Resistance genes and gene pyramids controlling rice blast pathogen populations in eight African countries

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Abstract

Background

The behavior of rice varieties under natural environments in fields often differs from the expected one. For developing varieties, breeders give then a particular importance to multi-local field screening to confirm the resistance of their germplasm. We assembled 81 accessions e.g. blast differential, traditional and improved varieties and tested them for resistance to blast (*Pyricularia grisea*) in eight African hot spots under different ecologies. We thus expected to identify accessions and genes or gene pyramids that provide durable resistance locally or across sites.

Methods

81 accessions (e.g. blast differential, traditional and improved varieties were tested in hot spots in Benin, Burkina Faso, Côte d'Ivoire, Madagascar, Mali, Rwanda, Togo and Uganda for resistance to leaf and neck blast. An Alpha design (randomized incomplete block) with four replications was used. Correlation between leaf blast and neck blast severity and between incidence and severity were analyzed.

Results:

From 2013 to 2016, multi-local screening tests were conducted at yje selected sites. Among the 81 rice accessions tested, seven accessions were consistently susceptible while 12 were resistant across locations and seasons. Interestingly, effective individual resistance genes (R genes) or gene pyramids efficient across the sites were identified. In addition, we noticed on some sites, changes in the responses of some rice accessions to the disease from one season to the other. Responses of some accessions also showed great variations from one site to another. In addition, several accessions sharing the same resistance genes exhibited different responses to blast. Regarding the neck blast, only fewer accessions could be assessed as very susceptible ones died at early stages. Although differential responses were observed in the four sites considered for the analysis, several accessions consistently resisted. In addition, results showed that leaf and neck blast resistances were correlated.

Conclusions

Results obtained provide useful information on the tested germplasm resistance. In addition, it was possible to identify resistant accessions and sometimes the R genes associated which were effective locally or across sites. Results also showed shifts in pathogenicity of the pathogen populations over seasons and sites. Finally, breeders can now use this valuable information for sustainable blast resistance breeding.

Background

Genetic control through the use of resistant varieties is undoubtedly the most economically efficient and environmentally friendly way to control diseases. Theoretically, it seems obvious that the development of resistant varieties with pyramid of resistant genes (R genes) capable of resisting blast is an option to have good yield [4, 5]. However, given the great genetic variability of *P. grisea* in space and time, resistance failures are encountered in the development programs for resistant varieties [6].

Therefore, one of the challenges for rice breeders and plant pathologists is to identify the resistance genes that hold consistently over time and in all environments. Thus, several collaborative programs to create blast differential varieties by incorporating R genes in a common rice susceptible background were conducted. This is the case, for example, of the monogenic lines developed by a collaborative initiative that involved the International Rice Research

Institute (IRRI) and the Japanese International Research Center for Agriculture Sciences (JIRCAS). These lines were developed through backcrossing the resistant donors with the known susceptible accessions CO39, Lijiang Xintuang Heigh (LTH) or US-2 as backgrounds targeting 14, 24 and 14 resistance genes, respectively [7, 8]. They help assess pathogen diversity in given localities and compare easily results, identify R genes in resistant accessions and pathogen races prevailing in study localities and deploy efficient R genes. This has made it possible to develop better strategies for controlling this economically important disease. Based on results obtained in Asia and partially in Africa, AfricaRice has developed a breeding program for improving blast resistance in its elite lines. This strategy relies on the introgression of *Pb1* and *pi21*, which provided durable resistance against the disease in Asia, into some elite lines using marker-assisted selection (MAS) [9].

In the process of this varietal development, it is necessary to carry out screening tests in natural environments in sites considered as hotspot of blast disease in Africa. Indeed, several studies have been carried out to identify hot spots and recommended for the screening of germplasm for resistance to the disease. This is how Séré et al. (10) and Odjo et al. (11) identified the best hotspots in Benin, Burkina Faso, Côte d'Ivoire, Ghana, Mali and Nigeria and later Idowu et al. (2013) in Nigeria. Other work in East Africa helped Chuwa et al. (12) identify four hotspots in Tanzania. This work also documented the resistance of varieties including those with introgressed R genes and the genetic variability of the strains present on the sites.

It is in the same dynamism that the work presented here was initiated in order to screen selected rice accessions in eight hot spots under different ecologies in Benin, Burkina Faso, Côte d'Ivoire, Mali, Madagascar, Togo, Uganda and Rwanda. The rice accession set tested is made up mainly of elite lines recently developed by AfricaRice and its partners, R genes pyramided lines, traditional varieties and blast differential varieties already used in previous projects in Asia and Africa.

The objective was to gain a better chracterize the pathogen's variability and identify R genes that consistently provide resistance locally and across sites. Specifically, the screening tests will allow 1) Identify resistant accessions and / or R genes that efficiently control the disease; 2) Indirectly assess the pathogenic diversity of the local pathogen's populations; and 3) document the resistance/susceptibility of the tested traditional varieties and elite lines that could serve as parents in breeding programs.

The information gathered by this study made it possible to update the information on the behavior of the differential varieties often used in projects for improving sustainable blast resistance breeding programs and to assess the resistance of improved and traditional accessions. It represents a wealth of information for plant pathologists and breeders and also provide information on the efficiency of known R genes and gene pyramids to control the disease in Africa.

Results

Leaf blast

Responses of the susceptible and resistant test accessions across sites

The combined ANOVA analysis across locations showed significant G X E effects ($p<0.05$) for the mean leaf blast scores obtained at all locations, meaning that accessions differed in their level of blast resistance/susceptibility at the different locations. The susceptible checks Maratelli and CO39 were susceptible at all sites while IRBLTA2-Pi was resistant in Burkina Faso but susceptible elsewhere. Five other accessions - IRBLb-B (*Pib*), IRBLKS-F5 (*Pik-s*), Shao Tiao-Tsao (*Pik-s*), IRBLa-C (*Pia*) and LTH - were also susceptible or moderately susceptible across all sites (Table 3A).

On the other hand, both resistant controls Tetep and Moroberekan remained resistant at all sites. In addition, 10 others - IR 56, IR 64, Pi-no.4, IRAT 13, IRAT 104, OU 244, ARICA 1, 2, 4 and WAB 56-104 - were either resistant or moderately resistant across all sites (Table 3B). These accessions have either only single R genes (e.g. Ou 244 with *Piz*), gene pyramids (e.g. Pi no. 4 with two R genes and Tetep with eight R genes) or have no known R genes (e.g. IRAT 104, ARICA 1-2, ARICA 4 and WAB56-104). These newly identified susceptible and resistant accessions can be used as controls in future trials.

Resistance/susceptibility of the remaining accessions

Several accessions - CT13432-3R (*Pi1, Pi2, Pi33, Pi54*), Fukuhikari [*Pita, Pik, Pi9(t)*, *Piz*), IR 72 [*Pita, Pib*], Kusabue [*Pik*, *Pish*], K1 |*Pita, Pi4(t)*], NP125 (*Pik*), Raminad (*Pi-ka*) and RIL 249 Moro [*Pi5(t)*] - were moderately susceptible at only one site. Others displayed susceptibility at two locations only; these include accessions ARICA 3 and ARICA 5, IRBLz5-CA (*Piz5*), K2 (*Pia, Pik-p, Pik*), NP125 (*Pik*) and Zenith (*Piz, MPiz, Pia, Pi1*) and other accessions with no known R gene. A third group of accessions - C101A51 [*Pi2(t)*, *Pia*, *Piz5*], Modan (*Pb1*), Owari Hata Mochi (*Pi21*), Toride 1 ((*Piz-t*, *Pish*) or Nipponbare (*Pia*, *Pi41*, *Pish*) - were moderately susceptible or susceptible at more than two locations (Table 3C) like C101LAC (*Pi1*+*Pia*+*Pi1b*+*Pi33*), Reiho (*Pita-2*, *Pia*, *Pish*), TCS 10 (no known R gene), IR1529 (*Pi33*) and ST1 *[Pif*, *Pi37(t), Pb1*] (Table 3C). .

Several of the accessions shared a single R gene and were expected to have comparable responses to the disease, especially when they were tested in the same locations- IRBL5-M and RIL249 Moro sharing *Pi5(t)*, IRBLa-C, C102TTP, Usen and IRBLa-A sharing *Pia*, IRBLks-F5, Shao Tiao-Tsao, and IRBLks-S sharing *Pik-s*, IRBLz-FU and Ou 244 sharing *Piz* and IRBLk-ka, Dular and NP125 sharing *Pik*. However, in Côte d'Ivoire and Rwanda, 75-1-127 (*Pi9*) was resistant while IRBL9-W (*Pi9t*) was susceptible. In Benin, IRBL5-M was susceptible while RIL249 Moro was resistant. Although IRBLa-C and IRBLa-A share the Pia gene, IRBLa-C was susceptible while IRBLa-A was resistant in trial 1 in Mali. Similarly, IRBLz-FU (*Piz*) was susceptible and Ou 244 (Piz) was resistant in trial 2 in Mali. Also, in the same trial conducted in Burkina Faso, IRBLk-ka (*Pi-ka*) was susceptible while NP125 (*Pi-ka*) was resistant. Conversely, both IRBLks-F5 and Shao Tiao-Tsao, which share the *Pik-s* gene, were consistently susceptible regardless of location and season.

Based on all the results obtained, gene options for protecting rice locally or across sites against blast are summarized in Table 3. They include only individual R genes and pyramids of two genes. Bigger pyramids were not included but some of them are shown in Tables 3B.

Blast populations

R genes that provided the same response at all the eight sites (not discriminant as shown in Table 3A,B,C) (e.g. IRBLks-F5 with Pik-s that was moderately susceptible or susceptible everywhere) were not selected for analyzing the blast populations present at the eight sites. Thirty accessions with single but different R genes were selected (Table 4). Two classes of interactions were made based on disease severity - compatible or "+" (Sev⌧3.0) where the pathogen was able to cause disease on the target accessions, and incompatible or "-" (Sev≤3.0) where the pathogen was unable to cause disease. Results obtained were then compared across seasons and sites and showed that the blast populations differed from one season to another at each site (Table 4). For example, in Benin, the numbers of defeated R genes in seasons 1, 2 and 3 were 24, 23 and 20, respectively. The results also indicated that Mali had the highest number (28) of R genes that failed while Uganda and Togo had the lowest (12). In Togo, 12 R genes failed in trial 1 and 17 in trial 2. In Côte d'Ivoire, 20 failed in trial 1 and 14 in trial 2. In Madagascar, 20 genes failed in trial 1 and 22 in trial 2. The analyses also confirmed the shifting of blast populations over seasons as shown earlier in Table 3A,B,C, and 4.

Neck blast

Severity data were collected in 4 countries (Benin, Côte d'Ivoire, Togo and Uganda) and results showed that no accession was scored susceptible across all the four countries (Table 5). Modan, our reference neck blast resistant reference accession harboring Pb1, resisted the disease in at all sites except in Côte d'Ivoire where it was susceptible. Ten accessions, including Ou 244, Toride 1, and IR 64 were resistant in all sites (Table 5). IRBL11-Zh was susceptible in two countries; while IRBL9-W was susceptible in trial 1 and moderately susceptible in trial 2 carried out in Côte d'Ivoire.

Relation between leaf and neck blast

Severity data for leaf and neck blast from trials in Benin, Côte d'Ivoire, Togo and Uganda were compared (Table 6). Most (76.5%) accessions that were resistant to leaf blast were also resistant to neck blast while only 14% were susceptible to neck blast, 3.0% moderately susceptible and 6.5% moderately resistant to neck blast. By contrast, 43.3% of the accessions that were susceptible to leaf blast were also susceptible to neck blast, 3.1% were moderately susceptible, 15.5% moderately resistant and 38.1% were resistant to neck blast. The following categories of accessions were identified: 1) susceptible to both leaf and neck blast (e.g. IRBLa-A in Côte d'Ivoire); 2) susceptible to leaf blast but resistant to neck blast (e.g. IRBL20-IR24 in Côte d'Ivoire); 3) resistant to leaf blast but susceptible to neck blast (e.g. IRAT 104 in Côte d'Ivoire); and 4) resistant to both diseases (e.g. IRAT 104 in Benin). The results show that resistance/susceptibility to both diseases is highly correlated (Table 6), with regression values of 0.54 for Benin, 0.41 for Togo, 0.39 and 0.59 for Côte d'Ivoire and 0.20 for Uganda.

Discussion

The highly variable pathogenicity in *M. grisea* [16, 17] might explain why resistant varieties sometimes became susceptible within two years after their release [18]. Sexual recombination cannot account for this high level of variability as fertile and compatible isolates do not exist in most rice growing regions [19–21] except in limited areas of the Himalayan foothills [22] where sexual reproduction was shown to occur. It has, therefore, become important to identify R genes or gene pyramids that hold against the disease over time. Several studies were conducted worldwide and also in African countries to evaluate the resistance of germplasm [10, 13, 23, 24]. However, different sets of differential accessions harboring known R genes were used in all these evaluation trials making it difficult to compare the results obtained. No attempt has so far been made to evaluate the same set of differential accessions under field conditions in a multi-country trial. The current initiative conducted by AfricaRice and its partners aimed for achieving this goal. It was expected to identify R genes that are consistent locally or across sites and simultaneously document pathogen variability.

In addition to the susceptible checks Maratelli, CO 39 and IRBLTA2-Pi, four test accessions - Lijiang Xintuan Heigh or LTH (harboring no known R gene), IRBLb-B (*Pib*), Shao Tiao-Tsao (*Pik-s*), IRBLa-C (*Pia*) and IRBLKS-F5 (*Pii*) - were consistently susceptible across locations and seasons (Table 3A). Similarly, accessions with R gene pyramids containing more than five R genes, such as Moroberekan could be used as resistant checks [19], IR64 was also resistant across all sites (Table 3B). The high level of resistance of these accessions might be due to the large number of R genes in the pyramids they harbor. According to Fukuoka et al (2015), such pyramids in association with some partial R genes they tested, conferred a strong, non-race specific and environmentally stable resistance to the pathogen. In addition, accessions Ou 244 (*Piz*), IR56 [*Pita*+*Pik*], IRAT 13 [*Pib*+*Pi8(t)*] with a few R genes as well as others, such as ARICA 1, 2 and 4, IRAT 104 and WAB56-104 with no known R genes, were also resistant. WITA 4, which is known to have a good level of blast resistance 26, 27), is one of the parents of ARICA 1 and 2. ARICA 4 has WAB 56-104 and Moroberekan as parents (Sie et al., unpublished). It is thus possible that ARICA 1 and 2 inherited their blast resistance from WITA 4 and ARICA 4 from WAB 56-104 and Moroberekan. Genetic analysis of the resistance of these accessions could provide useful information on the R genes involved. The highly variable resistance responses, ranging from very resistant to very susceptible, within and across the eight sites could be attributed to either the diversity of the pathogen or/and to the effects of G x E interactions.

This study has identified R genes that protect plants against the disease at each site and others that were efficient across sites. However, these findings must be confirmed using artificial inoculation of isolates originating from the trial sites.

If confirmed, the R genes that are consistently efficient across sites could be used by breeders to improve blast resistance in breeding lines. QTLs are generally believed to provide broad spectrum and stable resistance but some major genes (e.g. *Pi1, Piz-5 [Pi2], Pi5*, *Pi9, Pi40* and *pi21*) are also efficient [27–29]. However, it is necessary to test these accessions at more sites within each country to validate the results presented in this paper. For example, *Piz* was efficient at the Côte d'Ivoire site but was found ineffective in Madagascar at a high altitude site [31].

Contrary to expectations, accessions that share the same R gene did not always display the same responses. The presence of other R genes in these accessions might explain the differential reactions observed. Another hypothesis is that some of them don't bear the claimed R genes. This calls for other studies to clarify the differential responses. One option could be to artificially inoculate these accessions using isolates originating from the trial fields. In fact, these 81 tests accessions were inoculated under controlled conditions with 10 randomly selected isolates from the trial site in Benin and the results showed that only IRBLz-Fu and Ou 244 displayed the same results and were both resistant to all the isolates (Awande et al., unpublished). The use of other isolates is needed before valid conclusions can be drawn.

Accessions with pyramided R genes, such as IR56, IR64, as well as the resistant cultivar Tetep, were efficient across sites. Earlier studies reported that resistance was enhanced by the pyramid *Pi-b*+*Pi-kh* in the cultivar MR219 [32], *Pi-1*+*Pi-2* in Rongfeng B [32], *Pi9*+*Pita* in Pusa Basmati 1 [34], and *pi21*+ *Pi35* in Koshihikari [34]. In Africa, the R gene pyramiding approach has not yet been used for improving blast resistance in susceptible rice varieties. However, AfricaRice is currently introgressing *Pi21* and *Pb1* in improved lines/varieties although these genes were chosen because they provided stable and broad spectrum resistance to the disease in several countries, especially in Japan where the variety Modan (*Pb1*) was resistant for over 30 years on 50,000 ha [36]. Based on the results of the current study, we are now introgressing the R genes *Piz* (located on chromosome 6) and *Pi5(t)* (located on chromosome 9) [1] in susceptible varieties to test the efficacy of this R gene pyramid.

The blast population varied across and within sites. Variability was highest in Mali (27 genes out of 30 being defeated) and lowest in Uganda and Togo (only 12 genes being defeated). There is a need to test other sites and select the hottest ones for screening germplasm.

In Benin, Côte d'Ivoire, Togo and Uganda where data for both leaf and neck blast severity were collected, there was a positive correlation between the incidence and severity of the two diseases (data not shown). However, further investigations are needed, including artificial inoculation of rice genotypes with selected leaf and neck blast isolates at seedling and panicle stages before any strategy for leaf and neck blast resistance breeding can be recommended. Puri et al. (2008) had previously reported a positive correlation between leaf and neck blast resistance. Noenplab et al. (2005) found that leaf and neck blast were two different pathosytems and that two QTLs interacted additively to provide resistance to both diseases. However, Biloni and Lorenzi (2002) found that in Italy the two diseases were not always related. Ghatak et al. (2013) found that leaf isolates were less aggressive than neck isolates and concluded that neither population was specialized for infecting both organs. Their results suggest that the more aggressive isolates have a higher probability of infecting the necks at the vegetative stage and that a higher number of such isolates will be found on the necks. It has also been reported that neck blast is the most destructive form of the disease caused by *P. grisea* [42] and identifying sources of resistance to both leaf and neck blast will significantly and positively change the paradigm for breeding for blast resistance.

Conclusion

Several blast resistance screening trials have been conducted worldwide and resistance of germplasm documented. In Africa, trials were also conducted in hot spots using different sets of blast differentials. This made it difficult to compare the results. The present work was conducted using the same set of rice germplasm in all eight sites and during several seasons. Results obtained helped confirm the hotness of the test sites through the severe attacks observed on the susceptible controls, identify resistant and susceptible accessions, identify R genes that hold locally or across site and over seasons, document the differential responses of lines carrying the same R genes, characterize shifts in pathogenicity and show that leaf and neck blast resistances are correlated. This later result clearly showed that breeding for a strong leaf blast resistance will also protect the lines against neck blast whose evaluation is time consuming. It is recommended that the evaluation of differential lines initiated in this study should continue in the main African rice production regions. The information gathered will facilitate the selection of the most efficient R genes or gene pyramids.

Methods

Selection of trial sites

Thanks to pre-prospection in collaboration with the Plant pathologists of the National Agronomic Research Structure (NARS), trial sites were chosen in the rice fields of rice farmers and NARS experimental plots. Farmers and NARS partners have approved the trials to be conducted. These sites, easy to access, present symptomatic blast rice plants with high incidence and severity. For each site, meteorological and geographic data were collected (Table 1)

The germplasm used

The list and characteristics of the 81 accessions used are summarized in Table 2. They were selected by the corresponding author among the publicly available blast differentials used by plant pathologists. The germplasm is composed of the differential varieties, monogenic lines and other accessions developed by IRRI, JIRCA and AfricaRice. The seeds were obtained from CIRAD (Center for International Cooperation in Agronomic Research for Development), IRRI (the International Rice Research Institute) and the AfricaRice gene bank.

Experimental layout

The experimental design used was an Alpha network (randomized incomplete block with 81 entries, i.e. 9 x 9 accessions) with four replications. In our tests, nine incomplete blocks with nine elementary plots (accessions) for each replication were used. Each 0.1 m2 plot is made up of 18 plants in three rows (0.5 m) long 10 cm apart. Three susceptible accessions Maratelli, CO39 and IRBLTA2-Pi were used as spreader bands.

Soil preparation, sowing and plant maintenance

The majority of cultural practices such as soil preparation, sowing, fertilization, weeding and watering of different ecologies were being done according to the same routine procedure used by rice farmers. Spreader rows were sown/transplanted 2 weeks before the test entries. For more details see the additional file.

Scoring of symptoms

Leaf blast was scored using the modified IRRI scale [14]. The first leaf blast scoring was done as soon as the first symptoms were observed on the test accessions and at 7 days intervals thereafter, with a total of 5 scorings per trial. The mean leaf blast severity scores were calculated for each scoring session and trial as follows:

$Sev = (\Sigma Xi.Ni / TN)$.

Sev: the mean leaf blast score;

X : the rating category;

Ni : the number of plants showing symptoms in each rating category;

and TN : the total number of plants.

For neck blast, only mean severity data collected at harvest in each trial were used. The numbers of **attacked versus healthy necks** were recorded on the 12 inner plants in each plot and the percentage (incidence) was calculated.

The severity index was then calculated as follows:

$Sev: ((\Sigma NiXi / 3NP) * 100)$

Sev: the mean neck blast score

Ni=the number of plants in each severity score Xi of 0, 1, 2, 3,

NP=total number of panicles.

Accessions were then classified as resistant with:

$Sv \leq 10\%$; moderately resistant

10% ⊠$Sv \leq 30\%$; moderately susceptible

30% ⊠$S \leq 45\%$; and likely

$Sv > 45\%$.

For blast population analysis, only 30 accessions harboring single but different resistance genes were used. A gene that exhibited the same response at all sites (not discriminant) was excluded from this analysis. The responses of these accessions to blast infection were classified as incompatible (-) with $S \leq 3.0$ or compatible (+) with $S > 3.0$. The responses of all these accessions were then compared between seasons and across sites.

Statistical analysis

Data collected were subjected to an analysis of variance (ANOVA, mixed model) using GenSTAT statistical package, 14th edition [15]. Means of scores were calculated and compared with those of controls. Microsoft Excel was used to calculate simple correlation coefficients and regressions to determine the interactions between the mean severity of leaf blast and neck blast and between incidence and severity of neck blast.

Abbreviations

AfricaRice: Africa Rice Center

ARICA: Advanced Rice Varieties for Africa

MAS: marker-assisted selection

NARS: National Agronomic Research System

IRRI: International Rice Research Institute

CIRAD: Centre de coopération internationale en recherche agronomique pour le développement

JIRCAS: Japan International Research Center for Agricultural Sciences

IRAT : Institut de Recherches Agronomiques Tropicales et des Cultures Vivrières

Declarations

Ethics approval and consent to participate

Not applicable

Consent for publication

AfricaRice Deputy Director General-Director of Research has approved the submission of the paper for publication. All co-authors have also contributed to the drafting of the manuscript and have read and approved the final version of the paper.

Availability of data and materials

All raw data generated during and/or analysed during the current study are available in the Data Management Unit of AfricaRice and can be accessed by anyone upon request. These data collected in each country are also available from the NARS scientists.

Competing interests

The authors declare that they have no competing interests

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Authors' contributions

This project was designed by Dr. Silue and implemented by the NARS partners of the eight countries namely AS, OA in Benin, KK and KK in Togo, KAI and IO in Burkina Faso, RH, SM and RLM in Madagascar, AR and JL in Uganda, AK in Rwanda. All collected data were compiled by AS and OA. Their analysis and the drafting of the paper was done together with all authors. All co-authors have read and approved the final version of the paper. We have all agreed its submission to BMC-Plant Biology.

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Authors' information (optional)

References

1. Wang X, Lee S, Wang J, Ma J, Bianco T, Jia Y. Current advances on genetic resistance to rice blast disease. Rice-germplasm genet improv IntechOpen Ltd Lond. 2014:195–217.
2. Pennsi E. Armed and Dangerous: Sciences; New Series, 2010;327:804-805.
3. Séré Y, Fargette D, Abo ME, Wydra K, Bimerew M, Onasanya A, et al. 17 Managing the major diseases of rice in Africa. Realizing Africa Rice Promise. 2013:213.
4. Goto K, Kozaka T, Yanagita K, Takahashi Y, Suzuki H, Yamada M, et al. US-Japan cooperative research on the international pathogenic races of the rice blast fungus, *Piricularia oryzae* Cav., and their international differentials. Jpn J Phytopathol. 1967;33 Special:1–88.
5. Yamada M, Kiyosawa S, Yamaguchi T, Hirano T, Kobayashi T, Kushibuchi K, et al. Proposal of a new method for differentiating races of *Pyricularia oryzae* Cavara in Japan. Jpn J Phytopathol. 1976;42:216–219.
6. Agrios GN. Plant pathology 5th Edition: Elsevier Academic Press. Burlingt Ma USA. 2005;79–103.
7. Fukuta Y, Telebanco-Yanoria MJ, Imbe T, Tsunematsu H, Kato H, Ebron LA, et al. Development of new international standard differential variety series to integrate blast resistance of rice (*Oryza sativa* L). JIRCAS Res Highlights. 2003:16–17.
8. Fukuta Y, Cruz CMV, Kobayashi N. Development and characterization of blast resistance using differential varieties in rice. JIRCAS Work Rep. 2009. https://www.jircas.go.jp/en/publication/jircas_working_report/63. Accessed 17 Dec 2019.
9. Kumashiro T, Futakuchi K, Sié M, Ndjiondjop M-N, Wopereis MC. A continent-wide, product-oriented approach to rice breeding in Africa. Realiz Afr Rice Promise CABI Boston. 2013:69–78.
10. Séré Y, Onasanya A, Afolabi A, Mignouna HD, Akator K. Genetic diversity of the blast fungus, Magnaporthe grisea (Hebert) Barr, in Burkina Faso. Afr J Biotechnol. 2007;6. doi:10.5897/AJB2007.000-2410.
11. Odjo T, Kawasaki-Tanaka A, Noda T, Ahohuendo BC, Sere Y, Kumashiro T, et al. Pathogenicity analysis of blast (*Pyricularia oryzae* Cavara) isolates from West Africa. Jpn Agric Res Q JARQ. 2014;48:403–412.
12. Idowu OO, Salami AO, Ajayi SA, Akinwale RO, Sere Y. Varietal resistance of rice to blast fungus *Magnaporthe oryzae* at two sites in southwestern Nigeria. Afr J Biotechnol. 2013;12:5173–5182.
13. Chuwa CJ, Mabagala RB, Reuben MSOW. Pathogenic variation and molecular characterization of *Pyricularia oryzae*, Causal agent of rice blast disease in Tanzania. International. Journal of Science and Research. 2015; 4:1131-1139.
14. IRRI I. Standard evaluation system for rice. International Rice Research Institute. PO Box. 2002;933:1099.
15. Buysse W, Stern R, Coe R. GenStat discovery edition for everyday use. ICRAF Nairobi Kenya. 2004;114.
16. Ou SH, Nuque FL, Ebron TT, Awoderu VA. A type of stable resistance to blast disease of rice. Phytopathology. 1971;61:703–706.
17. Bonman JM. Pathogenic variability of monoconidial isotates of *Pyricularia oryzae* in Korea and in the Philippines. Plant Dis. 1987;71:5919–21.

18. Lin SC. Genetic analysis of minor gene resistance to blast in japonica rice. In: Rice Genetics I: (In 2 Parts). World Scientific; 1986. p. 451–469.
19. Khaled F, Prashanthi SK. Distribution of mating type alleles and fertility of Magnaportheoryzaeisolates in South India. International Journal of Advanced Research. 2016. http://www.journalijar.com/article/. Accessed 18 Dec 2019.
20. Silue D, Nottéghem J-L, Chaume J. Etude de la résistance spécifique d'*Oryza glaberrima* Steud à la pyriculariose du riz. Agron Trop. 1992;46:121–129.
21. Hemmati R, Javan-Nikkhahi M, Hedjaroude GA, Okhovvat SM, Moosanejad S. Fertility status and distribution of mating type alleles of the rice blast fungus, *Magnaporthe grisea* in northern Iran. Commun Agric Appl Biol Sci. 2004;69:537–539.
22. Saleh D, Xu P, Shen Y, Li C, Adreit H, Milazzo J, et al. Sex at the origin: an Asian population of the rice blast fungus *Magnaporthe oryzae* reproduces sexually. Mol Ecol. 2012;21:1330–44.
23. Baboy L, Mateso R, Sabiti K. Tests de résistance au champ vis-a-vis de la pyriculariose du riz au Zaire. Tropicultura. 1995;13:93–98.
24. Odjo T, Ahohuendo BC, Onasanya A, Akator K, Séré Y. Analysis of Magnaporthe oryzae population structure in Benin. Afr J Agric Res. 2011;6:6183–6188.
25. Fukuoka S, Saka N, Mizukami Y, Koga H, Yamanouchi U, Yoshioka Y, et al. Gene pyramiding enhances durable blast disease resistance in rice. Sci Rep. 2015;5:1–7.
26. Bouet A, Gbedie NA, Boka A, Kouassi N. Evaluation des variétés de riz prometteuses pour la résistance à quelques contraintes biotiques majeures et pour leurs performances agronomiques en Côte d'Ivoire. Int J Biol Chem Sci. 2015;9:2041-2056–2056.
27. Kazuki S, Vandamme E, Johnson J-M, Tanaka A, Senthilkumar K, Dieng I, et al. Yield-limiting macronutrients for rice in sub-Saharan Africa. Geoderma. 2019;338:546–54.
28. Fukuoka S, Okuno K. QTL analysis and mapping of pi21, a recessive gene for field resistance to rice blast in Japanese upland rice. Theor Appl Genet. 2001;103:185–90.
29. Jeon J-S, Chen D, Yi G-H, Wang GL, Ronald PC. Genetic and physical mapping of Pi5(t), a locus associated with broad-spectrum resistance to rice blast. Mol Genet Genomics. 2003;269:280–9.
30. Jeung JU, Kim BR, Cho YC, Han SS, Moon HP, Lee YT, et al. A novel gene, Pi40(t), linked to the DNA markers derived from NBS-LRR motifs confers broad spectrum of blast resistance in rice. Theor Appl Genet. 2007;115:1163–77.
31. Raboin LM, Ramanantsoanirina A, Dusserre J, Razasolofonanahary F, Tharreau D, Lannou C, et al. Two-component cultivar mixtures reduce rice blast epidemics in an upland agrosystem. Plant Pathol. 2012;61:1103–11.
32. Tanweer FA, Rafii MY, Sijam K, Rahim HA, Ahmed F, Ashkani S, et al. Introgression of Blast Resistance Genes (Putative Pi-b and Pi-kh) into Elite Rice Cultivar MR219 through Marker-Assisted Selection. Front Plant Sci. 2015;6. doi:10.3389/fpls.2015.01002.
33. Fu C, Wu T, Liu W, Wang F, Li J, Zhu X, et al. Genetic improvement of resistance to blast and bacterial blight of the elite maintainer line Rongfeng B in hybrid rice (*Oryza sativa* L.) by using marker-assisted selection. Afr J Biotechnol. 2012;11:13104-13114–13114.
34. Khanna A, Sharma V, Ellur RK, Shikari AB, Krishnan SG, Singh UD, et al. Marker assisted pyramiding of major blast resistance genes Pi9 and Pita in the genetic background of an elite Basmati rice variety, Pusa Basmati 1. Indian J Genet. 2015;75:417–425.

35. Yasuda N, Mitsunaga T, Hayashi K, Koizumi S, Fujita Y. Effects of pyramiding quantitative resistance genes pi21, Pi34, and Pi35 on Rice Leaf Blast Disease. Plant Dis. 2014;99:904–909.
36. Fujii K, Hayano-Saito Y, Arakawa M. Development and dissemination of rice cultivars with multiple resistance to diseases and insect pests in Japan. Plant Prot. 2005;59:226–230.
37. Koutroubas SD, Katsantonis D, Ntanos DA, Lupotto E. Blast fungus inoculation reduces accumulation and remobilization of pre-anthesis assimilates to rice grains. Phytopathol Mediterr. 2009;48:240–252.
38. Puri KD, Shrestha SM, Khhatri Chhetri GB, Joshi KD. Leaf and neck blast resistance reaction in tropical rice lines under green house condition. Euphytica. 2008;165:523.
39. Noenplab A, Vanavichit A, Toojinda T, Sirithunya P, Tragoonrung S, Sriprakhon S, et al. QTL Mapping for leaf and neck blast resistance in Khao Dawk Mali105 and Jao Hom Nin recombinant inbred lines. Kasetsart University; 2005.
40. Biloni M, Lorenzi E (Pavia U (Italy) D di E del T e degli AT. Relation between leaf and neck blast resistance in Italian rice varieties [*Oryza sativa* L. - Lombardy]. In: Atti delle Giornate Fitopatologiche (Italy). 2002.
41. Ghatak A, Willocquet L, Savary S, Kumar J. Variability in Aggressiveness of Rice Blast (*Magnaporthe oryzae)* Isolates originating from rice leaves and necks: A Case of pathogen specialization? PLoS ONE. 2013;8. doi:10.1371/journal.pone.0066180.
42. Zhu Y-Y, Fang H, Wang Y-Y, Fan JX, Yang S-S, Mew TW, et al. Panicle blast and canopy moisture in rice cultivar mixtures. Phytopathology^{TM}. 2005;95:433–8.

Tables

Table 1: Characteristics of the sites where each trial was conducted in the eight countries.

Countries	Trial no.	Site	Ecology	GPS coordinates	Date	Temperature**	Rainfall**	Relative humidity**	Disease scored
						Mini-maxi or mean in °C	Mini-maxi or mean in mm	Mini-Maxi in %	
Benin	1	Calavi	Upland	N06°25’133’’E002°19’665’’	Jun-Nov 13	25.9-27.5	0.5-118	81.2-86.0	Leaf/Neck
	2		Lowland	N06°25’322’’E002°19’604’’	Nov 13-Apr 14	27.5-29	25.4-107	78.0-82.0	Leaf/Neck
	3		Lowland	N06°25’322’’E002°19’604’’	May-Oct 14	26.0-28.0	109-235	81.0-87.0	Leaf/Neck
Togo	4	Kovié	Irrigated	N06°22’283’’E01°06’024’’	Oct 13-Feb 14	27.8-29 .6	4.2-159.0	72.0-79.0	Leaf/Neck
	5		Irrigated	N06°22’283’’E01°06’024’’	Jun-Oct 14	25.8-27.8	65.7-215.9	80.1-83.5	Leaf/Neck
Mali	6	Longorolla	Upland	N11°23'08.9"W05°39'42.6"	Jul-Oct 13	-*	283.0-355.0	-	Leaf/Neck
	7		Upland	N11°23'08.9"W05°39'42.6"	Jul-Oct 14	-	40.8-93.8	-	Leaf/Neck
Cote d’Ivoire	8	M’bé	Upland	N7°51'23.09"W5°06'43.98"	Jul-Oct 14	26.7-24.4	58.1-408.5	88.0-88.4	Leaf/Neck
	9		Upland	N7°51'23.09"W5°06'43.98"	May-Oct 15	19.4-35.2	45.2-298.0	58.4-100.0	Leaf/Neck
Burkina Faso	10	Farako-bâ	Upland	N11°09'23"W004°33'24"	Jul-Oct 14	29.9-31.1	46.8-322.0	85.9-89.7	Leaf/Neck
Madagascar	11	Ivory	Upland	S19°33’20.3’’E46°24’52.7’’	Nov 14-Mar 15	22.7-25.7	12-615	49.2-89.8	Leaf/Neck
	12	Ivory	Upland	S19°33’44.9’’E046°24’77.0’’	Dec 15-Mar 16	-	-	-	Leaf/Neck
Uganda	13	Namulonge	Upland	N00°31’30’’E32°36’54’’	Oct 14-Mar 15	23.0-26.0	52.0-152	53.8-68.8	Leaf/Neck
Rwanda	14	Kirimburi P8	Irrigated	S 1^{o}17’27.65’’ E 30^{o}18’.55.61	Nov 14-Apr 15	21.7-32.2	827	60.8-81.5	Leaf

*: Not recorded

**Mini/maxi during the trial period of the trials

Table 2: Characteristics of the 81 rice accessions used in the blast trials.

Accessions	Known resistance genes	Source	Reference
International differentials			
Caloro	*Pik-s, Pik-p*	AfricaRice	Yamasaki & Kiyosawa (1966)
Dular ACC	*Pik*	IRRI	’’
Kanto 51	*Pia, Pik*	IRRI	’’
NP125	*Pik*	AfricaRice	’’
RaminadStr 3	*Pi-ka*	’’	’’
Shao Tiao-Tsao	*Pik-s*	AfricaRice	’’
Usen	*Pita*	’’	Yamada et al. (1976)
Japanese differentials			
Aichi Asahi	*Pia, Pi19(t)*	IRRI	Yamada et al. (1976)
Chocoto	*Pia,Pik*	IRRI	’’
Fujisaka 5	*Pii, Pik-s*	AfricaRice	Kiyosawa (1984)
Fukuhikari	*Pita, Pik, Pi9(t), Piz*	AfricaRice	Cho et al. (2007)
K1	*Pita, Pi4(t)*	AfricaRice	Kiyosawa (1967, 1969)
2	*Pia, Pik-p, Pik*	’’	’’
K3	*Pik-h, Pik*	’’	’’
K59	*Pit, Pik-s*	AfricaRice	Kiyosawa (1972), Hayashi et al. (1998)
Kusabue	*Pik, Pish*	AfricaRice	’’
Pi n°4	*Pita-2, Pish*	’’	Kiyosawa (1969)
Toride 1	*Piz-t, Pish*	AfricaRice	Yamada et al. (1976)
Tsuyake	*Pik-m, Pi67*	AfricaRice	’’
Near-isogenic lines			
C101A51	*Pi2(t), Pia, Piz5*	IRRI	Mackill&Bonman (1992)
C101LAC	*Pi1, Pia, Pi1b, Pi33*	IRRI	Mackill&Bonman (1992); Hua et al. (2012)
C104LAC	*Pi1(t), Pia, Pi1b, Pi33*	IRRI	’’
C103TTP	*Pi1, Pi1b, Pi4-b*	’’	’’
C105TTP-1	*Pi4-a(t), Pi4-b*****	IRRI	Mackill&Bonman (1992)
C101TTP-6	*Pi4-b*	IRRI	’’’
CT13432-3R	*Pi1, Pi2, Pi33, Pi54*	AfricaRice	Divya et al. (2014)
IRI529	*Pi33*	’’	Mackill&Bonman (1992)
RIL249 Moro	*Pi5(t)*	IRRI,	Jeon et al. (2003)
Monogenic line, LTH background			
IRBL3-CP4	*Pi3*	IRRI	Tsunematsu et al. (2000), Fukuta et al. (2004), Hayashi &Fukuta (2009)
IRBL5-M	*Pi5(t)*	IRRI	’’
IRBL7-M	*Pi7(t)*	’’	’’
IRBL9-W	*Pi9(t)*	IRRI	’’
IRBL11-Zh	*Pi11(t)*	’’	Tsunematsu et al (2000)
IRBL12-M	*Pi12*	’’	Tsunematsu et al. (2000), Fukuta et al. (2004), Hayashi &Fukuta (2009)
IRBL19-A	*Pi19*	’’	’’
IRBL20-IR24	*Pi20*	’’	’’
IRBLa-A	*Pia*	’’	’’
IRBLb-B	*Pib*	’’	’’
IRBLa-C	*Pia*	IRRI	’’
IRBLi-F5	*Pii*	’’	’’
IRBLk-Ka	*Pik*	’’	Tsunematsu et al (2000)
IRBLkp-K60	*Pik-p*	’’	Tsunematsu et al. (2000), Fukuta et al. (2004), Hayashi &Fukuta (2009)
IRBLks-F5	*Pik-s*	’’	’’
IRBLsh-S	*Pish*	’’	’’
IRBLt-K59	*Pi(t)*	’’	’’

IRBLks-S	*Pik-s*	IRRI	‘’
IRBLta2-Pi	*Pita-2*	‘’	‘’
IRBLz-FU	*Piz*	‘’	‘’
IRBLzt-T	*Piz-t*	‘’	‘’
IRBL1-CL	*Pi1*	‘’	‘’
IRBLkh-K3	*Pik-h*	‘’	‘’
IRBLz5-CA	*Piz5*	IRRI	‘’
Newly improved lines			
ARICA 1	-	AfricaRice	Kumashiro et al. (2013)
ARICA 2	-	‘’	‘’
ARICA 3	-	‘’	‘’
ARICA 4	-	‘’	‘’
ARICA 5	-	‘’	‘’
Old varieties/cultivars			
75-1-127	*Pi9*	IRRI	Qu et al. (2006)
C102 TTP	*Pita*	IRRI	Mackill&Bonman (1992)
CO 39	*Pia, PiCo39(t)*	IRRI	Chauhan et al. (2002)
IR56	*Pita, Pik*	IRRI	Fukuta et al. 2007, Zhou et al. (2006)
IR64	*Pi20, Pita,Piz-t, Pib,Pik-s, Pi25(t), Pi27(t), Pi29(t), Pi30(t), Pi31(t), Pi32(t), Pi33(t), Pir2-3*	IRRI	Fukuta et al. (2007), Sallaud et al. (2003
IRAT 13	*Pib, Pi8(t)*	CIRAD	Kinoshita et al. (1994), Fukuta et al. (2009)
IRAT 104	-[***]	CIRAD	-
IR 72	*Pita, Pib*	IRRI	Fukuta et al. (2007)
Lijiang XintuanHeigh (LTH)	-	IRRI	Tsunematsu et al. (2000)
Maratelli	-	CIRAD	-
Milyang 23	*Pib, Pita, Pik-p*	AfricaRice	Cho et al. (2007)
Modan	*Pb1*	AfricaRice,	Hayashi et al (2010).
Moroberekan	*Pi5, Pi7(t), Pi10(t), Pi157, Pi44, Pi12, Pi12(t)*	AfricaRice	Séré et al. (2013)
Nipponbare	*Pia, Pi41, Pish*		Kawasaki-Tanaka &Fukuta (2014)
Ou 244	*Piz*	AfricaRice	Ou (1971)
OwariHataMochi	*Pi21*	AfricaRice	Fukuoka et al. (2009)
PNA 647F4-56	-	AfricaRice	Soko et al. (2010)
Reiho	*Pita-2, Pia, Pish*	AfricaRice	Kiyosawa et al. (1978)
Suito 11	-	AfricaRice	-
ST1	*Pif, Pi37(t), Pb1*		Ou, 1971;
TCS 10	-	IRRI	-
Tetep	*Pik-h, Pi1,Pita, Pi-4-b, Pitp(t), Pi5, Pita-2, Pik-p*	AfricaRice	Yamada et al. (1976), Mackill&Bonman (1992)
WAB56-104	-	AfricaRice	-
Zenith	*Piz, MPiz, Pia, Pi1*	IIRRI	Yamasaki &Kiyosawa (1966)

[*] : Accessions provided by International Rice Research Institute (IRRI), Philippines ; Centre International de Recherche pour le Développement (CIRAD), France, AfricaRice Plant Pathology laboratory or breeders, Benin.

[**]: Near-isogenic line developed at IRRI.

[***] : No gene known so far.

[****]: Synonymous to *Pita*.

[*****]: NERICA: New Rice for Africa; ARICA: Advanced Rice for Africa.

[******] : Differential monogenic lines developed through IRRI & JIRCAS collaboration.

Table 3: Differential, traditional and elite rice lines identified as susceptible or moderately susceptible (A) or resistant or moderately resistant (B) to leaf blast (*Magnaporthe oryzae*) across sites in Benin, Togo, Mali, Côte d'Ivoire, Burkina Faso, Madagascar and Uganda where trials were conducted from 2013 to 2015.

A	Benin			Togo		Mali		Côte d'Ivoire		Burkina Faso	Madagascar		Uganda	Rwanda
Susceptible or Moderately susceptible (R genes)	1*	2	3	4	5	6	7	8	9	10	11	12	13	14
CO 39 *Pia, PiCo39(t)*	S**	S	S	S	S	S	S	S	S	S	S	S	S	S
IRBLb-B *Pib*	MS	S	S	S	S	S	S	S	MS	MS	S	S	S	S
IRBLks-F5 *Pik-s*	S	S	S	MS	S	S	S	S	S	S	S	S	S	S
Maratelli -	S	S	S	S	S	S	S	S	MS	S	S	S	S	S
Shao Tiao-Tsao *Pik-s*	S	S	S	S	S	S	S	S	S	S	S	S	S	S
IRBLa-C *Pia*	S	S	S	MS	S	S	S	S	MS	S	S	S	S	MS
Lijiang XintuanHeigh (LTH) -	NT****	NT	S	NT	S	***	S	S	MS	S	S	S	S	S

B	Benin			Togo		Mali		Côte d’Ivoire		Burkina Faso	Madagascar		Uganda	Rwanda
Resistant or moderately resistant (R genes)	1[*]	2	3	4	5	6	7	8	9	10	11	12	13	14
Tetep *Pik-h, Pi1,Pita, Pi-4-b, Pitp(t), Pi5, Pita-2, Pik-p*	R	R	R	R	R	R	R	R	R	R	R	R	R	R
Moroberekan *Pi5, Pi7(t), Pi10(t),* *Pi157, Pi44, Pi12, Pi12(t)*	MR	R	R	R	R	R	R	R	R	R	R	MR	R	R
IR64 *Pi20, Pita,Piz-t, Pib,Pik-s, Pi25(t), Pi27(t), Pi29(t), Pi30(t), Pi31(t), Pi32(t), Pi33(t), Pir2-3*	MR	MR	R	R	R	MR	R	R	R	R	R	R	R	R
Pi n°4 *Pita-2, Pish*	NT	NT	R	NT	R	NT	R	R	R	R	MR	R	R	R
IR56 *Pita, Pik*	MR	MR	R	MR	R	-	R	R	R	R	R	R	R	R
IRAT 13 *Pib, Pi8(t)*	R	R	R	R	R	-	R	R	R	R	R	MR	R	R
Ou 244 *Piz*	*R*	*R*	*R*	*R*	*R*	*R*	*R*	*R*	*R*	*R*	*R*	*R*	*R*	*R*
ARICA 1 -	NT[*****]	NT	R	NT	R	NT	R	R	R	R	R	-	R	R
ARICA 2 -	NT	NT	R	NT	R	NT	MR	R	R	R	R	R	MR	R
ARICA 4 -	NT	NT	R	NT	R	NT	MR	R	R	R	R	R	R	R
IRAT 104 -	R	R	R	[****]	R	R	R	R	R	R	R	R	R	R
WAB56-104 -	R	MR	R	R	R	R	R	R	R	R	R	R	R	R

C	Benin			Togo		Mali		Cote d’Ivoire		Burkina Faso	Madagascar		Uganda	Rwanda
Other responses														
Accessions (R genes)	1*	2	3	4	5	6	7	8	9	10	11	12	13	14
C104LAC *Pi1(t), Pia, Pi1b, Pi33*	S**	S	S	MR	R	S	S	S	MR	MR	S	S	MR	R
C103TTP *Pi1, Pi1b, Pi4-b*	S	S	S	R	R	S	S	S	R	R	MS	S	R	R
IR 72 *Pita, Pib*	MS	R	R	R	R	R	R	R	R	R	R	R	R	R
C105TTP-1 *Pi4-a(t), Pi4-b*	S	MR	R	R	R	S	S	S	MS	R	S	S	S	MS
Chocoto *Pia,Pik*	MS	R	MR	R	R	S	S	MR	R	R	S	S	MR	S
C101TTP-6 *Pi4-b*	S	S	MS	R	MS	MR	S	MR	MR	MR	MS	S	MS	MR
IRI529 *Pi33*	MS	MR	R	R	MS	S	S	R	R	R	R	R	R	R
75-1-127 *Pi9*	S	MS	R	R	R	MS	S	R	R	R	R	R	R	R
IRBL5-M *Pi5(t)*	S	S	MS	MR	MR	MR	MS	MR	R	MR	MS	MR	R	R
IRBL7-M *Pi7(t)*	S	S	S	MR	S	MS	S	MS	R	MR	S	S	MS	MS
IRBL12-M *Pi12*	S	S	S	S	S	S	S	S	S	S	R	S	S	S
IRBL19-A *Pi19*	MR	MR	MR	R	R	MR	S	MS	MS	R	S	R	S	MS
IRBL20-IR24 *Pi20*	S	S	S	-***	S	S	S	R	R	S	MR	MS	R	MR
IRBLa-A *Pia*	S	S	S	MS	S	R	S	S	S	S	S	S	S	MR
IRBLi-F5 *Pii*	S	S	S	MS	S	S	S	S	MS	S	MS	MS	R	MS
IRBLkp-K60 *Pik-p*	S	S	S	MR	S	S	S	S	R	MR	S	S	R	MR
IRBLsh-S *Pish*	S	S	MR	R	R	S	S	MR	R	MR	R	MS	S	R
IRBLt-K59 *Pi(t)*	S	S	S	MS	S	S	S	S	S	S	S	S	R	S
IRBLta2-Pi *Pita-2*	S	S	S	S	S	S	S	S	R	S	S	S	S	S
IRBLz-FU *Piz*	R	R	R	MR	R	MR	S	MS	R	R	R	R	S	MS
IRBLzt-T *Piz-t*	S	S	MS	R	R	MS	S	MR	R	R	MS	MS	MS	R
IRBL1-CL *Pi1*	S	S	S	MS	MR	S	S	MS	MS	S	S	S	R	R
IRBLkh-K3 *Pik-h*	S	S	S	MR	S	S	S	S	S	S	S	MR	R	S
Nipponbare *Pia, Pi41, Pish*	S	MS	R	MS	R	S	S	R	R	S	R	R	MR	R
Aichi Asahi *Pia, Pi19(t)*	S	MR	R	S	MR	S	S	S	S	R	S	S	S	S
Zenith *Piz, MPiz, Pia, Pi1*	R	R	R	R	R	R	R	MR	R	R	MR	S	S	R
Dular ACC *Pik*	MR	MR	MS	MR	MS	MS	S	MR	R	MS	MR	MR	R	MR

Usen *Pita*	MS	MR	R	-	R	S	S	MS	MR	R	MS	S	R	MR
RaminadStr 3 *Pi-ka*	R	R	R	R	R	R	R	R	R	R	R	-	S	R
Suito 11 -	MS	MS	R	R	R	MR	S	R	R	R	MR	MR	R	R
OwariHataMochi *Pi21*	MS	MS	R	R	R	S	S	R	R	R	MR	MR	R	R
Modan *Pb1*	S	S	MS	R	R	MR	MR	R	R	R	R	MS	R	R
ST1 *Pif, Pi37(t), Pb1*	MS	R	R	R	R	MS	MR	R	R	R	R	R	MS	R
IRBLks-S *Pik-s*	S	S	MS	R	MS	S	S	MS	MS	S	MS	MR	R	S
Toride 1 *Piz-t, Pish*	S	MS	R	R	R	S	S	R	R	MR	R	R	R	MS
TCS 10 -	MR	MR	R	MR	S	S	MR	R	R	R	R	R	MS	MR
RIL249 Moro *Pi5(t)*	**R**	**R**	**R**	**-**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	MS	**R**	**R**
PNA 647F4-56 -	MS	R	MR	R	MR	S	S	MR	MR	R	MS	S	S	S
Fukuhikari *Pita, Pik, Pi9(t), Piz*	MR	MR	R	R	R	R	MR	R	R	R	R	MS	R	R
Milyang 23 *Pib, Pita, Pik-p*	S	S	S	-	MR	S	S	MR	MR	MR	R	R	MS	MR
Kanto 51 *Pia, Pik*	S	S	S	R	R	MS	S	S	R	R	S	MS	R	R
IRBL3-CP4 *Pi3*	S	S	S	MS	S	S	MS	S	S	S	S	S	S	MR
CT13432-3R *Pi1, Pi2, Pi33, Pi54*	R	R	R	R	R	R	R	R	R	R	R	R	MS	R
Tsuyake *Pik-m, Pi67*	S	S	S	R	R	-	S	S	R	MR	S	S	MS	R
NP125 *Pik*	MR	R	R	R	R	MR	S	R	R	R	MR	R	R	R
Fujisaka 5 *Pii, Pik-s*	S	S	S	MR	R	S	S	S	S	S	MR	MR	R	R
C101LAC *Pi1, Pia, Pi1b, Pi33*	MS	MR	R	R	R	R	MS	R	R	R	R	R	MS	R
IRBL9-W *Pi9(t)*	R	R	R	R	R	R	S	S	S	R	MR	R	S	R
Reiho *Pita-2, Pia, Pish*	MR	R	R	R	R	MR	MS	R	R	R	R	R	MS	R
C101A51 *Pi2(t), Pia, Piz5*	R	R	R	R	R	MS	S	R	R	S	R	R	R	MR
ARICA 3 -	NT****	NT	MS	NT	R	NT	S	R	R	R	R	-	S	R
ARICA 5 -	NT	NT	R	NT	R	NT	R	R	R	R	R	MS	MS	R
IRBLz5-CA *Piz5*	NT	NT	R	NT	R	NT	S	R	R	S	R	R	R	R
IRBL11-Zh *Pi11(t)*	NT	NT	S	NT	S	NT	S	S	MS	MS	R	MS	R	S
IRBLk-Ka *Pik*	NT	NT	S	NT	MR	NT	S	S	R	S	S	S	R	R
K59 *Pit, Pik-s*	NT	NT	R	NT	MS	NT	S	R	R	S	MS	MS	R	R
Kusabue	NT	NT	R	NT	R	NT	MS	R	R	R	R	R	R	R

Pik, Pish														
Caloro *Pik-s, Pik-p*	NT	NT	S	NT	S	NT	S	S	R	S	MS	MS	R	MR
K1 *Pita, Pi4(t)*	NT	NT	R	NT	R	NT	S	MR	R	R	MR	R	R	R
K2 *(Pia, Pik-p, Pik)*	NT	NT	R	NT	R	NT	S	R	R	MR	MR	MS	R	MR
K3 *Pik-h, Pik*	NT	NT	MS	NT	R	NT	S	MS	R	R	S	MS	R	R
C102 TTP *Pita*	NT	NT	MR	NT	R		S	S	S	MR	S	S	S	S

*1: Trial nos. 1, 2, 3 in Benin, 4 and 5 in Togo, 6 and 7 in Mali, 8 and 9 in Côte d'Ivoire, 10 in Burkina Faso, 11 and 12 in Madagascar, 13 in Uganda and 14 in Rwanda (for details see Table 1).

** Status of the accession: resistant (R) for Sev≤3.0; (moderately resistant (MR) for 3.0≤Sev≤4.0); moderately susceptible (MS for 4.0<Sev≤5.0; Susceptible (S) for Sev>5.0.

*** :Not germinated, destroyed by leaf blast, not flowered (being photosensitive), or destroyed by rats.

. **** NT: Not tested.

Accessions highlighted with the same color share the same resistance genes.

Legend

	Resistant or moderately resistant in all sites except one where it was susceptible or moderately susceptible
	Resistant or moderately resistant in all sites except two where it was susceptible or moderately susceptible

Table 4: Evidence of blast (*Magnaporthe oryzae*) populations that occurred at field sites in eight African countries (Benin, Togo, Mali, Côte d'Ivoire, Burkina Faso, Madagascar and Uganda) where blast differential rice lines harboring single genes were tested from 2013 to 2015.

		Benin			Togo		Mali		Côte d’Ivoire		BurkinaFFaso[a]	Madagascar		Uganda	Rwanda
Accessions (R genes)	Resistance genes	1[*]	2	3	4	5	6	7	8	9	10	11	12	13	14
C101TTP-6	*Pi4-b*	+	+	+	-	+	+	+	+	+	+	+	+	+	+
IRI529	*Pi33*	+	+	-	-	+	+	+	-	-	-	-	-	-	-
75-1-127	*Pi9*	+	+	-	-	-	+	+	-	-	-	-	-	-	-
IRBL5-M	*Pi5(t)*	+	+	+	+	+	+	+	+	-	+	+	+	-	-
IRBL7-M	*Pi7(t)*	+	+	+	+	+	+	+	+	-	+	+	+	+	+
IRBL12-M	*Pi12*	+	+	+	+	+	+	+	+	+	+	-	+	+	+
IRBL19-A	*Pi19*	+	+	+	-	-	+	+	+	+	-	+	-	+	+
IRBL20-IR24	*Pi20*	+	+	+	NT	+	+	+	-	-	+	+	+	-	+
IRBLa-A	*Pia*	+	+	+	+	+	-	+	+	+	+	+	+	+	+
IRBLb-B	*Pib*	+	+	+	+	+	+	+	+	+	+	+	+	+	+
IRBLi-F5	*Pii*	+	+	+	+	+	+	+	+	+	+	+	+	-	+
IRBLkp-K60	*Pik-p*	+	+	+	+	+	+	+	+	-	+	+	+	-	+
IRBLsh-S	*Pish*	+	+	+	-	-	+	+	+	-	+	-	+	+	-
IRBLt-K59	*Pi(t)*	+	+	+	+	+	+	+	+	+	+	+	+	-	+
IRBLta2-Pi	*Pita-2*	+	+	+	+	+	+	+	+	-	+	+	+	+	+
IRBLzt-T	*Piz-t*	+	+	+	-	-	+	+	+	-	-	+	+	+	-
IRBL1-CL	*Pi1*	+	+	+	+	+	+	+	+	+	+	+	+	-	-
IRBLkh-K3	*Pik-h*	+	+	+	+	+	+	+	+	+	+	+	+	-	+
Usen	*Pita*	+	+	-	NT	-	+	+	+	+	-	+	+	-	+
RaminadStr 3	*Pi-ka*	-	-	-	-	-	-	-	-	-	-	-	NT	+	-
OwariHataMochi	*Pi21*	+	+	-	-	-	+	+	-	-	-	+	+	-	-
Modan	*Pb1*	+	+	+	-	-	+	+	-	-	-	-	+	-	-
IRBLks-S	*Pik-s*	+	+	+	-	+	+	+	+	+	+	+	+	-	+
RIL249 Moro	*Pi5(t)*	-	-	-	NT	-	-	-	-	-	-	-	+	-	-
IRBL3-CP4	*Pi3*	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Ou 244	*Piz*	-	-	-	-	-	-	-	-	-	-	-	-	-	-
NP125	*Pik*	+	-	-	-	-	+	+	-	-	-	+	-	-	-
IRBL9-W	*Pi9(t)*	-	-	-	-	-	-	+	+	+	-	+	-	+	-
IRBLz5-CA	*Piz5*	NT	NT	-	NT	-	NT	+	-	-	+	-	-	-	-
IRBL11-Zh	*Pi11(t)*	NT	NT	+	NT	+	NT	+	+	+	+	-	+	-	+
Total number of genes overcome	*30*	**24/28**	**23/28**	**20/30**	**12/25**	**17/30**	**23/28**	**27/30**	**20/30**	**14/30**	**18/30**	**20/30**	**22/29**	**12/30**	**16/30**

*1: Trial nos. 1, 2, 3 in Benin, 4 and 5 in Togo, 6 and 7 in Mali, 8 and 9 in Côte d’Ivoire, 10 in Burkina Faso, 11 & 12 in Madagascar, 13 in Uganda and 14 in Rwanda (for details see Table 1).

[**‘’] -’’ = Sev≤3.0, ‘’+’’= S≥3.0.

[***] NT: Not tested.

[a] Burkina Faso

[b:] Madagascar

[c:] Uganda

[d:] Rwanda

Table 5: Differential, traditional and elite rice lines identified as resistant/susceptible to neck blast (*Magnaporthe oryzae*) based on their disease severity mean scores at sites in Benin, Togo, Côte d’Ivoire, and Uganda where trials were conducted from 2013 to 2015.

Accessions (R gene)	Benin 2,3*	Togo 4,5	Cote d'Ivoire 8,9		Uganda 13
IRI529	R**	R	-***	R	R
Pi33					
75-1-127	R	-	-	-	R
Pi9					
Modan	R	R	MR	S	R
Pb1					
RaminadStr 3	-	R	-	-	R
Pi-ka					
RIL249 Moro	R	R	-	-	R
Pi5(t)					
IRBLz5-CA	R	R	-	MR	R
Piz5					
IRBL11-Zh	R	R	S	S	R
Pi11(t)					
IRBL9-W	R	MR	S	MS	MR
Pi9(t)					
Ou 244	R	R	R	R	R
Piz					
IRAT13	R	R	MR	R	R
Pib, Pi8(t)					
Toride 1	R	R	R	R	R
Piz-t, Pish					
IR56	R	R	-	R	R
Pita, Pik	R	R		R	R
Nipponbare	R	R	R	R	R
Pia, Pi41, Pish					
IR64	R	R	-	R	R
Pi20, Pita,Piz-t, Pib,Pik-s, Pi25(t), Pi27(t), Pi29(t), Pi30(t), Pi31(t), Pi32(t), Pi33(t), Pir2-3					
Tetep	R	-	-	-	R
Pik-h, Pi1,Pita, Pi-4-b, Pitp(t), Pi5, Pita-2, Pik-p					
TCS 10	R	-	-	-	R
-					
CT13432-3R	R	R	R	R	R
Pi1, Pi2, Pi33, Pi54					
C101LAC	R	R	MR	R	R
Pi1, Pia, Pi1b, Pi33					
ARICA 1	R	R	-	-	R
-					
ARICA 2	R	-	-	R	R
-					
ARICA 3	R	R	-	R	R
-					
ARICA 4	R	R	R	R	R
-					
ARICA 5	R	R	MR	R	R
-					
Kusabue	R	R	R	R	R
Pik, Pish					
Pi n°4	R	R	R	R	R
Pita-2, Pish					
K2	R	R	R	R	R
Pia, Pik-p, Pik					
WAB56-104	R	R	MR	R	R

*: Trial number as indicated in Table 2.

**Sv= Neck blast severity: Resistant or R (0 - 15%); Moderately resistant or MR (16 - 30%); moderately susceptible or MS (31 - 45%); Susceptible or Sv (> 45%).

***: Not germinated, destroyed by leaf blast, not flowered (being photosensitive) or destroyed by rats.

Table 6: Analysis of the relationship between severities of leaf and neck blast on 81 selected rice accessions tested in five trials in Benin (1), Côte d'Ivoire(2), Togo (1) and Uganda (1) from 2013 to 2016.

Leaf blast reactions of accessions	No of interactions	**Neck blast reactions**							
		R**		MR		MS		S	
		No	%	No	%	No	%	No	%
Resistant*	200	153	76.5	13	6.5	6	3.0	28	14
Moderately resistant	28	15	53.6	0	0	3	10.7	10	35.7
Moderately susceptible	41	19	46.3	3	7.3	2	4.9	17	41.5
Susceptible	97	37	38.1	15	15.5	3	3.1	42	43.3
Missing	39								
Total	**405**	71		18		8		69	

*: 3.0 ≤Resistant; 3.1 >Moderately resistant≤ 4.0; 4.1 >Moderately susceptible≤ 5.0; Susceptible ≥5.1

**:*Resistant: 0 - 15%, Moderately resistant (16 - 30%), Moderately susceptible: 31 - 45%, Susceptible: > 45.