ISSN: 2518-2021 (Print), 2415-4474 (Online) Fundam Appl Agric 2017, 2(2): 243-246

Fundamental and Applied Agriculture

Journal homepage:www.f2ffoundation.org/faa

Plant genetics
ORIGINAL ARTICLE

Genetic analysis and agronomic performance of local rice genotypes under salinity stress

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ARTICLE INFO

Article history:

Received: 12 April 2017
Received in revised form: 01 May 2017
Accepted: 10 May 2017
Available online: 16 May 2017

Academic Editor: Md. Rashedur Rahman

Keywords:

Genetic diversity
Principal component
Rice genotypes
Salinity stress

ABSTRACT

Ten rice genotypes including seven landraces and three released varieties were used as plant material to study genetic divergence using multivariate analysis. Ten genotypes fell into three distinct clusters. The distribution pattern revealed maximum number of genotypes in cluster I and III while cluster II included minimum number of genotypes. The inter-cluster distances in all of the cases were higher than that of intra-cluster distances suggesting wider genetic diversity among the genotypes of different clusters. The intra-cluster distances in all the three clusters were low indicating the genotypes within the same clusters were closely related. Maximum genetic distance was observed between cluster I and cluster III. The genotype of cluster I with the cumulative ranking 1, for those traits like days to maturity, days to 50% flowering, plant height, panicle length, number of filled grains panicle^{-1}, Fertility percent and yield panicle^{-1}. In case of principal component analysis the first three components of the principal component with eigen values >1 contributed 83.00 percent variability existing in the rice genotypes for yield contributing traits in the study. Thus the results of principal component analysis revealed, wide genetic variability exists in this rice germplasm accessions. High salt tolerant traits with high genetic variability are expected to provide high level of gene transfer during breeding programs.

INTRODUCTION

Rice (*Oryza sativa* L.) is a self-pollinated cereal crop belonging to the family Gramineae (Poaceae) under the order Cyperales and staple food of more than 50% of the world's population (Aggarwal et al. 2002). Bangladesh stands fourth position for the production of rice and produced about 52.2 million tons (FAOSTAT 2014). But salinity is one of the major problems for rice cultivation in coastal areas. Therefore, development of salt tolerant cultivar has been considered as one of the strategies to increase rice production in coastal areas. Landraces of rice performed a very significant role in the food security and sustainable development of agriculture in coastal reason, in addition to their significance as genetic resource for rice genetic improvement (Tang et al. 2002). Rice landraces is not only endowed with genetic diversity but also represents a wealth of valuable genes (Sarma et al. 2003). Exploring diversity in a landrace collection is very important for identifying new genes and further improvement of the landraces (Jayamani et al. 2007). However, Bangladesh had abundant landraces of rice from time ancient. But, now rice diversity in Bangladesh is endangered all over the country due to extensive cultivation of modern varieties along with various intervention of rice habitat (Ahmed et al. 2010). Rice landraces need to be utilized for maintaining its diversity in rice field. Genetic diversity is the foundation for an efficient choice of parents for the variety development programme. Genetic diversity is a powerful tool to determine the genetic discrimination among the genotypes, which is used to identify appropriate parents for hybridization to develop high yielding potential variety (Bhatt 1970). But limited work has been done on genetic diversity for local landraces of Bangladesh.

However, Principal Component Analysis (PCA) is one of the tools available for summarizing and describing the inherent genetic variation in crop genotypes. This technique helps in identification of traits that help in distinguishing selected genotypes based on similarities in one or more traits and classify the genotypes into different groups (Ariyo 1987; Nair et al. 1998). The PCA has been used by (Nassir 2002; Ashim Chakravorty et al. 2013) in rice for partitioning observed

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variation and studying inter relationships among different traits. PCA helps to identify the traits with high variability. Therefore, the present investigation was undertaken to estimate the nature and magnitude of genetic diversity and the maximum number of variance with fewest number of principal component in rice genotypes.

METHODOLOGY

The study was conducted during the period from June to December 2015 at the experimental field of the Plant Breeding Division, Bangladesh Institute of Nuclear Agriculture (BINA), Mymensingh. Ten rice genotypes including seven landraces (Hogla, Dakh Shail, Kute Patnai, Ghunshi, Mondeshor, Tal Mugur, Nona Bokhra) and three released varieties (Binadhan-8, Binadhan-10 and BRRI dhan47) were used as plant material. Randomized Complete Block Design with five replications and three different salt treatments *viz.,* EC-6 dSm^{-1}, EC-8 dSm^{-1}, EC-12 dSm^{-1} with one control condition were used in this study. Management practices such as irrigation and fertilization were applied by following the standard procedures (IRRI 2002). Other intercultural operations were done whenever necessary. Morphological data were recorded at appropriate growth stage of rice plant following the standard evaluation system indicated by IRRI (IRRI 2002). The data were recorded on days to 50% flowering, days to maturity, plant height (cm), panicle length (cm), number of effective tillers $plant^{-1}$, number of filled grains $panicle^{-1}$, number of unfilled grains $panicle^{-1}$, fertility (%), 1000 seed weight (g) and yield $panicle^{-1}$ (g). Genetic diversity was worked out following principal component analysis (Rao 1964; Mahalanobis' 1936) generalized distance (D^2) analysis extended by (Rao 1952). Clustering of genotypes was done according to Tochers method (Rao 1952). Multivariate analysis viz. principal component analysis, cluster analysis were performed using GENSTAT 5.13 program.

RESULTS AND DISCUSSION

Analysis of Genetic Divergence

The analysis of variance (Table 1) revealed that the genotypes differed significantly from each other for all the characters studied indicating the presence of notable genetic variability among them. This implied that it would be judicious to classify the population on the basis of degree of divergence. 10 genotypes were grouped into three clusters (Table 2). The distribution pattern revealed maximum number of genotypes (4 genotypes) in cluster I and III. While cluster II included minimum number of genotypes (2 genotype). The minimum number of genotypes in cluster II was probably due to high correlation among most of the traits and duplication effect of the traits included in this study. It also revealed that no duplicate existed among the genotypes for the studied characters. (Fukuoka et al. 2006; Hossain 2008; Sarhadi et al. 2009 and Nascimento et al. 2011) found no duplicates from cluster analysis using Mahalanobis' D^2 statistics in rice. The clustering pattern also revealed that the genotypes constellated in the cluster were not originated from the same geographic region. Genotypes within the same cluster were originated from different geographic regions. This indicates that although genetic diversity is generally associated with geographical diversity, the former is not necessarily directly related to geographic distribution rather they did not follow the same trend and factors other than geographical isolation are also responsible for diversity which might be due to genetic drift, selection and continuous exchange of genetic materials among the countries of the world. Chakravorty et al. (2013) by evaluating 51 rice land races, Hosan et al. (2010) from a study on 20 landraces, Rajesh et al. (2010) assessing from 29 land races and Medhabati et al. (2013) by studying 37 wild and cultivated rice genotypes also found no parallel relationship between genetic and geographical diversity. Shanmugam and Rangasamy (1982) reported that grouping of materials of same origin into different clusters was an indication of broad genetic base in the genotypes belonging to that origin. Therefore, varieties originating from same place may have different genetic architecture or vice-versa. Statistical distances represent the index of genetic diversity among the clusters. The inter-cluster distances in all of the cases were higher than that of intra- cluster distances suggesting wider genetic diversity among the genotypes of different groups (Table 3). Similar trend was found by Iftekharuddaula et al. (2002). The intra-cluster D^2 values in all the three clusters were low indicating the genotypes within the same clusters were closely related. Maximum intra-cluster distance was observed in cluster I and minimum in cluster II denoting the genotypes under cluster I were most diversed and those of cluster II were comparatively similar.

The inter-cluster D^2 values ranged from 26.92 to 40.36 which indicates a wide range of diversity. Regarding the inter-cluster distance, maximum genetic distance was observed between cluster I and cluster III followed by cluster II indicating that genotypes of cluster I were far diversed from those of cluster III and the genotypes of cluster II from those of cluster III. Choosing of genotypes belonging to distant clusters were expected to execute maximum heterosis in crossing and to be used in hybridization program for obtaining a wide spectrum of variation among the segregants. Similar conclusions were also reported by Hossain et al. 2003. The minimum inter-cluster distance was observed between cluster I and cluster II followed by cluster II and cluster III denoting that the genotypes of these cluster were somewhat close. Similar trend were found by (Selvakumar et al.1989; Iftekharuddaula et al. 2002 and Sabesan et al. 2010) in rice.

Table 4 represents the mean values for all the ten morphological characters. The data revealed that different clusters exhibited the highest and lowest mean values of individual characters and none of the clusters showed the highest or lowest mean values of all the characters. However, the genotype of cluster I with the cumulative ranking 1, for days to maturity (146.05), days to 50% flowering (111.01), plant height (138.18 cm), panicle length (24.02), number of filled grains $panicle^{-1}$ (113.22), fertility (84.31%) and yield $panicle^{-1}$ (2.34). Similarly, the genotype of cluster III with the cumulative ranking 2, produced highest number of effective tillers $plant^{-1}$ (5.60) and number of unfilled grains $panicle^{-1}$ (27.16), while the genotype of cluster II with the cumulative ranking 3, produced highest 1000-Seed weight (25.01 g). Therefore, it may be possible to obtain the highest mean values for the maximum studied characters, if the genotypes of cluster I are crossed with the genotypes of cluster III, cluster II respectively. (Hosan et al. 2010; Mahalingam et al. 2012; Sohrabi et al. 2012 and Medhabati et al. 2013) reported similar trend of conclusions on rice using Mahalanobis' D^2 statistics.

Analysis of Principal Component

To find out independent impact of all the characters under study principal component analysis was directed. The first three components in the PCA analysis with Eigen values > 1 contributed 83.00 percent variability existing in the rice genotypes for yield contributing traits in the study (Table 5) indicates that the identified traits within the axes exhibited great influence on the phenotype of rice genotypes. PCA of quantitative traits found that, the first principal component accounted 50.03% of the total variability, where by days to 50% flowering (0.35), days to maturity (0.37), plant height (0.41), number of filled grains $panicle^{-1}$ (0.38) and yield $panicle^{-1}$ (0.41) were contributed positively. The second principal component accounted 19.79% of the total variability. The variable contributing most positively were number of effective tillers $plant^{-1}$ (0.60) and fertility percent (0.43). The third component accounted 13.18% of total variability in which the

Table 1. Analysis of variance for different morphological plant characters in ten rice genotypes

Characters	df	Days to 50% flowering	Days to maturity	Plant height (cm)	Panicle length (cm)	No. of effective tillers plant^{-1}	No. of filled grains panicle^{-1}	No. of unfilled grains panicle^{-1}	Fertility (%)	1000 seed weight (g)	Yield panicle^{-1} (g)
Replication	4	28.93	15.72	60.18	0.27	0.338	26.60	2.134	18.28	4.07	0.032
Genotypes (A)	9	2070.09**	2896.07**	15050.54**	96.72**	7.789**	11531.17**	1261.581**	1435.60**	251.71**	3.334**
Treatment (B)	3	105.17**	734.05**	3139.77**	250.04**	90.413**	30740.87**	7858.686**	14941.98**	725.27**	42.503**
A x B	27	28.27*	53.58**	220.75**	85.23**	2.202**	703.28**	599.999**	750.24**	84.79**	0.706**
Error	156	16.55	23.07	25.97	2.28	0.435	11.28	0.924	5.26	5.59	0.015

variable panicle length (0.52) and 1000 seed weight (0.77) contributed positively. In this study, we chose to follow the criterion used by Clifford and Stephenson (1975) and corroborated by (Guei et al. 2005), which suggested that the first three principal components are often the most important in reflecting the pattern of variability among accessions, and the characters associated with these are more useful in differentiating accessions. According to this criterion, the first three components account for more than 58.24 % of total variation giving a clear idea of the structure underlying the variables analysed. However, the criterion of (Raji 2002) was chosen to determine the cut off limit for the coefficients of the proper vectors; this criterion treated coefficients greater than 0.3 as having a large enough effect to be considered important, while traits having a coefficient less than 0.3 were considered not to have important effects on the overall variation observed in the present study. The phenotypic value of the each trait measures the importance and contribution of each component to total variance. Characters with high variability are expected to provide high level of gene transfer during breeding programs (Gana 2013; Varthini 2014).

Table 2. Distribution pattern of 10 rice genotypes in different clusters

Cluster number	No. of genotypes	Percent (%)	Name of genotypes
I	4	40	Hogla, Kute Patni, Ghunshi, Tal Mugur
II	2	20	Dakh Shail, Mondeshor
III	4	40	Nona Bokhra, Binadhan-8, Binadhan-10, BRRI dhan47

Table 3. Average intra (Bold) and inter cluster distance in 10 rice genotypes

Cluster	I	II	III
I	**15.04**	26.92	40.36
II		**11.94**	30.26
III			**14.13**

Table 4. Cluster mean for yield and yield contributing characters of 10 rice genotypes

Characters	Cluster I	Cluster II	Cluster III
Days to 50% flowering	111.01	114.88	95.56
Days to maturity	146.05	144.00	125.79
Plant height (cm)	139.18	138.30	87.69
Panicle length (cm)	24.02	22.78	21.74
No. of effective tillers plant^{-1}	5.23	4.35	5.60
No. of filled grains panicle^{-1}	113.22	68.44	69.29
No. of unfilled grains panicle^{-1}	19.66	20.13	27.16
Fertility (%)	84.31	67.26	72.12
1000 seed weight (g)	19.90	25.01	20.56
Yield panicle^{-1} (g)	2.34	1.93	1.59

Table 5. Principal components (PCs) for morphological traits of 10 rice genotypes

Characters	PC1	PC2	PC3
Days to 50% flowering	0.35	-0.30	0.06
Days to maturity	0.37	-0.20	-0.04
Plant height (cm)	0.41	-0.19	0.09
Panicle length (cm)	0.28	0.24	0.52
No. of effective tillers plant^{-1}	-0.13	0.60	0.11
No. of filled grains panicle^{-1}	0.38	0.30	-0.19
No. of unfilled grains panicle^{-1}	-0.19	0.19	0.23
Fertility (%)	0.30	0.43	-0.00
1000 seed weight (g)	-0.01	-0.25	0.77
Yield panicle^{-1} (g)	0.41	0.13	0.01
Eigen value	5.00	1.98	1.32
Variability (%)	50.03	19.79	13.18
Cumulative (%)	50.03	69.82	83.00

CONCLUSION

Genetic diversity among the genotypes Hogla, Kute Patni, Ghunshi, Tal Mugur and Nona Bokhra should be highlighted for the development of salt tolerant rice varieties and the phenotypic value of the each trait measures the importance and contribution of each component to total variance. Thus, the prominent characters coming together in different principal components and contributing towards explaining the variability and have the affinity to remain together into consideration during utilization of these characters in breeding program.

ACKNOWLEDGEMENTS

The first author is grateful to the Ministry of Science and Technology (MOST) for financial support to conduct this work.

CONFLICT OF INTEREST

The authors declare that there is no conflict of interests regarding the publication of this paper.

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