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Full Length Research Paper

Genetic diversity analyzed by quantitative traits among rice (*Oryza sativa* L.) genotypes resistant to blast disease

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Genetic diversity was studied for blast resistant and susceptible genotypes using 13 morphological characters. Plant height, days to flowering and maturity, panicle length, number of spikelet per panicle, number of filled grain per panicle, number of unfilled grain per panicle, 1000-grain weight and yield per hill were indicated as important contributors to genetic divergence in 14 rice genotypes. The first 3 principal components accounted for 78.72% of the total variation among resistant and susceptible rice genotypes. The genotypes were grouped into 7 clusters according to Mohalanobis's D^2 statistics and canonical vector analysis. On the basis of cluster distances, high yielding along with highly susceptible genotype, Bangladesh Rice Research Institute (BRRI) dhan29 could be crossed with resistant genotypes, BR 6017-3-3-4-1 and Zong-yu 7. Similarly, BRRI dhan28 could be crossed with Qing Liali No.1 for the development of blast resistant rice varieties with higher yield.

Key words: Blast disease, genetic diversity, quantitative traits, rice, resistant genotypes.

INTRODUCTION

Rice (*Oryza sativa* L.) is the staple food of more than 50% of the world's population (Zheng et al., 1995). About 40% of the world's population consumes rice as a major source of calorie (Banik, 1999). In Bangladesh, the rice is extensively cultivated over a large area and it covers 74% of the total calorie intake of the people. About 10.77 million hectares of land is used for rice cultivation, which produces 25.18 million metric tons of rice (BBS, 2003). Rice crops suffer from a number of diseases.

In Bangladesh, a total of 32 diseases have been identified of which 10 are considered as major (Latif et al., 2007). Among these diseases, rice blast caused by *Magnaporthe oryzae* is one of the most important widely important widely distributed plant diseases. Blast was first reported in Asia more than three centuries ago and is now present in over 85 countries. It is highly adaptable to environmental conditions and can be found in irrigated lowland, rain-fed upland or deepwater rice fields (Ou, 1985; Latif et al., 2011a).

Rice blast causes significant yield losses throughout South East Asia and South America. Major epidemics covering vast areas occur on a regular basis causing severe food storage to entire nations. Disease occurrence and severity vary by year, location and even within a field depending on environmental conditions and crop management practices. Yield losses estimate due to this devastating disease in the world have ranged from 1 to 50% (Scardaci et al., 2003).

Nowadays, use of chemicals is discouraged to save the environment. Therefore, emphasis has given on the host plant resistance which is economically viable and

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environment friendly technique for disease management. In Bangladesh, many resistant sources against blast pathogen have been identified from many improved varieties and local germplasm at Bangladesh Rice Research Institute. Some varieties such as BR3, BR5, BINA5 and BINA6 showed moderate resistance to leaf blast (Islam et al., 2001).

Blast resistant rice varieties are available, but this resistant is often either partial or controlled by a dominant single gene which is therefore inherently unstable to an onslaught by a genetically variable pathogen (McCouch et al*.*, 1994). Geographical variability of the blast pathogen has been extensively studied (Chen et al., 1995; Kumar et al., 1999; Mekwatanakern et al., 2000) in various countries. Genetic diversity is the essential to meet the diverse goals of plant breeding such as producing cultivars with increasing yield, genetic adoption, desirable quantity, pest and disease resistant (Nevo et al*.,* 1982). Quantitative classification offers a quantified degree of divergence among genotypes or populations, this serve as a sound basis of grouping any two or more genotypes based on minimum divergence between them (Sharma, 1997).

Although, resistance to blast is often short-lived, some cultivars are considered to possess durable resistance (Johnson, 1981). Durable resistance is thought to be associated with partial resistance, that is, in many cases under polygenic control (Wang et al*.,* 1994). For example, the rice cultivar, Monoberekan displays durable resistance to blast in upland conditions (Fomba and Taylor, 1994). The present study was undertaken to know the genetic diversity of blast resistant genotypes and selection of suitable parents for rice breeding programs to develop varieties with durable resistance.

MATERIALS AND METHODS

Experimental site

The study was conducted in two consecutive years at the experimental field of Plant Pathology Division, Bangladesh Rice Research Institute (BRRI), Gazipur, during the period of 2007 to 2008.

Genotypes and experimental design

A total of 14 genotypes including blast resistant and susceptible genotypes were used in the study (Rahman, 2008). Descriptions including names, sources and reaction types of the genotypes are given in Table 1. The experiment was laid out in a randomized complete block design with 4 replications.

Germination of seed

Seeds of all collected rice genotypes soaked in water separately for 48 h in clothes bag. Soaked seeds were picked out from water and wrapped with straw and gunny bag to increase the temperature for enhancing germination.

Seedling raising and transplanting

The seedlings of 14 genotypes were raised in earthen pots (30 × 30 cm). Then 30-day-old seedlings were transplanted in the experimental field. Recommended doses of fertilizers and other cultural practices were applied as and when necessary as recommended (BRRI, 2003).

Phenotypic data

Data were recorded on 13 quantitative characters, such as number of tiller per hill, tillering ability, plant height (cm), phenotypic acceptability, days to flowering, days to maturity, panicle length (cm), number of spikelet per panicle, number of filled grain per panicle, number of unfilled grain per panicle, 1000-grain weight (g), yield per hill (g) and disease index.

Analysis of data

Mean data (data of two consecutive years) of the 13 quantitative characters was analyzed by multivariate analysis using GENSTAT 5 (Beta) software program. Genetic diversity analysis involves several steps, that is, estimation of genetic distance between the varieties clustering and analysis of inter-cluster distance. Therefore, more than one multivariate technique is required to represent the results more clearly and it is obvious from the presentation of results of several researchers (Bashar, 2002; Uddin, 2001).

Principal component analysis (PCA)

Principal components were computed from the covariance or correlation matrix and genotype scores obtained from the first stage which has the property accounting for maximum variance and succeeding components with latent roots greater than unity (Jeger et al., 1983). The contributions of the different quantitative characters towards divergence are discussed from the latent vectors of the first two principal components. To divide the varieties of a data set into some number of mutually exclusive groups, clustering was done using non-hierarchical classification.

The algorithm is used to search for optimum values of chosen criterion. Starting from some initial classification of the varieties into required number of groups, the algorithm repeatedly transferred varieties from one group to another so long as such transfer improve the value of the criterion and the algorithm switches to a second stage which examines the effect of swapping two varieties of different classes.

Principal coordinate analysis (PCoA)

PCoA is equivalent to PCA, but it is used to calculate inter unit distances. Though, the use of dimension of PCA gives the minimum distance between each pair of the N point using similarity matrix (Digby et al., 1989).

Canonical vector analysis (CVA)

Canonical vector analysis (CVA) complementary to Mohalanobis's distance (D^2) statistics is a sort of multivariate analysis where canonical vector and roots representing different axes of differentiation and the amount of variation accounted for by each of such axes, are respectively derived. Canonical vector analysis finds linear combination of original variability than maximize the ratio of between groups to within groups' variation, thereby giving functions

Table 1. Name, source and reaction types of the resistant and susceptible genotypes.

Serial number	Variety	Sources	Reaction type
1	BR 6017-3-3-4-1	IRBN, INGER	Resistant
2	IR 45912-9-1-2-2	IRBN, INGER	Resistant
3	Zhong-yu 7	IRBN, INGER	Resistant
4	OM 1207	IRBN, INGER	Resistant
5	NR-11	IRBN, INGER	Resistant
6	IR 60913-42-3-3-2-2	IRBN, INGER	Resistant
7	SIPI 692033	IRBN, INGER	Resistant
8	Qing Liali No.1	IRBN, INGER	Resistant
9	NJ 70507	IRBN, INGER	Resistant
1	BR 14	BRRI	Resistant
11	BR 16	BRRI	Resistant
12	BRRI dhan28 (BR28)	BRRI	Moderately resistant
13	BRRI dhan29 (BR29)	BRRI	Highly susceptible
14	BRRI dhan36 (BR36)	BRRI	Moderately susceptible

BRRI= Bangladesh Rice Research Institute, IRBN= International Rice Blast Nursery, INGER=International Network for Genetic Evaluation of Rice.

of the original variables that can be used to discriminate between the groups. Thus, in this analysis a series of orthogonal transformation sequentially maximize the ratio of among groups to within group variation.

Computation of average intra-cluster distances

The average intra cluster distance for each cluster was calculated by taking all possible D^2 values within the members of a cluster obtained from PCoA. The formula used to measure the average intra-cluster distance was:

Intra-cluster distance = $\sum D^2 /n$

where, D^2 is the sum of distances between all possible combinations (n) of the genotypes included in a cluster. The square root of the D^2 values represents the distance (D) within cluster.

RESULTS AND DISCUSSION

Principle component analysis (PCA)

The PCA yielded eigenvalues of each principle component axes of coordination of genotypes with the first five axes totally accounted for 90.57% cumulative variation among the genotypes. The first three principal axes accounted for 78.72% of the total variation for 13 characters among 14 blast resistant and susceptible rice genotypes (Table 2).

Construction of scatter diagram

Based on the values of principal component score I and II obtained from the principal component analysis**,** a two dimensional scatter diagram using component score I as X axis and component score II as Y axis was constructed (Figure 1). The positions of the genotypes in the scatter diagram were apparently distributed into seven groups, which indicated that considerable diversity existed among the genotypes. The scattered diagram and genetic distances for blast resistant and susceptible rice genotypes of different clusters revealed that the genotype number 1, 2, 3, 4, 8, 12 and 14 were distantly located which suggesting more diverged from the rest of the genotypes (Figure 1 and Table 3).

Principal coordinate analysis (PCoA)

PCoA was performed on auxiliary of principal coordinate analysis. This analysis helped in estimating distances (D^2) for all possible 91 combinations between pairs of genotypes. The highest inter genotype distance was observed between the genotypes BR 6017-3-3-4-1 and Qing Liali No.1 (106.80) followed by Zhong-yu 7 and Qing Liali No.1 (95.70), Qing Liali No.1 and BRRI dhan36 (85.50), OM 1207 and Qing Liali No.1 (84.89). The tenth highest pair distance was 67.94 that was observed between genotypes Qing Liali No.1 and BR14. The lowest inter genotype distance (12.57) was observed between the genotypes Zhong-yu 7 and OM 1207. The tenth lowest pair distance 17.78 was observed between the genotypes IR 60913-42-3-3-2-2 and BRRI dhan28. The difference between the highest and lowest inter genotypes distance indicated the prevalence of variability among the 14 blast resistant and susceptible genotypes of rice (Table 3).

According to Sing and Chaudhaury (1985), the intra

Table 2. Eigen values and percentage of variation for corresponding 13 component characters in 14 blast resistant and susceptible rice genotypes.

Principle component characters	Eigen values	Percentage of total variation	Cumulative percentage
Number of tiller per hill	5.4042	45.03	45.03
Tillering ability	2.5163	20.97	66.00
Plant height	1.5259	12.72	78.72
Phenotypic acceptability	0.7964	6.64	85.36
Days to flowering	0.6247	5.21	90.57
Days to maturity	0.5000	4.17	94.74
Panicle length	0.2907	2.42	97.16
Number of spikelet per panicle	0.2331	1.94	99.10
Number of filled grain per panicle	0.0680	0.57	99.67
Number of unfilled grain per panicle	0.0249	0.21	99.88
1000-grain weight	0.0139	0.12	100.00
Yield per hill	0.0018	0.02	100.02
Disease index	0.0000	0.00	100.02

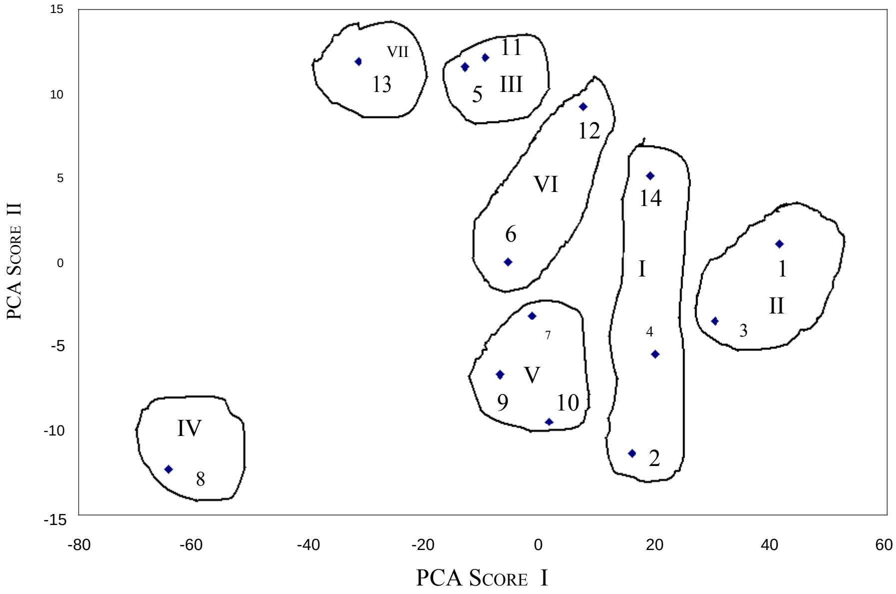

Figure 1. Scattered distribution of 14 blast resistant and susceptible genotypes based on their principal component scores superimposed with clustering.

cluster distances were computed by the values of inter genotypic distance matrix of PCoA. The inter cluster distances were larger than the intra cluster distances suggesting wider genetic diversity existed among the genotypes of different groups. The intra cluster distances in all the seven clusters indicated that the genotypes within the same cluster were closely related. The highest intra cluster distance was computed for cluster II (19.870) composed of two genotypes followed by cluster I (18.450) which composed of three genotypes. The lowest intra cluster distances were in clusters IV and VII (0.00, 0.00) followed by the cluster V (17.040) consisting of 1, 1 and 3 genotypes, respectively. However, the higher value (19.870) of intra cluster distance in cluster II indicated that the genotypes (2) that constituted this cluster might have diverged characters, which contributed to the formation of this cluster (Table 4).

Canonical variate analysis (CVA)

CVA was performed to obtain the inter cluster distances

Table 3. Ten of each lower and higher inter genotypic distance (D^2) between pairs of blast resistant genotypes.

10 Lower D^2 values	Genotypic combinations	10 Higher D^2 values	Genotypic combinations
12.57	Zhong-yu 7 and OM 1207	106.80	BR 6017-3-3-4-1 and Qing Liali No.1
14.65	SIPI 692033 and NJ 70507	95.70	Zhong-yu 7 and Qing Liali No.1
15.50	SIPI 692033 and BR14	85.50	Qing Liali No.1 and BRRI dhan36
15.60	OM 1207 and BRRI dhan36	84.89	OM 1207 and Qing Liali No.1
16.18	IR 60913-42-3-3-2-2 and SIPI 692033	80.99	IR45912-9-1-2-2 and Qing Liali No.1
16.77	NR-11 and IR 60913-42-3-3-2-2	75.68	Qing Liali No.1 and BRRI dhan28
17.69	NR-11 and BR16	73.69	BR 6017-3-3-4-1 and BRRI dhan29
17.78	IR 60913-42-3-3-2-2 and BRRI dhan28	67.94	Qing Lialy No.1 and BR14

Table 4. Average intra (Diagonal) and inter-cluster distances (D^2) for 14 blast resistant and susceptible rice genotypes.

Clusters	I	II	III	IV	V	VI	VII
I	18.450						
II	23.095	19.870					
III	37.155	50.755	17.690				
IV	83.793	108.250	59.585	0.000			
V	26.002	41.003	24.555	63.686	17.040		
VI	25.492	39.583	22.727	68.380	21.290	17.780	
VII	53.843	69.870	27.005	42.300	37.800	37.685	0.00

(Mahalanobis's D^2 values). These values of inter cluster distances (D^2) are presented in Table 4. Statistical distances represented the index of genetic diversity among the clusters. The inter cluster distances were bigger than the intra cluster distances suggesting wider genetic diversity among the genotypes of different clusters. Anandan et al. (2011) obtained larger inter cluster distances than the intra cluster distances in a multivariate analysis in rice.

The inter cluster distance was maximum between clusters II and IV (108.250) followed by the distance between clusters I and IV (83.793), clusters II and VII (69.870), clusters IV and VI (68.380), while the inter cluster distance was minimum between clusters V and VI (21.290) followed by the distance between cluster III and VI (22.727) (Table 4). The maximum values of inter cluster distance indicated that the genotypes belonging to cluster IV was far diverged from those of clusters II and I. Similarly, the higher inter cluster values between clusters IV and VI, clusters II and VII and clusters IV and cluster V indicated the genotypes belonging to each pair of cluster were far diverged. These relationships were also reflected in the scatter diagram (Figure 1). The genotypes belonging to the distant cluster could be used in hybridization programme for obtaining a wide spectrum of variation among the segregates. Similar report was also made (Bansal et al., 1999; Latif et al., 2011b; Norziha et al., 2011; Marker and Krupakar, 2009).

The genotypes belonging to the clusters II and IV, clusters I and IV having greater cluster distance and are recommended for inclusion in hybridization program for the development of blast resistant varieties as they are expected to produce good segregates. Thus, it could be suggested that crosses should be made between genotypes belonging to the distant cluster for higher heterotic response. Sinha et al. (1991) reported that the selection of parents from distantly placed clusters exhibited significantly high heterosis. Thus, heterosis could also be exploited by crossing between genotypes belonging to distant clusters like between genotypes of clusters II and IV, clusters I and IV, clusters II and VII, clusters IV and VI and clusters IV and V.

Non hierarchical clustering

Non hierarchical clustering using co-variance matrix grouped 14 blast resistant and susceptible rice genotypes into seven different clusters. These results confirmed the clustering pattern of the genotypes obtain through principal component analysis. Our results are in agreement with diversity analysis of 75 rice genotypes as described by Sawant et al. (1995) in their work. The pattern of distribution of genotypes into various clusters is given in Table 5. The distribution pattern indicated that the maximum number of genotypes (3) was found in clusters I and V. Cluster II, III and VI each consisted of two genotypes while clusters IV and VII each consisted

Table 5. Distribution of 14 blast resistant and susceptible rice genotypes in seven clusters.

Clusters	Numbers of genotypes	Name of genotypes
I	3	IR45912-9-1-2-2, OM 1207 and BRRI dhan36
II	2	BR 6017-3-3-4-1 and Zhong-yu 7
III	2	NR-11 and BR16
IV	1	Qing Liali No.1
V	3	SIPI 692033, NJ 70507 and BR14
VI	2	IR 60913-42-3-3-2-2 and BRRI dhan28
VII	1	BRRI dhan29

Table 6. Cluster means for 13 characters of 14 blast resistant and susceptible rice genotypes.

Characters	Clusters						
	I	II	III	IV	V	VI	VII
Number of tiller per hill	12.33	12.50	15.00	12.00	10.33	14.50	13.00
Tillering ability	5.00	5.00	5.00	5.00	5.00	5.00	5.00
Plant height (cm)	93.93	86.33	87.40	124.30	100.63	93.30	92.00
Phenotypic acceptability	3.00	4.00	3.00	3.00	3.00	3.00	3.00
Days to flowering	109.33	108.00	111.00	124.00	109.67	106.00	121.00
Days to maturity	142.67	141.50	150.50	160.00	151.00	139.00	154.00
Panicle length(cm)	22.67	20.50	22.00	30.00	21.33	23.00	28.00
Number of spikelet per panicle	129.67	116.50	155.00	187.00	143.67	144.50	166.00
Number of filled grain per panicle	103.00	93.00	118.00	145.00	113.00	115.00	135.00
Number of unfilled grain per panicle	23.33	23.50	37.00	42.00	30.33	29.50	31.00
1000-grain weight (g)	25.65	23.26	23.36	25.20	27.00	23.20	23.06
Yield per hill (g)	32.50	31.10	37.11	36.84	31.69	38.11	40.47
Disease index	3.00	2.00	2.50	3.00	3.00	3.75	7.00

of one genotype.

Intra cluster mean

Intra cluster mean for 13 characters are represented in Table 6. In case of number of tiller per hill, the highest intra cluster mean (15.00) was recorded in cluster III followed by cluster VI (14.50) and VII (13.00). Intra cluster mean for plant height was highest in cluster IV (124.30) followed by cluster V (100.63). Phenotypic acceptability had the highest for group mean in cluster II (4.00) followed by cluster mean (3.00) in clusters I, III, IV, V, VI and VII. Intra cluster mean for days to flowering was highest in cluster IV (124.00) followed by cluster VII (121.00). Intra cluster mean for days to maturity was highest in cluster IV (160.00) followed by cluster VII (154.00), cluster V (151.00) and cluster III (150.50). Intra cluster mean for panicle length was highest in cluster IV (30.00) followed by cluster VII (28.00).

The lowest intra cluster mean for this trait was observed in cluster II (20.50) followed by cluster V (21.33) and cluster III (22.00). Intra cluster mean for number of spikelet per panicle was highest in cluster IV (187.00) followed by cluster VII (166.00). Intra cluster mean for 1000-grain weight was highest in cluster V (27.00) followed by cluster I (25.65) and cluster IV (25.20). The lowest intra cluster mean for this trait was observed in cluster VII (23.06) followed by cluster VI (23.20), cluster II (23.26) and cluster III (23.36). Intra cluster mean for yield was highest in cluster VII (40.47) followed by cluster VI (38.11). The lowest intra cluster mean for this trait was observed in cluster II (31.10) followed by cluster V (31.69). Intra cluster mean for disease index was highest in cluster VII (7.00) followed by cluster VI (3.75). The lowest intra cluster mean for this trait was observed in cluster II (2.00) followed by cluster III (2.50).

The inter cluster distances of cluster IV and cluster II with other clusters were more or less higher than the inter cluster distances between the remaining cluster combinations (Table 4). The cluster mean of these two clusters for higher tillering ability, higher phenotypic acceptability and lower disease index were divergent. The highest plant height, days to flowering and maturity, panicle length, number of spikelet per panicle, number of filled grain per panicle and third highest for 1000-grain

Table 7. Latent vectors for 13 characters of 14 blast resistant and susceptible rice genotypes.

Characters	Vector 1	Vector 2
Number of tiller per hill	-0.1755	-0.2592
Tillering ability	0.0000	0.0000
Plant height	-0.0447	0.0551
Phenotypic acceptability	0.7852	-0.5403
Days to flowering	-0.0305	0.0839
Days to maturity	0.1001	0.0602
Panicle length	0.0050	0.2799
Number of spikelet per panicle	-0.2816	-0.1013
Number of filled grain per panicle	-0.1201	0.0652
Number of unfilled grain per panicle	0.0125	0.0073
1000-grain weight	-0.1113	0.0241
Yield per hill	-0.3363	-0.1846
Disease index	0.0254	-0.0517

weight was found in cluster IV while cluster VII had the highest yield per hill and disease index (Table 6). These indicated that the genotypes included in cluster II, cluster IV and VII were very important to contribute into the total divergence among the 14 blast resistant and susceptible genotypes for these characters.

Genotypes of cluster II had the highest tillering ability, the highest phenotypic acceptability and lower disease index revealed that the genotypes in cluster could be used to improve blast resistant variety.

The genotypes of cluster IV gave the higher mean for plant height, days to flowering and maturity, panicle length, number of spikelet per panicle, number of filled grain per panicle and number of unfilled grain per panicle and lower disease index. The highest cluster means for different characters in cluster IV indicated that the genotypes included in this cluster would offer good scope for improvement of rice resistant to blast through rational selection for these characters.

The genotypes of cluster VII produced the higher (third highest) mean for number of tiller per hill, second highest for panicle length, number of spikelets per panicle, number of filled grain per panicle, highest yield per hill and highest disease index. The result indicated that the genotypes in this cluster could be used to improve the variety with higher number of tiller per plant, good phenotypic acceptability and high yielding characters.

Contribution of characters towards divergence

The characters contributing maximum to the divergence are given greater emphasis for deciding the type of cluster for the purpose of further selection and the choice of parents for hybridization (Jagadev et al., 1995).

Contribution of characters towards divergence obtained by CVA is presented in Table 7. The values of vectors had positive values for days to maturity, panicle length and number of unfilled grain per panicle. These results indicated that three characters had the highest contribution towards the divergence among the 14 blast resistant and susceptible genotypes.

In vector 1, the important characters responsible for the genetic divergence in the major axis of differentiation were phenotypic acceptability, days to maturity, panicle length, number of unfilled grain per panicle and disease index having positive vector values while in vector 2 (the second axis of differentiation), plant height, days to flowering and maturity, panicle length, number of filled grain per panicle, number of unfilled grain per panicle and 1000-grain weight were important. These characters contributed to the total divergence in 14 genotypes of rice.

Alam et al. (2006) reported that days to heading, 1000-grain weight and yield per plant were the major contributors towards divergence in hull-less barley. Julfiquar (1985) also reported similar response for yield, 1000-grain weight, days to maturity and plant height in rice.

Plant height and grain yield considerably contributed to the total divergence reported (Vivekanondan and Subramaniam, 1993).

On the contrary, Chauhan and Chauhan (1994) reported that the contribution of 1000-grain weight was the highest followed by 50% flowering, panicle length and spikelet per panicle.

Singh et al. (1999) also reported that harvest index and number of filled grains per panicle contributed maximum to the divergence in rice.

Negative values in both vectors for number of tiller per hill, number of spikelet per panicle and yield per hill indicated that this character had the lowest contribution to the divergence.

Comparison of result based on different multivariate techniques

Results obtained from different multivariate techniques concluded that all techniques gave more or less similar results and one technique supplemented and confirmed the results of the other. The cluster pattern of D^2 analysis through non-hierarchical clustering had been taken care of by simultaneous variation in all the characters under this study. However, the distribution of genotypes in different clusters of the D^2 analysis had followed more or less similar trend of the principal component analysis.

The D^2 and principal component analyses were found to be the alternative methods in giving the information regarding the clustering pattern of genotypes. Nevertheless the CVA provided the information regarding the contribution of characters towards divergence of 14 blast resistant and susceptible rice genotypes.

Selection of genotypes for future hybridization purpose

Genotypes were to be selected on the basis of specific objectives. No common criterion was considered for the selection of genotypes. Genetically, distant parents are usually able to produce higher heterosis (Debnath et al., 2008; Mahmuda et al., 2008).

Considering magnitudes of genetic distance, contribution of different characters towards the total divergence, magnitude of genetic cluster means for different characters and performance of the genotypes were considered for hybridization program. The genotypes of cluster II could be selected for higher tillering ability, higher phenotypic acceptability and lower disease index.

The genotypes of cluster IV could be selected for higher plant height, higher panicle length, latest flowering and maturity, higher number of spikelet per panicle, higher number of filled grain per panicle, higher number of unfilled grain per panicle and higher (third highest) 1000-grain weight.

The genotypes of cluster VII could be selected for the highest yield per hill and higher disease index. The genotypes of clusters I, II and III could be selected for lower number of tillering per hill, earlier flowering and maturity, lower plant height, lower panicle length, lower number of spikelet per panicle, lower number of filled grain per panicle, lower number of unfilled grain per panicle, lower yield per hill and lower disease index.

The genotypes of cluster VI could be selected for early flowering and maturity, higher yield and lower disease index. Genetic distance between two clusters, II and IV was higher. So, considering the facts and to obtain the highest heterosis, crosses could be made among the genotypes of two clusters (II and IV), but this is not expected because those genotypes were resistant but to lower yielders. Therefore, high yielding along with highly susceptible BRRI dhan29 genotype could be crossed with resistant genotypes, BR 6017-3-3-4-1 and Zhong-yu7. On the other hand, genotype, BRRI dhan28 could be crossed with Qing Liali No.1 for the development of blast resistant along with high yielding rice varieties.

Conclusion

Multivariate analyses were performed for knowing the genetic diversity of 14 rice genotypes through PCA, PCoA and CVA using 13 quantitative characters. The genotypes were grouped into seven different clusters. The first three principal axes accounted for 78.72% of the total variation.

Genetic distance between clusters II and IV was higher. So, crosses could be made among the genotypes of the aforementioned clusters, but this is not expected because those genotypes were resistant but lower yielder. Therefore, to develop high yielding but blast resistant rice varieties, hybridizations should be made among the parents, BRRI dhan29, BRRI dhan28, BR 6017-3-3-4-1, Zhong-yu7 and Qing Liali No.1.

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