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Studies on Genetic Parameters in Breeding Lines of Aerobic Rice

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ABSTRACT

Genetic variability is a pre-requisite for selection in the plant breeding program. The present study was carried out with an objective of estimating the genetic parameters, diversity, association among variables, cause-effect relationship and Principal components to provide basis for selection of parents in the hybridization program. A total of sixty rice breeding lines along with check MTU 1010 were evaluated in Randomized Complete Block Design with two replications. Seven quantitative traits were recorded to study the genetic parameters. The GCV was lower for all the traits than PCV. Higher PCV and GCV was recorded of productive tillers per plant. Plant height recorded highest heritability and lowest heritability was observed for productive tillers per plant. Productive tillers per plant, number of filled grains per

L.V. Subba Rao Indian Institute of Rice Research, Rajendranagar, Hyderabad 500030, Telangana, India Email: ramyarathod.5@gmail.com *Corresponding author panicle, plant height and number of panicles per sqm showed high heritability coupled with high genetic advance as percent of mean indicating selection of these traits in the aerobic breeding program will be effective to attain stable rice genotypes. Positive and significant association was found for number of panicles per sqm, productive tillers per plant, number of filled grains per panicle and 1000-grain weight with grain yield. UPGMA dendrogram grouped sixty one genotypes into five clusters. The maximum genotypes 24 were recorded in cluster three and cluster one with minimum of 4 genotypes. The Si values were higher for cluster four, two and one indicating good clusters formation and closer relationship among the members of clusters. The first four components accounted for 83.89% of total variation and more den 0.5 Eigen values through PCA. This suggests the presence of large genetic variability, which gives wider options for breeder during selections.

Keywords Aerobic, Rice, Variability, Association, Path analysis.

INTRODUCTION

Rice (*Oryza sativa* L.) is the second most widely consumed food crop in the world next to wheat. It is an important cereal, which feeds more than one third of the world's population serving as the staple food

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for nearly 3.2 billion people. It is the principle food for more than half of the world's population (Sasaki and Burr 2000). It is mostly grown under submerged soil conditions and requires more water compared to other crops. Rice crop is growing under a range of water applications ranging from 3000 to 5000 litres of water to produce 1 kg of rough (unmilled) rice in an irrigated lowland production system (Tuong and Bouman 2003).

Around 1300–1500 mm is a typical amount of water needed for irrigated rice in Asia. Irrigated rice receives an estimated 34–43% of the total world's irrigation water, or about 24–30% of the entire world's developed fresh water resources (www.irri.org). The declining water availability and increasing cost of water threaten the production of irrigated rice. Unpredictable rainfall pattern is a major constraint in the lives of poor farmers under rainfed situations. In the coming years water crisis is the major issue over the world bringing irrigated rice cultivation to an edge. There is an immediate need to develop an alternative viable approach to cultivate rice with minimum water.

Aerobic rice cultivation is a water saving approach aims at combining drought tolerance of upland rice and yield potential of lowland rice. In this system rice is established in un-puddle and un-flooded conditions by direct seeding like other cereals wheat, maize and barley. Aerobic rice cultivation requires 50% less water requirement compared to transplantedrice (Bouman et al. 2005). Aerobic rice is a boon to farmers who cannot access to grow rice under flooded conditions. This approach reduces the water requirement by reduction in loss due to seepage, percolation and evaporation. Aerobic rice production enhances oxygen availability in the root zone. The oxygen enhances root development, which results in stronger, more resilient rice plants, with increased tolerance to drought, extended submergence and pest infestations (Thakur et al. 2016, Wu et al. 2015, Chang et al. 2016). Keeping in mind the coming years of water scarcity, it is time to save water and make a shift from irrigated paddy cultivation to aerobic rice cultivation (Lal et al. 2013). Planned breeding experiments to develop varieties cultivable under aerobic condition with high yield potential is the major goal to the plant breeders.

Sl. No.	Breeding lines	Sl. No.	Breeding lines
1	G-3911	32	3912
2	G-3901	33	G-3903
3	G-3927	34	G-3954
4	G-3960	35	G-3956
5	G-3944	36	G-3910
6	G-3952	37	G-3943
7	G-3947	38	G-3905
8	G-3928	39	G-3937
9	MTU 1010	40	G-3920
10	G-3963	41	G-3919
11	G-3906	42	G-3907
12	G-3957	43	G-3934
13	G-3949	44	G-3959
14	G-3915	45	G-3909
15	3926	46	G-3938
16	3930	47	3922
17	G-3961	48	3933
18	G-3940	49	G-3951
19	G-3942	50	G-3939
20	G-3935	51	G-3917
21	G-3921	52	G-3929
22	G-3953	53	G-3916
23	G-3924	54	G-3925
24	G-3925	55	G-3955
25	G-3950	56	G-3932
26	G-3923	57	G-3936
27	G-3945	58	G-3931
28	G-3913	59	G-3904
29	G-3914	60	G-3908
30	G-3962	61	G-3946
31	3902		

Table 1. List of aerobic rice breeding lines.

MATERIALS AND METHODS

Planting material

Sixty one aerobic rice breeding lines from all over India were evaluated in initial varietal trial -1- aerobic, AICRP during the wet season (WS) -2019 at Regional sugarcane and Rice Research Station Rudrur, Nizamabad, Telangana (Table 1).

Soil physico-chemical properties

The soil of experimental cite was clay loam having good nutrient supply and water holding capacity with an organic carbon content of 1.25%, pH – 7.5 and electric conductivity 0.67dS/m.

Weather conditions

The weather data were recorded from 29th to 47th

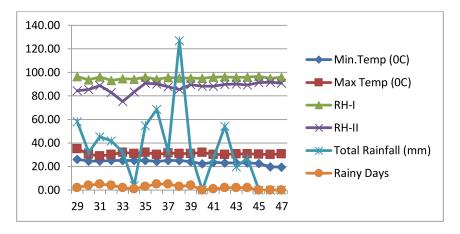


Fig. 1. Weather data based on standard weeks from time of sowing to harvest of the crop.

standard week of crop growth as shown in Fig. 1.The mean minimum and maximum temperature ranged from 19.43°C to 26.14°C and 35.14°C to 30.57°C respectively. The relative humidity ranged from 95.31 % to 87.59 %. The crop growth period received a total rainfall of 655.3 mm and maximum rainfall of 359.3 mm was recorded during maximum tillering stage of the crop and 128 mm during grain filling stage. A total of 45 rainy days were recorded from time of sowing to harvest i.e., 19.7.2019 to 28.11.2019.

Planting method

Sixty one breeding lines were direct seeded in the plots in RCBD (Randomized Complete Block Design) with two replications. The plot size was 6 sqm with a spacing of 20 cm \times 15 cm. The sowing was done on 19th July, 2019, 120 kg N ha⁻¹ was top dressed in four equal splits at 2, 5, 8 and 11 weeks after sowing respectively, 60 kg P ha⁻¹, 20 kg K₂O ha⁻¹ and 20 kg ZnSO₄ ha⁻¹ was applied at direct seeding. Remaining 20 kg K₂O was applied with the last split of N. Weeds were controlled by one application of pre-emergence herbicide Pendimethalin, post-emergence herbicide metsulfuron methyl 10% + chlorimuron ethyl 10% WP application at 20-25 DAS and supplemented with hand weeding. All the prophalytic measures were taken to protect the crop from pest and diseases.

Observations

In each replication, five plants of each genotype were selected randomly and were tagged all the observations except days to 50% flowering recorded on these plants. Seven yield related traits viz., days to 50% flowering (DFF), plant height (PH), productive tillers per plant (PT/P), number of filled grains per panicle (NFG/P), 1000-grain weight (TW) and grain yield per plant (GY) was recorded.

Statistical data analysis

The genotypic and phenotypic coefficients of variation, heritability were calculated according to the formula given by Falconer (1981). The genetic advance was computed following the formula suggested by Johnson *et al.* (1955). Pearson's correlation coefficients and cause –effect relationship were computed to evaluate the relationship among the observed variables. Clustering was carried out by using Unweighted Pair Group Method with Arithmetic Mean (UPGMA) method (Ward *et al.* 1963). Principal component analysis was performed using correlation matrix to examine the percentage contribution of each trait to total genetic variation by the software SAS version 9.2. The silhouette plot was analyzed using R software version 4.0.1.

RESULTS AND DISCUSSION

PCV, GCV, heritability and genetic advance

The conducted research study unveiled that days to 50% flowering ranged from 78.0 days to 111.0 days with a mean of 94.0 days, 59.0 cm to 120.0 cm

Sl. No. Traits	Mean	Range		Coefficient of variation (%)		(Heritability	Genetic advance as per cent of mean	
	1110000	Min	Max	PCV	GCV	(hbs - %)	(%)	
1	DFF	94.0	78.0	111.0	7.42	7.22	94.63	14.48
2	PH	89.0	59.0	120.0	13.06	12.91	97.71	26.28
3	NP/m ²	278.0	209.0	364.0	12.54	11.82	88.80	22.95
4	PT/P	8.0	5.0	12.0	20.08	21.01	82.40	33.68
5	NFG/P	140.0	97.0	212.0	15.99	15.36	92.27	30.40
6	TW	22.2	16.4	25.7	8.21	7.83	90.88	15.38
7	GY	3330.0	2350.0	5350.0	14.76	13.87	88.26	26.84

Table 2. Genetic variability, heritability and genetic advance of quantitative traits. DFF - Days to 50% flowering , PH - plant height(cm), PT/P - productive tillers per plant , NFG/P - number of filled grains per panicle , TW - 1000-grain weight (g) and GY - grain yieldper plant (g).

for plant height with a mean of 89.0 cm, number of panicles per sqm with a mean of 278.0 ranged from 209.0 to 364.0, range of 8.0 to 5.0 productive tillers per plant with a mean 8.0, 140.0 to 97.0 number of filled grains per panicle having mean of 140.0, the 1000-grain weight ranged from 16.4 g to 25.7 g with range 22.2 g and grain yield ranged from 2350.0 kg/ ha to 5350.0 kg/ha with a mean 3330.0 kg/ha.

The phenotypic coefficient of variation (PCV) was higher for all the seven quantitative traits than the genotypic coefficient of variation (GCV) as shown in Table 2. This may be explained by the higher genotypes by environment interaction for these traits, similar observations were made by Kavitha and Reddy (2002). The higher PCV and GCV (>20%) was observed for productive tillers per plant (20.08% and 21.01%) respectively. This indicated greater scope for improvement through selection in environments showing high PCV and GCV. These results are in similarity with Mamata et al. (2018), Rathod et al. (2020). Moderate PCV and GCV (10-20%) was recorded for number of filled grains per panicle (15.99% and 15.36%), grain yield/ha (14.76% and 13.87%), plant height (13.06% and 12.91%) and number of panicles per sqm (12.54% and 11.82%) respectively. These characters exhibited moderate phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) values, are likely to allow reasonable scope of improvement through selection in respective environment owing to their moderate genetic variability (Garg et al. 2011, Tiwari et al. 2011). Days o 50% flowering (7.42% and 7.22%) and 1000- grain weight (8.21% and 7.83%) showed lower PCV and GCV indicating little scope of improvement in these traits due to lack of requisite variability.

The heritability (h_{bs}) estimates ranged from 82.40% to 97.71%. The highest heritability was observed for plant height (97.71%), followed by days to 50% flowering (94.63%), number of filled grains per panicle (92.27%), 1000-grain weight (90.88%), number of panicles per sqm (88.80%), grain yield/ ha (88.26%) and lowest heritability (82.40%) was recorded for productive tillers per plant. Genetic advance as percent mean (GAM) was highest for productive tillers per plant (33.68) followed by number of filled grains per panicle (30.40), plant height (26.28) and number of panicles per sqm (22.95). Medium GAM was recorded for days to 50% flowering (14.48) and 1000-grain weight (15.38).

In the present study, productive tillers per plant, number of filled grains per panicle, plant height and number of panicles per sqm showed high heritability coupled with high genetic advance as percent of mean. This is in agreement with Abebe et al.(2017) and Mamata et al. (2018) for plant height, Rathod et al.(2020) for productive tillers per plant and number of filled grains per panicle. This indicates that the environment has a minor influence on the expression of these traits and these traits are controlled by additive gene action as suggested by Panse (1957). Therefore, these traits could be selected by breeders in early generations and will be effective. High heritability with moderate genetic advance as percent mean was recorded for days to 50% flowering and 1000-grain weight. This is an indication that additive gene action

Traits	DFF	PH (cm)	NP/m ²	PT	NFG/P	TW (g)	GY (kg/ha)
DFF	1.00	0.35**	0.06	0.14	0.11	0.14	0.10
PH (cm)		1.00	0.11	0.04	-0.09	-0.09	0.02
NP/m ²			1.00	0.70**	0.25	0.30**	0.45**
PT/P				1.00	0.42**	0.52**	0.66**
NFG/P					1.00	0.31**	0.49**
TW (g)						1.00	0.54**
1 (5)						1.00	0.01

 Table 3. Correlation coefficients of yield and yield attributing characters.

governs those traits and selection will be rewarding (Roychowdhury and Tah 2011).

Correlation studies

Character association studies primary importance is to know the suitability of various characters for selection, because selection of a particular trait may induce desirable or undesirable changes in the associated characters. Grain yield/ha had positive significant association with number of panicles per sqm (0.45^{**}) , productive tillers per plant (0.66**), number of filled grains per panicle (0.49**) and 1000-grain weight (0.54^{**}) as shown in Table 3. Results suggests that, while improving grain yield due care is given to component traits viz., number of panicles per sqm, productive tillers per plant, number of filled grains per panicle and 1000-grain weight as these traits are positively associated with grain yield, indirect selection for these traits might improve the grain yield (Fig. 2). These are in similarity with Rathod et al. (2020) for productive tillers per plant, number of filled grains per panicle and 1000-grain weight.

Cause and effect analysis

The total correlation between yield and its component characters may be some times misleading, as it might be an over-estimate or under-estimate because of its association with other characters. If relationship is due to multiple effects of gene (s) it is difficult to separate these effects by selecting a particular character. Hence, indirect selection by correlated response may not be sometimes fruitful. When many characters are affecting a given character, splitting total correlation into direct and indirect effects of cause as devised by Wright (1921). With this background, the direct and indirect effects of different yield contributing traits

on yield were estimated using genotypic correlation coefficients and are tabulated and represented below (Table 4). The highest positive direct effect on grain yield was exhibited by productive tillers per plant (0.61) followed by number of filled grains per panicle (0.31), 1000-grain weight (0.24) and plant height (0.08) indicating selection of these characters will bring direct improvement in grain yield per plant. The results are in parallel with Lakshmi et al.(2017) for plant height, Lakshmi et al. (2017), Rathod et al. 2020 for productive tillers per plant, number of filled grains per panicle and 1000-grain weight. Days to 50% flowering and number of panicles per sqm exerted negative direct effect on grain yield per plant. The results are in uniformity by Lakshmi et al. (2017), Rathod et al. (2020) for days to 50% flowering.

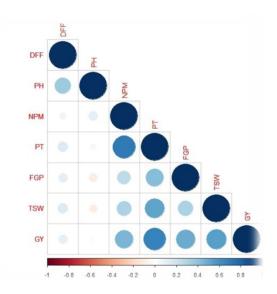


Fig. 2. Correlogram depicting the association between yield and yield attributing traits.

Traits	DFF	PH (cm)	NP/m ²	PT/P	NFG/P	TW (g)	GY (kg/ha)
DFF	-0.03	0.03	0.09	0.07	0.03	0.03	0.12
PH (cm)	-0.01	0.08	-0.02	0.01	-0.02	-0.02	0.02
NP/m ²	-0.02	0.01	-0.16	0.48	0.06	0.08	0.51**
PT/P	0.05	0.02	-0.13	0.61	0.09	0.13	0.73**
NFG/P	0.04	-0.08	0.04	0.24	0.31	0.08	0.48**
TW (g)	0.05	-0.06	0.05	0.34	0.08	0.24	0.81**

Table 4. Direct and Indirect effects of yield and yield attributing traits.

Cluster analysis of aerobic rice genotypes

Hierarchical cluster analysis of some yield contributing traits is depicted in Fig. 3. Five main clusters were identified. Cluster 1 had minimum genotypes 4 with 2 sub-clusters 1a with one genotype which is most diversified among the genotypes and 1b having three genotypes. Genotype of cluster 1 has good yield attributing traits such as dwarf plant type (3906, 3915, 3955), number of filled grains per panicle and high grain yield (3955). Cluster 2 has 5 genotypes with sub-clusters 2a having two genotypes and 2b with three genotypes. 2a had genotype having characters such as dwarf plant type, number of productive tillers per plant and 1000-grain weight (3630), 2b had genotype with good 1000-grain weight (3937). Cluster 3 recorded maximum genotypes 24 grouped under sub-clusters 3a with fifteen genotypes and 3b having nine genotypes which are superior for early duration, panicle length, number of filled grains per panicle, number of panicles per sqm 1000-gain weight and grain yield (3901, 3911, 3927, 3944, 3910, 3924, 3913, 3946, 3922). Grouping of these in one cluster indicated their parental relationships. Cluster 4 had 20 genotypes with 10 genotypes in sub-cluster 4a and 10 genotypes in sub-cluster 4b. This cluster had genotypes with good number of panicles per sqm (G-3952, G-3925, G-3904, G-3907). Eight genotypes are present in cluster 5 with sub-clusters 5a and 5b. Good character early duration genotypes (G-3939, G-3917, G-3934) was observed in cluster 5.

Silhouette plot

The silhouette plot helps to identify clusters visually based on their formation and relationship. The plot was constructed using sixty one aerobic genotypes as given in Fig. 4. The cluster 4 has highest S_i values, followed by cluster 2 (0.15) and cluster 1(0.12) indicating good formation of clusters and the genotypes in the clusters are closer to each other. The cluster 1 has one genotype with negative value, followed by two in cluster 2, one in cluster 3, two in cluster 4 and 1 in cluster 5. The negative values indicate the genotypes are the outliers i.e., they does not belong to the cluster.

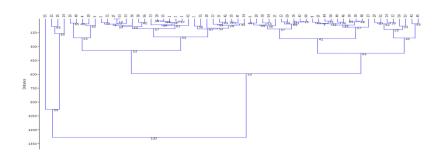
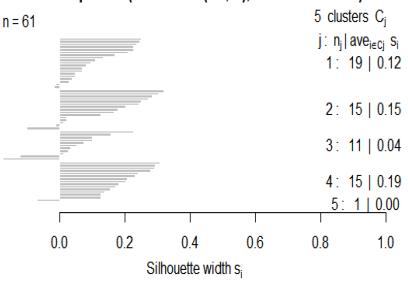


Fig. 3. Dendrogram representing distribution of 61 aerobic rice genotypes based on morphological traits (from left of the figure is cluster 1: sub-cluster 1a and 1b, cluster 2: sub-cluster 2a and 2b, cluster 3: sub-cluster 3a and 3b, cluster 4: sub-cluster 4a and 4b, cluster 5: sub-cluster 5a and 5b).



Silhouette plot of (x = cutree(hc, 5), dist = distance)

Fig. 4. Silhouette plot to identify clusters visually among sixty one aerobic rice genotypes.

Principal component analysis

PCA analysis was performed with seven quantitative traits and indicated that first four components accounted for 83.89% of total variation and more than 0.5 eigen values (Table 5). The 1st principal component accounted for 42.21% of total variance and featured number of productive tillers per plant (0.51) as principal trait, followed by grain yield (0.48), number of panicles per sqm (0.41) and 1000 grain weight (0.40). 2nd principal component accounted for19.25% of total variance featuring plant height (0.73) as principal trait, followed by days to 50% flowering (0.64). Traits number of productive tillers per plant (-0.64) in negative direction. The 3rd principal component recorded 12.62% and 4th principal component with 9.81% of total variance. These components was loaded mainly by trait number of

Table 5. Eigenvalues, % variance and cumulative % variance of morphological traits.

Traits	PC 1	PC 2	PC 3	PC 4
Eigen value	2.95	1.34	0.88	0.68
% variance	42.21	19.25	12.62	9.81
cumulative variance %	14.30	28.60	42.90	57.1
Days to 50% flowering	0.13	0.64	0.40	-0.15
Plant Height (cm)	0.03	0.73	-0.23	0.18
Number of panicles/m2	0.41	0.06	-0.59	0.05
Number of productive tillers per plant	0.51	-0.64	-0.23	-0.02
Number of filled grains per panicle	0.36	-0.15	0.45	0.71
1000-grain weight (g)	0.40	-0.11	0.27	-0.65
Grain yield (g)	0.48	0.06	0.06	0.03

Average silhouette width : 0.13

CONCLUSION

The materials of the present study exhibited high level of variability for productive tillers per plant, number of filled grains per panicle, plant height and number of panicles per sqm. There was direct positive significant association of grain yield per plant with number of panicles per sqm, productive tillers per plant, number of filled grains per panicle and 1000-grain weight, selection would be effective to increase yielding ability. Productive tillers per plant, number of filled grains per panicle and 1000-grain weight showed highest positive direct effect on grain yield per plant. Sixty one breeding lines were grouped into five main clusters. Cluster 3 has maximum genotypes twenty four having good agronomic traits early duration, number of filled grains per panicle, number of panicles per sqm, 1000-grain weight and grain yield. PCA identified days to 50% flowering, plant height, number of panicles per sqm and productive tillers per plant as main components contributing towards the total variation existing in the present breeding material.

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