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Genetic Diversity of INGER Rice Genotypes Based on Morphological Characters and Bacterial Blight Resistance

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ABSTRACT

Bacterial blight disease (causal organism: *Xanthomonas oryzae* pv. *oryzae*) is an economically significant menace to rice cultivation in Bangladesh as well as in the world, which reduces significant yield loss in rice and hampers food security. The most sustainable strategy to fight this disease is the adoption of disease-resistant cultivars. The morphological trait and nature of diversity of 92 bacterial blight-resistant INGER (International Network for Genetic Evalu-ation of Rice) genotypes collected from the International Rice Research Institute (IRRI, Philippines) were analyzed to explore for sources of resistance. Artificial inoculation by *BXO9*, a virulent race of *Xoo* was used to evaluate and screen those genotypes in the field. Twelve genotypes, out of 92 had resistance, and another 12 had moderately resistance. Eleven morphological traits including disease data of each genotype were recorded and found noticeable diversity among the genotypes. Pearson's correlation analysis among genotypes revealed that yield per hill is positively correlated with number of tiller per hill, number of effective tiller per hill, number of spikelets per panicle, number of filled spikelets per panicle and thousand grain weight. In cluster analysis, 15 major groups were obtained in 92 rice genotypes by using Euclidean distance and the UPGMA method. Cluster-1 comprises single genotypes SVIN310, which showed resistant reaction to bacterial blight disease had the highest tiller number, effective tiller number, number of spikelets per panicle, filled spikelets per panicle and thousand-grain weight. In PCA analysis, the first four principal components narrated around 77.32% variation. Among 92 genotypes, G1 (SVIN310), G23 (SVIN018), G70 (SVIN012), G75 (SVIN054), G33 (SVIN007), G48 (SVIN006), G80 (SVIN049), G90 (BRRI dhan84), G30 (SVIN290) near to the vector line of yield per hill are highly and positively responsive to the yield per hill. Considering all of these, cluster-1 having genotype SVIN310 with resistant phenomena would be the potential genotype for further use in a breeding programme.

Key words: Bacterial blight, Disease resistance, Diversity analysis, INGER, Rice

INTRODUCTION

Rice (*Oryza sativa* L.), is the ancient domesticated and widely cultivated crop in the world (Ainsworth, 2008). From 2001 to 2025 the overall demand for rice will increase by 25% to bear the increasing population (Maclean *et al.*, 2002; Kabir *et al.*, 2020). In Bangladesh, rice security is equivalent to food security (Kabir *et al.*, 2020; Mamun *et al.*, 2021). Bangladesh which is recognized as one of the top climate vulnerable countries in the world, also facing the risk of climate change like severe drought, salinity, uneven precipitation, severe cold, and the emergence of diseases and pests (Mezanur-Rahman *et al.*, 2016; Mamun *et al.*, 2018; Rahman *et al.*, 2021; Aziz *et al.*, 2022). During the life cycle, rice faces different

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biotic and abiotic stresses like diseases, insects, submergence and salinity, etc. (Ara *et al*., 2015; Morshed *et al*., 2023). In Bangladesh, so far 32 diseases of rice is reported, and among them blast (Nihad *et al*., 2022), bacterial blight (Rashid *et al*., 2021), sheath blight (Latif *et al*., 2022), false smut (Nessa *et al*., 2015) and tungro (Nihad *et al*., 2021; Hore *et al*., 2022) diseases are the major threat of rice production. Enormous yield losses by rice diseases of bacterial, fungal, and viral hamper rice production (Ullah *et al*., 2012). Bacterial Blight (BB) is one of the most disastrous rice diseases, which causes up to 50% yield loss in severe cases that are mostly dependent on variety, growth stage, geographical site, and ecological conditions (Liu *et al*., 2014). Bacterial blight (BB) is first discovered in Fukuoka province, Japan in 1884 (Ou, 1985). Both inbred and hybrid varieties can be severely affected by BB disease and can cause significant yield loss (Anik *et al*., 2022; Akter *et al*., 2022). There is no doubt bacterial blight disease is a destructive disease, which can cause a serious problem and reduces yield in severe cases. Moreover, location wise variation of bacterial races makes it difficult to control and to date, 12 races of bacterial blight pathogen with diverse pathogenicity have been identified in Bangladesh (Rashid *et al*., 2021). There are many different means of management like the use of some chemicals and antibiotics to control bacterial blight but it harms our environment and health. No effective chemical was found yet to give to the farmers for the management of BB in Bangladesh (Rahman *et al*., 2018). Even, though bacterial blight is controlled by several measures, resistant variety is considered the durable and nature-friendly approach to control the disease (Nihad *et al*., 2020; Akter *et al*., 2022). Screening is the main gateway through which a breeder can identify the source of resistan genes and use them to develop durable disease-resistant rice varieties. According to, Anik *et al*., 2022 it is the prerequisite to find out the potential resistant genotypes based on yield contributing morphological traits and nature of genetic diversity to develop a durable BB resistant variety. Thorough screening is obligatory to identify the resistant source from huge diverse populations. In plant breeding, genetic diversity plays a fundamental role to rescue resistant sources so breeders can develop stable variety after further screening and selection (Mazid *et al*., 2013a; Nihad *et al*., 2021). Researchers are always interested to identify a resistant cultivar to uncover available resistance genes against BB disease. It is reported that using gene pool, genome structure, and transferring desirable traits to plants is the most effective way for crop advancement (Nihad *et al*., 2021; Anik *et al*., 2022). Understanding and assessing genetic diversity is mandatory, which is the basis of plant breeding. A gene pool having diversified genetic resources is the prerequisite for initiating breeding programmes (Sivaranjani *et al*., 2010; Nihad *et al*., 2020). The objective of this experiment to evaluate the INGER rice genotypes against bacterial blight pathogen to find resistant sources against bacterial blight disease of Bangladesh.

MATERIALS AND METHODS

The experiment was set up in the research plot of BRRI, Gazipur during Boro 2018 following randomized complete block design (RCBD) with three replications. Ninety two rice germplasms (including resistant and susceptible checks) were obtained from International Rice Research Institute (IRRI) and Bangladesh Rice Research Institute (BRRI) to screen against bacterial blight disease. In every plot of each genotype, 15 plants were allowed to grow till harvesting. The plot size of each plot was 0.75m^2. Fertilizers were given in BRRI recommended doses and other intercultural practices were done in time as

necessary. Five plants of each genotype were inoculated by a virulent race of *Xanthomonas oryzae* pv. *oryzae (Xoo)* by leaf clipping method at the maximum tillering stage.

Bacterial blight pathogen inoculation

A virulent *Xoo* isolate BXO9 (Khan *et al.*, 2009) was used for inoculation by following a well known leaf clipping method (Kauffman *et al.*, 1973). With an incubation period of 72 hours at 28°C, bacterial inoculum was prepared on Peptone Sucrose Agar (PSA) and mixed with distilled water for proper dilution. The suspension optical density (OD) absorbance was read at 600 nm and the concentration was adjusted to OD_{600} = 1. This value is equivalent to bacterial concentration of around 3.3×10^8 colony forming units per milliliter (cfu/mL). After dipping the scissors into the solution, about 3-4 cm healthy leaf portion from the top was cut for bacterial blight pathogen inoculation.

Data collection

Data of 11 morphological traits were documented from three hills of each genotype including disease reaction to bacterial blight disease. Plant height (PH, cm), number of tiller per hill (NTH^{-1} , no.), effective tiller per hill (ETH^{-1}, no.), days to 80% flowering (DF, day), days to maturity (DM, day), panicle length (PL, cm), number of grains per panicle (NGP^{-1}, no.), number of filled spikelet per panicle (FSP^{-1}, no), number of unfilled spikelet per panicle (USP^{-1}, no), thousand grains weight (TGW, g) and disease score (DS, no.) (Table 1) were the considerable traits for data collection. The disease data was collected at 14 days after inoculation from all leaves of three hills. Disease reaction was classified according to the standard evaluation scale of IRRI (IRRI, 2013) (Table 1). All susceptible, moderately susceptible and highly susceptible genotypes were considered as susceptible in this study.

Table 1. Disease scale for differentiate genotypes based on disease reaction.

Score	Disease Affected Leaf Area (%)	Description
1	1-5	Resistant
3	6-12	Moderately Resistant
5	13-25	Moderately Susceptible
7	26-50	Susceptible
9	>50	Highly Susceptible

Statistical analysis

Correlation, cluster and principal component analysis were done by using R programing software. Cluster analysis and dendrogram were prepared by using the Euclidean distance and UPGMA method. The principal coordinate analysis (PCoA) of 92 rice entries was done by EIGEN and PROJ modules of NTSYS-pc software.

RESULTS

Reaction of INGER genotypes to *Xoo*

Among 92 genotypes, 12 genotypes showed resistant, 12 showed moderately resistant and others genotypes showed susceptible reaction to bacterial blight disease (Table 2).

Table 2. List of INGER materials and disease reactions to *Xoo*.

Code	ID	Source of collection	Disease reaction	Code	ID	Source of collection	Disease reaction
G1	SVIN310	IRRI	R	G47	SVIN002	IRRI	S
G2	SVIN288	IRRI	R	G48	SVIN006	IRRI	S
G3	SVIN323	IRRI	R	G49	SVIN016	IRRI	S
G4	SVIN314	IRRI	R	G50	SVIN023	IRRI	S
G5	SVIN318	IRRI	R	G51	SVIN010	IRRI	S
G6	SVIN309	IRRI	R	G52	SVIN328	IRRI	S
G7	SVIN324	IRRI	R	G53	SVIN300	IRRI	S
G8	SVIN313	IRRI	R	G54	SVIN019	IRRI	S
G9	SVIN316	IRRI	R	G55	SVIN011	IRRI	S
G10	SVIN317	IRRI	R	G56	SVIN042	IRRI	S
G11	SVIN048	IRRI	MR	G57	SVIN030	IRRI	S
G12	SVIN312	IRRI	MR	G58	SVIN325	IRRI	S
G13	SVIN044	IRRI	MR	G59	SVIN013	IRRI	S
G14	SVIN005	IRRI	MR	G60	SVIN032	IRRI	S
G15	SVIN322	IRRI	MR	G61	SVIN043	IRRI	S
G16	SVIN045	IRRI	MR	G62	SVIN326	IRRI	S
G17	SVIN026	IRRI	MR	G63	SVIN329	IRRI	S
G18	SVIN305	IRRI	MR	G64	SVIN003	IRRI	S
G19	SVIN315	IRRI	MR	G65	SVIN304	IRRI	S
G20	SVIN307	IRRI	MR	G66	SVIN034	IRRI	S
G21	SVIN321	IRRI	MR	G67	SVIN035	IRRI	S
G22	SVIN050	IRRI	MR	G68	SVIN031	IRRI	S
G23	SVIN018	IRRI	S	G69	SVIN038	IRRI	S
G24	SVIN327	IRRI	S	G70	SVIN012	IRRI	S
G25	SVIN302	IRRI	S	G71	SVIN008	IRRI	S
G26	SVIN303	IRRI	S	G72	SVIN014	IRRI	S
G27	SVIN285	IRRI	S	G73	SVIN319	IRRI	S
G28	SVIN020	IRRI	S	G74	SVIN292	IRRI	S
G29	SVIN024	IRRI	S	G75	SVIN054	IRRI	S
G30	SVIN290	IRRI	S	G76	SVIN046	IRRI	S
G31	SVIN291	IRRI	S	G77	SVIN036	IRRI	S
G32	SVIN287	IRRI	S	G78	SVIN022	IRRI	S
G33	SVIN007	IRRI	S	G79	SVIN051	IRRI	S
G34	SVIN289	IRRI	S	G80	SVIN049	IRRI	S
G35	SVIN037	IRRI	S	G81	SVIN029	IRRI	S
G36	SVIN306	IRRI	S	G82	SVIN299	IRRI	S
G37	SVIN028	IRRI	S	G83	BRRI dhan28	BRRI	S
G38	SVIN009	IRRI	S	G84	BRRI dhan29	BRRI	S
G39	SVIN041	IRRI	S	G85	BRRI dhan50	BRRI	S
G40	SVIN039	IRRI	S	G86	BRRI dhan58	BRRI	S
G41	SVIN033	IRRI	S	G87	BRRI dhan63	BRRI	S
G42	SVIN021	IRRI	S	G88	BRRI dhan74	BRRI	S
G43	SVIN047	IRRI	S	G89	BRRI dhan81	BRRI	S
G44	SVIN004	IRRI	S	G90	BRRI dhan84	BRRI	S
G45	SVIN351	IRRI	S	G91	IRBB60	IRRI	R
G46	SVIN040	IRRI	S	G92	IRBB65	IRRI	R

R: Resistant, MR: Moderately Resistant, S: Susceptible, SVIN: Source of Variation INGER, G: Genotype.

Pearson's correlation coefficient

Correlation analysis revealed the relationship among the studied traits to take decision to design an effective breeding schedule. Effective tiller per hill had significant positive (0.92***) correlation with the total tiller per hill (Fig. 1). Additionally, number of filled spikelets (0.84***) as well as unfilled spikelets (0.67***) had positively related with total number of filled spikelets per panicle. From this study, it is showed that panicle length (0.59***) had positively correlated with plant height and yield per hill is positively correlated with number of spikelets per panicle (0.59***), number of filled spikelets (0.6***) and thousand grain weight (0.36***). Yield per hill also positively correlated with number of tiller per hill (0.6***) and number of effective tiller per hill (0.7***).

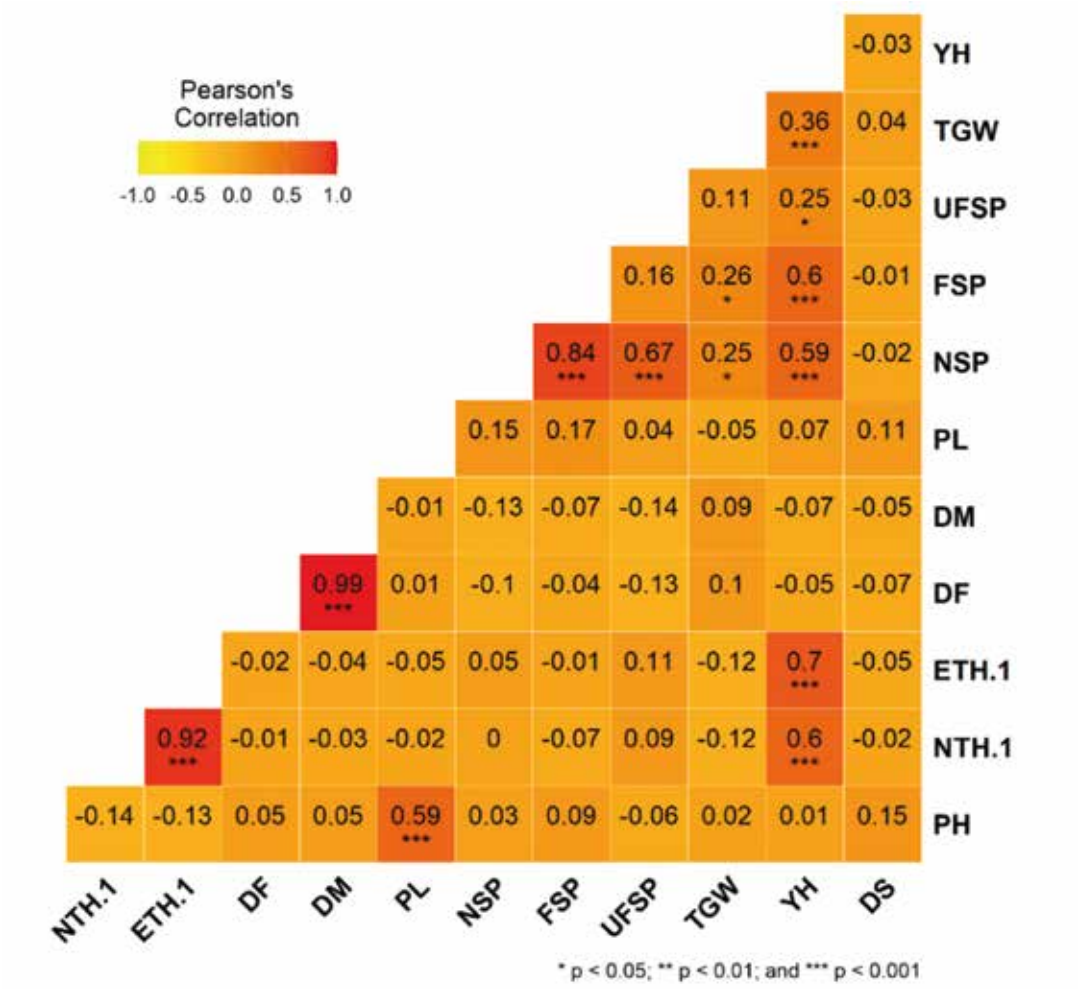

Fig. 1. Correlogram represented the relationship among the studied traits.

Here, PH: Plant height, NTH^{-1}: Number of tiller per hill, ETH^{-1}: Effective tiller per hill, DF: Days to 50% flowering, DM: Days to maturity, PL: Panicle length, NSP^{-1}: Number of spike-lets per panicle, FSP^{-1}: number of filled spikelets per panicle, UFSP^{-1}: Number of unfilled spikelets per panicle, TGW: Thousand grains weight, DS: Disease severity.

Cluster analysis

Based on multivariate analysis of morphological characters, 15 major groups were observed among 92 rice genotypes (Fig. 2 and Table 3). Cluster 3 had the highest number of genotypes (47), which comprised 51.08% of the studied genotypes. Clusters having the single genotype (clusters 1, 2, 7, 8, 9, 11, 13, 14 and 15) were considered the smaller groups compared to others. Clusters 10 was comprised of two genotypes, whereas, groups 4 and 12 containing three genotypes. On the other hand, the second largest cluster was group 6 as it comprised of 19 genotypes and cluster 5 containing nine genotypes.

Fig. 3 presents clusterwise mean data of studied parameters. Cluster-1 had the highest average number of tiller per hill, effective tiller per hill, number of spikelets per panicle, filled spikelets per panicle and thousand grain weight. Cluster-4 had the highest yield per hill. Cluster-11 had also the highest number of tiller per hill and cluster-12 had the highest number panicle length. Based on disease severity, cluster 1 and cluster 11 found as resistant to bacterial blight disease. Genotype of cluster 13 found as moderately resistant (Fig. 3).

Table 3. Number of cluster and respective genotypes found from Euclidean distance and UPGMA method cluster analysis.

Cluster	Genotype	Designation
1	G1	SVIN310
2	G70	SVIN012
3	G2, G3, G4, G6, G17, G18, G12, G13, G14, G16, G20, G21, G22, G23, G25, G27, G28, G35, G37, G38, G40, G41, G42, G44, G45, G46, G47, G49, G50, G53, G60, G64, G65, G72, G74, G75, G76, G79, G81, G85,G86, G87, G88, G89, G90, G91, G92	SVIN288, SVIN323, SVIN314, SVIN309, SVIN026, SVIN305, SVIN312, SVIN044, SVIN005, SVIN045, SVIN307, SVIN321, SVIN050, SVIN018, SVIN302, SVIN285, SVIN020, SVIN037, SVIN028, SVIN009, SVIN039, SVIN033, SVIN021, SVIN004, SVIN351, SVIN040, SVIN002, SVIN016, SVIN023, SVIN300, SVIN032, SVIN003, SVIN304, SVIN014, SVIN292, SVIN054, SVIN046, SVIN051, SVIN029, BRRI dhan50, BRRI dhan58, BRRI dhan63, BRRI dhan74, BRRI dhan81, BRRI dhan84, IRBB60, IRBB65
4	G24, G26, G36	SVIN327, SVIN303, SVIN306
5	G5, G8, G62, G71, G82, G78, G80, G30, G34	SVIN318, SVIN313, SVIN326, SVIN008, SVIN299, SVIN022, SVIN049, SVIN290, SVIN289
6	G9, G10, G31, G32, G66, G67, G68, G69, G51, G52, G54, G57, G59, G61, G63, G19, G77, G15, G29	SVIN316, SVIN317, SVIN291, SVIN287, SVIN034, SVIN035, SVIN031, SVIN038, SVIN010, SVIN322, SVIN019, SVIN030, SVIN013, SVIN043, SVIN329, SVIN315, SVIN036, SVIN328, SVIN024
7	G83	BRRI dhan28
8	G55	SVIN011
9	G84	BRRI dhan29
10	G43, G56	SVIN047, SVIN042
11	G7	SVIN324
12	G48, G33, G58	SVIN006, SVIN007, SVIN325
13	G11	SVIN048
14	G73	SVIN319
15	G39	SVIN041

Fig. 2. Circular dendrogram showing the cluster wise genotypes distribution of 92 rice genotypes.

PH	NTH.1	ETH.1	DF	DM	PL	NSP	FSP	UFSP	TGW	YH	DS	
92.44	26	23.94	109.33	139.33	24.4	141.67	113.33	28.33	25.33	32.88	1	Cluster 1
74.67	20.78	18.44	116.17	146.17	23.03	75.33	59.5	15.83	19.33	20.96	7	Cluster 2
84.6	16.07	15.47	103.4	133.4	24	87.4	74.4	13	20.6	23.87	5.38	Cluster 3
82.6	21.43	18.9	117.4	147.4	25.04	94.6	79.4	15.2	23.2	34.83	8.33	Cluster 4
83.53	16.87	16.2	103	133	23.76	131.8	95.8	36	21	32.9	5.22	Cluster 5
83.25	15.08	13.83	114.5	144.5	25.75	118.75	74	44.75	19.75	20.18	6.16	Cluster 6
90.6	16.3	16.02	115.9	145.9	23.68	90.4	73.6	16.8	20.1	23.69	9	Cluster 7
88.5	22.58	20	114.83	144.83	25.43	96.83	78.75	18.08	19.83	31.03	5	Cluster 8
74.11	21.11	20.11	118	148	20.4	97	65.33	31.67	22.67	29.78	7	Cluster 9
88.33	12.9	11.48	115.14	145.14	25.3	114.29	96	18.29	23.86	26.2	6	Cluster 10
79.8	26	22.13	105.8	135.8	22.8	81	63	18	20.8	29	1	Cluster 11
93.67	17.17	16.67	103	133	28.15	88.25	71.5	16.75	20.25	23.83	5.66	Cluster 12
79.22	15.99	15.04	103.11	133.11	23.2	90.56	72.22	18.33	20.44	22.26	3	Cluster 13
96.11	15.2	13.11	113.33	143.33	26.36	77.89	66	11.89	21.44	18.29	7	Cluster 14
80.68	13.73	12.47	114.8	146.4	22.11	73.4	59.8	13.6	21.4	15.81	7	Cluster 15

Fig. 3. Cluster wise mean of the studied parameters of 92 rice genotypes.
Here dark green indicates the highest value and dark purple indicates the lowest value, PH: Plant height, NTH^{-1}: number of tiller per hill, ETH^{-1}: effective tiller per hill, DF: days to 50% flowering, DM: days to maturity, PL: panicle length, NSP^{-1}: number of spikelets per panicle, FSP^{-1}: number of filled spikelets per panicle, $UFSP^{-1}$: number of unfilled spikelets per panicle, TGW: 1000-grain weight, DS: Disease severity.

Principal component analysis (PCA)

PCA biplot analysis revealed that variability of number of tiller and effective tiller per plant, number of grain per panicle and yield per hill were high in the 92 genotypes (Fig. 4). Yield contributing characters i.e., number of tiller and effective tiller per plant, number of grain per panicle, filled and unfilled grain and thousand grain weight are positively related with yield per hill of the genotypes. The genotypes G1 (SVIN310), G23 (SVIN018), G70 (SVIN012), G75 (SVIN054), G33 (SVIN007), G48 (SVIN006), G80 (SVIN049), G90 (BRRI dhan84), and G30 (SVIN290) that are close to the yield per hill vector line respond positively and highly to it. Resistant, moderately resistant and susceptible genotypes also showed the diversified position in PCA biplot analysis. First four principal components justified about 77.32% of the variability and showed a high correlation. The PC1, PC2, PC3 and PC4 described about 25.9%, 17.2%, 18.85 % and 15.37 % of the total variability (Table 4). In PC3, NTH^{-1} (0.72%), ETH^{-1} (0.72%), DF (0.63%) and DM (0.62%) were the most important contributing characters. On the other hand, NSP^{-1} (0.89%), FSP^{-1} (0.72%), $UFSP^{-1}$ (0.6%) is important parameters for the first PC. PH (0.81%) and PL (0.83%) is the most important trait for PC4 (Table 4).

Table 4. Eigen vectors and eigen values of the first four principal components.

Variable	Principal component			
	PC1	PC2	PC3	PC4
Eigen value	2.387	2.017	1.886	1.537
Percent	25.9	17.2	18.855	15.368
Cumulative	23.867	44.038	62.893	78.261
PH	0.103	0.283	0.017	0.819
NTH^{-1}	0.197	-0.606	0.722	0.123
ETH^{-1}	0.232	-0.601	0.721	0.111
DF	-0.485	0.575	0.634	-0.071
DM	-0.509	0.569	0.619	-0.081
PL	0.171	0.257	-0.013	0.836
NSP^{-1}	0.889	0.350	0.150	-0.142
FSP^{-1}	0.720	0.431	0.123	-0.098
$UFSP^{-1}$	0.609	0.021	0.100	-0.122
TGW	0.282	0.426	0.108	-0.290

Note. PH: Plant height, NTH^{-1}: number of tiller per hill, ETH^{-1}: effective tiller per hill, DF: days of 50% flowering, DM: days to maturity, PL: panicle length, NSP^{-1}: number of spikelets per panicle, FSP^{-1}: number of filled spikelets per panicle, $UFSP^{-1}$: number of unfilled spikelets per panicle, TGW: 1000-grain weight.

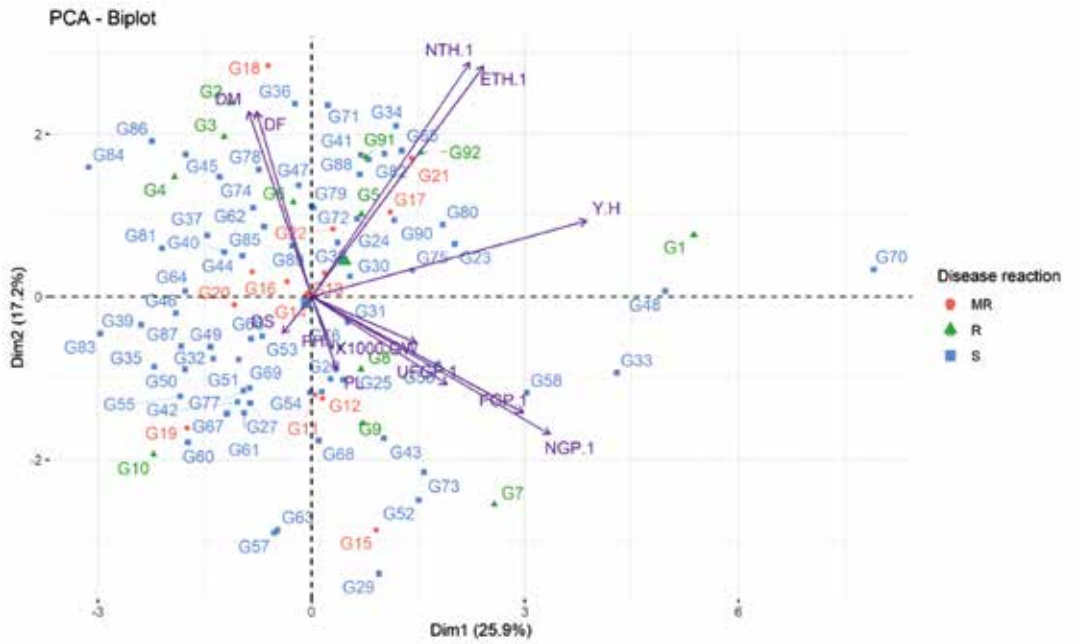

Fig. 4. PCA biplot of 92 rice genotypes based on morphological characters and disease reaction. Here, PH: Plant height, NTH^{-1}: number of tiller per hill, ETH^{-1}: effective tiller per hill, DF: days of 50% flowering, DM: days to maturity, PL: panicle length, NSP^{-1}: number of spikelets per panicle, FSP^{-1}: number of filled spikelets per panicle, $UFSP^{-1}$: number of unfilled spikelets per panicle, TGW: 1000-grain weight, DS: Disease severity.

Principal coordinate analysis (PCoA)

PCoA plot depicted the spatial dispersal of the genotypes (Fig. 5). SVIN319 (G73), SVIN012 (G70), BRRI dhan29 (G84), SVIN022 (G78), SVIN299 (G82) were found far away from center of the cluster. The rest of the genotypes were placed more or less near to the center (Fig. 5). In this case, center means that point where cluster center exists. In this point, at least one number for each parameter is present. Contour lines between each genotype and the center characterized Eigen vectors for the respective genotypes. The information generated from these results explained that genotypes those are far away from center are more genetically diverse and genotypes those are placed in near to the center are less diverse.

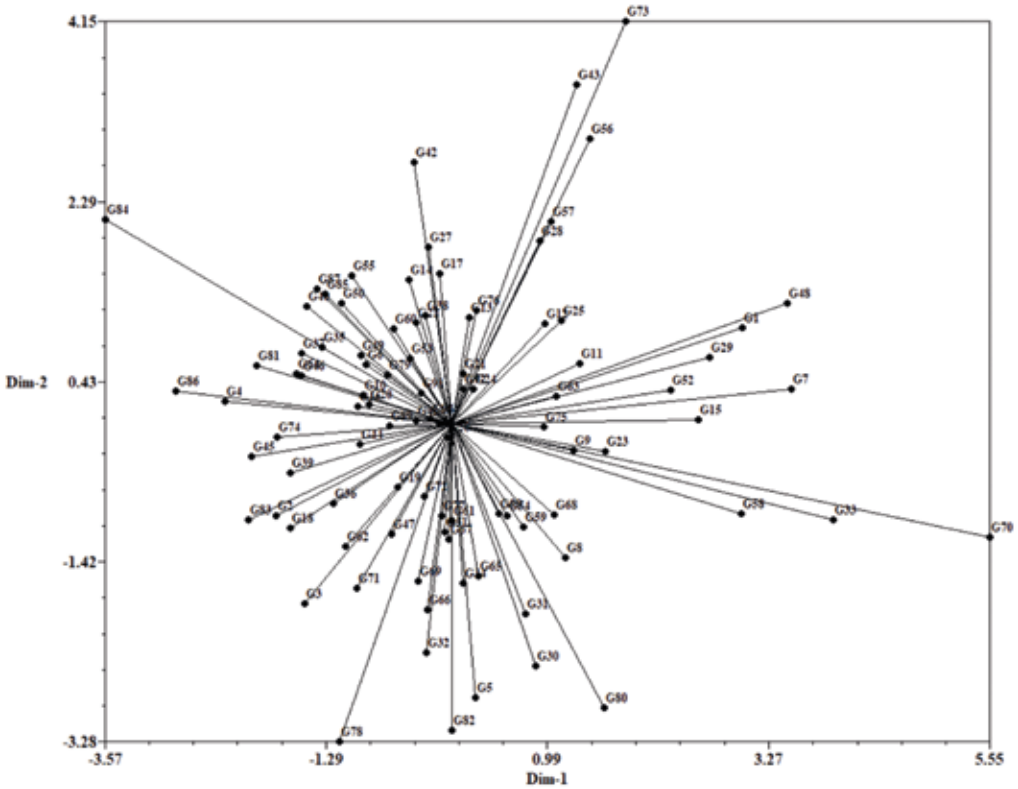

Fig. 5. Two-dimensional PCoA plot of 92 genotypes.

DISCUSSION

Revealing of diversity analysis based upon morphological traits and disease reaction are important to initiate resistant breeding programme. Yield is a quantitative trait and it regulates by so many factors. Indirect factors are plant height, growth duration, effective tiller number, length of panicle, seed length, seed setting and direct factors are panicle number, grains per panicle, filled grains and thousand grain weight (Sakamoto & Matsuoka, 2008; Huang *et al.*, 2011). Therefore, for improving yield related traits by direct selection sometimes become complicated and time demanding. Moreover, indirect selection is much easier and less time consuming. Consequently, it is suitable to use strongly correlated traits (Ahmadikhah *et al.*, 2008). Thousand grain weight is positively correlated with filled spikelets per panicle. All of those traits can contribute in enhancing yield of a genotype. Positive relationship between TGW and grain yield was described by Tsuzuki and Umeki, 1990. Furthermore, strong and significant relationship between yield and TGW also stated by the researchers (Mirza *et al.*, 1992; Efendi *et al.*, 2015). Significant relationship was found between filled spikelets and rice yield in this study, which corroborate with Ullah *et al.*, 2011. Additionally, panicle per hill positively correlated with rice yield which is similiar to the results of Abarshahr *et al.*, 2011. On the other hand, plant height has no significant relationship with the yield of the studied genotypes. Sarawgi *et al.*, 2013

described analogous results. Plant height and some other indirect traits have significantly weak relationship compared to the direct traits (Hairmansis *et al*., 2013). Mohaddesi *et al*., 2010 found that plant height and grain yield have a significant positive correlation.

By cluster analysis, 15 clusters were found from the distance analysis of the morphological traits of the studied genotypes. Based on 11 phenotypic traits 58 rice entries were grouped into four clusters reported by Ahmadikhah *et al*., 2008. Based on 20 morphological traits, 23 rice lines were divided into ten different groups (Veasey *et al*., 2008). The UPGMA dendrogram divided 41 bacterial blight resistant and susceptible rice varieties into six major clusters based on 13 agronomic traits (Mazid *et al*., 2013b).

First four principal components of the present study described around 77.2% of variation. Lasalita Zapico *et al*., 2010 also noted 82.7% of the total variability in 32 upland rice geno-types, which is almost similar to the results of our study. Eigenvectors specified the contribution of agronomic characters for percentage of variation to the principal components (Latif *et al*., 2011). Moreover, 70.99% variability was described by four principal components derived from the analysis of 11 phenotypic traits of 94 rice entries (Nihad *et al*., 2021). Caldo *et al*., 2016 noted the first 10 principal components described for 67% of total variability of the agronomic traits.

Principal coordinate analysis display the spatial dispersal of the varieties based on their relatedness (Nihad *et al*., 2021). Genotypes near to the centroid indicates they have similar characteristics, whereas genotypes distant from centroid indicates diverse characteristics (Nihad *et al*., 2021). Siddique *et al*., 2017 reported that the landraces distantly positioned from the center point were more diverse while the rice entries located near to the centroid carried more or less similar genetic composition and these findings support the result of the present study. Nevertheless, genotypes having broader deviation could be utilized as donor parents for hybridization to advance bacterial blight resistant variety.

CONCLUSION

Information generated from this study might be helpful for breeders to select resistant materials considering yield contributing character for durable bacterial blight resistant variety development. In Pearson's correlation coefficient, it is showed that yield per hill is positively correlated with number of spikelets per panicle (0.59***), number of filled spikelet (0.6***), thousand grain weight (0.36***), number of tiller per hill (0.6***) and number of effective tiller per hill (0.7***). Cluster 1 comprising single genotypes (SVIN310) showed the highest number of tiller, effective tiller, number of filled spiklets per panicle. PCA biplot analysis revealed that variability of number of tiller and effective tiller per plant, number of spikelets per panicle and yield per hill were high among the 92 genotypes. Yield contributing characters i.e., number of tiller and effective tiller per plant, number of spikelets per panicle, filled spikelets per panicle and thousand grain weight are positively related with yield per hill of the genotypes. Out of 92 INGER genotypes G1 (SVIN310), G23 (SVIN018), G70 (SVIN012), G75 (SVIN054), G33 (SVIN007), G48 (SVIN006), G80 (SVIN049), G90 (BRRI dhan84), G30 (SVIN290) near to the vector line of yield per hill are highly and positively responsive to the yield per hill. The mentioned genotypes could be used in hybridization programme to develop high yielding variety. In another words, the entry G1 (SVIN310) which have both yield potential and bacterial blight resistance phenomena could be used as resistant source to develop bacterial blight resistant variety.

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