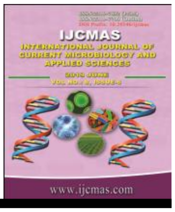
Int.J.Curr.Microbiol.App.Sci (2019) *8*(6): 1577-1583

EXCELLENT PUBLISHERS

International Journal of Current Microbiology and Applied Sciences
ISSN: 2319-7706 **Volume 8 Number 06 (2019)**
Journal homepage: http://www.ijcmas.com



Original Research Article https://doi.org/10.20546/ijcmas.2019.806.189

Genetic Divergence Studies in Rice (*Oryza sativa* L.) Hyrids for Yield, Yield Component Traits and Quality Parameters

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ABSTRACT

Keywords

Rice hybrids, Genotypes, Clusters and D^2 analysis

Article Info

Accepted:
15 May 2019
Available Online:
10 June 2019

Genetic divergence was assessed among 20 rice hybrids with 15 characters from different eco-geographical regions of India using Mahalanobis' D^2 analysis. The experimental materials were evaluated during *kharif*- 2017 at Agricultural College Farm, Bapatla, Andhra Pradesh, India. The 20 rice hybrids were grouped into 5 clusters. Out of five clusters, maximum number 9 of genotypes are in cluster I. Cluster II is second largest with 6 genotypes followed by cluster IV with 3 genotypes. Clusters III and V possess one genotype each. The pattern of distribution of genotypes from different eco-geographical regions into various clusters was at random indicating that geographical diversity and genetic diversity were not related. Based on the *perse* performance and cluster mean values of characters, it can be concluded that, the hybrid S-8001 which is present in the cluster II is found to be superior over other hybrids and checks in the present study by having high mean values for the economically important characters *viz.*, number of total grains per panicle, number of productive tillers per plant and grain yield per plant.

Introduction

The slogan 'Rice is life' aptly describes the importance of rice in food and nutritional security. Rice (*Oryza sativa* L.) is the world's second most important cereal crop and staple food for more than 60% of the global population providing about 75% of the calorie and 55% of the protein intake in their average daily diet. In India, rice is grown in 44.0 mha with the production of 108.50 mt and productivity of 2.4 t/ha. during 2016-17 (Directorate of Economics & Statistics, 2016-17). Maintaining stable rice production is extremely important to feed the constantly growing population. For the estimated population of 1.63 billion people by the year 2050 with a per capita rice consumption of 225 to 275 g/day, country would require 133 to 162 M t of rice (Directorate of Rice Research, 2013). In the present scenario the rice productivity has reached a plateau.

In order to achieve the expected targets, we have to develop the varieties with higher yield potential by breaking the existing yield plateau through utilizing more diversified parents in breeding programmes.

The success of any plant breeding programme largely depends on the existence of diversity among the genotypes (Allard, 1960). This helps in the choice of parents for hybridization in yield improvement programmes. Hence, estimation of genetic diversity for yield and its components among genotypes is important for planning the future hybridization programme. The use of Mahalanobis' D^2 statistics for estimating genetic divergence has been emphasized by Sarawgi and Bisne (2007). Hence, the present investigation was carried out in the southern block of Agricultural College Farm, Bapatla to ascertain the value and magnitude of genetic diversity of 20 rice genotypes and to select suitable genotypes.

Materials and Methods

The present investigation was carried out during *kharif*, 2017 at Agricultural College Farm, Bapatla. The experimental material consisted of twenty genotypes (15 Hybrids + 5 Checks) of Rice (*Oryza sativa* L.) obtained from Indian Institute of Rice Research (IIRR), Rajendranagar, Hyderabad, Telangana, which were sown in nursery beds and transplanted into the main field in Randomized Block Design in three replications with a spacing of 15 x 15 cm.

Single plant observations were recorded on five plants selected at random per genotype per replication for characters *viz*., plant height (cm), number of productive tillers per plant, panicle length (cm), number of total grains per panicle, grain yield per plant (g) and their means were used for statistical analysis. However, observations on days to 50% flowering, days to maturity were recorded on plot basis and all grain quality parameters *viz.*, hulling percentage, milling percentage, head rice recovery percentage, L/B ratio, water uptake, kernel elongation ratio, volume expansion ratio and amylose content were done as per DRR laboratory manual on rice grain quality procedures. Genetic divergence analysis was done following the D^2 statistics proposed by Mahalanobis (1936).

Results and Discussion

The analysis of variance showed significant differences among the genotypes for all the characters. The 20 genotypes were grouped into 5 clusters using the Tocher's method with the criterion that the intra cluster average D^2 values should be less than the inter cluster D^2 values. The distribution of 20 genotypes into 5 clusters is presented in Table 1. The distribution of 20 genotypes into 5 clusters was at random with maximum number of 9 genotypes in cluster I. Cluster II is the second largest with 6 genotypes followed by cluster IV with 3 genotypes. As could be seen from the results that cluster III and V were solitary clusters. The formation of distinct solitary clusters may be due to the fact that geographic barriers preventing gene flow or intensive natural and human selection for diverse and adoptable gene complexes must be responsible for this genetic diversity. These results were in accordance with Dutta *et al.,* (2011), Vennila *et al.,* (2011), Chakravorty and Ghosh (2012), Singh *et al.*, (2012), Karuppaiyan *et al.*, (2013), Manohara and Singh (2013), Allam *et al.,* (2014), Bhadra and Roy (2014), Ramanjaneyulu *et al.,* (2014), Beevi and Venkatesan (2015), Kumar *et al.*, (2015), Bharathi *et al.*, (2016), Chandramohan *et al.*, (2016) and Ashok *et al.*, (2017).

The maximum intra cluster D^2 value was 95.18 for cluster IV followed by 90.27 for cluster II, 41.08 for cluster I, while it was zero for clusters III and V as shown in Table 2. The high intra cluster distance in cluster IV indicated the presence of wide genetic diversity among the genotypes *viz.*, HRI-195, RTNRH-11 and NS-6816. Cluster mean values showed wide range among the genotypes studied, which indicates the presence of variation among the genotypes studied. The maximum inter cluster D^2 values was observed between cluster II and V (444.87) followed by cluster I and V (267.50). Intra and inter cluster distance of 20 rice genotypes are showed in the Figure 1.

Table.1 Clustering pattern of 20 genotypes of rice (*Oryza sativa* L.) by Tocher's method

Cluster No.	No. of genotypes	Name of the genotypes
I	9	MEPH-143, 27P63 (NCH-2), BPT-5204(NCV-2), CRHR-115, NK-23831, W+GL-14(NCV-1), US-308, CRHR-116, CRHR-118
II	6	PHI-17108, CRHR-119, JKRH-3333 (NCH-1), S-8001, Indam-200-043, NPH-2899
III	1	RRX-135
IV	3	HRI-195, RTNRH-11, NS-6816
V	1	ADT-49 (ZCV)

Table.2 Average intra and inter cluster D^2 values among five clusters in 20 rice (*Oryza sativa* L.) genotypes

Cluster No	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	**41.08**	127.17	88.74	152.36	267.50
Cluster II		**90.27**	229.30	176.61	444.87
Cluster III			**0.00**	227.43	168.70
Cluster IV				**95.18**	226.74
Cluster V					**0.00**

Diagonal bold values indicate intra cluster distances

Table.3 Mean values of five clusters by Tocher's method for 20 genotypes of rice (*Oryza sativa* L.)

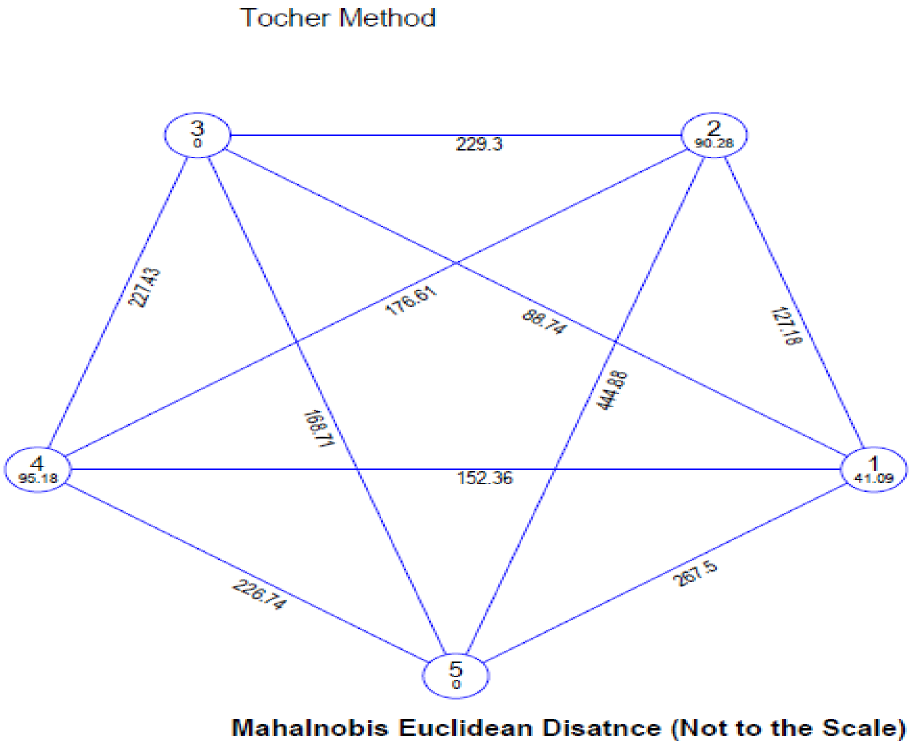
Character / Cluster number	Days to 50% Flowering	Days to Maturity	Plant Height (cm)	Number of productive tillers/ Plant	Panicle Length (cm)	No. of total grains/ Panicle	Hulling %	Milling %	Head Rice Recovery	Volume Expansion Ratio	Water Uptake	L/B Ratio	Kernel Elongation Ratio	Amylose Content	Grain yield/ plant (g)
Cluster I	98.55	127.88	131.65	18.00	**24.37**	311.07	83.07	72.22	59.66	**3.625**	112.03	**2.97**	1.78	23.40	46.85
Cluster II	100.66	129.38	128.45	18.38	**22.60**	**369.38**	84.61	74.05	61.94	3.661	**225.00**	2.81	1.77	22.84	**54.33**
Cluster III	**102.00**	**130.00**	114.60	**15.33**	23.36	244.66	**87.33**	**77.00**	**73.66**	3.707	**103.33**	**2.53**	**1.87**	**24.60**	**28.66**
Cluster IV	**88.00**	**117.00**	**136.02**	**19.22**	23.64	350.33	82.55	72.11	56.33	**3.703**	198.88	2.78	**1.68**	**22.77**	41.00
Cluster V	89.66	119.00	**96.66**	18.33	22.76	**220.00**	**82.33**	**70.00**	**54.00**	3.647	115.00	2.90	1.80	23.10	29.00

Bold figures are indicated maximum and minimum mean values for each character.

Table.4 Contribution of different characters towards genetic divergence among 20 genotypes of rice (*Oryza sativa* L.)

Character	Percent contribution towards divergence
Days to 50% Flowering	13.68
Days to Maturity	0.00
Plant Height (cm)	13.16
Number of productive tillers/ Plant	0.53
Panicle Length (cm)	0.00
Number of total grains/ Panicle	4.74
Hulling %	0.53
Milling %	0.00
Head Rice Recovery (%)	2.63
Volume Expansion Ratio	0.00
Water Uptake	42.11
L/B Ratio	6.84
Kernel Elongation Ratio	5.26
Amylose Content (%)	0.53
Grain Yield/ Plant (g)	10.00

Fig.1 Intra and Inter cluster distances of 20 rice (*Oryza sativa* L.) genotypes in five clusters based on Tocher method



The cluster mean values for 15 characters are presented in Table 3. The data indicated a wide range of mean values between the characters. The cluster I is having highest mean value for panicle length and L/B ratio; cluster II for number of total grains per panicle, water uptake and grain yield per plant; cluster III for days to 50% flowering, days to maturity, hulling percentage, milling percentage, head rice recovery percentage, kernel elongation ratio and amylose content; cluster IV for plant height (cm), number of productive tillers per plant and volume expansion ratio. Cluster mean values showed wide range among the genotypes studied, which indicates the presence of variation among the genotypes studied (Table 4).

Based on the *perse* performance and cluster mean values of characters, it can be concluded that, the hybrid S-8001 which is present in the cluster II is found to be superior over other hybrids and checks in the present study by having high mean values for the economically important characters *viz.*, number of total grains per panicle, number of productive tillers per plant and yield per plant.

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How to cite this article:

Devi, M., D.P.B. Jyothula, B. Krishnaveni and Rao, V.S. 2019. Genetic Divergence Studies in Rice (*Oryza sativa* L.) Hyrids for Yield, Yield Component Traits and Quality Parameters. *Int.J.Curr.Microbiol.App.Sci*. 8(06): 1577-1583. doi: https://doi.org/10.20546/ijcmas.2019.806.189