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RESEARCH ARTICLE

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Evaluation of indigenous rice germplasm for identification of durable bacterial blight (*Xanthomonas oryzae* pv. *oryzae*) resistance sources in Bangladesh

Abstract:
Bacterial blight disease caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) is one of the most devastating biotic stresses of rice in all rice growing countries of the world. Find out the resistant source is the first step for the development of resistant rice variety through breeding techniques. In this experiment, one hundred land races including susceptible check Purbachi and resistance check IRBB65 were screened both in seedling and maximum tillering stages. BXO9, a representative isolate of the major races of BB pathogen of Bangladesh was used for inoculation. The results were analyzed through multivariate analysis viz. Principal component analysis (PCA), Principal coordinate analysis (PCO), Canonical vector analysis (CVA) and Cluster analysis (CLSA) using GENSTAT 5. The genotypes were grouped into ten clusters based on lesion length on leaves, relative lesion length and leaf area damaged. In nursery experiment, cluster VI contained 4 genotypes including Purbachi and cluster I comprised 2 entries including IRBB65. In field experiment, cluster V contained 9 land races including Purbachi and cluster I contained 7 land races including IRBB65. In nursery experiment SUNGWALA, PAJRE and in field experiment MATHIA and HARMA SHAIL (1) showed resistance against *Xoo*. However, further research is necessary for the confirmation of these materials as resistant source both at seedling and maximum tillering stages using molecular markers.

Keywords: Bacterial blight, resistance source, land races

Introduction:

Bacterial blight (BB), caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) is one of the most destructive diseases in the major rice growing countries of Asia, including Bangladesh [1,2]. The disease is a serious problem, as rice is grown under irrigated and high fertilizer input conditions that are conducive to disease development [3]. In severe epidemics, yield reduction ranging from 20% to 40% directly attributed to BB infection, is common [4]. Breeding for disease resistance is the most effective, economic and also eco-friendly method for controlling of BB elsewhere. Several germplasm donors carrying diverse genes for BB resistance have been used to develop BB resistant varieties. Some climatic factors such as rainfall, humidity, temperature, flood and stormy weather during the rice growing season along with high nitrogenous fertilizer application for increasing the yield of HYV causes the occurrence and the severity of BB in Bangladesh [2,4-6].

Japan as well as International rice research institute of Philippines has been studied about the pathogenicity of *Xoo* and resistance genes in rice cultivar [7]. Six BB pathogen races with some aggressive virulent strain were identified in 2009 in Bangladesh [14]. In Bangladesh, severe outbreak of BB was occurred in both hybrid and inbred varieties in Boro 2007-08 [8]. Control of the disease with copper compounds, antibiotics, and other chemicals has not proven effective. Enhancing host resistance is considered as the most effective strategy to achieve disease resistance in rice. However, the high degree of pathogenic variation in *Xoo* often causes the breakdown of resistance [9, 10]. Development of resistant varieties is considered the most cost-effective and eco-friendly approach to protect rice from biotic and abiotic stresses for ensuring the yield stability. Studies have demonstrated that pyramiding multiple resistant genes in one cultivar is the sustainable way for long time resistance against the BB [11-13]. Resistant breeding to *Xoo* in Bangladesh is still in an early developmental stage [14]. To assist the rice breeding program against bacterial leaf blight in Bangladesh search for resistant sources is essential. The present study was undertaken to identify the resistant source(s) of rice against the major race of Bacterial Blight pathogen in Bangladesh.

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Materials and Methods:

The experiment was conducted in both nursery and field conditions at Bangladesh Rice Research Institute (BRRI), Gazipur during T. Aman 2011 season.

Collection of test materials (land races and check varieties)

One hundred rice land races were obtained from the Genetic Resources and Seed (GRS) Division, BRRI and two check rice varieties (Purbachi as susceptible and 'IRBB65' as resistant check) were also included in the screening test for comparison.

Inoculum preparation and Inoculation of test entries

BXo9, a virulent and major race of *Xoo* [14] was collected from the Plant pathology Division, BRRI for inoculation. The isolate was cultured on Peptone Sucrose Agar (PSA) medium for 24-48 hours at 28ºC. Before inoculation the concentration of the bacterial suspension was adjusted to 10^8 to 10^{10} CFU/ml using distilled water. The leaf clipping inoculation method [15] was adopted in this experiment.

Nursery trial

Pre germinated seeds of 102 tested materials were seeded in the nursery bed maintaining line to line distance 10 cm and line length 1 m with continuous seeding in line. Susceptible check (Purbachi) was seeded at every 10 lines interval. At 40 days after seeding, 50% of all tested materials were inoculated with BXo9.

Field trial

Field screening was also conducted by using the rest 50% seedlings of the nursery bed following IRRI method. The test entries were planted in the field maintaining susceptible check (Purbachi) at every 10 lines interval and transplanted 5 hills of each entry in a line. All the test entries were inoculated with BXo9 at maximum tillering stage.

Collection and Analyses of data

A total of 20 inoculated rice leaves were randomly selected from each entry in both nursery and field trial. Data on lesion length, relative lesion length and leaf area damaged were recorded at 14 days after inoculation (DAI). Lesion length was measured by using a measuring scale. The relative lesion length was computed using the following formula [16].

$$\text{Relative lesion length \%} = \frac{\text{Lesion length}}{\text{Length of the leaf}} \times 100$$

Mean data of each character was subjected to multivariate analysis following Principal component analysis (PCA), Principal coordinate analysis (PCO), Canonical vector analysis (CVA) and Cluster analysis (CLSA) using GENSTAT 5.

Principal component analysis (PCA)

Principal component analysis is one of the multivariate techniques to know the interrelationships among several characters and can be done from the sum of squares and product matrix for the characters. Principal components were computed from the correlation matrix and genotypic scores obtained for the first component and succeeding components with latent roots greater than unity [17]. The first component has the property of accounting for maximum variance.

Principal Coordinate analysis (PCO)

Principal coordinate analysis is equivalent to PCA but it is used to calculate inter-unit distances. Through the use of all dimensions of *p* it gives the minimum distances between each pair of the N points using similarity matrix [18]. Inter-distances between genotypes were studied by PCO.

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Canonical Vector Analysis (CVA)

Canonical vector analysis (CVA) complementary to D^2 statistic 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, respectively and derived. Canonical vector analysis finds linear combination of original variability than maximize the ratio of between groups to within group's variation, thereby giving functions of the original variables that can be used to discriminate between the groups.

Cluster Analysis (CLSA)

Genotypes were divided into groups on the basis of a data set into some number of mutually exclusive groups. The clustering was done using non- hierarchical classification. In Genstat, the algorithm is used to search for optimal values of the chosen criterion.

Computation of average Intra-cluster distance

Computation of Average Intra-Cluster distance for each cluster was calculated by taking possible D^2 values within the members of a cluster obtained from the PCO after the clusters were formed. The formula utilized was $\Sigma D^2/n$, where ΣD^2 is the sum of distances between all possible combinations (n) of the genotypes included in a cluster found from the equation n (n-1)/2. The square root of the average D^2 values represents the distance (D) within cluster.

Results and Discussion:

Screening land races against bacterial blight (BB) pathogen in seedling nursery

Reaction of land races to the BB pathogen

Mean values of lesion length, relative lesion length and leaf area damaged by the BB pathogen were shown in Table 1. Variations in three parameters on 102 genotypes including 2 checks indicated the existence of genetic diversity among the tested land races. The lesion length ranges from 0.65 to 8.96 cm. The lowest and highest lesion length were found on the resistant check variety 'IRBB65' (0.65 cm.) and susceptible check 'Purbachi' (6.17 cm.), respectively. The relative lesion length ranged from 2.55 to 76.86%, where highest relative lesion length was recorded at 'GOUTI (2)' followed by 'NEEL KONTHI'. Conversely, the lowest value of the parameter was found on IRBB65. The maximum leaf area damaged (63.08%) was recorded from 'MIRJA MUKHI' followed by 'NEEL KONTHI'.

Genetic diversity among the tested land races

Non-hierarchical clustering of genotypes

The computations from distance matrix gave non-hierarchical clustering among 102 test rice genotypes including 2 check varieties and grouped them into ten clusters (Table 2). The distribution pattern indicated that cluster V was comprised of the highest number of 18 tested entries followed by cluster II and cluster VII. Each of cluster III and cluster IV contained eleven entries; and I, VI, VIII, IX and X were comprised of two, four, seven, ten and twelve entries, respectively. Among the tested materials, resistant check 'IRBB65' was placed in cluster I. The inclusion of susceptible check 'PURBACHI' in cluster VI indicated that this variety is totally different from other entries used in this study (Table 2).

Construction of scatter diagram

On the basis of principal axes I and II from the principal component analysis, a two dimensional scatter diagram using component score I as X-axis and component score 2 as Y-axis was constructed (Fig 1). The distribution of genotypes in scattered diagram was distributed into 10 clusters which revealed existence of considerable diversity among the tested genotypes.

Principal Coordinate Analysis (PCO)

The highest inter genotypic distance was 4.3033 observed between GOUTI (2) and IRBB65 (resistance check) and the lowest distance of 0.0238 was observed between SOLDELA and DIGHA. Differences between the highest and lowest

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inter genotypic distances indicated the prevalence of genetic diversity among the 102 land races. The statistical distances represent the index of genetic diversity among the clusters (Table 3).

Canonical variant analysis (CVA)

Canonical Variant Analysis was performed to obtain the inter cluster distances (Mahalanobis's D^2 value). The values of inter cluster distance (D^2) were presented in Table 4. Statistical distances represented the index of genetic diversity among the clusters. The inter cluster distance was maximum between cluster I and cluster VI followed by the distance between cluster I and cluster III. The minimum inter cluster distance was observed between cluster VII and cluster X. The maximum intra-cluster distance was noticed from the cluster I followed by cluster VIII and cluster X. The minimum was found in cluster V followed by cluster III (0.2257). Differences in cluster means existed for almost all the characters studied. In cluster I, it contained lowest value of all the studied characters (lesion length, relative lesion length and damaged leaf area) and cluster VI contained the highest value (Table 5).

Higher inter and intra cluster distances indicate higher genetic variability among genotypes between and within clusters, respectively. The relationships were also reflected in the scatter diagram (Fig. 1).

Contribution of different characters towards divergence of the genotypes

Relative contribution towards divergence is presented in Table 6. Vector I and Vector II values were obtained from Principal Component Analysis (PCA). In first axis vector I, all the studied characters had negative impact towards divergence. In vector II, lesion length had negative impact; and relative lesion length and leaf area damaged had positive impact towards divergence.

Screening land races against BB pathogen in field condition

Reaction of land races to the BB pathogen

Mean values of lesion length, relative lesion length and leaf area damaged by the BB were shown in Table 7. Variations in three parameters on102 genotypes indicate the existence of genetic diversity among the tested land races. The lesion length ranges from 0.6 to 44.6 cm, where the lowest and highest lesion length was found on rice germplasm MATHIA (Acc. No. 523) and SALLA (Acc. No. 455), respectively. The relative lesion length ranged from 1.34 to 100.0% among the test landraces. The highest relative lesion length was recorded at BASH PHUL, BUNA DHAN, DUDHSAR followed by Purbachi while the lowest value of the parameter was found on MATHIA. Again, the maximum (100%) leaf area damaged was recorded from BUNA DHAN followed by BASH PHUL.

Genetic diversity among the tested land races

Non-hierarchical clustering of genotypes

The distribution pattern indicated that cluster II was comprised of the highest number of 20 tested entries followed by cluster X and cluster VII. Cluster I, cluster VI and cluster VIII contained seven entries; cluster III and V were comprised of nine entries; cluster IV contained one and cluster IX contained eleven entries. Among the tested materials, resistant check 'IRBB65' was placed in cluster I. The inclusion of susceptible check 'Purbachi' in cluster V indicated that this variety is totally different from other entries used in this study (Table 8). It may be concluded that these results were confirmatory with the clustering pattern of the genotypes obtained through Principal Component Analysis (PCA).

Construction of scatter diagram

On the basis of principal axes I and II from the Principal Component Analysis, a two dimensional scatter diagram using component score I as X-axis and component score 2 as Y-axis was constructed (Fig. 2). The distribution of genotypes in scattered diagram was distributed into 10 clusters which revealed existence of considerable diversity among the tested genotypes.

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Principal Coordinate Analysis (PCO)

The highest inter genotypic distance was 6.261 observed between KASIA PHUL (2) and MATHIA. The lowest distance of 0.018 was observed between BALAN and SHIL KUMOR (2). Differences between the highest and lowest inter genotypic distances indicated the prevalence of genetic diversity among the 102 land races (Table 9).

Canonical Variant Analysis (CVA)

Canonical Variant Analysis was performed to obtain the inter cluster distances (Mahalanobis's D^2 value). The values of inter cluster distance (D^2) were presented in Table 10. Statistical distances represented the index of genetic diversity among the clusters. The inter cluster distance was maximum between cluster I and cluster IV followed by the distance between cluster II and cluster IV. The minimum inter cluster distance was observed between cluster III and cluster VII. The maximum intra-cluster distance was noticed from the cluster I followed by cluster II and cluster X. The minimum was found in cluster IV (0.00) followed by cluster III (0.194). Differences in cluster means existed for almost all the characters studied. In cluster I, it contained lowest value of all the studied characters and cluster IV contained the highest value (Table 11).

The intra-cluster distances ranged from 0.00 to 1.323 (Table 10). Intra-cluster distances in all clusters were more or less low which indicated genotypes within the same cluster were closely related. The highest intra-cluster distance was recorded in cluster I containing seven genotypes followed by cluster II. The lowest intra-cluster distance was observed in cluster IV having only one genotype. It was favored to decide that intra-cluster diversity was the highest in cluster I *i.e.*, more heterogeneous and intra-cluster diversity was the lowest in cluster IV and because of containing one genotype it is homogenous.

Higher inter and intra cluster distances indicate higher genetic variability among genotypes between and within clusters, respectively. The relationships were also reflected in the scatter diagram (Fig. 2).

Contribution of different characters towards divergence of the genotypes:

Relative contribution towards divergence was presented in Table 12. Vector I and Vector II values were obtained from Principal Component Analysis (PCA). In first axis vector I, all the studied characters had positive impact towards divergence. In vector II, lesion length and relative lesion length had negative impact and leaf area damaged had positive impact towards divergence. The character that showed positive value in both vectors contributed most towards divergence. In the present study, all the characters showed positive value first vector; two characters showed negative value and one character showed positive value in second vector. Mean lesion length and Relative lesion length showed positive value in vector I and negative value in Vector II.

Variations in mean Bacterial Blight severities of the tested 102 materials to the major race BXO9 of BB pathogen (*Xoo*), were found indicating the existence of genetic variability for BB resistance among the tested materials.

In nursery trial, land race SUNG WALA comprised in cluster I with resistant check IRBB65. It is clear from the Table 5 that the lowest intra cluster means for mean lesion length, relative lesion length and leaf area damaged were obtained from cluster I. The other cluster VIII maintained minimum distance (D^2=6.357) from cluster I. Therefore, more emphasis should be given on these clusters for selecting BB resistant rice genotype(s), which may be useful for developing durable BB resistant rice cultivars.

The characters (Lesion length, Relative lesion length and Leaf Area Damaged) showed positive value in both vectors contributed most towards divergence. In case of nursery trial, one character showed negative value in both the vectors; and other two characters showed positive value in one vector and negative value in other vector. Relative lesion length and Leaf Area Damaged showed negative value in vector I and positive value in Vector II. It indicates that relative lesion length and leaf area damaged contributed the highest for divergence. Moreover, mean lesion length showed negative

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value in vector II indicating the character contributed lowest for divergence in the studied materials. So, considering the resistant potentiality at seedling stage, SUNG WALA (Acc. No. 494) from cluster I and PAJER (Acc. No. 423) from cluster VIII may select as resistant sources.

In field trial, among the tested materials, resistant check 'IRBB65' was placed in cluster I along with KHOMON DHAN, JOTA GANJ, HARMA SHAIL (1), KALI RAY, BANSH PHUL (2) and MATHIA. The inclusion of susceptible check 'Purbachi' in cluster V indicated that this variety is totally different from other entries used in this study (Table 8). Due to the lowest intra cluster means for mean lesion length, relative lesion length and leaf area damaged were obtained from cluster I (Table 11). Therefore, more emphasis should be given on this cluster for selecting BB resistant rice genotype(s), which may be useful for the development of durable BB resistant rice cultivars.

Again, in case of field trial, only Leaf Area Damaged showed positive value in both the vectors thus it contributed most towards divergence. Other two characters Lesion Length and Relative Lesion Length showed negative value in vector II indicating the character contributed lowest for divergence in the studied materials. Therefore, MATHIA and HARMA SHAIL (1) may select for using resistant sources because of their lowest response to the BB pathogen and comprised in cluster I. Genotypes belonging to the distant clusters could be used in hybridization program for obtaining a wide spectrum of variation among the segregates [19]. It is more beneficial if crossing might be carried out between genotypes belonging to different groups if their genetic distances (D^2) were greater than 12.5 [20]. Thus it could be suggested that crosses might be made between genotypes belonging to the distant clusters for higher heterotic response (Table 10).

In the present study, the inter cluster distances between cluster I and IV with other cluster suggesting that crossing of genotypes of cluster I and IV with desirable genotypes of other clusters would express heterotic effect.

Conclusion:

The information generated in this study would be very useful for the development of durable resistant rice cultivar against different races of the bacterial blight pathogen in Bangladesh. Results revealed that the inter cluster distances were larger than the intra cluster distances and wider genetic diversity among the test entries. In nursery experiment, PAJRE and in field experiment, MATHIA and HARMA SHAIL (1) showed resistance against *Xoo* due to highest varietal distance (D), which may use for crossing program for the development of BB resistant rice variety.

Authors' contributions:

All authors are contributed equally in this research work.

Table 1. Disease development on land races including checks after inoculation with *Xanthomonas oryzae* pv. *oryzae* in nursery

Sl. No.	Acc. No.	Variety Name	Mean Lesion Length	Relative lesion length (%)	Leaf Area Damaged (%)
01	417	GOUTI(2)	7.88	76.86	52.73
02	418	SUNA MUKHI	3.94	44.23	26.43
03	419	SUNA SHAIL (4)	3.55	39.78	21.25
04	420	DHOLA DEPA	5.64	46.37	33.18
05	421	JHULON	2.80	26.82	14.46
06	422	BOKOL SHAIL	3.02	31.59	15.07
07	423	PAJRE	2.09	23.01	13.10
08	424	BINNA PHUL	3.76	39.59	23.12
09	425	KHOMON DHAN	3.95	39.52	27.53
10	426	JOTA GANJ	3.48	28.60	23.08

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11	427	HARMA SHAIL (1)	3.23	37.55	45.00
12	428	HARMA SHAIL (2)	2.20	29.14	27.50
13	429	KALI RAY	3.95	30.26	25.18
14	430	NAGRA DHAN	3.41	46.23	35.71
15	431	GAINJA	3.00	30.77	27.50
16	432	BADA DHAN	2.23	29.77	12.88
17	433	BUCHI	4.08	25.65	14.05
18	434	BOWAL DOH	3.98	36.13	19.00
19	435	MOHINI SHAIL	3.03	40.47	26.25
20	436	NEEL KONTHI	5.90	65.56	53.33
21	437	KATI SHAIL	4.80	45.24	35.57
22	438	KATIK SHAIL	4.67	54.59	49.29
23	439	HORMA	7.26	53.42	40.75
24	440	KAISA PHUL	3.40	36.96	30.00
25	442	SOLDELA	5.01	37.65	23.85
26	443	JOLA	4.60	29.58	19.00
27	444	TANGUL	5.58	42.40	35.00
28	445	BANSH PHUL (1)	2.54	23.09	16.88
29	446	BANSH PHUL (2)	5.49	48.79	40.00
30	447	TEPA KHULA	4.48	43.73	41.92
31	448	KASIA PHUL (2)	6.16	52.29	49.00
32	449	BAWAI JHAKI	6.47	40.88	40.00
33	450	BAS KOLOM	5.28	32.94	38.67
34	451	DOLA GOCHA	8.96	39.20	28.40
35	453	KALI BUNI	3.88	31.57	23.13
36	454	KOLOM DEPA	5.50	38.46	44.50
37	455	SALLA	3.72	33.84	28.89
38	456	KOLOM	6.19	47.73	37.45
39	457	BABU SHAIL	5.36	48.86	38.46
40	458	BUTA SHAIL	8.08	57.05	40.75
41	459	MOHON BHOG	5.38	49.90	28.89
42	460	PENGUN	3.98	27.65	25.00
43	461	NOYON MONI	4.63	29.66	19.68
44	462	BETO	6.64	46.97	33.50
45	463	RANJAY	4.94	48.31	34.62
46	464	NIDAN SHAIL	4.14	41.73	30.00
47	465	HASH RAJ	4.47	33.01	21.94
48	466	BASH PHUL	6.25	48.56	29.50
49	467	GUJA BALAM	4.56	40.62	24.00
50	468	MIRJA MUKHI	5.28	64.93	63.08
51	469	LAIJAN	7.03	51.79	42.25
52	470	KALAM BASHIR	3.44	29.00	17.50
53	471	SUNGAIL	6.94	49.55	31.75
54	472	HIDA	7.00	56.91	44.00
55	473	HIDA (2)	5.63	39.38	32.27
56	475	SHULI	6.78	41.07	26.00
57	477	KRISNA CHURA	4.19	34.72	36.50

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58	479	AJOL DIGA (2)	5.83	43.53	31.67
59	480	KAKUA	5.42	40.23	40.33
60	485	HANSA	7.02	42.14	40.85
61	486	KANJAL	3.90	23.19	12.14
62	487	LALHIDA	6.73	36.51	35.33
63	488	MATI GOROL (2)	5.13	34.41	21.36
64	489	DIGHA (3)	6.68	36.74	37.83
65	490	DIGHA	5.06	37.14	23.41
66	491	DIGHA	4.99	42.88	28.94
67	492	BHUJON KURPUR	4.04	20.20	25.00
68	493	KAGOL GOOR	5.85	39.02	31.47
69	494	SUNG WALA	4.90	15.50	5.20
70	495	PATH KOLA	6.17	34.24	18.10
71	496	HANS KUL	5.56	33.37	19.40
72	498	KALA RAY	6.02	31.52	18.00
73	499	DUDH SAR	7.16	45.29	28.70
74	500	CHANDA AMAN	6.79	33.26	36.33
75	501	LAL AMAN	5.93	36.02	39.14
76	502	LAU JAN	6.48	39.42	42.75
77	503	NARA ASWINA	2.82	38.94	30.00
78	504	BUNA DHAN	4.31	30.11	20.00
79	507	SHORIGHA PANA	4.25	32.71	21.43
80	508	BEGUN BICHI	4.10	28.87	30.00
81	513	BHASHA MANIK	5.91	50.13	40.50
82	514	KOCHU DHOLA	3.68	35.56	31.25
83	515	SUNGA WALA	2.90	30.93	25.50
84	516	BALAN	2.73	31.06	26.43
85	518	KONEKCHUL	6.70	39.41	31.43
86	519	HORINKHUR PANATI	3.91	28.42	25.71
87	520	GANJIA	5.04	42.42	30.91
88	521	DUDHSAR	3.84	29.57	20.56
89	522	HALDI JAON	4.40	39.40	27.50
90	523	MATHIA	5.98	57.50	38.00
91	525	MUKUT SHAIL	5.78	42.00	33.77
92	529	BAN KOLOM	5.89	37.74	30.45
93	531	GANJIA	5.69	38.26	33.33
94	532	GANJIA	4.60	42.40	40.83
95	536	SAFA HAR (3)	7.04	49.21	40.63
96	537	KAL NANIA	3.14	22.64	17.69
97	539	KARTIK SHAIL (LAL)	5.57	42.57	33.33
98	549	SHIL KUMOR (2)	5.58	44.64	35.00
99	559	SHUL PAN	6.64	51.27	32.50
100	574	HUNUMAN JOTA	5.73	47.51	30.42
101	S. CK	PURBACHI (**)	6.17	62.45	50.46
102	R. CK	IRBB65 (*)	0.65	2.55	3.50

Note: (*) indicates lowest lesion length and (**) highest lesion length among the tested materials.

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Table 2. Distribution of land races with 2 check varieties in ten clusters

Cluster	Member	Name of variety
I	2	SUNG WALA, IRBB 65
II	14	BOKOL SHAIL, BOWAL DOH, JOLA, KALI BUNI, NOYON MONI, HASH RAJ, KALAM BASHIR, MATI GOROL (2), PATH KOLA, HANS KUL, KALA RAY, BUNA DHAN, SHORIGHA PANA, DUDHSAR
III	11	KATIK SHAIL, HORMA, BANSH PHUL (2), KASIA PHUL, BABU SHAIL, BUTA SHAIL, LAIJAN, HIDA, BHASHA MANIK, MATHIA, SAFA HAR (3)
IV	11	HARMA SHAIL (1), TEPA KHULA, BAWAI JHAKI, BAS KOLOM, KOLOM DEPA, KAKUA, HANSA, DIGHA (3), LAL AMAN, LAU JAN, GANJIA
V	18	DHOLA DEPA, NAGRA DHAN, KATI SHAIL, TANGUL, KOLOM, MOHON BHOG, BETO, RANJAY, BASH PHUL, SUNGAIL, AJOL DIGA (2), DUDH SAR, GANJIA, MUKUT SHAIL, KARTIK SHAIL (LAL), SHIL KUMOR (2), SHUL PAN, HUNUMAN JOTA
VI	4	GOUTI(2), NEEL KONTHI, MIRJA MUKHI, PURBACHI
VII	13	SUNA MUKHI, SUNA SHAIL (4), BINNA PHUL, KHOMON DHAN, MOHINI SHAIL, SOLDELA, DOLA GOCHA, NIDAN SHAIL, GUJA BALAM, SHULI, DIGHA, DIGHA, HALDI JAON
VIII	7	JHULON, PAJRE, BADA DHAN, BUCHI, BANSH PHUL (1), KANJAL, KAL NANIA
IX	10	JOTA GANJ, HARMA SHAIL (2), KALI RAY, GAINJA, PENGUN, BHUJON KURPUR, BEGUN BICHI, SUNGA WALA, BALAN, HORINKHUR PANATI
X	12	KAISA PHUL, SALLA, HIDA (2), KRISNA CHURA, LALHIDA, KAGOL GOOR, CHANDA AMAN, NARA ASWINA, KOCHU DHOLA, KONEKCHUL, BAN KOLOM, GANJIA

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Table 3. Ten higher and ten lower inter genotypic distance among the 100 land races along with 2 check varieties in nursery

Sl. No.	Genotypic combination	Genotypic Distances
10 higher inter genotypic distance		
1	GOUTI (2) & IRBB65	4.3033
2	MIRJA MUKHI & IRBB65	4.1686
3	NEEL KONTHI & IRBB65	4.1041
4	PURBACHI & IRBB65	4.0509
5	BUTA SHAIL & IRBB65	3.9596
6	HIDA & IRBB65	3.9483
7	KASIA PHUL (2) & IRBB65	3.9102
8	HORMA & IRBB65	3.8740
9	KATIK SHAIL & IRBB65	3.8624
10	MATHIA & IRBB65	3.8204
10 lower inter genotypic distance		
1	SOLDELA& DIGHA	0.0238
2	JOLA & NOYON MONI	0.0340
3	MUKUT SHAIL & KARTIK SHAIL (LAL)	0.0364
4	PENGUN & HORINKHUR PANAH	0.0404
5	HIDA (2) & KAGOL GOOR	0.0417
6	HIDA (2) & GANJIA	0.0431
7	BANSH PHUL (2) & BABU SHAIL	0.0433
8	TEPA KHULA & GANJIA	0.0452
9	KAGOL GOOR & BAN KOLOM	0.0459
10	TANGUL & MUKUT SHAIL	0.0468

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Table 4. Average intra (Diagonal) and inter cluster distances (D^2) of 100 exotic rice genotypes with 2 check varieties (Inter-group distances)

	I	II	III	IV	V	VI	VII	VIII	IX	X
I	**2.0216**									
II	9.251	**0.2629**								
III	19.759	10.661	**0.2257**							
IV	16.6	8.285	4.492	**0.2633**						
V	15.881	6.688	4.025	3.913	**0.2122**					
VI	26.377	17.257	6.690	10.519	10.597	**0.2584**				
VII	12.791	3.557	7.233	5.753	3.225	13.751	**0.3180**			
VIII	6.357	3.104	13.631	10.938	9.684	20.177	6.532	**0.3436**		
IX	10.148	2.756	9.850	6.612	6.288	16.377	3.859	4.461	**0.2796**	
X	13.622	4.956	6.259	3.347	3.016	12.862	2.706	7.721	3.669	**0.3302**

Table 5. Cluster mean for 3 characters in 100 land race genotypes along with 2 check varieties

	I	II	III	IV	V	VI	VII	VIII	IX	X
Mean lesion length	2.78	4.52	6.31	5.55	5.73	6.36	4.78	2.97	3.43	5.09
Relative lesion length	9.03	31.89	52.78	39.14	46.14	67.45	40.25	24.88	28.59	36.97
Leaf Area damaged	4.35	19.58	42.15	41.07	32.86	54.90	25.90	14.46	26.09	32.27

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Table 6. Characters contribution towards divergence

Characters	Vector I	Vector II
Mean Lesion Length	-0.5321	-0.8345
Relative Lesion Length	-0.6083	0.2594
Leaf Area Damaged	-0.5888	0.4862

Table 7. Disease development on 100 land races and 2 check varieties after inoculation with *Xanthomonas oryzae* pv. *oryzae* in field.

Sl. No.	Acc. No.	Variety Name	Mean Lesion Length (cm)	Relative Lesion Length (%)	Leaf Area Damaged
01	417	GOUTI(2)	28.5	59.50	53
02	418	SUNA MUKHI	20.9	50.98	21.9
03	419	SUNA SHAIL (4)	14.8	37.47	28
04	420	DHOLA DEPA	8.98	22.34	16
05	421	JHULON	33.2	79.43	80
06	422	BOKOL SHAIL	15.5	42.12	14
07	423	PAJRE	18.2	46.55	18.6
08	424	BINNA PHUL	11.5	30.38	14.6
09	425	KHOMON DHAN	8.2	19.25	5.2
10	426	JOTA GANJ	7.3	15.15	7.2
11	427	HARMA SHAIL (1) (*)	1.5	3.59	2.6
12	428	HARMA SHAIL (2)	10.8	27.69	8.2
13	429	KALI RAY	6	14.02	6
14	430	NAGRA DHAN	24.4	64.89	26
15	431	GAINJA	26.2	56.71	41
16	432	BADA DHAN	16.8	35.74	21
17	433	BUCHI	10.8	21.34	19.6
18	434	BOWAL DOH	15.4	39.29	15
19	435	MOHINI SHAIL	12.4	27.19	12
20	436	NEEL KONTHI	31.6	71.82	60
21	437	KATI SHAIL	12	27.03	9
22	438	KATIK SHAIL	21.8	52.91	32
23	439	HORMA	32.6	68.49	52
24	440	KAISA PHUL	27	64.59	48.2
25	442	SOLDELA	32.6	81.50	70
26	443	JOLA	33.2	66.67	50
27	444	TANGUL	36.9	73.51	39

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28	445	BANSH PHUL (1)	30	66.08	41
29	446	BANSH PHUL (2)	5.2	11.26	5
30	447	TEPA KHULA	22.3	44.60	36
31	448	KASIA PHUL (2)	33.8	81.45	39
32	449	BAWAI JHAKI	20	43.10	7
33	450	BAS KOLOM	42.7	77.64	18
34	451	DOLA GOCHA	28.4	56.35	32
35	453	KALI BUNI	30.6	61.45	42
36	454	KOLOM DEPA	37.4	74.50	62
37	455	SALLA (**)	44.6	88.49	27
38	456	KOLOM	44.2	81.55	26.6
39	457	BABU SHAIL	27	59.21	28
40	458	BUTA SHAIL	29	72.50	57
41	459	MOHON BHOG	15.7	35.68	15
42	460	PENGUN	21.5	41.99	8.6
43	461	NOYON MONI	30.4	74.51	36
44	462	BETO	41.8	80.69	77
45	463	RANJAY	33.6	77.06	73
46	464	NIDAN SHAIL	31.4	63.82	51
47	465	HASH RAJ	39.8	66.56	47
48	466	BASH PHUL	29.6	100.00	89
49	467	GUJA BALAM	32.2	60.53	34.6
50	468	MIRJA MUKHI	27.2	62.67	33
51	469	LAIJAN	17	72.03	20
52	470	KALAM BASHIR	13	25.19	16
53	471	SUNGAIL	12	26.91	23
54	472	HIDA	27.8	55.16	47
55	473	HIDA (2)	29.2	54.48	44
56	475	SHULI	27.8	67.15	48
57	477	KRISNA CHURA	26.8	77.01	51
58	479	AJOL DIGA (2)	28.4	86.06	65
59	480	KAKUA	21.2	47.96	39
60	485	HANSA	15.4	34.07	11
61	486	KANJAL	11	24.55	18
62	487	LALHIDA	29.4	69.01	46
63	488	MATI GOROL (2)	23.4	90.00	72
64	489	DIGHA (3)	24.6	61.19	57
65	490	DIGHA	9.4	20.52	21
66	491	DIGHA	22	47.01	38
67	492	BHUJON KURPUR	12.4	27.80	21
68	493	KAGOL GOOR	11.8	26.34	16
69	494	SUNG WALA	35.2	73.03	65

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70	495	PATH KOLA	12.6	25.30	15
71	496	HANS KUL	16.8	40.00	24
72	498	KALA RAY	31.8	67.95	57
73	499	DUDH SAR	37.8	75.30	57
74	500	CHANDA AMAN	17.6	44.00	25
75	501	LAL AMAN	15.6	40.00	30
76	502	LAU JAN	19.4	45.54	32
77	503	NARA ASWINA	18.4	53.49	38
78	504	BUNA DHAN	30	100.00	100
79	507	SHORIGHA PANA	31.4	74.06	48
80	508	BEGUN BICHI	20	38.31	34
81	513	BHASHA MANIK	14.8	31.90	26
82	514	KOCHU DHOLA	19.6	60.12	30
83	515	SUNGA WALA	8	21.74	8
84	516	BALAN	23	52.75	39
85	518	KONEKCHUL	18.6	41.33	23
86	519	HORINKHUR PANATI	9.4	19.75	17
87	520	GANJIA	17.2	39.27	26
88	521	DUDHSAR	45	100.00	38
89	522	HALDI JAON	13.6	25.95	25
90	523	MATHIA	0.6	1.34	4
91	525	MUKUT SHAIL	20.6	41.04	8
92	529	BAN KOLOM	28.6	61.11	42
93	531	GANJIA	16.2	32.40	20
94	532	GANJIA	15	31.38	19
95	536	SAFA HAR (3)	18	44.33	13.4
96	537	KAL NANIA	11.2	26.54	10
97	539	KARTIK SHAIL (LAL)	17.4	43.07	12
98	549	SHIL KUMOR (2)	23	53.74	39
99	559	SHUL PAN	24.6	62.12	36
100	574	HUNUMAN JOTA	19.2	53.93	35
101	S. CK (**)	PURBACHI	32.8	93.71	82
102	R. CK (*)	IRBB65	1.71	4.50	3.59

Note: (*) indicates lowest lesion length and (**) indicates highest lesion length.

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Table 8. Distribution of 100 land races with 2 check varieties in ten clusters (Field)

Cluster	Member	Name of variety
I	7	KHOMON DHAN, JOTA GANJ, HARMA SHAIL (1), KALI RAY, BANSH PHUL (2), MATHIA, IRBB65
II	20	DHOLA DEPA, BINNA PHUL, HARMA SHAIL (2), BUCHI, MOHINI SHAIL, KATI SHAIL, KALAM BASHIR, SUNGAIL, KANJAL, DIGHA, BHUJON KURPUR, KAGOL GOOR, PATH KOLA, BHASHA MANIK, SUNGA WALA, HORINKHUR PANATI, HALDI JAON, GANJIA, GANJIA, KAL NANIA
III	9	NEEL KONTHI, HORMA, KOLOM DEPA, BUTA SHAIL, KRISNA CHURA, SUNG WALA, KALA RAY, DUDH SAR, SHORIGHA PANA
IV	1	LAIJAN
V	9	JHULON, SOLDELA, BETO, RANJAY, BASH PHUL, AJOL DIGA (2), MATI GOROL (2), BUNA DHAN, PURBACHI
VI	7	TANGUL, KASIA PHUL (2), BAS KOLOM, SALLA, KOLOM, NOYON MONI, DUDHSAR
VII	14	GOUTI(2), GAINJA, KAISA PHUL, JOLA, BANSH PHUL (1), KALI BUNI, NIDAN SHAIL, HASH RAJ, HIDA, HIDA (2), SHULI, LALHIDA, DIGHA (3), BAN KOLOM
VIII	7	NAGRA DHAN, DOLA GOCHA, BABU SHAIL, GUJA BALAM, MIRJA MUKHI, KOCHU DHOLA, SHUL PAN
IX	11	KATIK SHAIL, TEPA KHULA, KAKUA, DIGHA, LAL AMAN, LAU JAN, NARA ASWINA, BEGUN BICHI, BALAN, SHIL KUMOR (2), HUNUMAN JOTA
X	17	SUNA MUKHI, SUNA SHAIL (4), BOKOL SHAIL, PAJRE, BADA DHAN, BOWAL DOH, BAWAI JHAKI, MOHON BHOG, PENGUN, HANSA, HANS KUL, CHANDA AMAN, KONEKCHUL, GANJIA, MUKUT SHAIL, SAFA HAR (3), KARTIK SHAIL (LAL)

Table 9. Ten higher and ten lower inter genotypic distances among the land races along with 2 check varieties

Sl. No.	Genotypic combination	Genotypic Distances
10 higher inter genotypic distance		
1	KASIA PHUL (2) & MATHIA	6.261
2	BUNA DHAN & MATHIA	5.656
3	BASH PHUL & MATHIA	5.589
4	HARMA SHAIL (1) & LAIJAN	5.576

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5	BETO & MATHIA	5.565
6	MATHIA & PURBACHI	5.558
7	DUDHSAR & MAHTIA	5.447
8	JHULON & MATHIA	5.445
9	SOLDELA & MATHIA	5.385
10	KOLOM DEPA & MATHIA	5.347
	10 lower inter genotypic distance	
1	BALAN & SHIL KUMOR (2)	0.018
2	KAKUA & DIGHA; KAISA PHUL & SHULI	0.048
3	HORMA & JOLA	0.050
4	KALI BUNI & BAN KOLOM	0.066
5	KALAM BASHIR & PATH KOLA	0.067
6	SHULI & LAL HIDA	0.073
7	SOLDELA & RANJAY; TEPA KHULA & DIGHA	0.075
8	BANSH PHUL (1) & KALI BUNI; KOLOM DEPA & SUNG WALA	0.078
9	PENGUN & MUKUT SHAIL	0.080
10	HORMA & NIDAN SHAIL	0.081

Table 10. Average intra and inter cluster distances (D^2) of 100 land races along with 2 check varieties (Inter-group distances) in field

	I	II	III	IV	V	VI	VII	VIII	IX	X
I	**1.323**									
II	3.54	**0.497**								
III	14.03	10.51	**0.194**							
IV	50.03	47.26	40.39	**0.00**						
V	17.44	13.94	3.56	39.47	**0.2999**					
VI	14.72	11.36	4.80	36.73	6.89	**0.4334**				
VII	11.79	8.26	2.24	41.69	5.75	5.16	**0.219**			
VIII	10.35	6.90	4.61	41.10	8.12	4.54	2.84	**0.254**		
IX	8.40	4.87	5.63	43.87	9.09	7.21	3.39	2.78	**0.2407**	
X	6.22	2.98	8.42	44.29	11.96	8.50	6.23	4.22	3.16	**0.4846**

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Table 11. Cluster mean for 3 characters in 100 land races along with 2 check varieties in field

	I	II	III	IV	V	VI	VII	VIII	IX	X
Mean lesion length	4.36	11.84	32.62	71.00	31.71	39.66	29.58	26.20	20.54	17.67
Relative lesion length	9.87	26.11	72.74	87.61	72.03	82.45	62.39	60.84	48.20	41.18
Leaf Area damaged	4.80	16.72	56.56	80.00	78.67	31.94	46.94	31.37	35.64	17.15

Table 12. Characters contribution towards divergence

Characters	Vector I	Vector II
Mean Lesion Length	0.6133	-0.3053
Relative Lesion Length	0.6014	-0.4175
Leaf Area Damaged	0.5121	0.8559

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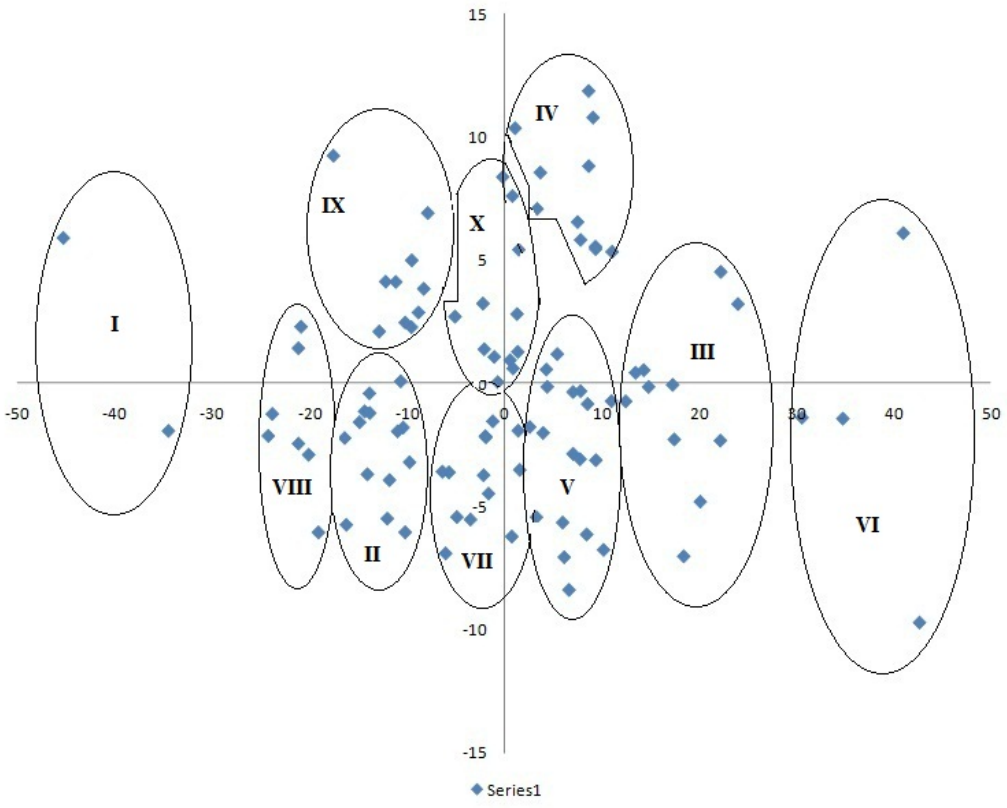

Figure 1. Scatter diagram of 100 land races along with 2 check varieties based on their principal component scores superimposed with clustering (Nursery).

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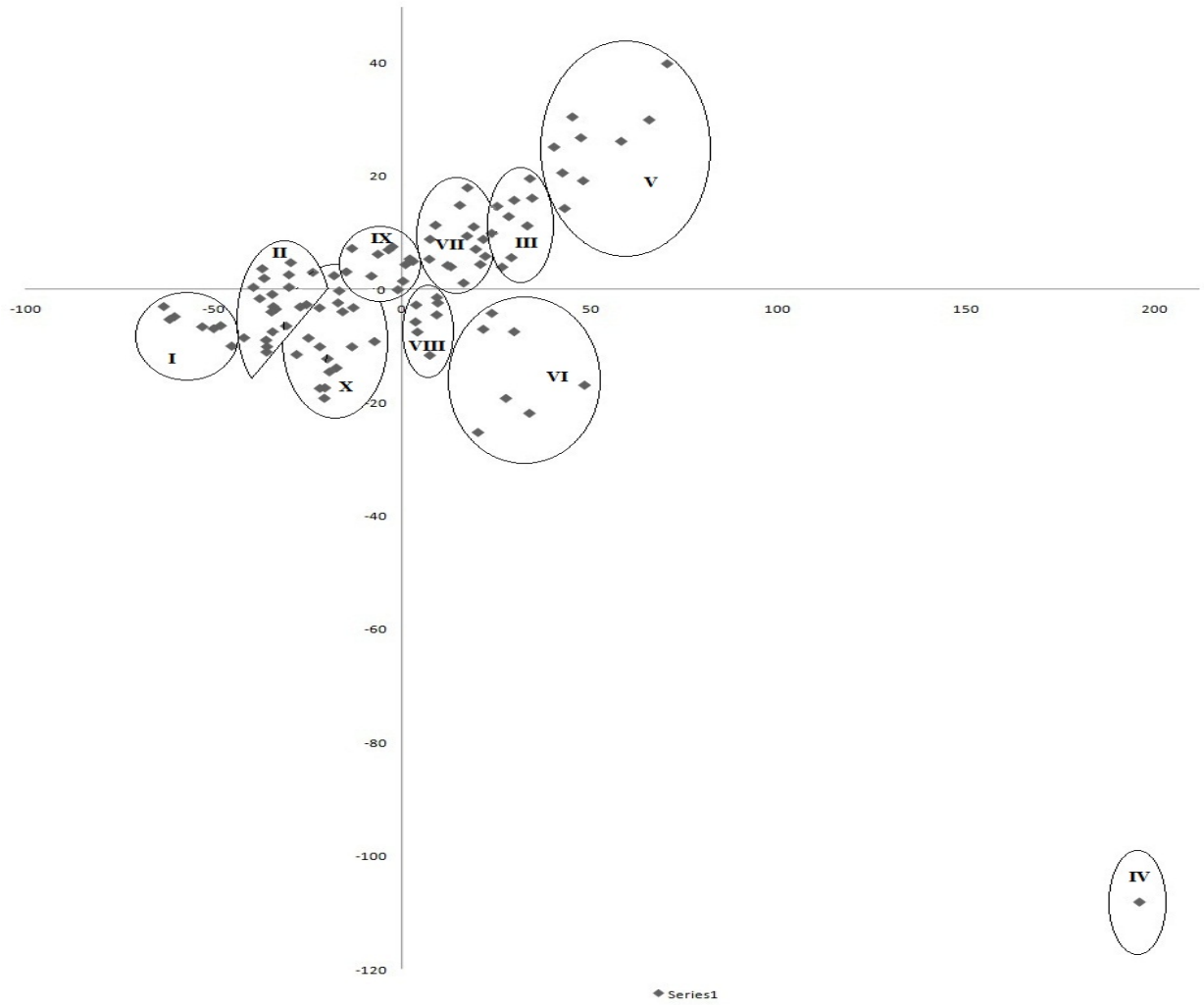

Figure 2. Scatter diagram of 100 land races along with 2 check varieties based on their Principal Component Scores superimposed with clustering (Field).

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Author(s) & Affiliations

ABM Muzahidul Islam[1], J Rozalin Rahman[2], SAI Nihad[3], R Akter[3], HA Dilzahan[3], MZ Islam[4], MR Bhuiyan[3], MH Kabir[2], MM Rashid[3], MR Islam[5], MA Latif[3] and MAI Khan[3,*]

[1]RAB-4, Mirpur, Dhaka, Bangladesh;
[2]Department of Agricultural Extension, Bangladesh;
[3]Plant Pathology Division, Bangladesh Rice Research Institute, Gazipur, Bangladesh;
[4]Genetic Resources and Seed Division, Bangladesh Rice Research Institute, Gazipur, Bangladesh;
[5]Department of Plant Pathology, Bangladesh Agricultural University, Mymensingh, Bangladesh.