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Study of Genetic Diversity for Rice Genotypes under Aerobic Condition

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ABSTRACT

An experiment was conducted to study genetic diversity in rice genotypes under aerobic condition using of D^2 statistic by Tocher method. The Thirty (30) rice genotypes were grouped into seven clusters indicated the presence of wide genetic diversity among them. The grouping of genotypes showed no clear relationship with their geographic origins. Out of 22 different traits, kernel breadth and kernel length were observed to be major contributors to genetic diversity in the rice genotypes. Maximum inter cluster distances were recorded between cluster 4 and cluster 5 followed by cluster 2 and cluster 4, cluster 4 and cluster 7, cluster 3 and 5. Cluster 1 exhibited the highest intra-cluster distance (52.68). In this study, the inter-cluster distances were higher than the intra-cluster distances, which shows the presence of considerable divergence among the genotypes. Genotypes belonging to these clusters can be used for future hybridization program to improve yield potential under aerobic condition.

Keywords Rice, Aerobic rice, Genetic diversity, D^2 analysis.

INTRODUCTION

Rice is one of the most important cereal grains, feeding over half the global population (Fukagawa N. K. and Ziska 2019). Demand of food is steadily increasing with growing population, but rice cultivation is facing multiple challenge like limited cultivated area, water scarcity, climate change. More improved rice cultivars need to develop for accomplish future demand by combining different attributes like yield potential, grain quality and resistance to both biotic and abiotic stress (Ali *et al.* 2011). Around 55% of the total rice growing area comes under irrigated condition and provide about 75% production (Kumar *et al.* 2015). Rising water scarcity, imposes to develop alternative rice growing systems that require less water, without much compromising with grain yield.

Aerobic rice cultivation is a water saving technology. It can save around 50% of irrigation water as compared to lowland rice (Dey *et al.* 2018). In aerobic

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cultivation, seeds are sown directly into non-puddled soil without standing water, and the soil is maintained in an aerobic (well-aerated) condition throughout the crop's growing period. In this method, seed requirement is also very low, 6-8 kg ha^{-1} as compared to 62.5 kg ha^{-1} in low land rice. It is environment friendly approach as it reduced greenhouse gas (methane) emission. Aerobic rice cultivar also should be responsive to high input, tolerance for moisture stress, weed competitiveness and lodging tolerance (Anandan *et al.* 2016). For selection of parents and development of better recombinants, breeder should have knowledge about genetic divergence among available genotypes in any crop improvement program. It helps breeders to decide suitable breeding strategies for their future crop improvement. The importance of genetic divergence study for selection of desirable parental lines for hybridization purpose were highlighted by different researchers like (Chandra and Nilanjaya 2016, Nivedha *et al.* 2024). Considering the above facts, this experiment was conducted to evaluate genetic divergence of the rice genotypes under aerobic condition.

MATERIALS AND METHODS

In the present field experiment, thirty (30) rice genotypes were sown under dry direct seeded condition during *kharif* 2018 and *kharif* 2019 using Randomized Block Design (RBD) with three (3) replications. Each genotype was sown in 5 m length row with spacing 20 × 15 cm. To maintain aerobic field condition, field was irrigated immediately after sowing to ensure proper germination and subsequently irrigation was given once at 5-7 days interval. The plots were kept without standing water throughout crop season. Standard cultural practices and plant protection measures were implemented to promote a uniform and healthy crop stand. Data were recorded from randomly selected five (5) plants of each genotype on 22 different parameters viz., days to 50% flowering, plant height (cm), leaf length (cm), leaf width (cm), number of tillers plant^{-1}, panicle length (cm), number of grains panicle^{-1}, grain yield (g) plant^{-1}, days to maturity, biological yield (g) plant^{-1}, 1000 seed weight (g), harvest index (%), root length (cm), root volume (ml), root fresh weight (g) plant^{-1}, root dry weight (g) plant^{-1}, kernel length (mm), kernel breadth (mm), kernel length-breadth ratio, brown rice (%), milled rice (%) and head rice recovery (%).

RESULTS AND DISCUSSION

In the present study, D^2 analysis based on 22 different characters clustered the 30 rice genotypes into seven clusters (Table 1). Different researchers also studied genetic diversity under aerobic or direct seeded condition like, Chandra and Nilanjaya (2016) had clustered 25 rice genotypes into 6 clusters under aerobic condition. Kumari *et al.* (2016) analyzed 24 rice germplasms under aerobic condition and grouped into 5 clusters. Tripathi *et al.* (2017) clustered 32 rice genotypes into 7 clusters under direct seeded condition. The genotypes within same cluster are considered to be closely related to each other. Out of seven clusters, cluster 1 was the largest with 21 genotypes, cluster 2 contained three genotypes and cluster 4 included two genotypes. Only one genotype was present in each of the remaining clusters. Clustering of different rice genotypes in different group are presented in Fig. 1. Inter- and intra-cluster distances are presented in Table 2. Maximum inter cluster distances were recorded between cluster 4 and 5 (188.07) followed by cluster 2 and cluster 4 (180.46), cluster 4 and cluster 7 (143.06), cluster 3 and 5 (141.11).

Table 1. Cluster group of 30 rice genotypes using D^2 statistic.

Cluster	No. of genotypes	Genotypes
I	21	R 1986-296-2-86-1, RP 6191-HHZ1-Y4-Y1-Y1, RP 5955-15-1-1-1-1, AAGP 9412, CR 3948-2-1-2-2-1, CR Dhan-201, TRC 2015-5, PAU2K10-23-53-14-52-20-0-4, IR 99784-11-8-1-2, CR 3997-8-IR 91648- B- 89-B-5-1,IR91326-19-2-1-2, OM6377, RP Bio 4918-B-B-2215, IR 95812- CR 3948- 1-2-1-2, IR95780-43-1-1-1, RCPR 25- IR88964-24-2-1-4, RP 5587- B-B-B 210-1, OR 2537-1, RP5591-123-16- 2, IR99784- 255-91-1-5, TRC 2015 -15
II	3	IR14L521, RDR- 1158, NVSR-2107
III	1	R 1973-206-2-86-1
IV	2	RP 5594- 410- 53-4-2, CR 3983-53-1-2-1-2-IR95786
V	1	HKR-48
VI	1	OR2568-4
VII	1	Govind

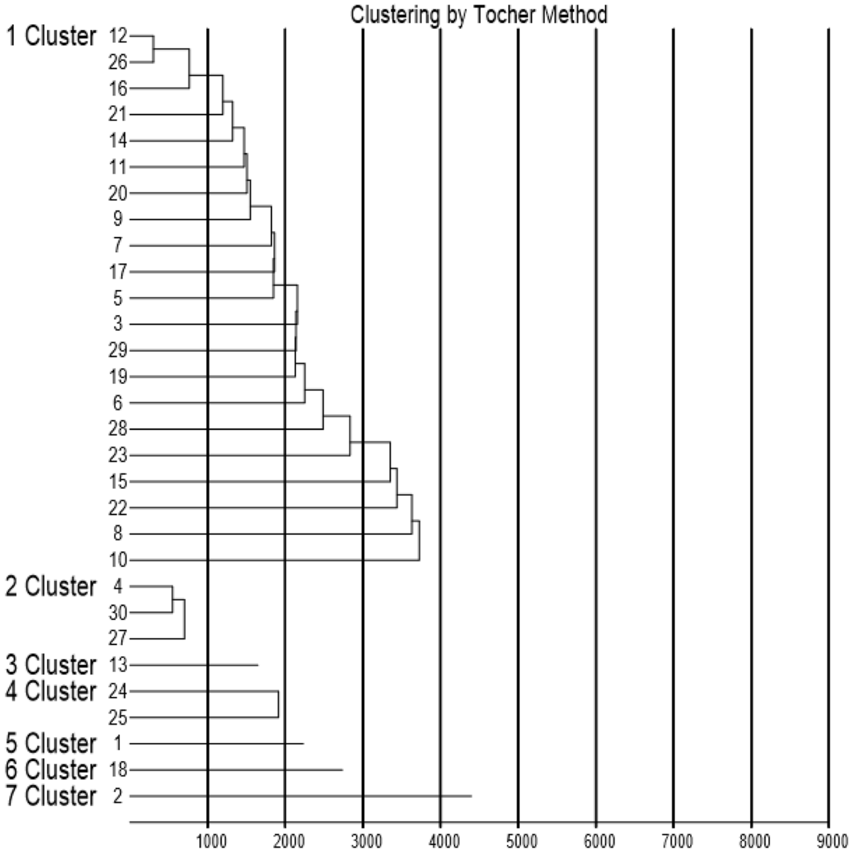

Fig. 1. Clustering pattern of 30 rice genotypes using D^2 statistic.
(1-HKR-48, 2-Govind, 3-OM6377, 4-IR14L521, 5-IR91326-19-2-1-2, 6- IR95780-43-1-1-1, 7-IR 99784-11-8-1-2, 8-IR99784-255-91-1-5, 9-PAU2K10-23-53-14-52-20-0-4, 10-TRC 2015 -15, 11-CR Dhan-201, 12-R 1986-296-2-86-1, 13-R 1973-206-2-86-1, 14-CR 3948-2-1-2-2-1, 15-OR 2537-1, 16-RP 5955-15-1-1-1-1, 17-CR 3997-8-IR 91648- B- 89-B-5-1, 18-OR2568-4, 19-IR 95812- CR 3948-1-2-1-2, 20-TRC 2015-5, 21-AAGP 9412, 22-RP5591- 123-16- 2, 23-RP 5587- B-B-B 210-1, 24-RP 5594- 410- 53-4-2, 25-CR 3983-53-1-2-1-2- IR95786, 26-RP 6191- HHZ1-Y4-Y1-Y1, 27-NVSR-2107, 28-RCPR 25- IR88964-24-2-1-4, 29-RP Bio 4918-B-B-2215, 30-RDR- 1158).

The maximum intra-cluster distance was observed in Cluster 1 (52.68). In this study, the inter-cluster distances were higher than the intra-cluster distances, it indicates the presence of considerable divergence among the genotypes. Similar findings regarding inter- and intra-cluster distances in rice have been

Table 2. Intra and inter cluster distances (D^2) among seven clusters in rice genotypes grown under aerobic condition.

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7
Cluster 1	52.68	77.73	78.37	126.75	86.73	78.68	83.64
Cluster 2		29.76	129.03	180.46	76.34	113.53	120.47
Cluster 3			0.00	71.62	141.11	88.78	108.47
Cluster 4				43.76	**188.07**	119.45	143.06
Cluster 5					0.00	119.65	75.97
Cluster 6						0.00	96.44
Cluster 7							0.00

Table 3. Cluster means for 22 different yield and quality parameters of rice genotypes.
(DF= Days to 50% flowering, PH= Plant height, LL= Leaf length, LW= Leaf width, TN= Number of tillers / plant, PL= Panicle length, GN= Number of grains / panicle, DM= Days to maturity, TW=1000 seed weight, RL= Root length, RV= Root volume, RFW= Root fresh weight / plant, RDW= Root dry weight / plant, KL= Kernel length, KB= Kernel breadth, KLBR= Kernel length-breadth ratio, BR%= Brown rice (%), MR%=Milled rice %, HRR%= Head rice recovery (%), GY= Grain yield / plant, BY=Biological yield / plant, HI= Harvest index).

	50% DF	PH	LL	LW	TN	PL	GN	DM	TW	RL	RV
Group.1	89.98	111.32	39.96	1.02	10.73	24.68	131.20	119.98	26.04	16.80	29.94
Group 2	89.22	117.62	47.28	1.13	14.11	25.42	142.16	119.22	30.39	21.09	42.64
Group 3	91.83	106.32	39.78	1.01	11.74	23.90	106.71	121.83	21.67	14.73	25.29
Group 4	103.08	97.46	33.08	1.03	10.07	23.17	140.82	133.08	16.49	14.64	29.29
Group 5	86.50	107.19	41.94	1.12	13.43	25.98	129.71	116.50	25.67	17.34	35.50
Group 6	79.50	100.81	32.65	0.96	9.84	21.35	99.70	109.50	24.92	13.06	13.55
Group 7	81.17	93.49	34.49	1.25	10.08	24.33	100.04	111.17	23.42	14.94	14.91
	RFW	RDW	KL	KB	KLBR	BR	MR	HRR	GY	BY	HI
Group.1	30.10	9.79	6.19	1.99	3.12	79.75	66.41	59.85	21.31	51.78	40.71
Group 2	42.83	16.32	6.58	2.09	3.15	80.88	69.39	65.51	32.78	62.74	52.42
Group 3	25.38	7.98	5.78	1.72	3.38	81.24	68.07	61.06	16.46	47.90	33.72
Group 4	29.39	9.42	4.98	2.05	2.43	78.07	65.10	59.06	16.11	54.17	30.59
Group 5	35.69	9.85	6.99	1.98	3.53	77.61	66.20	60.21	24.13	69.97	34.31
Group 6	13.73	4.64	5.02	2.50	2.01	79.99	70.26	60.22	15.72	37.97	41.28
Group 7	14.90	4.51	6.27	1.89	3.33	78.42	63.62	43.78	11.44	33.44	34.01

reported by various researchers (Vennela *et al.* 2017, Behera *et al.* 2018 and Takar *et al.* 2024).

Table 4. Relative contribution of different yield and quality parameters towards genetic divergence in rice genotypes grown under aerobic condition.

Source	Times ranked 1st	Contribution %
Days to 50% flowering	0	0.00%
Plant height	3	0.69%
Leaf length	0	0.00%
Leaf width	0	0.00%
Number of tillers per plant	0	0.00%
Panicle length	1	0.23%
Number of grains per panicle	1	0.23%
Days to maturity	0	0.00%
1000 seed weight	5	1.15%
Root length	0	0.00%
Root volume	9	2.07%
Root fresh weight per plant	1	0.23%
Root dry weight per plant	3	0.69%
Kernel length	92	21.15%
Kernel breadth	171	39.31%
Kernel length-breadth ratio	22	5.06%
Brown rice (%)	2	0.46%
Milled rice %	3	0.69%
Head rice recovery (%)	38	8.74%
Grain yield per plant	16	3.68%
Biological yield per plant	29	6.67%
Harvest index	39	8.97%

The genetic divergence among 30 genotypes grown under aerobic condition was also supported by cluster means for 22 different parameters (Table 3). An aerobic rice cultivar is expected to combine the drought-resistant traits of upland varieties with the high-yielding characteristics of lowland cultivars (Dey *et al.* 2018). Desirable traits of aerobic rice cultivation like root parameters (root length, root volume, root fresh weight and root dry weight) and yield components (grain numbers/panicle, test weight, grain yield/plant and harvest index) were observed in genotypes of cluster 2.

Number of times each of twenty-two (22) traits appeared in first rank and its respective contribution % under aerobic condition towards genetic divergence is presented in Table 4. Kernel breadth contributed maximum towards genetic divergence (39.31%), followed by kernel length (21.15%), harvest index (8.97%), head rice recovery (8.74%), biological yield per plant (6.67%), kernel length-breath ratio (5.06%), grain yield per plant (3.68%), root volume (2.07%), 1000 seed weight (1.15%), plant height (0.69%), milled rice (0.69%), root dry weight per plant (0.69%), brown rice (0.46%), panicle length (0.23%), number of grains per panicle (0.23%) and root fresh weight/plant (0.23%). Hence, Kernel breadth and Kernel length were found to be major contributors to genetic diversity in the present study. To create wide range variability and transgressive segregations, crossing should be done between diverse genotypes belong to different clusters (Dey *et al.* 2020).

In the present study, we recommend crossing between genotypes from cluster 4 (RP 5594- 410-53-4-2, CR 3983-53-1-2-1-2-IR95786) and genotypes from cluster 5 (HKR-48) and 2 (IR14L521, RDR- 1158, NVSR-2107) for hybridization program. Further evaluation may help to select desirable genotypes from cluster 2 for aerobic cultivation due to desirable combination of root parameters and yield contributing traits.

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