan *et al.*(2020); Prakash *et.al.* (2022).

Table v: Cluster mean of the characters

CHARACTERS	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
HEIGHT (cm)	122.58	127.92	142.4	138.2	138.96	109.27	125.6	83.6
TILLER/PLANT	12.79	10.58	9.2	9.4	11.76	17.4	11.5	29.6
DAYS TO 50% FLOWERING	129.1	126.78	140.4	139.8	137.56	105	135.7	107.8
LEAF AREA (cm^2)	75.79	73.96	65.93	60.88	92.57	65.25	70.62	68.39
FLAG-LEAF LENGTH (cm)	40.59	39.98	51.44	34.72	42.38	49.23	44.86	44.46
FLAG-LEAF WIDTH (cm)	1.71	1.82	1.78	1.6	2.05	1.87	1.43	2.44
TOTAL CHLOROPHYLL CONT. (mg/g)	4.15	2.21	4.34	2.28	4.53	2.83	3.22	4.2
GRAIN LENGTH (mm)	8.63	8.47	8	8.5	8.72	7.05	9.55	7.96
GRAIN WIDTH (mm)	3.15	3.07	2.24	3.86	3.39	2.64	3.5	2.86
L/B RATIO	2.8	2.78	3.6	2.21	2.63	2.67	2.8	2.79
HARVEST INDEX	35.86	35.13	34.4	39.02	45.79	46.08	33.69	56.81
LENGTH of PANICLE (cm)	26.02	27.31	31.55	20.36	30.22	24.44	31.24	21.8
1000 SEEDS WEIGHT (gm)	24.03	26.74	18.43	22.44	30.48	19.15	16.28	15.61
SPIKELET/PANICLE	199.11	238.34	339.8	366.4	310.76	174.87	427.9	99.6
%GRAIN FILLING	86.78	88.78	93.21	92.56	87.87	89.57	93.96	95.06
SPIKELET DENSITY	7.67	8.91	10.79	18.01	10.22	7.15	13.76	4.58
SPIKELET/PLANT	2033.73	2369.6	2642.2	3591.6	3453.24	3056.93	3951.5	2866.8
PANICLE/PLANT	10.12	9.85	7.8	9.8	11	17.47	9.2	28.8
GRAIN YIELD/PLANT	458.43	589.8	356.76	736.3	1036.39	899.66	522.44	1251.06

The yield potential of any genotype should not be ignored at the time of selection of the parental lines. It's crucial to meticulously analyze the selection of a specific cluster from which genotypes are chosen for a breeding program, as well as the selection of a particular genotype from the chosen cluster. When selecting genotypes from distant clusters, it's essential to consider their mean values for different traits as well, to generate promising breeding material.

Figure 1: Dendrogram (constructed based on genetic divergence) showing clusters



Based on the current study, it is recommended that parental lines chosen from clusters II, IV, VII, and VIII be utilized in a hybridization program. Hybridization between divergent parents is expected to yield broad variability, potentially resulting improved progeny. These four clusters also had maximum number of highest cluster means for experimental characters.

IV. CONCLUSION

Varietal improvement in any crop heavily relies on selecting parents with high genetic divergence in hybridization, as this increases the likelihood of achieving maximum heterosis and generating a broad spectrum of variability in segregating generations. The findings of the present study reveal significant genetic divergence among the evaluated rice genotypes. Genotypes grouped under clusters II, IV, VII, VIII exhibited the highest inter cluster distances. The highest intra-cluster distance was observed in cluster VI, followed by cluster V. Cluster I was the largest, containing 24 genotypes. This divergence indicates the presence of valuable genetic variability, which can be judiciously utilized in future breeding programs. The focus on using genotypes from divergent clusters helps safeguard against genetic erosion It also holds considerable promise for the development of superior rice cultivars with enhanced yield potential, improved grain quality and better adaptability in the region's diverse agro-ecological conditions. This approach aligns with the objectives, particularly in regional food security and resource-constrained farming systems, where access to quality seeds and climate adapted varieties is limited. Therefore, it is advisable to include genotypes from clusters II, IV, VII, and VIII, (which exhibit the highest cluster distance), in a hybridization program, as they are anticipated to yield desired segregates.

Furthermore, the development and dissemination of such improved rice cultivars can contribute directly to strengthening the local seed system, increasing farmer's income and promoting sustainable agricultural practices. Agricultural extension services can also utilize these research findings and use such scientifically selected parent lines among local research stations, progressive farmers and seed growers. This led to the transfer of knowledge from research institutions to the grassroots level.

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