academicJournals

Vol. 12(33), pp. 5173-5182, 14 August, 2013
DOI: 10.5897/AJB2012.2959
ISSN 1684-5315 ©2013 Academic Journals
http://www.academicjournals.org/AJB

African Journal of Biotechnology

Full Length Research Paper

Varietal resistance of rice to blast fungus *Magnaporthe oryzae* at two sites in southwestern Nigeria

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Accepted 26 July, 2013

This study was conducted to elucidate the performance of varieties with known resistance genes of rice at two sites and assess the efficiency of the two sites for screening rice genotypes for blast resistance. Thirty-four (34) varieties plus one local check were screened for resistance to rice blast disease caused by a fungus (*Magnaporthe oryzae*) at Ibadan and Ikenne under natural infection for two years. The experiment was laid out using randomized complete block design with four replicates. Data were collected on disease development and severity using standard evaluation scale. Data were subjected to analysis of variance and the effect of genotype, environment, and their interaction were further analyzed using genotype main effect plus genotype-by-environment (GGE) biplot. Results revealed that the thirty-five varieties responded differently to blast infection and the two sites were significantly different from each other. Genotype-by-environment interaction was significant and had the highest contribution to the total sum of squares for disease development and severity scores. GGE biplot revealed that only Moroberekan was resistant to blast fungus across years and sites. In conclusion, although, the two sites are found in the same agroecology, Ibadan was identified as a better site for screening rice genotypes for blast resistance than Ikenne.

Key words: Blast fungus, disease severity, genotype-by-environment interaction, genotype-by-environment (GGE) biplot, rice.

INTRODUCTION

Rice (*Oryzae* spp.) is the most important staple food in the world today (Hawksworth, 1985) which has become part of everyday diet of many households. Currently, the population of people eating rice is about three billion, which is about half of the total world population. Rice is a staple food for over half the world's people and has the second largest cereal production after maize with over 685 million tons recorded in 2008 (FAOSTAT). At the beginning of the 1990s, annual production was around 350 million tons and by the end of that century, it had reached 410 million tons. According to the International Food Policy Research Institute (IFPRI), rice production needs to increase by 38% by 2030 in order to meet the demands of the growing world population. Nigeria is West Africa's largest producer of rice, producing an average of 3.2 million tons of paddy rice for the past 5 to 6 years

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Abbreviation: ANOVA, Analysis of variance; **DAP,** days after planting; **GGE,** genotype main effect plus genotype by environment interaction; **IRRI,** International Rice Research Institute; **SES,** standard evaluation scale.

(WARDA, 1996). Rice cultivation is widespread within the country, extending from the northern to southern zones with most rice grown in the eastern and middle belt of the country. Rice production is constrained by many biotic and abiotic factors such as: crop management techniques (low –input and use of machinery) by small scale rice farmers, as well as lack of water control techniques, soil fertility, location, pests and diseases. Blast is a major threat to rice production in the tropics. Rice blast is a disease caused by *Magnaporthe oryzae* B. Couch (anamorph: *Pyricularia oryzae* Cavara) (Couch and Kohn, 2002). It belongs to the family Magnaporthaceae: order, Magnaporthales: class, Sordariomycetes: phylum, Ascomycota and kingdom, Fungi.

Rice blast is a problem almost everywhere that rice is grown. It is one of the main pathological threats to rice crop worldwide (Chadha and Gopalakrishna, 2005). The disease symptoms appear on the aerial parts of the plant. Most infections occur on the leaves, causing diamond-shaped lesions with a gray or white center to appear, which can consume the whole leaves and causing the death of the plant at any stage of growth and on the panicles, which turn white and die before being filled with grain. *M. grisea* is host specific to rice, although, certain strains that do not attack rice can harm weeds in the rice field. Blast is considered the principal disease of rice because of its wide distribution and high incidence under favourable conditions (Lavanya and Gnanamanikam, 2000).

Although, losses due to blast are difficult to estimate because of the compounding effects of environmental factors, high yield losses up to 80% have been recorded (Ou, 1985) and this usually occur when the pathogen (virulent) found the environmental conditions favourable, that is, relatively high humidity (up to 85% and above), high or excessive nitrogen fertilizer application, presence of dew and drought stress, conditions which tend to favor epidemic situation.

In Nigeria, rice blast disease was first recorded in Port Harcourt (River state) in 1956 (Awoderu, 1972) and later in Badeggi (Niger State) in 1958 and in Irrua in 1963. Since then, blast has been reported whenever and wherever rice is grown. The use of resistant varieties is the most economical and effective way of controlling rice blast mainly in resource-poor farmers' fields. Unfortunately, the causal fungus is able to overcome this resistance within two to three years after these plants are cultivated widely (Lavanya and Gnanamanickham, 2000). The breakdown in resistance has been attributed to the high variability of the pathogen and there are numerous reports that this diversity may be due to continuous generation of novel pathogenic variation and the knowledge of the genetic variation within and among populations is of prime importance in understanding the population biology of the pathogenic fungi (Xia et al., 2000).

Inadequate screening methods could indirectly be linked with the rapid breakdown of resistance; cultivars may be considered resistant; although, they are susceptible to existing pathogen sub-populations that are not represented in the screening nurseries used for varietal evaluation (Chen et al., 1995). Moreover, as blast disease is dependent on the prevailing environmental conditions (Sere et al., 2011), a rice variety that exhibit blast resistance in one locality may be completely susceptible in another. The use of near isogenic lines (NILs) provides an opportunity to characterize resistance genes phenoltypically (Mackhill and Bonman, 1992). Therefore, information on the efficiency of the screening sites is fundamental to the development of strategies to increase durability of resistance to rice blast.

The objectives of this study were to: a) elucidate the phenotypic performance of the near isogenic lines (NILs) in the two sites; and b) assess the efficiency of the two sites for screening rice genotypes for blast resistance under natural conditions.

MATERIALS AND METHODS

Genetic materials

Thirty-four (34) varieties with known resistance genes and one local variety of rice used for this study were obtained from the Genebank of the International Rice Research Institute (IRRI), through Plant Pathology Unit, Africa Rice Center, Cotonou. The varieties and the resistant genes they carry are listed in Table 1.

Experimental site

The study was carried out at International Institute of Tropical Agriculture (IITA) Station in Ibadan (7° 23' N, 3° 55' E, altitude of 204 m asl, 1500 m rainfall), Oyo State and Institute of Agricultural Research and Training (IAR&T) Station at Ikenne in Ogun State (6° 87′ N, 3° 7′ E, altitude of 60 m, about 1500 m rainfall). The two locations have history of high incidence of blast disease and are among the blast screening locations in Nigeria.

Field layout and experimental design

A land area of 7 × 15 m was ploughed and harrowed at each location. The plots were laid out using a randomized complete block design with 4 replications. Each entry was sown in 3 rows of 50 cm each with 10 cm spacing between rows and between holes leaving an alley of 1 m in-between blocks. Three to four seeds were sown per hole. Three infecting rows were planted between replications 1, 2, 3 and 4 fifteen (15) days before the entries were planted in order to increase and homogenize the inoculum. At the emergence of the seedling of these rows, infected leaves were collected in the diseased plants, scratch in small pieces and disseminated between the rows. At two weeks after planting, seedlings were thinned to one plant per stand. Missing stands were also filled from the extra seed planted in front of each variety. Two plants in the center of each variety were tagged as plant 3 and 4 (P3 and P4) and used for the data collection throughout the experiment. Weeding was done starting from three weeks after planting until it was no more necessary. NPK fertilizer was applied at planting at the rate of 200 kg/ha on infecting rows and 334 kg/ha on test entries. Urea was applied at the rate of 300 and 500 kg/ha of urea at 21 days after

Table 1. Varieties and lines used and their respective resistance genes.

Code	Name	Type*	Resistance gene
V1	IRBL 1-CL	Monogenic line	Pi1
V2	IRBL 11-ZH	Monogenic line	Pi11
V3	IRBL 12-M	Monogenic line	Pi12
V4	IRBL 19-A	Monogenic line	Pi19
V5	C103 TTP	NIL	Pi1b
V6	IRBL 20-IR 24	Monogenic line	Pi20
V7	IRBL 3-CP 4	Monogenic line	Pi3
V8	IR 1529	Variety	Pi33
V9	IRBL 5-M	Monogenic line	Pi5
V10	Moroberekan	Variety	Pi5(t), Pi7
V11	IRBL 7-M	Monogenic line	Pi7
V12	75-1-127	Variety	Pi9
V13	IRBL 9-W	Monogenic line	Pi9
V14	CO39	P-NILs	Pia
V15	IRBLA-A	Monogenic line	Pia
V16	Aichi Asahi	Variety	Pia + Pi19
V17	NipponBare	Variety	Pia + Pish
V18	IRBLB-B	Monogenic line	Pib
V19	St1	Variety	Pif
V20	IRBLI-F5	Monogenic line	Pii
V21	IRBLK KA	Monogenic line	Pik
V22	IRBLKH-K3	Monogenic line	Pik-h
V23	Tetep	Variety	Pikh+ Pi-1 +Pita + Pitp?
V24	IRBLKM TS	Monogenic line	Pik-m
V25	IRBLKP-K60	Monogenic line	Pik-p
V26	IRBLKS-F5	Monogenic line	Pik-s
V27	IRBLSH-S	Monogenic line	Pish
V28	IRBLT-K59	Monogenic line	Pit
V29	IRBLTA CP 1	Monogenic line	Pita
V30	IRBLTA 2-PI	Monogenic line	Pita-2
V31	IRBLZ FU	Monogenic line	Piz
V32	IRBLZ 5-CA $^{(R)}$	Monogenic line	Piz-5
V33	IRBLZT-T	Monogenic line	Piz-t
V34	LTH	P-ML	
V35	IRBLKS CO/CO	NIL as susceptible check)	Piks

* NIL = Near Isogenic Line; P-NIL = Recurrent parent for the Near Isogenic Lines; P-ML= Recurrent parent for the monogenic lines

sowing to infecting row and test entries, respectively.

Disease evaluation

The plants were examined twice a week, in order to ascertain the exact date of first appearance of symptoms on the varieties tested. Starting from the appearance of the first symptoms in each variety, evaluation was done in the two central holes), the number of leaves, number of tillers and the number of the following four types of lesions bs, bg, bG and pG. Disease progress was evaluated at the sampling times based on the percentage of diseased leaf area. Data were collected on the number of leaves on each rice plant from 3 weeks after planting. Starting from 21 days after planting, the blast symptoms were scored once a week using the standard evaluation scale (SES) of International Rice Research Institute (IRRI) (Table 2).

Statistical analysis of data

Data collected on disease severity and number of susceptible lesions was subjected to analysis of variance (ANOVA) to test for differences among the varieties and between the two screening sites. Means were separated using LSD. Scores and counts were log-transformed before subjecting to ANOVA. Entry means of blast severity at each screening site that were generated from the ANOVA were further analyzed using genotype main effect plus

Table 2. Standard evaluation scale of rice blast disease.

Scale	Description
0	No typical susceptible lesion observed.
1	Small brown specks (bs) of pin-point size without sporulating centre.
3	Small roundish to slightly elongated, necrotic grey spots, about 1 to 2 mm in diameter, with a distinct brown margin (bg).
5	Typical susceptible blast lesions 3 mm or longer, infecting less than 10% of the leaf area.
7	Typical susceptible blast lesions infecting 11 to 50% of the leaf area.
9	More than 75% leaf area affected.

Source: International Rice Research Institute (IRRI, 1980), Phillipines.

genotype by environment interaction (GGE) biplot analysis (Yan et al., 2000; Yan, 2001).

This software was used to partition significant genotype by environment interaction (GEI) obtained from ANOVA into their respective eigen values to investigate the performance and stability of varieties in the various environments, and to test for the discriminating power of the different testing sites. The biplots were constructed using Model 3 of the GGE Biplot software (Yan, 2001). In the model, the data were not transformed ('transform = 0'), not standardized ('scale = 0'), and were environment-centered ('centering = 2'). The polygon and the vector views of the GGE biplot were constructed based on genotype-focused singular value partitioning ('SVP = 2'), which rendered them appropriate for visualizing the relationships among environments.

The GGE biplot statistical model equation is presented as follows:

$$Y_{ij} - Y_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij}$$

Where, Y_{ij} is the average yield of genotype *i* in environment *j*, Y_j is the average yield across all genotypes in environment *j*, λ_1 and λ_2 are the singular values for PC1 and PC2, ξi_1 and ξi_2 are the PC1 and PC2 scores, for genotype *I*, η_{j1} and η_{j2} are the PC1 and PC2 scores, for environment *j*, ε_{ij} is the residual of the model associated with the genotype *i* in environment *j*.

The polygon view of the GGE biplot revealed which genotype is best for which environment. The biplot decomposes the significant GEI obtained in the analysis of variance to expose the pattern of the interaction that exists between the set of environments and the genotypes studied. In the biplot, genotypes found at the vertex of the polygon are considered the best for the environment or set of environments which fell within the sector. The lines from the origin of the figure divide the polygon into sectors.

RESULTS

Analysis of variance

Results of the combined ANOVA performed across the two sites for 2009 and 2010 showed significant difference for variety, site, year and interactions for the two growth traits, disease severity and at all levels of blast disease development (Table 3). Contribution of the different sources of variation to the observed total variation revealed that error, that is unaccounted sources of variation made the highest contribution to the total sum of squares (Table 3). For growth parameters, variety effect made the highest contribution (approximately 10% for number of tillers and 9% for number of leaf) to total sum of squares, followed by the G × E interaction effects (approximately 6% for number of tiller and 8% for number of leaf). When the genotype by environment interaction was partitioned into its components for number of tillers, year × variety had the highest contribution of 3.07% to the G × E interaction, followed by variety × site (1.93) and year × site × variety (1.35); whereas, the contribution of year × site was the lowest contribution (0.07). For number of leaf, variety × year contributed (2.50), variety × site 2.18, year × site 1.55 and variety × year × site 1.47. For disease development, G × E interaction had the highest contribution (approximately 16%) to the total sum of squares. When partitioned into its components (for pG), year × site has the highest contribution of 5.16, followed by variety × site × year (4.79), then, variety × year (2.91) while variety × site gave the lowest contribution of 2.62. For leaf blast severity (LBS) score, contribution of variety effect to the total sum of squares was the highest (approximately 26%), followed by G × E interaction effect (approximately 25%).

When partitioned into its components, year × site effect had 12.99 which is the highest contribution at 77 days after sowing, variety × site gave 4.41, variety × year × site gave 4.38 and variety × year gave 3.53 to the total G × E interaction at 77 days after sowing (Table 4). The G × E for LBS at 21 days after planting contributed 21.37% to the total sum of squares, when partitioned into its components; variety × year and variety × site contributed10.69 each to the GEI while variety × site × year and year × site had no contribution to the GEI effect at 21 days after sowing.

For LBS 98, GEI contributed approximately 17% to the total sum of squares, of which 10.55 was from variety × site × year effect, 3.56 was from variety × year effect, 2.53 was from variety × site and only 0.19 was from year × site effect.

For LBS49, GEI contributed approximately 14% into the total sum of squares. When partitioned into its components, year × site gave 4.35, followed by variety × site with 3.54, variety × year gave 3.32 and variety × year × site gave 2.95 into the contribution into the GEI.

The contribution of year effect was greatest for LBS and moderate for all other traits. In comparison, site effect contributed more in relative terms to blast symptom

Table 3. Proportion of sum of squares accounted for by sources of variation from the combined analysis of variance of the growth traits, level of disease development and severity of 35 rice varieties evaluated under natural blast infection at Ikenne and Ibadan in 2009 and 2010.

Source		Number of tiller	Number of leaf	bs	bg	bG	pG	Leaf blast severity (LBS)			
								21	49	77	98
Year	1	2.39**	4.08**	2.47**	1.14**	2.64**	4.36**	2.47	12.58**	8.33**	0.48**
Site	1	3.51**	1.85**	8.30**	5.14**	2.59**	2.99**	2.47**	0.00	1.10**	0.21**
VAR	34	9.97**	8.62**	4.34**	2.37**	2.10**	4.35**	21.21**	9.20**	14.67**	25.66**
G × E	103	6.43	7.71	11.74	15.21	11.49	15.49	21.37	14.16	25.31	16.84
Year*site	1	0.07*	1.55**	2.69**	9.26**	5.79**	5.16**	0.00	4.35**	12.99**	0.19**
VAR *year	34	3.07**	2.50**	2.14**	1.80**	1.80**	2.91**	10.69**	3.32**	3.53**	3.56**
VAR* site	34	1.93**	2.18**	3.48**	2.17**	2.13**	2.62**	10.69**	3.54**	4.41**	2.53**
VAR*year* site	34	1.35**	1.47**	3.42**	1.98**	1.77**	4.79**	0.00	2.95**	4.38**	10.55**
Error	312	55.88	56.62	51.97	48.11	64.21	72.03	57.89	62.63	49.51	48.22

*, ** - significant at 0.05 and 0.01 levels of probability, respectively; ns – not significant. bs, Hypersensitive lesion; bg, susceptible lesion; bG and pG, highly susceptible lesion.

Table 4. Mean values for growth traits, level of disease development and severity of 35 rice varieties evaluated under natural blast infection at Ikenne and Ibadan in 2009 and 2010.

Trait	Ibadan	Ikenne	LSD
Number of tillers	1.33	1.11	0.03
Number of leaves	2.31	2.095	0.45
bs	0.63	1.515	0.07
bg	0.02	0.82	0.05
bG	0	0.32	0.03
pG	0.045	0.17	0.02
LBS21	0.32	0.12	0.07
LBS49	0.74	0.45	0.08
LBS77	1.39	1.245	0.07
LBS98	1.89	1.86	0.04

development. As a proportion of the total observation, variety effect contributed less than 5% to symptom, 9.97% to number of tillers, 8.62 to leaf, but 9.20 to 25.66 to leaf blast severity. Similarly, the greatest contribution of G × E was to LBS ranging from 14 to 25, then to disease development 11.49 to 15.49; whereas, the corresponding contribution to number of tillers and number of leaf was 6.43 and 7.71, respectively. There were significant difference between the means of all the growth traits and disease development traits at the two locations, whereas, there were no significant difference between the leaf blast severity parameters taken in the year 2009 and 2010.

The graphs of the pattern of resistance/susceptibility of selected varieties showed no significant difference between the resistant varieties and the susceptible varieties at Ikenne until 77 days after sowing (Figure 1); whereas, there was a significant difference between the resistant and susceptible varieties at Ibadan site by 49 days after sowing (Figure 1).

Biplot analysis of the blast infection pattern at Ikenne and Ibadan

The results presented in Figure 2 showed the polygon view of the GGE biplot analysis. In the biplot view, the genotypes located at the vertex (vertex genotype) of the polygon were the best for the locations that fell within the sector. Therefore, the figure showed that (V12) (75-1-127 *Pi9*) was the vertex genotype in the sector where (IK09) Ikenne in 2009 fell; while V10 (Moroberekan) was the vertex genotype in the sector where Ikenne in 2010, Ibadan in 2009 and Ibadan in 2010 were found (Figure 2). Figure 3 presented a vector view of the GGE biplot showing the discriminating ability and representativeness of the testing site. The biplot also revealed the repeatability of the sites for testing rice genotypes for blast resistance. In the biplot, the length of the environment vectors approximates the standard deviation within each environment. This means that the longer the environment vector, the more discriminating the environment. In addition,

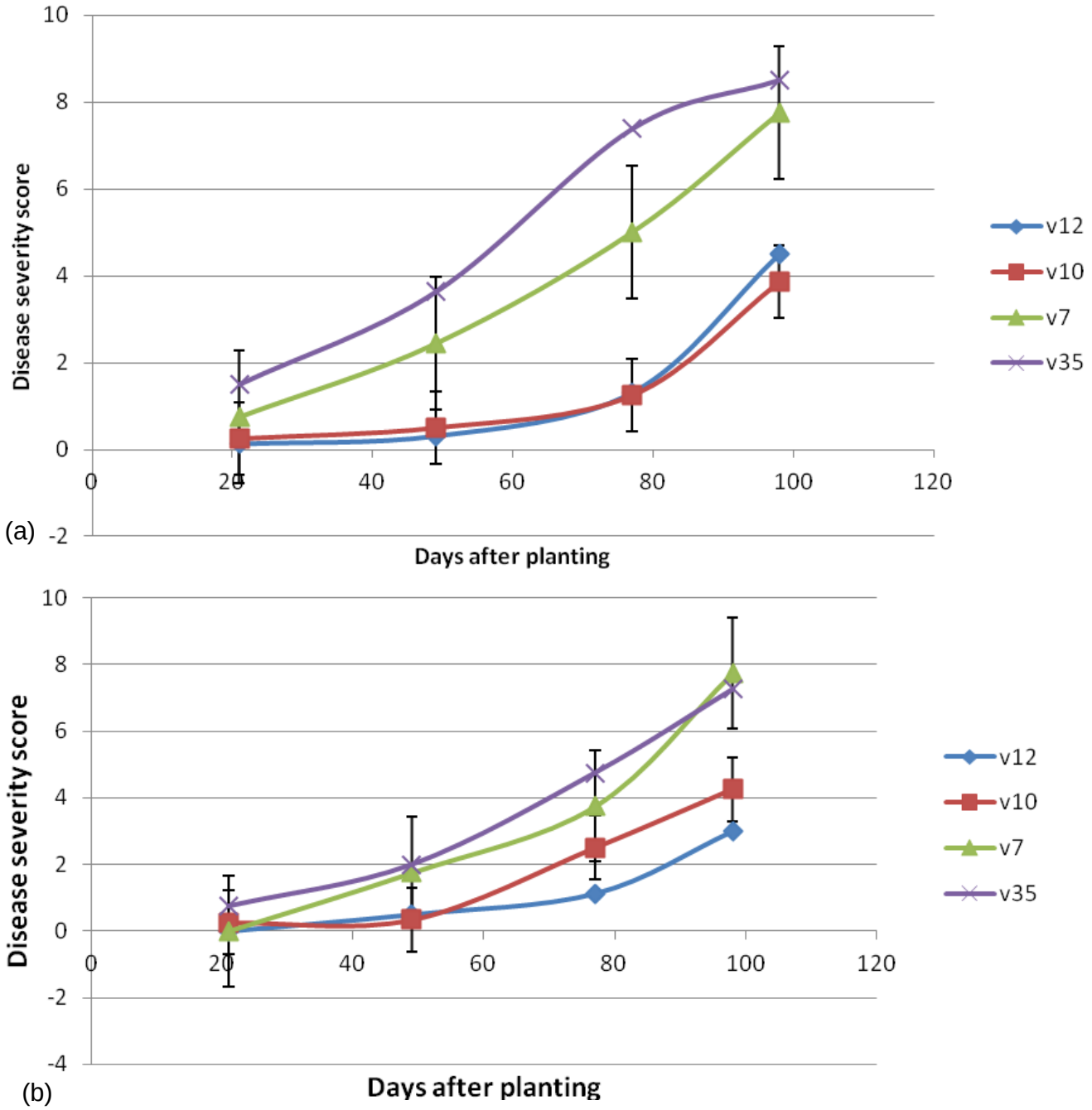

Figure 1. Pattern of blast resistance/susceptibility of two selected resistant and two selected susceptible varieties; (a) at Ikenne and (b) at Ibadan from 21 to 98 days after planting.

the angle between the vector of an environment and the average environment (small circle on the single-arrow horizontal line) axis is a measure of the representativeness of the environment. Furthermore, the cosine of the angle between any two environment vectors is a measure of their correlation coefficient between them. Figure 3 shows that Ikenne in 2010 was the most discriminating environment, indicating that it is most efficient in screening for rice blast.

Ibadan in 2009 and Ibadan in 2010 were moderately discriminating. The biplot showed that the year had little effect on the performance of the varieties at Ibadan site as revealed by an acute angle between Ibadan in 2009 and Ibadan in 2010 and relatively equal vector length in the biplot, indicating that Ibadan is moderately repeatable. Results for Ikenne however, showed that Ikenne in

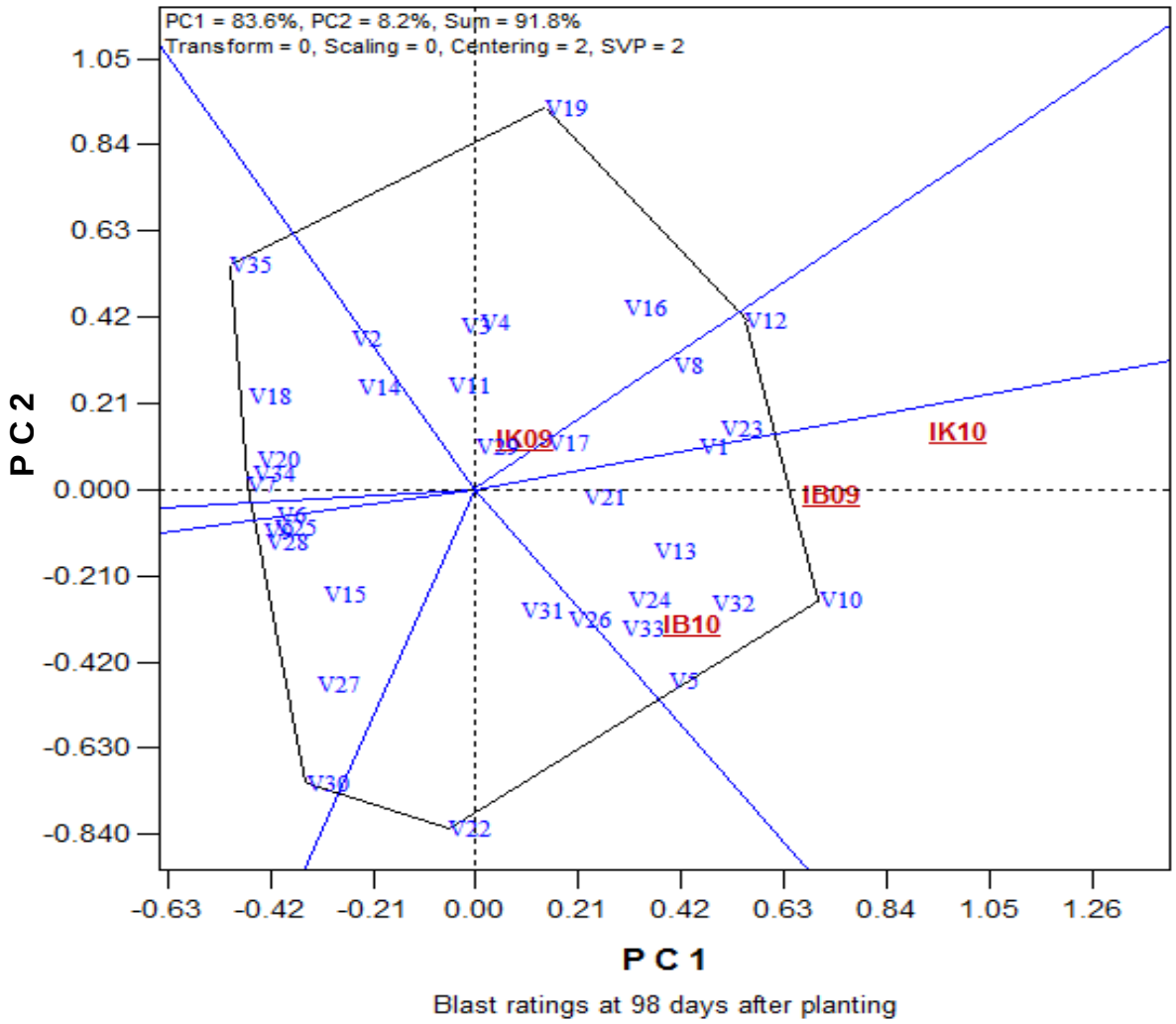

Figure 2. Polygon view of GGE biplot, showing which variety is resistant in the study environment. The two principal components (PC1 and PC2) explained 91.8% of the total GGE variation. The genotypes are in blue colour and environments are in red colour. The guidelines indicate zero values for the two axes respectively. IB09 = Ibadan, 2009; IB10 = Ibadan 2010; IK09 = Ikenne, 2009; IK10 = Ikenne, 2010.

2009 was less discriminating than Ikenne in 2010; in fact, the least discriminating among the four test environments. The indication of this is that the two locations are not correlated and the results from the two environments were not consistent with each other. Disease severity index of the 35 varieties at the two locations showed that at Ibadan, only ten varieties (V10) Moroberekan, (V32) IRBLZ5-CA(R), (V12) 75-1-127, (V24) IRBLKM-TS, (V13) IRBL9-W, (V5) C103TTP, (V1) IRBL1-CL, (V23) Tetep, (V33) IRBLZT-T and (V8) IR1529) of the 35 varieties were resistant while twelve varieties (V10) Moroberekan, (V12) 75-1-127, (V8) IR1529, (V24) IRBLKM-TS, (V23) Tetep, (V13) IRBL-9-W, (V16) Aichi-Asahi, (V1) IRBL1-CL, (V29) IRBLTA-CP-1, (V17) NipponBare, (V19) St1 and (V32) IRBLZ5-CA(R) showed resistance at Ikenne (Table 4).

DISCUSSION

The varieties evaluated exhibited differential but characteristic responses to the rice blast fungus as it has been reported earlier (Odjo et al., 2011). The contrasts of the two sites were unexpected at least to the extent and magnitude observed, because the two sites were in the same agro-ecological zones and is expected to share similar macroclimatic conditions. Nevertheless, the differences suggest that site specific microclimatic factors and the variability associated with them are more in blast screening than apparent macroclimatic factors in the choice of site for blast screening. Furthermore, there may be possibility of the presence of different strains of blast fungus at the two sites since the genotypes used in this study were special varieties, each carrying specific

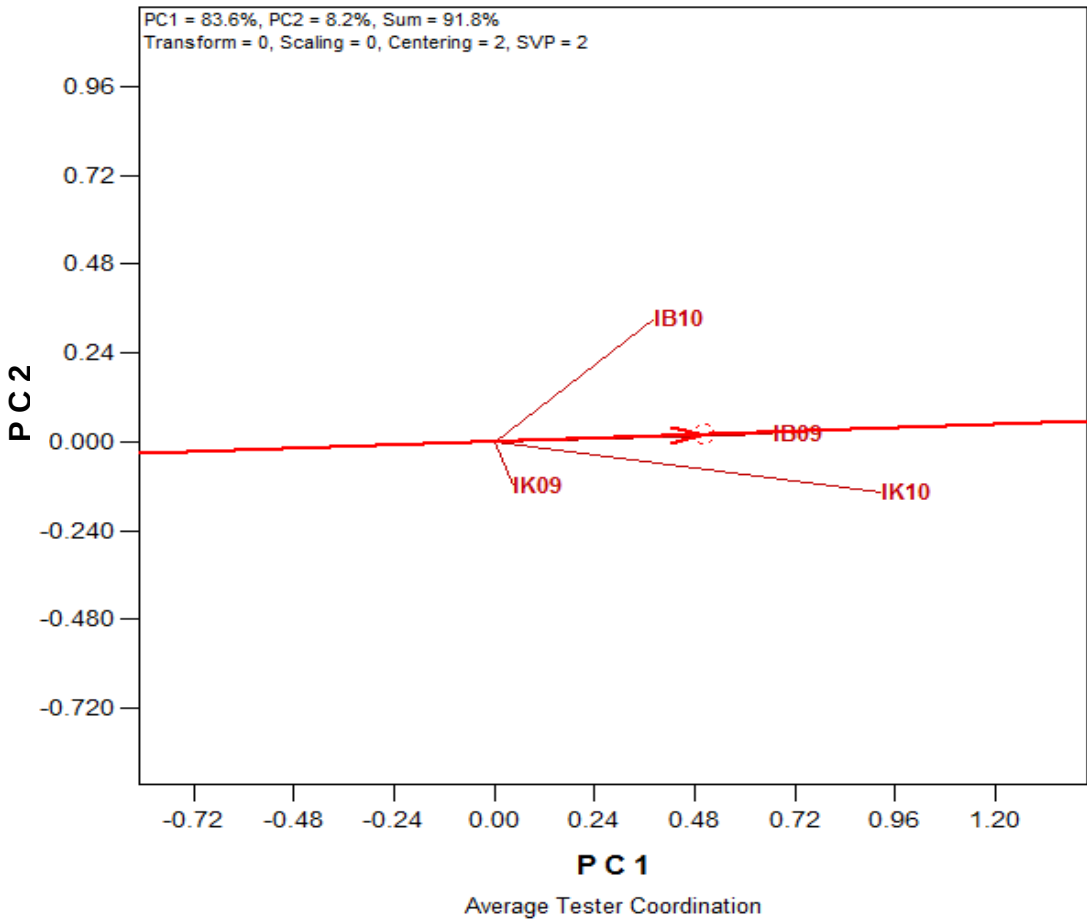

Figure 3. A vector view of GGE biplot showing the discriminating ability and representativeness of testing sites for blast fungus in southwestern Nigeria.

known resistant genes. According to Sere et al. (2003), it is important that the performance of a variety be viewed in relation to the biotic and abiotic parameters of the environment (or precisely of the site and ecological niches) that have been targeted. However, further study on genetic diversity of the blast inoculum collected from the two sites is needed to confirm this observation. In the statistical model used for this study, although, there were significant effects for all main factors and interaction effects, it is interesting to note that among the known sources of variation, GEI consistently had highest contribution to the total sum of squares for all levels of disease development and severity scores except at 98 days after planting. For growth traits, however, variety had the highest contribution to total sum of squares. This is an indication that blast disease development and severity scores were greatly conditioned by environmental factors while growth traits were controlled by the genotypic effect of the variety. This result is expected because the evaluation was carried out under a natural infection conditions on the field. Different trends may be observed if evaluation has been done in the screen house conditions or under artificial inoculation on the field. The pattern of disease severity differed at the two locations. At Ikenne, the difference between resistant and susceptible varieties were not significant until about 98 days after planting while difference became significant by around 78 days at Ibadan. The two selected susceptible varieties had similar response to blast from the first stage (21 DAP) to 98 days at Ikenne whereas at Ibadan, the pattern of response of the two susceptible varieties were significantly different especially at 77 days. For the two resistant varieties, the pattern of blast disease severity at Ibadan was similar at all stages but significantly different at Ikenne. This result indicate that despite the fact that two resistant varieties possessed different resistant genes for blast resistance, their ability to express resistance is greatly conditioned by environmental factors at Ikenne than at Ibadan. (V10) Moroberekan expressed outstanding resistance at Ikenne while the environmental factors at Ibadan did not permit the outstanding performance of the variety. By implication, Moroberekan (V10) is the most suitable variety in terms of blast resistance for farmers' cultivation in the southwestern region of Nigeria.

Since tillering is an essential factor when estimating yield (Jaffuel and Dauzat, 2005), it then implied that (V8)

IR1529, (V23) Tetep, (V19) St1, (V16) Aichi-Asahi and (V29) IRBLTA-CP-1 would be high yielding varieties while (V22) IRBLKH-K3, (V28) IRBLT-K59 and (V10) Moroberekan would be poor yielding ones. The implication of the inclusion of (V10) Moroberekan among poor-yielding variety, which was earlier identified as resistant to blast, is that blast resistance in rice does not necessarily imply high yielding. However, breeders are advised to use (V10) Moroberekan as a veritable source germplasm to introgress blast resistance into some elite high-yielding varieties adapted to this region. The thirty five varieties responded differently to blast infection at the two sites within the two years of research. At Ikenne, only three varieties (V10) Moroberekan, (V12) 75-1-127 and (V8) IR1529 were moderately resistant to blast fungus both in 2009 and 2010 while six varieties (V10) Moroberekan, (V24) IRBLKM-TS, (V23) Tetep, (V32) IRBLZ5-CA(R), (V5) C103TTP and (V13) IRBL9-W were moderately resistant to blast during the two years. Across years and locations, only V10 (Moroberekan) was resistant to blast fungus. This result is expected since Moroberekan is known to have a durable resistance to blast. It possess two vertical resistance genes (*Pi5* on chromosome 4 and *Pi7* on chromosome 11), but also quantitative trait loci (QTLs) for partial resistance on eight chromosomes (Wang et al., 1994).

Moreover, at least six major blast resistance loci have been identified in Moroberekan (Chen et al., 1997). It could therefore be said that it exhibited horizontal resistance to blast fungus. It has been reported in the literature that Moroberekan has been cultivated without severe blast damage for many years in upland areas of West Africa (Ahn and Seshu, 1987; Fomba and Taylor, 1994). Considerable progress towards understanding the genetic basis of durable resistance to rice blast in Moroberekan has been made in a series of studies. The identification of at least six major genes and ten quantitative trait loci (QTLs) in Moroberekan provides strong circumstantial evidence that durability of blast resistance is a function of the combination of major genes qualitative resistance and QTLs for partial or quantitative resistance (Huang et al., 1997). The major genes *Pi5(t)* and *Pi7(t)* were identified in the F7 population derived from a cross between Moroberekan (of the *japonica* subspecies) and CO39 (of the *indica* subspecies) (Wang et al., 1994). Field performance of the lines carrying *Pi5(t)* and *Pi7(t)* suggested that *Pi5(t)* and *Pi7(t)* conditioned broad resistance spectrum (Ziegler et al., 1995). Combination of carefully characterized major genes and QTLs would contribute to the consistent development of cultivars with durable resistance.

The significant G × E interaction from the combined ANOVA justified the use of GGE biplot to further analyze the interaction components. The biplots analyzed interaction at the different stages of disease development and severity that different varieties had outstanding resistance to blast at different stages. This also means that different genes conferred resistance to blast at different levels of disease development/severity. (V28) IRBLT-K59 was the best at the Ibadan in 2009, Ikenne in 2009 and Ikenne in 2010 while (V31) IRBLZ-FU at Ibadan in 2010 at 21 DAP. This implies that (Pit and Piz) genes are more efficient for blast tolerance at this stage. At 49 and 77 DAP, however, (V32) IRBLZ5-CA(R) was the best at IK09 Ikenne in 2009 and Ikenne in 2010, (V23) Tetep at Ibadan in 2009 and (V10) Moroberekan at Ibadan in 2010. This also implies that (Piz-5, Pikh + Pi-1 + Pita + Pitp) and *Pi5(t)* and *Pi7(t)* genes controlled blast resistance at this stage. The results at 98 DAP showed that it is only (V10) Moroberekan that carried through the resistance. The discriminating ability and representativeness of the locations revealed that the two vectors of Ibadan had moderately high discriminating ability and the angles between the two vectors revealed that Ibadan had moderately high representativeness. On the other hand, Ikenne in 2010 had high discriminating ability whereas Ikenne in 2009 had a short vector. The implication of this is that the two vectors are not correlated (Yan et al., 2007). Generally, the result shows that Ibadan is a better test location for screening for rice blast resistance than Ikenne.

In conclusion, the results of the research showed that the two testing sites were not the same even though they are in the same ecological zone (rainforest). The differences could be site specific such as the amount of rainfall and soil characteristics. The blast disease development and severity scores were greatly conditioned by environmental factors while growth traits were largely genotypic effect of the varieties. The performance of the thirty five varieties should be viewed in relation to the biotic and abiotic parameters of the environment. Ibadan had moderate discriminating ability in the two years while Ikenne site had a high discriminating ability in one year and low ability in the other year (showing inconsistency); the consistency of Ibadan site makes it a better site for screening for blast resistance than Ikenne. Moroberekan (V10) was resistant to blast fungus across year and location while V35 (local check) and V7 (IRBL3-CP 4) were highly susceptible to blast fungus at the two sites. However, further study on genetic diversity of the blast inoculums collected from the two sites to confirm this observation is underway.

ACKNOWLEDGEMENTS

The authors of this paper wish to acknowledge the financial support of the African Rice Centre and technical assistance of its field staff. The authors also acknowledge the contributions of Dr B. O. Odu to the write-up.

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