

GGE BIPLLOT ANALYSIS OF PERFORMANCE IN FARMERS' FIELDS, DISEASE REACTION AND GRAIN QUALITY OF BACTERIAL LEAF BLIGHT-RESISTANT RICE GENOTYPES

RODANTE E TABIEN^{1*}, STANLEY OMAR PB SAMONTE²,
MARLOU C ABALOS¹ & ROLANDO C SAN GABRIEL¹

¹Philippine Rice Research Institute, Science City of Muñoz, Nueva Ecija, Philippines; *Current address: Texas A&M University Agricultural Research and Extension Center, 1509 Aggie Drive, Beaumont, TX 77713, USA. ²Department of Horticulture, Crop Science Cluster, College of Agriculture, UP Los Baños, College, Laguna 4031

The current technology of using DNA markers facilitated the pyramiding of bacterial leaf blight (BLB) resistance genes, selection and development of five elite lines after three backcrosses. These DNA marker-aided selection (MAS)-derived lines were evaluated for yield and grain qualities in farmers' fields in 15 environments in 2000-2002, after inoculation with nine races of BLB pathogen in the screen house. GGE biplot analyses were conducted to identify the stable genotype for deployment as well as the suitable areas for its commercial grain production. Analysis on grain quality and disease reaction also aimed to determine donor parents for the trait and identify BLB races that will be useful in further screening for resistance. Results showed AR32-19-3-3 has the best yielding line for deployment in Nueva Ecija, Baler and Eastern Samar provinces. It has the best package of resistance to all BLB races and the grain traits commonly found in IR64, the most popular quality rice in the Philippines. It is a good donor for grain quality traits such as amylose content and grain shape. GGE biplot analyses pinpointed the best in this line, thus supporting the varietal release of AR32-19-3-3 in 2006, currently called NSIC Rc142 - 'Tubigan 7.' Among the lines, AR32-4-58-2 is a good donor for high milling recovery, head rice and crude protein content. Race 6 is the best representative race for inoculation among BLB races, while races 1 and 5 are good for BLB resistance screening.

bacterial leaf blight, disease resistance, GEI, GGE biplot, grain quality, rice

INTRODUCTION

Bacterial leaf blight (BLB), caused by *Xanthomonas oryzae* pv *oryzae*, is one of the most devastating diseases in the rice production areas of the Philippines and several Asian countries. The causal pathogen, which infects rice at the seedling stage, is known as *kresak* and causes leaf blighting at maximum tillering and heading stages; it is endemic to several provinces of the Philippines, particularly in the Visayas. It significantly reduces grain yield and grain quality during severe infection.

Breeding for resistance is one of the options to combat BLB. Towards this end, more than 30 major genes and several quantitative trait loci (QTLs) have

been identified for BLB resistance. Some of these genes have been mapped and tagged, and the corresponding linked DNA markers have been located or developed. These markers are the new tools in transferring or pyramiding BLB genes.

A project of the International Rice Research Institute (IRRI) and the Asian Biotechnology Network (ARBN) was conceptualized and subsequently funded by the Asian Development Bank (ADB) to use DNA markers in rice breeding. Collaborators from Asian rice-growing countries, ie, Indonesia, India, China, Vietnam, Thailand, and the Philippines transferred or pyramided the resistance genes into their popular varieties and these are now ready for evaluation. Some of the collaborators released MAS-derived lines as

new varieties (Leung et al 2004).

Yields of rice in BLB-endemic areas are not stable due primarily to the genotype of the varieties and the environmental factors that favor or inhibit development and spread of the disease. Resistance genes *xa5*, *xa13*, and *Xa21* provide effective control even for various races of BLB, while high relative humidity and low temperature are both critical in the disease cycle of BLB (Singh et al 2001). Use of resistant varieties and their proper deployment spatially and temporally are generally recommended to increase yields in BLB-endemic areas and preserve the effectiveness of resistance genes (Leung et al 2004).

Yield can be attributed to genotype (G), environment (E), and genotype x environment interaction (GEI). Although major BLB resistant (R) genes are generally effective and less affected by the environment, yield being a complex trait may not be determined solely by the presence of the R gene. Moreover, GEI may be large that yields become unpredictable. Genotypic performance can be analyzed using multi-location or multi-environment trials (MET) and several approaches have been used to evaluate genotypic stability and yield performance.

Recently, the GGE biplot analysis was proposed to study MET and GEI (Yan 1999, Yan et al 2000, Yan 2001). It is a graphical display of two important parts of variation, G and GEI, which are relevant in genotype evaluation. It is constructed using the principal components PC1 and PC2 obtained after single-value partitioning (Yan 2002).

PC1 represents the proportional cultivar response across locations and is considered as the genotype axis, while PC2 represents the disproportional cultivar response across location and is called the genotype by environment axis or non-genotype axis (Yan et al 2000, Laffont et al 2007). Genotypes with high PC1 values give higher average yields, and locations with large PC1 and near zero PC2 are useful in identifying high-yielding genotypes.

GGE biplots can identify cultivars with high yield

and high stability, and identify environments that can discriminate genotypes or that can serve as representative environments of the whole region (Ma et al 2004, Yan & Tinker 2004, Navabi et al 2005, Samonte et al 2005, Dardanellia et al 2006).

Furthermore, the biplot can be useful in determining breeding objectives and selecting sites (Yan & Hunt 2001), visualizing trait relations (Yan & Rajcan 2002, Navabi et al 2005, Yan & Tinker 2005, Dardanellia et al 2006), determining specific and general combining ability, best cross, group and parents in diallel (Yan & Hunt 2002), investigating QTL-environment patterns (Yan & Tinker 2005), and studying genotype susceptibility and/or race/isolate virulence groups (Yan & Falk 2002). GGE biplot can be used in both replicated plots and on-farm strip plots (Yan et al 2002).

At the Philippine Rice Research Institute (PhilRice), several elite lines with one or more BLB resistance genes, particularly *Xa4*, *xa5* and *Xa21*, have been undergoing various yield trials. While waiting for the national coordinated testing, five elite lines were evaluated in on-farm strip plots. This study used GGE biplot analysis to evaluate the performance of these elite lines, which had either single or a combination of *xa5*, *Xa21* and *Xa4* resistance genes, in farmers' plots for yield, grain quality data, reaction to nine BLB races, and to identify the best rice genotype for deployment and best areas for commercial rice production. Analysis of grain quality and disease reaction aimed to determine important traits and BLB races that will be useful in setting breeding objectives.

MATERIALS AND METHODS

Genotypes for Evaluation

Five elite lines and two check varieties were used in this study (Table 1). The elite lines, pyramided for BLB resistance genes, were selected after three and four backcrosses to IR64 and BPI Ri-10, respectively (Tabien et al 2003). Both AR32-19-3-3 and AR32-19-

3-4 reached the multi-location adaptation trial, which is the last phase before varietal release. IR64 served as check for yield and grain quality, while PSB Rc28 served as BLB susceptible check.

Treatments and Cultural Management

The elite lines and check varieties were evaluated using farmer strip plots in towns and provinces reported to have BLB. The disease was seasonally present in these areas, but worse during the wet season. Farmer leaders willing to conduct trials were selected as farmer-cooperators to facilitate the introduction of the BLB resistant lines in these areas.

In each site, farmer cooperators shared 0.25 ha of their irrigated land for the growth and evaluation of the elite lines and check cultivar of their choice (IR64 or PSB Rc28). Cultural management was based on the farmer's practice, except for fertilizer that was based on the recommendation of the Bureau of Soils and Water Management.

Data on yields from each site were obtained from five 1-m² plots. For three years (2000 to 2002), the entries were evaluated in 15 sites. In most environments (year x location combinations), the entries were evaluated during the wet season when BLB was prevalent.

BLB Resistance and Physio-Chemical Grain Evaluation

The same reactions to BLB races as reported in an earlier paper in this journal (Tabien et al 2003) were used in the data analysis. These were taken as follows: all entries (including IR24 as susceptible check) were grown in the screen house at the PhilRice Headquarters in Maligaya, Muñoz, Ecija, for inoculation.

At 21 days after seeding, 20 seedlings of each entry were transplanted at 20 x 20 cm rows to plots. At maximum tillering, 2-3 tillers were separated and assigned to each race. At inoculation, BLB inoculum suspension of 1 x 10⁹ cells/mL was prepared and the suspension was introduced into each plant using the

leaf clip inoculation method. At 14 days from inoculation, the lesion length from the tip of the cut leaves was measured from the three uppermost leaves.

Harvests from a dry season trial at Nueva Ecija during the 2001 wet season (WS) were used for grain quality test. Physical and chemical grain attributes of the samples were measured following the standard protocol of the National Cooperative Test for rice (NCT 1996). The same grain test results reported in an earlier paper in this journal (Tabien et al 2003) were used in the biplot analysis.

Genotype x Environment (Location) Interaction

The SREG model analysis of grain yield was performed using the SAS (SAS Institute 1999) programs written by Burgueño et al (2001). The SREG linear-bilinear model is represented by:

$$\bar{y}_{ij} = \mu + \delta_j + \sum_{k=1}^l \lambda_k \alpha_{ik} \gamma_{jk} + \bar{\varepsilon}_{ij}$$

where \bar{y}_{ij} is the mean of the i^{th} cultivar in the j^{th} environment for g genotypes and e environments ($i = 1, 2, \dots, g$ and $j = 1, 2, \dots, e$); μ is the overall mean; δ_j is the site effect; λ_k ($\lambda_1 \geq \lambda_2 \geq \dots \geq \lambda_l$) are scaling constants (singular values) that allow the imposition of orthonormality constraints on the singular vectors for cultivars, $\alpha_k = (\alpha_{1k}, \dots, \alpha_{gk})$ and sites, $\gamma_k = (\gamma_{1k}, \dots, \gamma_{ek})$; α_{ik} and γ_{jk} for $k = 1, 2, 3, \dots$ are called "primary," "secondary," "tertiary," . . . etc. effects of the i^{th} cultivar and j^{th} site, respectively; $\bar{\varepsilon}_{ij}$ is the residual error assumed to be normally and independently distributed ($0, \sigma^2/r$) (where σ^2 is the pooled error variance and r is the number of replicates). In the SREG model, the main effects of cultivars (G) plus the GE interaction were absorbed into the bilinear terms (Burgueño et al 2001, Crossa et al 2002).

The GGE biplot methodology, which is composed of two concepts, the biplot concept (Gabriel 1971) and GGE concept (Gauch & Zobel 1996, Yan et al 2000), was used to visually analyze the results of SREG analysis of MET data. This methodology uses a biplot to show the two factors (G plus GE) that are

important in genotype evaluation and that are also the sources of variation in SREG model analysis of MET data (Yan et al 2000, Yan et al 2001). The GGE biplot shows the first two principal components, PC1 and PC2, also referred to as primary and secondary effects, respectively (Yan et al 2000). In this study, GGE biplots were used to compare the performance of different genotypes at an environment, compare the performance of a genotype at different environments, compare the performance of two genotypes at all environments, identify the highest yielding genotypes at the different mega-environments, and identify ideal cultivars and test locations.

Three data subsets were analyzed to present a comparison of environments with the common checks IR64 (the standard check for yield and grain quality) and PSB Rc28 (BLB susceptible check), and comparison among MAS-derived lines in different environments.

Host x Pathogen Interaction

Lesion length data from Tabien et al (2003) were analyzed similar to yield-location analysis, with PC1 and PC2 values plotted in biplots. The distribution of the races and genotype in the polygon drawn on races that are farthest from the biplot origin indicates relationships and groupings.

Genotype x Grain Quality Traits Interaction

Data for the GGE biplot analysis of physical and chemical traits of the grains for each genotype were obtained from Tabien et al (2003). Similar analysis as above was conducted.

RESULTS AND DISCUSSION

Genotype x Environment (Location) Interaction

IR64 vs MAS-Derived Lines

The GGE biplot for the grain yield of 6 rice genotypes in nine environments with IR64 as check showed that the first principal component (PC1)

explained 38.5% of the G and GEI effects, while PC2 explained 30.5%, for a total of 69.0% (Figure 1). The amount of variation explained was 4x the amount of total GGE explained by just the genotypic effect alone. Three MAS-derived lines and IR64 formed the vertices of the polygon, indicating their responsiveness to the nine environments evaluated. Among the entries, AR32-19-3-3 and AR32-4-33-1 showed the best yield responses.

Analysis of the adaptation of rice genotypes in nine locations revealed through the location distribution along the genotype line, a line passing from the genotype vertex to the biplot origin, that IR64 performed best at PhilRice (Muñoz, Nueva Ecija) and San Jorge (Samar), AR32-19-3-3 performed best at Talavera and Cabanatuan (towns in Nueva Ecija), and AR32-4-33-1 performed best in the island of Mindoro, Northern Samar, and Iloilo. AR32-19-3-2 was not the best cultivar for any of the environments tested. Further analysis showed that the nine locations can be grouped into three mega-environments (each having a common best performing genotype). These were: a) Abra, Mindoro, Samar and Iloilo for AR32-4-33-1, b) PhilRice, San Jorge of Samar for IR64, and c) Cabanatuan and Talavera of Nueva Ecija for AR32-19-3-3.

These results reflect the current popularity of IR64 among farmers in Nueva Ecija, one of the major rice-growing provinces of the Philippines, and in the island of Samar. For the MAS-derived lines, the best line, AR32-19-3-3, is also well-suited in Nueva Ecija like its recurrent parent (IR64). Having been backcrossed to IR64 three times, AR32-19-3-3 is about 87.5% genetically like IR64; thus, it performed as well as IR64. During an earlier evaluation of the five MAS-derived lines in Nueva Ecija, AR32-19-3-3 was the popular choice among the farmers, and the seed exchanges propelled its popularity.

Comparison of IR64 with the MAS-derived entries using the perpendicular line to the linking line between IR64 and MAS-derived line being compared as shown in Figure 2 (eg, IR64 vs AR32-19-3-3)

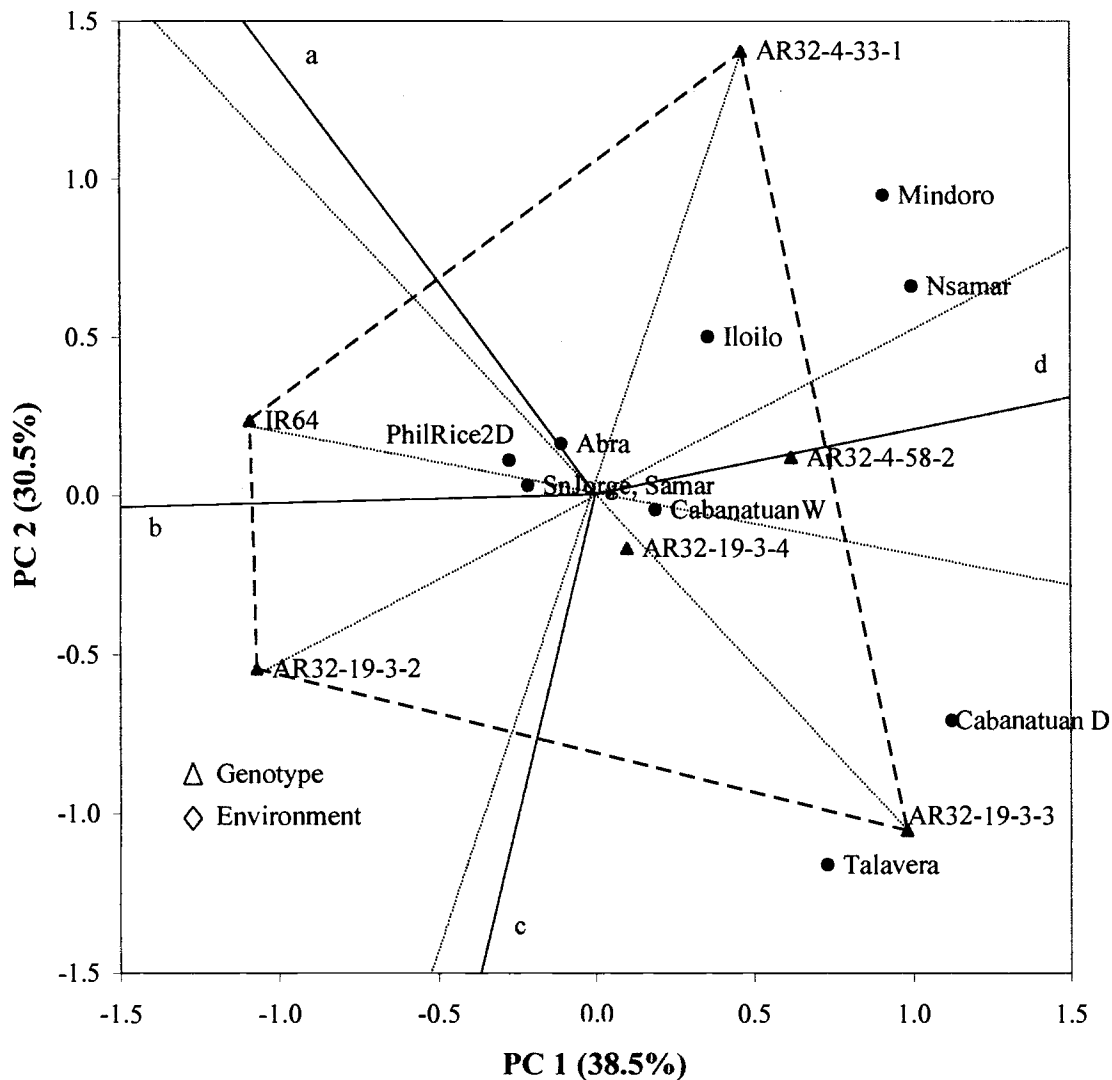


Figure 1. Biplot of genotypes that performed best in each of the environment. Lines a to d divided the graph into 4 sectors showing specific environment for the winning genotype(s).

revealed that both AR32-19-3-3 and AR32-4-33-1 yielded better than IR64 in six out of nine locations (Mindoro, Northern Samar, Iloilo, Cabanatuan D, Cabanatuan W, and Talavera NE), while AR32-19-3-2 was better than IR64 in three locations (Cabanatuan D, Cabanatuan W and Talavera NE). Using the mean environment axis in the biplot as shown in Figure 2, following Samonte et al (2005), the highest yielding entry in this subset was AR32-19-3-3, followed

closely by AR32-4-33-1 and AR32-4-58-2. These entries had higher yields than IR64. Furthermore, the two most stable lines among entries and relative to IR64 were AR32-4-58-2 and AR32-19-3-4. The biplot indicated that of the five MAS-derived lines, four had higher yields and two had more stable yields than IR64 across locations. These results showed the advantage of having resistance gene for the endemic disease. IR64 has no xa5 and Xa21 genes for BLB

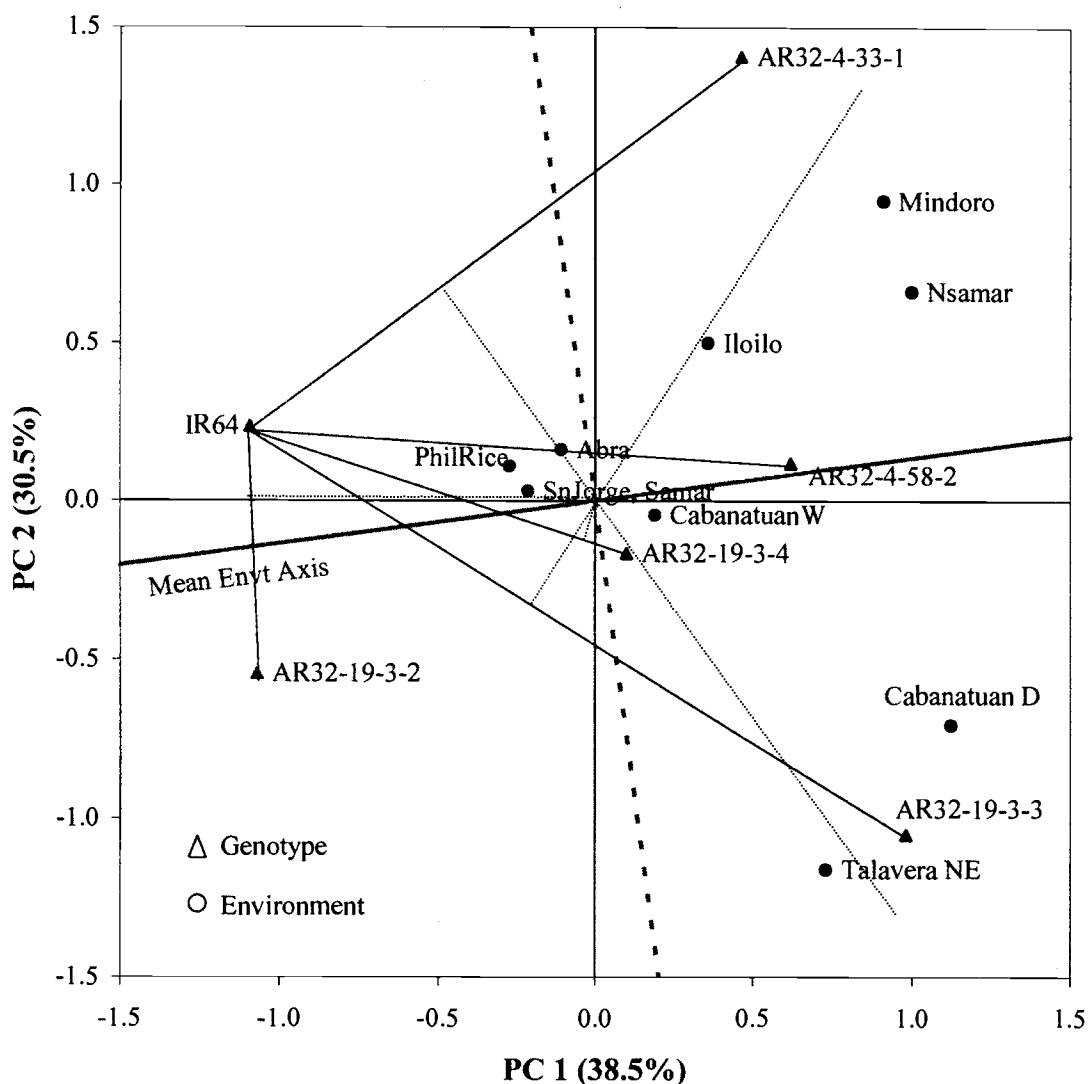


Figure 2. Biplot showing the yield performance and stability of IR64 compared with MAS-derived lines in each environment

resistance, thus resulting in a relatively lower performance under high disease pressure.

The relationship of sister lines AR32-19-3-3 and AR32-19-3-4 are shown in the biplot, as the two were clustered in the same mega-environment. These sister lines have the same BLB genes, and they were produced from three backcrosses to IR64, making

them similar in genetic background to IR64, but with two more BLB resistance genes. These BLB genes are the major differences between the sister lines and IR64. This was clearly reflected in their high yield advantage over IR64 (IR64 = 2.2 t/ha, AR32-19-3-3 = 4.62 t/ha, AR32-19-3-4=4.53 t/ha) in BLB-endemic areas.

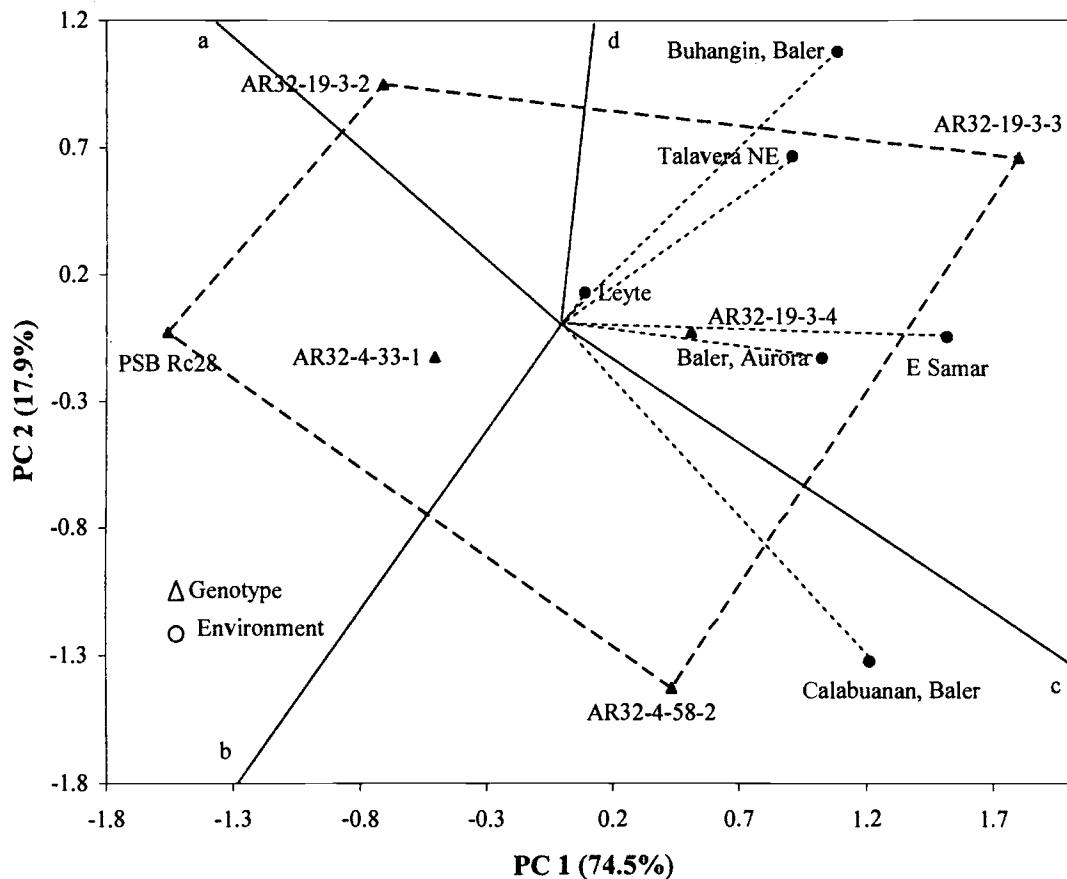


Figure 3. Biplot showing the performance of PSB Rc28 compared with MAS-derived lines in each environment. All genotypes are ranked based on their performance in specific environment

PSB Rc28 vs MAS-Derived Lines

This analysis included six environments that had the BLB-susceptible PSB Rc28 planted together with the MAS-derived lines. The distribution of the test entries showed that three MAS lines and PSB Rc28 form the vertex genotypes (Figure 3). These genotypes found at the vertex were very responsive to six environments, with AR32-19-3-3, the farthest genotype from the biplot origin, being the most responsive genotype.

To determine the rank of each MAS-derived line in each location and to know its position relative to the average yield in each site, a location line was made

between site point and the biplot center of origin. A perpendicular line to this location line passing the center of origin was drawn as shown in Figure 3. For each location line, the rank of the MAS-derived line can be determined by drawing another perpendicular line from the point of a MAS-derived line to the location line. The MAS-derived line farthest from the biplot origin (more positive) is ranked first.

In five sites, AR32-19-3-3 ranked first in grain yield in all but one location, while PSB Rc28 ranked last in all but one location. Line AR32-19-3-4 was consistently above the average in yield in all locations and always below its sister line, AR32-19-3-3.

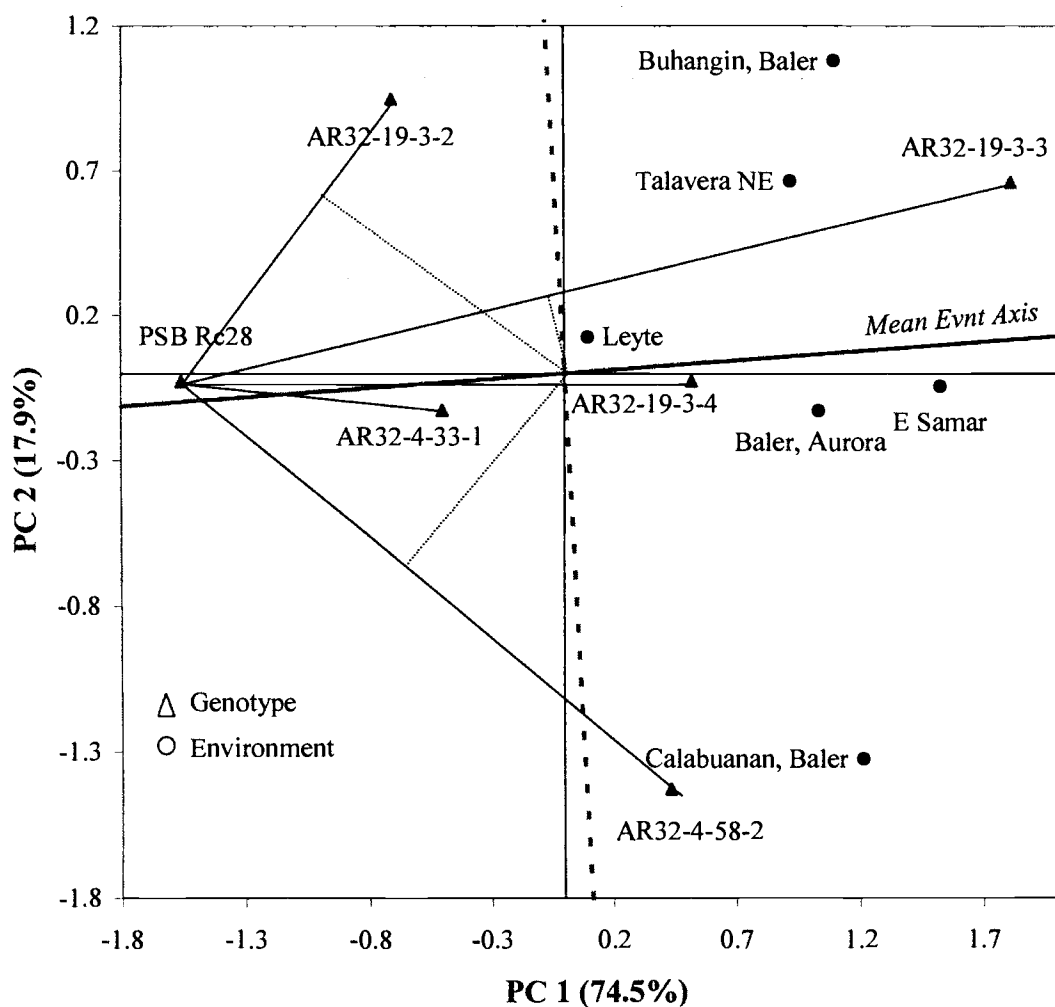


Figure 4. Biplot showing the yield performance and stability of PSB Rc28 compared with MAS-derived lines in each environment

However, AR32-4-33-1 was consistently below average in yield for each site. The other MAS-derived lines were either above or below average in yield depending on location. These results showed that the yields of MAS-derived lines were better than the susceptible check for all locations, and that AR32-19-3-3 was consistently the best among the MAS-derived lines. Adaptation analysis revealed that AR32-19-3-3 was the highest-yielding genotype for the mega-environment that consisted of Leyte, Samar,

Buhangin, Talavera, and Baler, while AR32-4-58-2 was best for the other mega-environment that consisted of Calabuanan. It can be noted that MAS-derived lines without Xa21, a resistance gene effective against most BLB races, performed like the susceptible PSB Rc28. As shown in Figure 4, the two top-yielding entries were AR32-19-3-3 and AR32-19-3-4, which were sister lines that contained the Xa21 gene. The top two stable lines, being closer to the mean environment axis and with very low PC2

values, were AR32-19-3-4 and AR32-4-33-1. All MAS-derived lines were high-yielding and more stable than the susceptible PSB Rc28. These results further revealed the advantage of having resistance genes in endemic areas for BLB.

Although the six environments were different from the above nine sites analyzed having IR64 as check, AR32-19-3-3 and its sister line were still the best and both were also adapted to locations near to where IR64 performed best.

Performance of MAS-Derived Lines

The GGE biplot of the grain yield of 5 MAS-derived lines in 15 environments accounted for 77.2% of the variation due to genotype and genotype x environment interaction. Checks were excluded from analysis since they were not in all locations.

Four lines formed the vertices of the polygon (Figure 5) and each line was the highest-yielding genotype in its mega-environment. The four mega-environments were composed of seven, three, three, and two locations, respectively. Adaptation analysis showed that AR32-19-3-3 was best in Buhangin, AR32-19-3-2 in PhilRice, AR32-4-58-2 in Mindoro, and AR32-4-33-1 in Iloilo. AR32-19-3-3 was best in seven locations (Buhangin-Baler, LaTorre-Talavera, Eastern Samar, Baler-Aurora, Calabuanan-Baler, Cabanatuan D, and Northern Samar), three for AR32-4-58-2 (Northern Samar, Mindoro, Abra, and Calabuanan), four for AR32-19-3-2 (PhilRice, Leyte, San Jorge-Samar, and Cabanatuan W) and two for AR32-4-33-1 (Iloilo and Abra).

GGE biplot analysis showed that AR32-19-3-4 was the most stable line but AR32-19-3-3 was an ideal genotype, as it was both the highest-yielding and a stable line (Figure 6). In contrast, AR32-19-3-2 was the least desirable. The exclusion of the check varieties did not change the distribution of the genotypes in the biplot graph, with AR32-19-3-3 consistently leading the group in grain yield.

In addition to these farmers' trials at several locations, both AR32-19-3-3 and AR32-19-3-4 were

also evaluated in the national variety evaluation trials at 15 to 22 locations, where after two years, AR32-19-3-4 was dropped, while AR32-19-3-3 was advanced and eventually released as new rice cultivar NSIC Rc142, 'Tubigan 7' in 2006 (Manalo 2006). GGE biplot analysis clearly revealed the differences between the sister lines and identified AR32-19-3-3 as the best for varietal release. The common basis of varietal release was two-year multi-location trials in more sites, but the small scale farmers' yield trials provided the same information, and the biplots showed the clear advantages of the best line.

To determine the ideal location for evaluation of BB resistant lines, PC1 and PC2 scores were considered. The two best places having the lowest PC2 (a representative of the 15 environments) and highest PC1 (an environment that can discriminate genotypes) were Eastern Samar and Baler, respectively. These can be candidate sites for future evaluation of BLB resistant lines. Biplot analysis can be applied to assist in determining the best place to grow and deploy this new cultivar. As reflected in the biplot (Figure 5), AR32-19-3-3 (NSIC Rc142) will perform best in the mega-environment composed of Baler, Nueva Ecija, and Eastern part of Samar, while lower yield is expected in Mindoro, Northern Samar and Iloilo. Breakdown of resistance is common in endemic areas and the identified sites can be the source of a new virulent race. Proper deployment, both temporally and spatially, should be practiced in these locations to prolong effectiveness of the resistance genes and the cultivar itself.

Host x Pathogen Interaction, Resistance to BLB

The GGE biplot analysis largely explained the variation (89%) in lesion length that is due to genotype and genotype x race interaction effects. Figure 7 showed the four entries forming the vertices of the polygon. IRBB 21, the donor for Xa21 gene, was the most stable, thus found near the biplot origin, together with two other MAS lines. As shown in the same graph, AR32-19-3-4 was the most responsive to

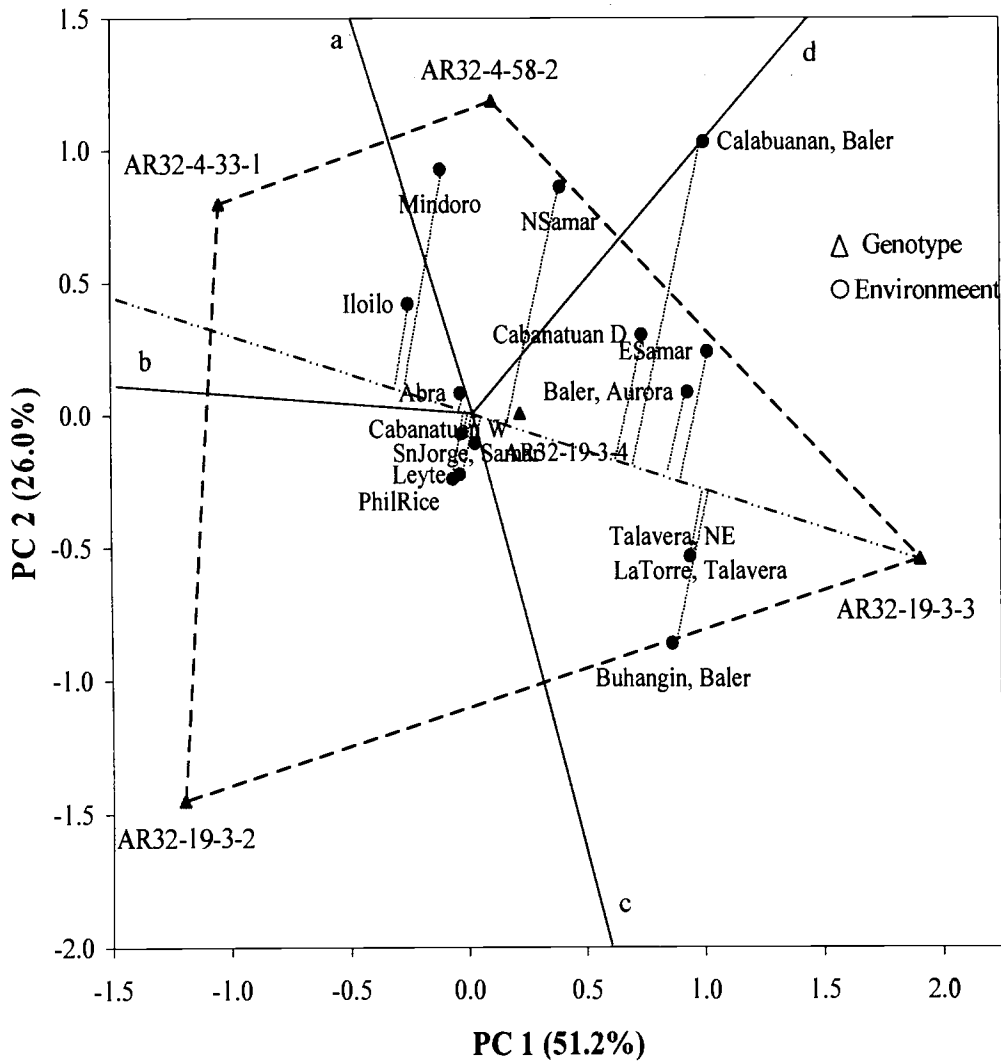


Figure 5. Biplot showing the ranking of MAS-derived lines based on yield performance in a specific environment

nine races of BLB found in the Philippines, followed by AR32-4-58-2, AR32-19-3-3 and the highly susceptible, IR24.

There were three groups of races formed (races in sector c-d for AR32-19-3-3, races in sector b-c for AR32-19-58-2 and races in sector a-d for AR32-19-3-4). There were five races for AR32-19-3-3 (race 1, 3, 6, 7, and 8), one for AR32-19-58-2 (race 5), and three for AR32-19-3-4 (race 2, 4, and 9). This result

indicated that the nine races of BLB in the Philippines can be grouped into three classes. Each line had varying degrees of resistance and this is reflected by the distribution of the race along the entry line (vertex of the line to the center of origin). For instance, AR32-19-3-3 had increasing lesions in the following race order: 1, 5, 7, 8, 3, 4, 9, 6, and 2. Among entries, biplot analyses revealed that AR32-19-3-3 is an ideal genotype with the best resistance followed by AR32-

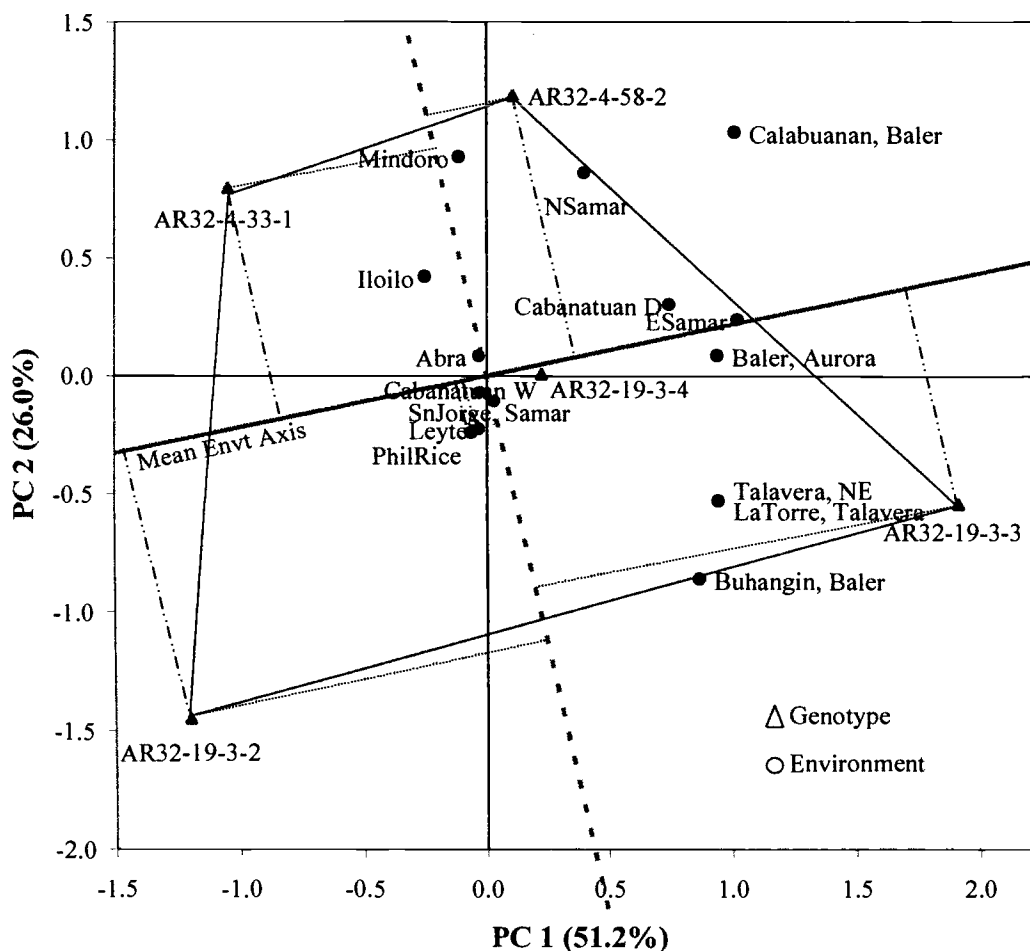


Figure 6. Biplot showing the yield performance and stability of MAS-derived lines

19-3-4. The most stable was the BLB resistant donor, IRBB21. Among the races, races 7 and 1 were found the most discriminating races while race 6, reported as the most virulent race in the Philippines, was found to be a good representative of the nine races in screening for BLB resistance. This result supports the current practice of using races 1 and 6, two of the most common races of BLB in country, in screening for BLB resistance.

The analysis further supports the choice of AR32-19-3-3 as the best line for both yield and BLB resistance. These results were consistent with those obtained in India. The pyramided lines evaluated in 31

sites were all resistant and Xa21 proved to be the most effective resistance gene. Inoculation with 17 races from India and six races from the Philippines showed that pyramided lines had high levels of resistance (Singh et al 2001).

Genotype x Grain Quality Traits Interaction

The biplot analysis in Figure 8 showed that 77% of the total variation can be explained by the PC1 and PC2 obtained. Since the biplot explained most of the variations, correlation between two traits following Yan et al (2002) was estimated. The graph showed several negative relationships (nearly obtuse angle)

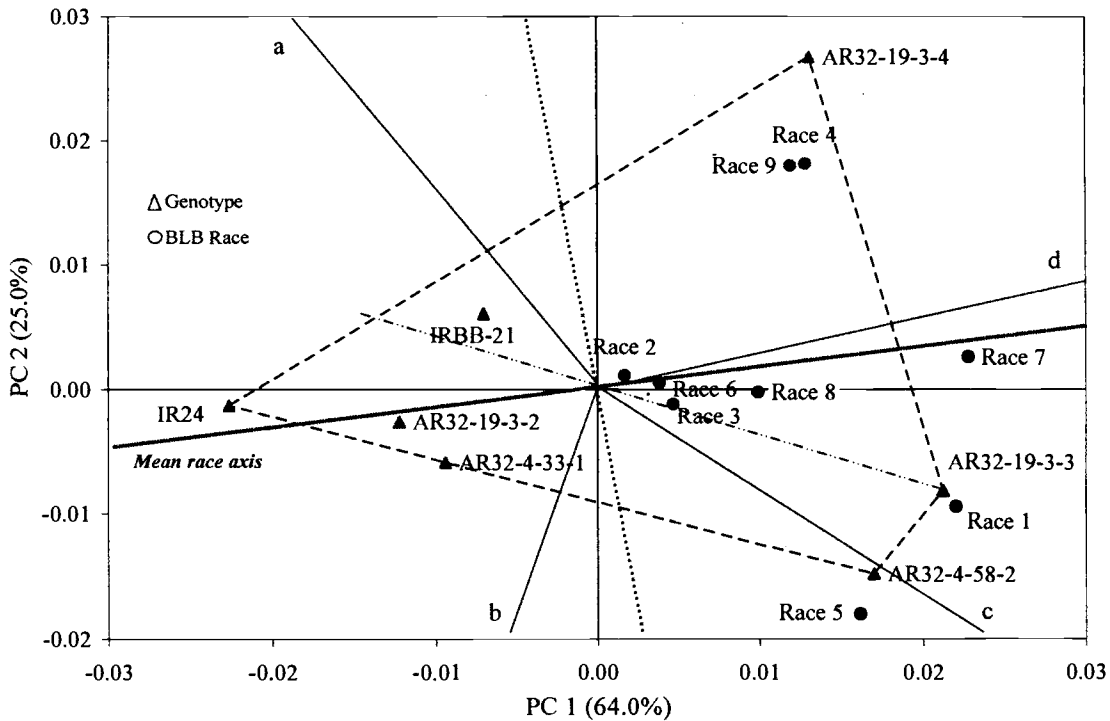


Figure 7. Biplot of genotypes based on their performance and reaction to the 9 races of BLB

and these were between gel consistency (GC) and shape (SHP), GC and milling recovery (MR), amylose content (AC) and chalky grain (CG), moisture content (MC) and head rice (HR), moisture content (MC) and crude protein (CP).

A nearly positive correlation of $\cos 0^\circ = 1$ was obtained between CP and HR, and SHP and MR. Other strong positive correlations having acute angles were GS and AC, GS and MR, MC and AC, GS and SHP, HR and GT, CP and GT, CG and CP, and CG and HR. Several instances of no-correlation (right angle) were noted such as between grain size (GS) and gelatinization temperature (GT), CP and GC, HR and GC, CP and SHP, CP and MR, and HR and SHP.

Aside from correlation between traits, the biplot can also be a tool to compare genotypes and identify good parents with several desirable traits. As shown in

the graph, IR64 had the highest AC, GS, and MC while AR32-4-58-2 had the highest CP, HR, GT, SHP, and MR. AR32-4-33-1 had the highest GC and CH. The highest value may not always be the best for these traits; thus, interpretation should be relative to the trait being considered. For instance, AC should be between 20 to 25%; CG should be lower than 10%; GC should be at 41 to 60% and SHP at 2.00 and above.

The associated traits close to the three vertex genotypes are their best or worst traits that can be either selected for or avoided in varietal development. For high protein, milling recovery and head rice, AR32-4-58-2 is the best donor, while IR64 is a good donor for amylose content and grain size. AR32-4-33-1 is a donor for softer rice but should be avoided as a parent due to the problem of chalkiness in this line.

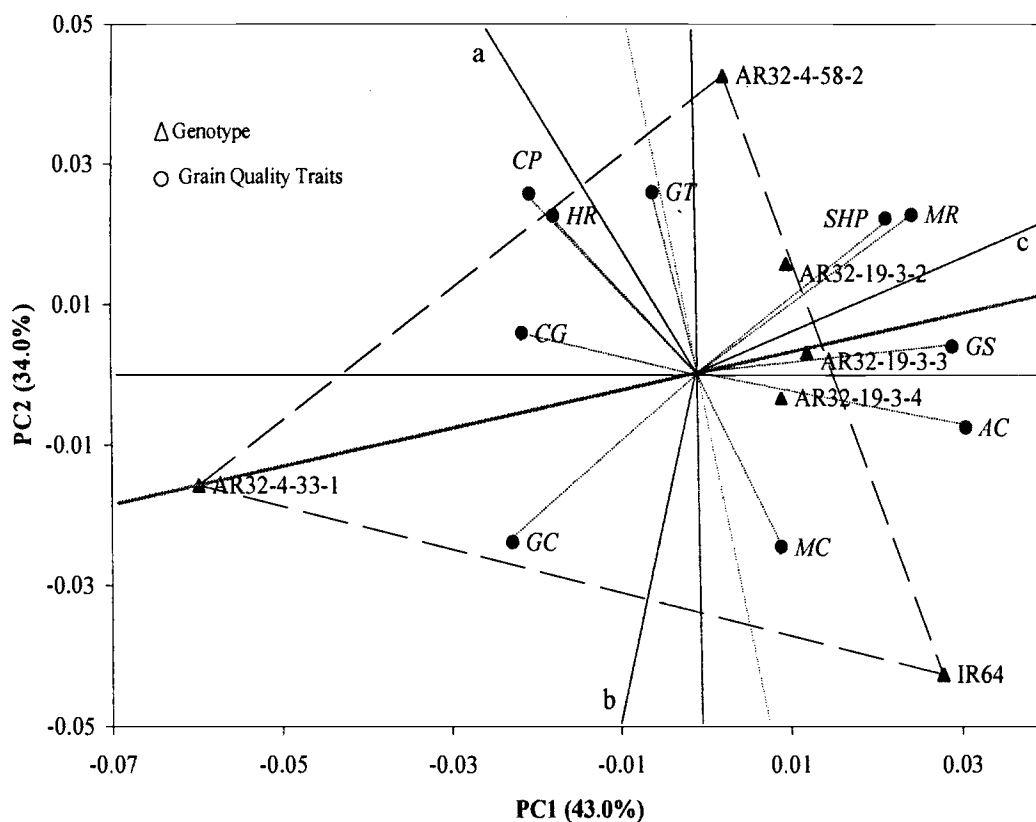


Figure 8. Biplot of the interaction between genotypes and grain quality traits

Abbreviations: GS = grain size, SHP = seed shape, HR = head rice, CG = chalky grains, GT = gelatinization temperature, GC = gel consistency, CP = crude protein, MC = moisture content, AC = amylose content, MR = milling recovery.

Cultivar IR64 has been the standard check for grain and milling qualities in the Philippines and its milled rice commands a higher price in the market. As two of the criteria for potential cultivar release, grain and milling traits should be comparable or better than IR64. The lines that are similar to IR64 based on grain and milling traits are AR32-19-3-3 and AR32-19-3-4, which are both progenies of backcrossing with IR64.

CONCLUSION

The results showed the practical use of the GGE

biplot graph in evaluating performance of elite lines in various tests having different objectives. The GGE biplot was able to identify the high-yielding genotype, the best location for its deployment, the most resistant genotype, and the best in grain and milling quality traits. It was able to separate also the nearly same sister lines and was able to identify the most virulent race and the best race of the pathogen for resistance evaluation. Foremost, the GGE biplot was able to select the same genotype previously selected in another experiment for varietal release; thus, this analysis supports the varietal release of NSIC Rc142.

Acknowledgment

The authors would like to acknowledge the assistance extended by the area extension workers and technicians for identifying locations and cooperators, and the farmer cooperators for allowing us to use their fields, growing the MAS-derived lines and control entries, and helping us gather the yield data.

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Table 1. Pedigree and Xa gene present in five elite lines and check varieties evaluated in on-farm strip plot

Cultivar/Line	Pedigree	Estimated Xa gene
AR32-19-2	IR64*3//IRBB5-21/PSB Rc14	Xa4, xa5
AR32-19-3	IR64*3//IRBB5-21/PSB Rc14	Xa4, xa5, Xa21
AR32-19-4	IR64*3//IRBB5-21/PSB Rc14	Xa4, xa5, Xa21
AR32-4-33-1	BPI Ri10*4/IRBB5-21	xa5
AR32-4-58-2	BPI Ri10*4/IRBB5-21	xa5
IR64		Xa4
PSB Rc28		none

Table 2. Reaction of IR24, IRBB 21 and five MAS-derived lines to 9 races of bacterial leaf blight *

Lines	Genetic Background	<i>BLB Races</i>								
		<i>1</i>	<i>2</i>	<i>3</i>	<i>4</i>	<i>5</i>	<i>6</i>	<i>7</i>	<i>8</i>	<i>9</i>
<i>Lesion length (cm)</i>										
IR24	BLB S check	31	24	16	24	11	21	8	28	19
IRBB21	BLB R check	5	2	2	2	3	5	3	5	3
AR32-4-33-1	BPI Ri-10	5	8	9	8	2	15	3	2	6
AR32-4-58-2	BPI Ri-10	1	7	6	3	1	6	1	2	4
AR32-19-3-2	IR64	4	13	14	7	3	19	3	7	5
AR32-19-3-3	IR64	1	4	2	2	1	4	1	2	2
AR32-19-3-4	IR64	2	8	9	1	5	6	1	2	1

*Data from Tabien et al 2003

Table 3. Physico-chemical analysis of IR64 and five MAS-derived lines with bacterial leaf blight resistance genes, 2001 WS*

Physico-Chemical Traits	Rice Lines					IR64 cultivar
	AR32-4-33-1 (BPI RI10 background)	AR32-4-58-2 (BPI RI10 background)	AR32-19-3-4 (IR64 background)	AR32-19-3-3 (IR64 background)	AR32-19-3-2 (IR64 background)	
Grain Size (mm)	6.10	6.40	6.60	6.54	6.64	6.50
Grain Shape (mm)	3.00	3.20	3.10	3.10	3.10	3.10
Head Rice %	58.74	56.94	58.70	57.31	56.68	48.38
Chalky Grains %	23.30	13.24	10.80	11.42	11.98	-
Gel Temperature	4.33 L/Hi	6.75 L/I	4.17 L/I/Hi	3.50 L/I/Hi	3.50 HI/I	3.50 HI/I
Crude Protein %	8.13	8.30	7.88	7.32	7.36	-
Gel Consistency*	90.00	43.00	56.00	54.00	65.00	67.00
Moisture content %	11.47	11.46	11.18	11.30	11.50	12.10
Amylose %	11.78	18.16	18.16	18.24	17.29	23.22
Milling Recovery %	66.87	71.62	71.05	70.88	70.87	69.25

*Grain Size (mm): 6.60-7.49 - Long; 5.50-6.59 - Medium; 5.49 below - Short. Grain Shape (mm): 3.10 above - Slender; 2-3 - Intermediate; 1.99 below - Bold. Head Rice %: 71% above - Premium; 65%-70% - Grade 1. Chalkiness: 11.80-23.30 - Grade 3. Gel consistency: 25-40 - Hard; 41-60 - Medium; 61-100 - Soft. Amylose %: 10.1-20 - Low; 20.1-25 - Intermediate; 25% above - High. Milling Recovery%: 70.1% above - Premium; 65.1-70% - Grade 1. * Grain quality data taken from Tabien et al 2003*