17 Managing the Major Diseases of Rice in Africa

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Introduction

Rice is the principal food grain consumed by almost half of the world's population (Khush, 2005), making it the most important food crop currently produced (Cottyn *et al.*, 2001). Rice is increasingly becoming a regular staple for the populations of sub-Saharan Africa (SSA). Rice availability and prices impact directly on the welfare of the poorest consumers in the region, many of whom are resource-poor farmers depending on rice as both a staple food and a source of income. It is therefore not surprising that rice is a major component of the food-security and poverty-alleviation strategies of many SSA countries. Against this background, any improvement in rice productivity will contribute significantly to achieving a higher level of regional and household food security, while responding to the needs of the poorest by enhancing their diet both quantitatively and qualitatively and by providing additional income opportunities (Seck *et al.*, 2012).

The 2007–2008 crisis in rice availability and price prompted African countries to develop initiatives to increase their domestic production by increasing the area under rice cultivation or increasing the productivity per unit area by using high-yielding varieties and fertilizers. However, both development of new areas for rice cultivation and intensification face prevailing and unpredictable challenges, among which diseases are likely to feature prominently.

This chapter gives an overview of the rice diseases identified in Africa and their importance, and then focuses on the three major ones. We describe what is known about pathogen variability and show how that knowledge can be used to create varietal resistance as part of an integrated approach to disease management.

Major Rice Diseases and Their Importance in Africa

Diseases of rice

Various studies have inventoried rice diseases in SSA (Roger, 1958, Notteghem and Baudin, 1981; Akinsola *et al.*, 1982, Mbodj *et al.*, 1984; Séré, 1988a,b,c; Sy and Séré, 1996).

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At a very early stage, research on rice diseases was conducted in the framework of an integrated pest management (IPM) approach. As early as 1979, a seminar on the integrated management of rice pests was organized by the Africa Rice Center (AfricaRice) in Bobo-Dioulasso (Burkina Faso). A further seminar in 1981 at Fendall, Liberia (ADRAO, 1982), and a series of training workshops gave impetus to the IPM approach.

Three categories of rice pathogens are identified (Sy and Séré, 1996): (i) **major pathogens** (Plates 9a, 9b, 10 and 11) – blast fungus (*Magnaporthe oryzae*), *Rice yellow mottle virus* (RYMV) and the bacterium responsible for leaf blight (*Xanthomonas oryzae* pv. *oryzae*), the prevalence of which (by rice ecosystem) was defined by the Integrated Pest Management (IPM) Task Force (Table 17.1); (ii) **secondary pathogens** – responsible for brown spot (*Bipolaris oryzae*), leaf scald (*Gerlachia oryzae*) and sheath blight (*Rhizoctonia solani*); and (iii) other **pathogens classified as minor** – responsible for false smut (*Ustilaginoides virens*), narrow brown spot (*Cercospora jansenea*), sheat rot (*Sarocladium oryzae*), bakanae disease (*Fusarium moniliforme*), bacterial leaf streak (*Xanthomonas oryzae* pv. *oryzicola*) and grain discoloration (caused by a complex of fungi). Two further pathogens which inflict minor yield losses – *Sclerophtora macrospora* and *Corallocytostroma oryzae* – have also been identified in Africa (Séré, 1988a,c). Moreover a pathogen responsible for red stripe (El-Namaky, 2011) was recently described (Plate 12).

Despite many efforts to develop integrated management of rice diseases based on varietal resistance, unexpected epidemic explosions still appear – such as blast in Kenya in 2008 (Séré *et al.*, 2011) and RYMV in Rwanda in 2009 (Ndikumana *et al.*, 2011).

Rice blast

Rice blast is caused by an ascomycete fungus *Magnaporthe oryzae* (anamorph: *Pyricularia oryzae*) (Couch and Kohn, 2002). The symptoms (elliptical grey-white lesions) appear on the aboveground organs of the rice plant: the most frequently described are leaf, node and neck blast. Neck blast (Plate 9b) is considered more destructive than leaf blast (Plate 9a) (Zhu *et al.*, 2005).

Rice blast has been widely and intensively studied both globally and in Africa, because the interaction between rice and the blast pathogen has both practical and theoretical interest. The practical interest is related to the importance of rice in human nutrition and the importance of unpredictable yields losses caused by blast worldwide (Jia *et al.*, 2009). The theoretical interest is linked to the fact that the blast pathogen is considered as a model for investigation by plant pathologists (Valent, 1990).

According to Bidaux (1978) rice blast was first reported in Africa in 1922. It is the most widespread disease in SSA. In Burkina Faso, surveys in farmers' fields indicated that intensifying rice cultivation (use of fertilizer and modern, but susceptible, varieties) may lead to increased yield losses due to blast, reducing an important part of the benefit created by intensifying rice cultivation (Séré *et al.*, 2011). Yield losses of 1–22% were recorded in rainfed lowland, and 4–45% in irrigated systems in the south and west of the country. Yield losses of up to 44% (equivalent to 2 t/ha) were recorded in the irrigated perimeter of Vallée du Kou (Séré *et al.*, 2011).

In many countries, blast inflicts significant damage: heavy yield losses (up to 100%) were reported by farmers in Ghana (Nutsugah *et al.*, 2004) and in some locations in The Gambia (Jobe *et al.*, 2002); in Sierra Leone, losses in excess of 80% were reported in susceptible cultivars and accessions in experimental plots (Fomba and Taylor, 1994). In Nigeria, blast outbreaks have been reported to cause rice yield losses of about

Table 17.1. Importance of major rice diseases across rice ecosystems in West Africa. (Adapted and corrected from Fakorede and Yoboué, 2001).

Disease	Upland	Lowland	Irrigated	
			Forest and savannah	Sahel
Blast	++	+	+	–
RYMV	–	+	+	++
Bacterial blight	–	–	+	+

Key: from – no disease to ++ high pressure.

35–50% and, in a serious outbreak of the disease, up to 100% of yield may be lost (WARDA, 1999a,b). Yield losses of 20–30% have been recorded in Benin (Vodouhe *et al.*, 1981), 36–63% in Burkina Faso (Séré, 1981), 64% in Togo (Akator *et al.*, 1981) and up to 80% in Côte d'Ivoire (Delassus, 1973).

Rice yellow mottle disease

First recorded in 1966 at Otonglo near Lake Victoria, Kenya (Bakker, 1970), *Rice yellow mottle virus* (RYMV) (genus *Sobemovirus*) is now a major biotic constraint of rice, present in most of the rice-growing countries in Africa (Abo *et al.*, 1998; Kouassi *et al.*, 2005; Séré *et al.*, 2008b; Traoré *et al.*, 2009; Ndikumana *et al.*, 2011).

RYMV disease is characterized by mottling and yellowing symptoms of various intensities depending on genotype and time of infection. Infected plants show pale yellow mottling on their leaves, stunted growth, fewer tillers, asynchronous flower formation, poor panicle exsertion, spikelet discoloration and sterility (Plate 10). In severe cases, affected plants may die. Yield loss ranges from 10% to 100%, depending on the timing of the infection and the type of variety (Abo *et al.*, 1998; Kouassi *et al.*, 2005).

RYMV disease is transmitted when the sap of infected leaves comes into contact with the cells of healthy leaves – for example, leaf contact in closely spaced plants, contaminated hands of field workers, rice stubble incorporated into the soil, and intertwining of rice roots. RYMV is not transmitted through rice seeds (Konate *et al.*, 2001; Abo *et al.*, 2004). Many insects are vectors of RYMV, including *Dicladispa gestroi*, *Trichispa sericea*, *Chaetocnema* spp., *Sessilia pussila*, *Chnootriba similis*, other beetles belonging to the family Chrysomelidae; the long-horned grasshoppers *Conocephalus merumontanous* and *Con. longipennis*; the short-horned grasshoppers, *Oxya hyla*, *Paratettix* sp., *Zonocerus variegatus*, *Euscyrtus* sp., *Cofana spectra*, *Cof. nimacuata*, *Locris rubra* and *L. maculate* (Abo *et al.*, 1998; Nwilene, 1999).

The increasing incidence and importance of RYMV in Africa is attributed to the cultivation of new highly susceptible exotic rice varieties mostly from Asia (Thresh *et al.*, 2001) and the availability of water through irrigation which allows for sequential planting and maintenance of higher crop intensity without dry-season gaps, which favours increase of both insect vectors and alternative hosts (Traoré *et al.*, 2009). The RYMV epidemic at the beginning of the 1990s in West Africa was the result of intensification of rice cultivation (Traoré *et al.*, 2009).

Bacterial blight

Bacterial blight of rice, caused by *Xanthomonas oryzae* pv. *oryzae*, is another major biotic constraint to rice production and productivity. The disease was first observed in Africa (Mali) by Buddenhagen *et al.* (1979). In the following years, it was reported from Senegal (Trinh, 1980), Cameroon (Notteghem and Baudin, 1981), Niger (Reckhaus, 1983), Madagascar and Nigeria (Buddenhagen, 1985), Burkina Faso (Séré and Nacro, 1992) and Tanzania (Ashura *et al.*, 1999), and later from Benin, Guinea, The Gambia, Mozambique, Rwanda and Uganda (Onasanya *et al.*, 2009; El-Namaky, 2011).

The pathogen enters the host plant through natural openings at the leaf tip or margins (Ou, 1985) or through wounds. The pathogen reaches the xylem, where it multiplies and spreads throughout the plant, resulting in systemic infection (Huang and Cleene, 1989; Gnanamanickam *et al.*, 1999).

Typical bacterial blight symptoms (Plate 11) include leaf blight, pale yellow leaves and wilting (named 'kresek' symptom). Leaf blight is most common between maximum tillering and maturity stages. However, kresek – the most devastating manifestation of the pathogen – is most commonly observed at seedling stage, with seedlings being most susceptible in the 21 days after transplanting.

The pathogen mainly attacks rice, but also infects other *Oryza* species and wild hosts (Li *et al.*, 1985). In Niger, an extensive study at 23 sites revealed bacterial blight infection on *Brachiaria* sp., *Cyperus esculentus*, *C. rotondus*, *Dactyloctenium aegyptium*, *Echinocloa* sp., *Eulesine indica*, *Kyllinga squamulata*, *Leersia hexandra*, *Oryza barthii*, *O. longistaminata*, *Panicum lactum*, *P. repens* and *Pennisetum pedicelatum* (AfricaRice, 2010).

A survey carried out in several West African countries revealed yield loses of 2.7–41.0%

(Awoderu *et al.*, 1991) and a disease incidence of 70–85% in farmers' fields (Séré *et al.*, 2005). The introduction of a high-yielding but susceptible variety from Taiwan to the bacterial blight pathogen in the mid-1990s drew scientists' attention to the importance of this disease (Ouedraogo *et al.*, 2007). Complete crop failures have occurred in Burkina Faso (Ouedraogo *et al.*, 2007).

Variability of Rice Disease Pathogens in Africa

Rationale

In addition to the identification and prioritization of rice pathogens in Africa, research activities were pursued to develop IPM, mainly through the collaborative network implemented by AfricaRice and its national (NARS) partners called the IPM Task Force (WARDA, 2002). Priority was placed on varietal resistance as the main component of an IPM strategy (WARDA, 1999a,b). As information on pathogen diversity is essential for adequate utilization of resistant varieties and for developing strategies to increase the durability of resistance (Xia *et al.*, 2000), research activities were undertaken to better understand the structure of pathogen populations.

Rice blast

Blast pathogen diversity at pathological level is usually analysed by infecting 'differential' varieties with different isolates of the pathogen. However, in Africa, blast-trapping nurseries were developed and implemented, not only to identify efficient resistance genes, but also to characterize rice-growing areas (especially screening sites) in terms of the structure of their blast pathogen populations (Séré *et al.*, 2007, 2011). Such nurseries appeared to be an effective tool for characterizing the virulence spectrum of blast populations using limited equipment and labour (Séré *et al.*, 2007). The best sites for screening for durable resistance were identified (Séré *et al.*, 2007) and efficient resistance genes were found. For instance, the

virulence genes that overcome the blast-resistance genes of rice *Pi9*, *Pit* and *Piz-5* are not present or are extremely rare in five countries – Benin, Burkina Faso, Guinea, Mali and Nigeria (Séré *et al.*, 2011). The results from field screening in Africa of varieties with resistance genes to Asian blast pathogens suggested a difference between blast pathotypes on the two continents (Séré *et al.*, 2007).

The development of molecular tools offered new opportunities for analysing the blast fungus diversity to help effective deployment of resistance and to identify shifts in races or population structures (Javan-Nikkhah *et al.*, 2004; Chen *et al.*, 2006). A tremendous amount of knowledge on blast pathogen population diversity has been accumulated throughout the world, especially with the identification of disperse-repetitive DNA sequences called MGR (Hamer and Givan, 1990). Studies in West Africa focused on describing the extent of blast pathogen diversity (lineages and pathotypes) in and around key sites in Burkina Faso, Côte d'Ivoire, Ghana and Nigeria: the persistent dominant lineages and major pathotype groups were identified (Chipili *et al.*, 1999). However, such studies were conducted in few countries in Africa (Chipili *et al.*, 1999; Nutsugah *et al.*, 2008) in comparison to what was done elsewhere in the world. Consequently, the research needs to be continued on a larger scale throughout Africa.

RYMV

Several hundred RYMV isolates from cultivated rice and wild *Poaceae* were collected in more than ten countries and stored in isolate banks mainly at the Institut de recherche pour le développement (IRD, France) and AfricaRice. All the isolates were serologically typed with both polyclonal and monoclonal antibodies. The coat protein gene of some isolates representative of the geographic distribution and of the serological variability was sequenced. These studies indicated that RYMV is a variable virus, and that there are several strains with different geographical distributions and pathogenic properties (N'Guessan *et al.*, 2000; Pinel *et al.*, 2000). Five major serotypes were described and named Ser1, Ser2, Ser3, Ser4 and Ser5. Comparing the

molecular and immunological typing of RYMV isolates, Fargette *et al.* (2002b) found that molecular typing is consistent with immunological typing. However, Ser5 includes two strains (S5 and S6), leading to the identification of six strains: S1, S2 and S3 are West African isolates, while S4, S5 and S6 are from East Africa.

Phylogenetic analyses were performed, not only to analyse the genetic relationships between the isolates, but also to assess the links between geographic and genetic distances. The most basal strains were in East Africa. Phylogenetic inferences showed that the centre of origin of RYMV was in East Africa, possibly within the Eastern-Arc mountains biodiversity hot spot, and that successive strain radiations had occurred from the east to the west of the continent. Altogether, the data suggested that RYMV originated from wild *Poaceae* and infected cultivated rice only recently (Fargette *et al.*, 2004).

The evolution rate of RYMV was calculated from sequences of the coat protein gene of isolates collected from rice over a 40-year period in different parts of Africa. The results show that an RNA plant virus such as RYMV evolves as rapidly as most RNA animal viruses (Fargette *et al.*, 2008).

Bacterial blight

Xanthomonas oryzae pv. *oryzae* is a Gamma proteobacterium. The pathogen is a Gram-negative rod with round ends of 0.5–0.8 × 1.0–2.0 μm. The pathogen fails to grow on L-alanine as exclusive carbon source and 0.2% vitamin-free casamino acids, but it is insensitive to 0.001% cupric nitrate, which differentiates it from *X. oryzae* pv. *oryzicola* (the cause of rice bacterial leaf streak) (Vera Cruz *et al.*, 1984).

Although studies have not been as extensive in Africa as in Asia, the pathogen does show high pathogenic variability in Africa. Séré *et al.* (2005) found that four Malian isolates from different origins reacted differently on four varieties (Bouaké 189, BG90-2, NERICA 1 and NERICA 4). Isolate 1 (from Molodo) is virulent on three varieties and isolate 3 (from Nango) was not virulent on any of the four varieties. Two isolates (2 and 4, from Ndebougou and Niono, respectively) were virulent on two varieties.

None of the four isolates developed a compatible reaction on NERICA 1.

Another pathotyping analysis carried out with 50 strains of *X. oryzae* pv. *oryzae* isolated from seven West African countries on 18 near-isogenic rice lines (NILs) resulted in the description of two pathotypes of the pathogen, *Pta* and *Ptb*, having three and two pathotype sub-groups, respectively (Onasanya *et al.*, 2009). A similar study carried out on 47 isolates from 25 locations in Niger revealed three major pathogroups (AfricaRice, 2010).

Gonzalez *et al.* (2007) evaluated 16 African strains of *X. oryzae* pv. *oryzae*, using differential varieties. They identified three new races (A1, A2 and A3) of *X. oryzae* pv. *oryzae* among African isolates, none of which has been described in Asian populations of the pathogen.

A pathotyping analysis carried out with 23 strains collected from West Africa and with reference strains from Asia against seven rice differential lines with monogenic resistance genes identified two pathogroups, PI and PII. The latter comprised the more virulent strains of the pathogen, which comprised 61% of the strains tested (Bimerew, 2010).

Trapping nurseries were used in a bacterial blight-prone environment in West Africa to analyse the interaction between resistance genes and a natural pathogen population (AfricaRice, 2010). None of the Malian races of *X. oryzae* pv. *oryzae* induced susceptible reactions in the rice lines bearing resistance genes *xa5*, *Xa7*, *Xa14*, *Xa18* or *Xa21*, or one of the associations *Xa4+xa5*, *xa5+Xa21* or *xa13+Xa21*. The *X. oryzae* pv. *oryzae* races that induce susceptible reaction to *Xa1*, *Xa2*, *xa7*, *xa8*, *Xa11*, *Xa14*, IR24 (*Xa18* and other), *Xa21*, the associations *Xa4+Xa21* and *Xa4+xa5+xa13+Xa21* were rare in Niger. In Burkina Faso, lines with resistance gene *Xa7* or the four pyramided genes (*Xa4+xa5+xa13+Xa21*) were resistant or moderately resistant to the natural population of *X. oryzae* pv. *oryzae* over 2 years, as was Gigante, while lines with *xa3*, *Xa10*, *Xa11*, *Xa4+xa5*, *Xa4+xa13* or *xa5+xa13* were moderately resistant.

Molecular techniques were used to characterize the genetic diversity among African strains of *X. oryzae* pv. *oryzae*. A study carried out using multilocus sequence analysis of *X. oryzae* pv. *oryzae* strains isolated from Africa based on *atpD*, *dnaK*, *gyrB* and *efp* housekeeping

genes demonstrated that African strains are distinct from Asian ones (Bimerew, 2010), indicating that African strains are genetically distant from Asian ones. White *et al.* (1995) and Gonzalez *et al.* (2007) previously reported a difference between African and Asian strains of *X. oryzae* pv. *oryzae*.

Integrated Management of Rice Diseases in Africa

Background

Genetic control receives the most attention among the control measures to be used against rice pathogens, because it is the easiest method for farmers to adopt and the principal component of the IPM strategy (WARDA, 1999a,b). Based on the known interactions between pathogens and plant hosts, screening methods were developed and used to characterize rice varieties developed by breeders. In order to reinforce the resistance, other control measures were also investigated (WARDA, 1999a,b).

Rice blast

Genetic control

HOST–PATHOGEN RELATIONSHIP. Two kinds of host–pathogen relationship are described for the blast pathogen and rice.

In the vertical system, the relationship between virulence genes of the rice pathogens and resistance genes of rice varieties is explained by the gene-for-gene theory (Kiyosawa, 1980; Silué *et al.*, 1992).

The vertical resistance is controlled by few genes of major effect (Wang *et al.*, 1994; Liu *et al.*, 2002; Sallaud *et al.*, 2003; Chen *et al.*, 2004). They are responsible for a qualitative, complete and non-durable resistance. More than 70 *Pi* genes have been identified (Dai *et al.*, 2007; Lin *et al.*, 2007; Ballini *et al.*, 2008), some of which have been molecularly characterized (Suh *et al.*, 2009). Markers for many blast resistance genes (e.g. *Pi1*, *Pi2* [or *Piz-5*], *Pita*, *Pit*, *Pi7*, *Pi9*, *Pi1* and *Pib*) are now available (Khush and Brar, 2004).

Although no comprehensive study of the durability of the major genes has been carried out in Africa, an analysis of the virulence of the blast population in Benin by planting lines and varieties bearing known major resistance genes each month from September 2007 to October 2008, gives an indication of the efficiency of some resistance genes over a year. For instance, the variety 75-1-127 (with *Pi9*) and Moroberekan (*Pi7* + *Pi5* and other major genes and quantitative trait loci (QTLs) according to Chen *et al.*, 1997) remained efficient in each monthly trial, while IRBLz5-CA/CO (*Piz5*) failed in the 11th month (August 2008) and other NILs were efficient only during the first 2 to 4 months (Table 17.2). Resistance of *Pi9* and *Piz5* was confirmed in trials conducted at Ouèdèmè (Benin) in 2009 and 2011 (Table 17.3). However, in the hot spot of Longorola (Sikasso) in Mali, *Pi9* was susceptible while *Piz5* was resistant (Ayeko, 2012).

When the vertical resistance fails against a blast strain, the severity of the disease will depend on the ability of the variety to slow the epidemic either by reducing the size of the lesions or by reducing the production of new spores. This aptitude is conferred by what is known as 'horizontal resistance'. Scientists agree that this system is stable and durable (Wang *et al.*, 1994). However, this type of resistance has low heritability because of strong environmental influence on the expression of the resistance genes (Wang *et al.*, 1989). It is generally polygenic, but durable resistance has also been shown to be also conferred by major genes like *Pi40* (Suh *et al.*, 2009) and the recessive gene *pi21* (Fukuoka and Okuno, 2001).

MANAGEMENT OF THE RESISTANCE. The two kinds of resistance can exist together in the same cultivar. For example, Moroberekan, a traditional West African cultivar, is known to have a durable resistance to blast. It possesses two vertical resistance genes (*Pi5* on chromosome 4 and *Pi7* on chromosome 11), but also 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 is therefore important, when screening varieties for blast resistance, to know whether the resistance is complete and non-durable or partial and long-lasting.

Table 17.2. Efficiency of blast resistance genes in 13 month planting dates of varieties and NILs with different resistance genes

Variety or NIL	Resistance gene	Planting date						
		Oct 07	Nov 07	Dec 07	Jan 08	Feb–Aug 08	Sep 08	Oct 08
IRBL5-M/CO	Pi5(t)	S	S	S	S	S	S	S
Co39	Pia	S	S	S	S	S	S	S
IRBLkp-K60/CO	Pik-p	S	S	S	S	S	S	S
IRBLks-CO/CO	Piks	S	S	S	S	S	S	S
C102 TTP	Pita	S	S	S	S	S	S	S
C104 PKT	Pi3	**R**	S	S	S	S	S	S
IRBLzt-IR56/CO	Piz-t	**R**	S	S	S	S	S	S
IRBL7-M/CO	Pi7	**R**	S	S	S	S	S	S
Nato	Pii	**R**	S	S	S	S	S	S
IRBL1-CL/CO	Pi1	**R**	**R**	S	S	S	S	S
C101 LAC	Pi1 + Pi1b + Pi33	**R**	**R**	S	S	S	S	S
C101 A51	Pi2 (= Piz5)	**R**	**R**	S	S	S	S	S
St 1	Pif	**R**	**R**	S	S	S	S	S
IRBLkh-K3/CO	Pik-h	**R**	**R**	S	S	S	S	S
IRBLb-IT13/CO	Pib	**R**	**R**	S	S	S	S	S
IRBLta2-IR64/CO	Pita-2	**R**	**R**	S	S	S	S	S
IRBLsh-Fu/CO	Piz	**R**	**R**	S	S	S	S	S
IRBLkm-Ts/CO	Pik-m	**R**	**R**	S	S	S	S	S
IR1529	Pi33	**R**	**R**	**R**	**R**	S	S	S
K 59	Pit	**R**	**R**	**R**	**R**	S	S	S
Shwetasoke	?	**R**	**R**	**R**	**R**	S	S	S
IRBLz5-CA/CO	Piz-5	**R**	**R**	**R**	**R**	**R**	S	S
Moroberekan	Pi5 + Pi7 + Pi10(t) + Pi157 + QTLs	**R**	**R**	**R**	**R**	**R**	**R**	**R**
75-1-127	Pi9	**R**	**R**	**R**	**R**	**R**	**R**	**R**

R, resistant; S, susceptible.

Table 17.3. Reaction of blast resistance genes against natural population at Ouèdèmè in Benin. (Adapted from Ayeko, 2012.)

Variety or monogenic line	Resistance gene(s)	Reaction under natural conditions	
		2009	2011
Moroberekan	Pi5 + Pi7 + Pi10(t) + Pi157 + QTLs	R	R
IRBL 9-W	Pi9	R	R
IRBLZ 5-CA (R)	Piz-5	R	R
IRBLZT-T	Pizt	R	R

A procedure to characterize the nature of the resistance of rice varieties was designed at AfricaRice (Séré et al., 2004, 2011). It consists of, first, evaluating a large number of varieties in order to identify entries with low disease score and, second, characterizing the nature of the resistance of those entries in order to ascertain whether their low disease score is due to vertical or horizontal resistance.

In order to make the resistance to blast durable, it is possible to pyramid several vertical resistance genes (Hittalmani et al., 2000). Moreover the utilization of multi-lines composed of a mixture of varieties with different resistance genes (Wolfe, 1985; Zhu et al., 2000)

enables the reduction of disease pressure and ensures stability of blast control. The combination of vertical resistance genes and partial ones is what makes the durability of resistance possible, as in the case of Moroberekan (Wang *et al.*, 1994).

Other control measures

In Africa, several efficient fungicides have been identified: benomyl and edifenphos (Delassus, 1973), tricyclazol (Mbodj, 1989), kitazin and thiophanate-methyl (Séré, 1981). In Burkina Faso (Séré *et al.*, 2011), seed treatment with systemic products can ensure efficient protection at low cost, mainly when associated with foliar treatment. However, such control measures should be used only when it is necessary to save a crop – for instance, in experiments where it is essential for any reason to secure the yield of a susceptible variety or line in a blast-prone environment.

Environmental factors influence the expression of blast, including temperature, humidity, leaf wetness, nitrogen fertilization and drought. Crop management practices that minimize the negative impact of such factors can be used in blast management. For instance, in farmers' fields, blast incidence increases with increasing nitrogen supply (Séré *et al.*, 2011). To ensure improved management of nitrogen, split application is better than single application (Kürschner *et al.*, 1992).

Moreover, longer duration of leaf wetness (which is related to duration of high relative humidity of the atmosphere) appeared to increase neck blast damage in farmers' fields in Burkina Faso (Séré *et al.*, 2011). Therefore, planting rice so that the reproductive stage occurs in late October, when the relative humidity becomes low, was recommended and used to reduce neck blast. Comparing a susceptible variety (FKR 16) with a resistant one (FKR 48) at different planting dates with and without chemical protection (Séré *et al.*, 2011) indicated that using chemical products on the susceptible variety reduced the incidence of blast from 22.9% to 5.2%. Without any chemical, it is possible to reduce disease incidence by planting the same susceptible cultivar earlier (3.6% incidence) or later (6.4% incidence).

RYMV

Genetic control

Two kinds of resistance to RYMV have been described. A partial resistance associated with delayed virus accumulation in the host was found in *Oryza sativa* subsp. *japonica* cultivars (Albar *et al.*, 1998). Partial resistance in these cultivars is associated with tolerance, which is characterized by low symptom severity despite the high virus content at the late stage of infection (Ioannidou *et al.*, 2003). Partial resistance is polygenic and linked to major QTLs on chromosomes 7 and 12 (Pressoir *et al.*, 1998).

The second type is a high resistance characterized by the absence of symptoms, a low amount of virus and a limited impact on yield (around 5%). This high resistance is controlled by a recessive gene (Ndjiondjop *et al.*, 1999). Four alleles of the locus *RYMV1* have been identified: *rymv1-2* in *O. sativa* cv. Gigante (Ndjiondjop *et al.*, 1999; Albar *et al.*, 2003) and cv. Bekarosaka (Rakotomalala *et al.*, 2008), *rymv1-3* in *O. glaberrima* accession TOG 5681 (Albar *et al.*, 2006), *rymv1-4* (Albar *et al.*, 2006) in *O. glaberrima* accession TOG 5672, and *rymv1-5* (Thiemélé *et al.*, 2010) in *O. glaberrima* accession TOG 5674. TOG 5672, known to possess *rymv1-4*, also carries a second resistance gene on the locus *RYMV2* (Thiemélé *et al.*, 2010).

Recurrent backcrossing has been used by AfricaRice breeders to introgress the resistance genes into the background of elite varieties. However, the emergence of resistance-breaking RYMV isolates is a matter of concern. Such resistance-breaking isolates are found in natural populations of RYMV (Konate *et al.*, 1997; Sorho *et al.*, 2005; Traoré *et al.*, 2006). Moreover, resistance-breaking strains can emerge after serial inoculation of virus-resistant plants, illustrating the ability of RYMV for host adaptation (Fargette *et al.*, 2002a).

The genetic basis of the resistance-breaking phenomenon has been analysed (Fargette *et al.*, 2002a; Hébrard *et al.*, 2006, 2008; Pinel-Galzi *et al.*, 2007; Poulicard *et al.*, 2010; Traoré *et al.*, 2006). The Virus Protein genome link (VPg) encoded by the ORF2a of RYMV was identified as the virulence factor (Hébrard *et al.*, 2006). A single mutation in the VPg of a strain is sufficient for it to break the resistance. For instance,

the ability to overcome the *rymv1-2* or *rymv1-3* alleles appeared to be associated with polymorphism in the VPg sequence at position 49, a site that is under very strong positive selection (Pinel-Galzi *et al.*, 2007). A threonine residue confers a strong ability to break *rymv1-3* resistance, whereas strains possessing glutamic acid at this position are more adapted to *rymv1-2* resistance breaking (Traoré *et al.*, 2010).

At AfricaRice, screening for resistance is conducted in a screen house through mechanical inoculation of the last expanded leaves of 21-day-old seedlings. The disease symptoms are evaluated on all the rice plant's leaves, to determine the ability of the varieties to control virus movement within the plant. Susceptibility of rice cultivars can vary with plant age, with plants developing a kind of resistance at adult stage manifested by recovery ability (e.g. variety PNA 647F4-56) (Soko *et al.*, 2010). Even in the field, the recovery ability of PNA 647F4-56 was observed by farmers in Mali who indicated that the growth cycle became longer (Séré, 2005, unpublished observation).

The potential of using three insect vectors (*Oxya hyla*, *Locris rubra* and *Cnootriba similes*) to screen rice varieties was investigated. The results revealed that although there are some differences between the mechanical screening and the insect vector methods, both methods screen the varieties in the same way and, therefore, insects can be used to screen for RYMV resistance (Séré *et al.*, 2008a).

Integrated management

The amount of inoculum is important in determining the impact of a disease (Sorho *et al.*, 2005; Traoré *et al.*, 2009). Therefore, phytosanitation involving isolation of nurseries and removal of infected weeds and rice ratoons can reduce disease incidence and decrease the risk of emergence of virulent isolates (mainly resistance-breaking isolates) (Sorho *et al.*, 2005). Resistant cultivars should be associated with prophylactic measures within an integrated disease management approach (Traoré *et al.*, 2009). The insect vectors play an important role in transferring RYMV from surrounding contaminated rice or weeds to new rice fields (Nwilene, 1999) – their control should be part of the integrated approach to RYMV control.

Bacterial blight

Genetic control

RICE–PATHOGEN INTERACTION. Resistance gene products of the host recognize the presence of avirulence (*avr*) gene products of the pathogen, resulting in a rapid defence response and an incompatible interaction, restricting the pathogen to the site of inoculation.

Host plants have strategies to recognize pathogen attacks and activate defence mechanisms, resulting in the expression of various degrees of resistance to infection, manifested as vertical resistance controlled by major genes specific to a particular pathogen race, or quantitative (horizontal) resistance controlled by many genes and effective against a number of races.

HOST RESISTANCE. More than 30 resistance genes have been identified worldwide from cultivated and wild rice (Sun *et al.*, 2004; Niño-Liu *et al.*, 2006). These resistance genes encode different classes of proteins, such as nucleotide-binding site leucine-rich repeat (NBS-LRR) proteins and receptor kinase (RK). Additionally, the differential expression of resistance genes after infection indicates that rice has developed different strategies to overcome bacterial blight infection (Song *et al.*, 1995; Yoshimura *et al.*, 1998; Gu *et al.*, 2005).

Africa is endowed with some indigenous species of *Oryza* (including *O. barthii*, *O. longistaminata* and *O. glaberrima*), which can be used as potential sources of resistance to bacterial leaf blight. Vikal *et al.* (2007) report that out of 84 accessions of *O. glaberrima* evaluated against seven pathotypes of *X. oryzae* pv. *oryzae* in Punjab (India) over a period of 3–4 years, 13 showed a resistant to moderate resistant reaction to all pathotypes. Similarly, five and four accessions of *O. barthii* and *O. longistaminata*, respectively, also showed resistance to moderate resistance to these pathotypes. The broad-spectrum resistance gene, *Xa21*, is also found in *O. longistaminata* (Yoshimura *et al.*, 1998). Besides looking for other sources of resistance genes, it is also possible to combine two or more resistance genes by gene pyramiding, thereby improving the resistance spectrum and durability of a cultivar. Huang *et al.* (1997) report that rice varieties with two, three and four resistance genes have a wider spectrum and a higher level of resistance than varieties with only a single resistance gene.

Curiously, IR24 – the recurrent parent of the NILs developed by the International Rice Research Institute (IRRI) to analyse the pathological diversity of the bacterial blight pathogen and which was susceptible in Asia – is resistant to some African populations (AfricaRice, 2010). This means that the *Xa18* and other resistance genes that IR24 harbours (Liu *et al.*, 2007; Wu *et al.*, 2007) are efficient against some African bacterial blight pathogen strains.

The susceptibility of Gigante to bacterial blight is to be taken into consideration in breeding for resistance to RYMV, because in breeding programmes Gigante is used as parent to transfer RYMV resistance into many varieties.

Integrated management

The management of bacterial blight is also based on using resistant varieties. However, as the major genes alone are not able to ensure durable resistance, it is important to pyramid several genes (Gnanamanickam *et al.*, 1999) and/or add genes for partial resistance (Huang *et al.*, 1997).

Moreover, cultural practices can reduce bacterial blight severity. For instance, farmers in Niger used to burn crop residues after harvesting heavily infected fields, destroying the surrounding weeds that serve as a reservoir of the pathogen and thereby reducing inoculum (AfricaRice, 2010). Management of fertilizers, particularly nitrogen, is another cultural practice to be used, because increasing the level of N increases bacterial blight severity. A survey in farmers' fields in northern Benin indicated that the higher the quantity of urea applied, the greater the disease severity (AfricaRice, 2010). However, the impact of N depends on the time it is applied and the time infection occurs (Basso, 2010). When applied after infection, there is no increase in disease severity (Basso, 2010).

Conclusion: Challenges and Opportunities for Integrated Management of Rice Diseases in Africa

In order to develop integrated management strategies against rice diseases based on the utilization of resistant varieties, research on rice diseases in Africa focused on the following questions:

- What pathogens infect rice in Africa?
- Which are the most important of these that need particular attention?
- What control measures can be used in an IPM approach to reduce their impact on yield?

Next, research zoomed into the three major pathogens that cause greatest yield losses in the absence of any control measure. Although pertinent information was generated, some gaps remain to be filled.

For blast, it will be important to describe the blast population structure throughout Africa to better advise on the development and deployment of resistant cultivars. Moreover, the possible existence of new resistance genes in local cultivars has to be examined. Partial resistance needs to be considered, particularly in association with vertical resistance, as the stability of the resistance of varieties like Moreberekan and Tetep seems to be linked with such associations. It will be important to investigate the possibility of pyramiding major resistance genes (Hittalmani *et al.*, 2000). Moreover, the utilization of multilines to stabilize the resistance to blast disease (Wolfe, 1985; Zhu *et al.*, 2000) needs to be evaluated under African conditions. The impact of management practices on the disease needs to be evaluated in order to develop an IPM system.

There have been tremendous achievements in studies related to RYMV through collaborative research involving NARS, AfricaRice and advanced institutions (mainly IRD). The diversity in countries not yet sampled has to be investigated. It will be important to look for new resistance genes in local cultivars, mainly *O. sativa* subsp. *indica* and *O. glaberrima*, and in related species. The genetic background of RYMV pathogenicity needs deeper investigation, especially the resistance-breaking mechanism. It will also be important to assess the genetic background of the recovery ability, in order to ascertain whether it is a plant resistance mechanism or an environment-dependent condition and to see whether it can be used as a component of integrated management of RYMV.

Relatively less progress has been made in research on bacterial blight compared to advancement in the two other main rice diseases in Africa. However, a capacity in bacterial

research is being built in Africa and needs to be supported. There is a need for further characterization of the population structure in order to better understand the differences between the Asian and African situations. There is also a need to find a susceptible variety in Africa in order to build an appropriate set of NILs adapted to the continent and then accelerate the analysis of pathological diversity of the bacterial blight pathogen in Africa and the identification of resistance genes among African rice cultivars.

Climate change is expected to affect agriculture, mainly through higher temperatures, elevated carbon dioxide concentration, and changes in rainfall patterns, all of which will affect weed, pest and disease dynamics. Research should envisage future climate scenarios that could influence rice–pathogen relationships (including the emergence of pathogens that are considered as minor today). Using experiments and simulation models (Savary *et al.*, 2006, 2011, 2012), it should be possible to know which pathogens could negatively impact productivity of the crop under changing conditions, and then pre-emptively develop possible options to mitigate the impact of climate change on rice diseases and rice resistance to them.

References

Abo, M., Sy, A. and Alegbejo, M. (1998) *Rice yellow mottle virus* (RYMV) in Africa: evolution, distribution, economic significance and sustainable rice production and management strategies. *Journal of Sustainable Agriculture* 11, 85–111.

Abo, M.E., Alegbejo, M.D. and Sy, A.A. (2004) Evidence of non-transmission of *Rice yellow mottle virus* through rice seed. *Tropicultura* 22(3), 116–121.

ADRAO (1982) *Gestion intégrée des déprédateurs du riz en Afrique de l'Ouest. Concepts, techniques et application de la gestion intégrée des déprédateurs du riz en Afrique de l'Ouest*. Association pour le développement de la riziculture en Afrique de l'Ouest, Monrovia, Liberia.

AfricaRice (2010) Characterization of the pathogen population structure of bacterial leaf blight of rice in West Africa as a prerequisite for the identification and deployment of durable resistance. Final Report of a BMZ-funded project. Africa Rice Center, Cotonou, Benin.

Akator, K.S. (1981) Méthodes de lutte contre la pyriculariose du riz au Togo. In: *Proceedings of the Symposium on Rice Resistance to Blast*, Montpellier, France, 18–21 March. Service de Pathologie Végétale, Montpellier, France, pp. 43–50.

Akinsola, E.A., Ouayogode, B. and Akintayo, I. (eds) (1982) *Integrated Pest Management in Rice in West Africa*. West Africa Rice Development Association, Fendall, Liberia.

Albar, L., Lorieux, M., Ahmadi, N., Rimbault, I., Pinel, A., Sy, A., Fargette, D. and Ghesquière, A. (1998) Genetic basis and mapping of the resistance to *Rice yellow mottle virus*. I. QTLs identification and relationship between resistance and plant morphology. *Theoretical and Applied Genetics* 97, 1145–1154.

Albar, L., Ndjiondjop, M.-N., Esshak, Z., Berger, A., Pinel, A., Jones, M., Fargette, D. and Ghesquière, A. (2003) Fine genetic mapping of a gene required for *Rice yellow mottle virus* cell-to-cell movement. *Theoretical and Applied Genetics* 107, 371–378.

Albar, L., Angratz-Reyser, M., Hébrard, E., Ndjiondjop, M.N., Jones, M. and Ghesquière, A. (2006) Mutations in the eIF(iso)4G translation initiation factor confer high resistance of rice to *Rice yellow mottle virus*. *Plant Journal* 47, 417–426.

Ashura, L.K., Mabagala, R.B. and Mortensen C.N. (1999) Isolation and characterization of seed-borne pathogenic bacteria from rice (*Oryza sativa* L.) in Tanzania. *Tanzania Journal of Agricultural Sciences* 2(1), 71–80.

Awoderu, V.A., Bangura, N. and John, V.T. (1991) Incidence, distribution and severity of bacterial diseases on rice in West Africa. *Tropical Pest Management* 37, 113–117.

Ayeko, A.A. (2012) Etude de la résistance de cultivar de riz *Oryza glaberrima* a la pyriculariosecausee par *Magnaporthe oryzae* dans les écosystèmes de Ouèdèmè (Benin) et de Longorola (Mali). Diplôme d'Ingénieur Agronome, 6ème Promotion, Faculté d'Agronomie, Université de Parakou, Benin.

Bakker, W. (1970) Rice yellow mottle, a mechanically transmissible virus disease of rice in Kenya. *Netherlands Journal of Plant Pathology* 76, 53–63.

Ballini, E., Morel, J.B., Droc, G., Price, A., Courtois, B., Notteghem, J.L. and Tharreau, D. (2008) A genome-wide meta-analysis of rice blast resistance genes and quantitative trait loci provides new insights into partial and complete resistance. *Molecular Plant–Microbe Interactions* 21, 859–868.

Basso, A. (2010) Bioécologie de *Xanthomonas oryzae* pv *oryzae* (Ishiyama) Swing *et al.*, responsable de la maladie des raies bactériennes. Doctoral thesis, Université Abdou Moumouni de Niamey, Niger.

Bidaux, J.-M. (1978) Screening for horizontal resistance to rice blast (*Pyricularia oryzae*) in Africa. In: Buddenhagen, I.W. and Persley, G.J. (eds) *Rice in Africa*. Proceedings of a conference held at the International Institute of Tropical Agriculture, Ibadan, Nigeria, 7–11 March 1977. Academic Press, London, New York, San Francisco, pp. 159–174.

Bimerew, M. (2010) Metabolic diversity and molecular characterization of *X. oryzae* pv. *oryzae* strains from West Africa. MSc thesis, Leibniz University of Hannover, Germany.

Buddenhagen, I.W. (1985) Rice disease evaluation in Madagascar. *International Rice Commission Newsletter* 34, 74–78.

Buddenhagen, I.W., Vuong, H.H. and Ba, D.D. (1979) Bacterial blight found in Africa. *International Rice Research Newsletter* 4, 11.

Chen, D., Wang, G.L. and Ronald, P.C. (1997) Location of the rice blast resistance locus *Pi5(t)* in Moroberekan by AFLP bulk segregant analysis. *Rice Genetics Newsletter* 14, 95–98.

Chen, X.W., Li, S.G., Xu, J.C., Zhai, W.X., Ling, Z.Z., Ma, B.T., Wang, Y.P., Wang, W.M., Cao, G., Ma, Y.Q., Shang, J.J., Zhao, X.F., Zhou, K.D. and Zhu, L.H. (2004) Identification of two blast resistance genes in a rice variety, Digu. *Journal of Phytopathology* 152, 77–85.

Chen, Q.H., Wang, Y.C. and Zheng, X.B. (2006) Genetic diversity of *Magnaporthe grisea* in China as revealed by DNA fingerprint haplotypes and pathotypes. *Journal of Phytopathology* 154, 361–369.

Chipili, J., Sreenivasaprasad, S., Séré, Y. and Talbot, N.J. (1999) Characterization of the rice blast pathogen populations at screening sites in West Africa. In: Sreenivasaprasad, S. and Johnson, R. (eds) *Major Fungal Diseases of Rice: Present status and perspectives*. Kluwer Academic, Netherlands.

Cottyn, B., Regalado, E., Lanoot, B., De Cleene, M., Mew, T.M. and Swings, J. (2001) Bacterial populations associated with rice seed in the tropical environment. *Phytopathology* 91(3), 282–292.

Couch, B.C. and Kohn, L.M. (2002) A multilocus gene genealogy concordant with host preference indicates segregation of a new species, *Magnaporthe oryzae*, from *M. grisea*. *Mycologia* 94(4), 683–693.

Dai, L.Y., Liu, X.L., Xiao, Y.H. and Wang, G.L. (2007) Recent advances in cloning and characterization of disease resistance genes in rice. *Journal of Integrative Plant Biology* 49(1), 112–119.

Delassus, M. (1973) Lutte chimique contre la pyriculariose du riz en Casamance (Sénégal). In: Séminaire ADRAO sur la protection des plantes en riziculture, Monrovia, Libéria, mai 1973. Association pour le développement de la riziculture en Afrique de l'Ouest, Monrovia, Liberia, pp. 220–225.

El-Namaky, R. (2011) Technical progress report on the Green Super Rice (GSR) project. Africa Rice Center, Cotonou, Benin.

Fakorede, M.A.B. and Yoboué, N. (comp.) (2001) *Summary of WARDA/NARS Task Forces Activities 1991–1997*. West Africa Rice Development Association, Bouaké, Côte d'Ivoire.

Fargette, D., Pinel, A., Traoré, O., Ghesquière, A. and Konaté, G. (2002a) Emergence of resistance-breaking isolates of *Rice yellow mottle virus* during serial inoculations. *European Journal of Plant Pathology* 108, 585–591.

Fargette, D., Pinel, A., Halimi, N., Brugidou, C., Fauquet, C.M. and Van Regenmortel, M.H.V. (2002b) Comparison of molecular and immunological typing of isolates of *Rice yellow mottle virus*. *Archives of Virology* 147, 583–596.

Fargette, D., Pinel, A., Abubakar, Z., Traoré, O., Brugidou, C., Fatogoma, S., Hébrard, E., Choisy, M., Séré, Y., Fauquet, C. and Konaté, G. (2004) Inferring the evolutionary history of *Rice yellow mottle virus* from genomic, phylogenetic, and phylogeographic studies. *Journal of Virology* 78, 3252–3261.

Fargette, D., Pinel, A., Rakotomalala, M., Sangu, E., Traoré, O., Sérémé, D., Sorho, F., Issaka, S., Hebrard, E., Séré, Y., Kanyeka, Z. and Konaté, G. (2008) *Rice yellow mottle virus*, an RNA plant virus, evolves as rapidly as most RNA animal viruses. *Journal of Virology* 82, 3584–3589.

Fomba, S.N. and Taylor, D.R. (1994) Rice blast in West Africa: its nature and control. In: Zeigler, R.S., Leong, S.A. and Teng, P.S. (eds) *Rice Blast Disease*. CAB International, Wallingford, UK and International Rice Research Institute, Los Baños, Philippines, pp. 343–356.

Fukuoka, S. and Okuno, K. (2001) QTL analysis and mapping of *pi21*, a recessive gene for field resistance to rice blast in Japanese upland rice. *Theoretical and Applied Genetics* 103, 185–190.

Gnanamanickam, S.S., Priyadarisini, V.B., Narayanan, N.N., Vasudevan, P. and Kavitha, S. (1999) An overview of bacterial blight disease of rice and strategies for its management. *Current Science* 77, 1435–1444.

Gonzalez, C., Szurek, B., Manceau, C., Mathieu, T., Séré, Y. and Verdier, V. (2007) Molecular and patho-typic characterization of new *Xanthomonas oryzae* strains from West Africa. *Molecular Plant–Microbe Interactions* 20, 534–546.

Gu, K.Y., Yang, B., Tian, D.S., Wu, L.F., Wang, D.J., Sreekala, C., Yang, F., Chu, Z.Q., Wang, G.L., White, F.F. and Yin, Z.C. (2005) *R* gene expression induced by a type-III effector triggers disease resistance in rice. *Nature* 435, 1122–1125.

Hamer, J.E. and Givan, S. (1990) Genetic mapping with dispersed repeated sequences in the rice blast fungus mapping the *SMO* locus. *Molecular and General Genetics* 223, 487–495.

Hébrard, E., Pinel-Galzi, A., Bersoult, A., Siré, C. and Fargette, D. (2006) Emergence of a resistance-breaking isolate of *Rice yellow mottle virus* during serial inoculations is due to a single substitution in the genome-linked viral protein VPg. *Journal of General Virology* 87, 1369–1373.

Hébrard, E., Pinel-Galzi, A. and Fargette, D. (2008) Virulence domain of the RYMV genome-linked viral protein VPg towards rice *rymv1-2*-mediated resistance. *Archives of Virology* 153, 1161–1164.

Hittalmani, S., Parco, A., Mew, T.V., Zeigler, R.S. and Huang, N. (2000) Fine mapping and DNA marker assisted pyramiding of the three major genes for blast resistance in rice. *Theoretical and Applied Genetics* 100, 1121–1128.

Huang, J.S. and Cleene, D.M. (1989) How rice plants are infected by *Xanthomonas campestris* pv. *oryzae*. In: *Bacterial Blight of Rice*. International Rice Research Institute, Manila, Philippines, pp. 31–42.

Huang, N., Angeles, E.R., Domingo, J., Magpantay, G., Singh, S., Zhang, G., Maravadivel, K.N., Bennett, J. and Khush, G.S. (1997) Pyramiding of bacterial blight resistance genes in rice: marker-assisted selection using RFLP and PCR. *Theoretical and Applied Genetics* 95, 313–320.

Ioannidou, D., Pinel, A., Brudgidou, C., Albar, L., Ahmadi, N., Ghesquiere, A., Nicole, M. and Fargette, D. (2003) Characterisation of the effects of a major QTL of the partial resistance to *Rice yellow mottle virus* using a near-isogenic-line approach. *Physiological and Molecular Plant Pathology* 63, 213–221.

Javan-Nikkhah, M., McDonald, B.A., Banke, S. and Hedjaroude, G.-A. (2004) Genetic structure of Iranian *Pyricularia grisea* populations based on re-PCR fingerprinting. *European Journal of Phytopathology* 110, 909–919.

Jia, Y., Lee, F.N. and McClung, A. (2009) Determination of resistance spectra of the *Pi-ta* and *Pi-k* genes to U.S. races of *Magnaporthe oryzae* causing rice blast in a recombinant inbred line population. *Plant Disease* 93, 639–644.

Jobe, L.M.S., Sanyang, S. and Daeboe, M.L. (2002) Response of some improved exotic rice varieties to blast disease, *Pyricularia oryzae* in The Gambia 2000/2001. Paper presented at the Second Regional Rice Research Review (4Rs), Bouaké, Côte d'Ivoire, 9–12 April.

Kaku, H. (2004) Histopathology of red stripe of rice. *Plant Disease* 88, 1304–1309.

Khush, G.S. (2005) What it will take to feed 5.0 billion rice consumers in 2030. *Plant Molecular Biology* 59, 1–6.

Khush, G.S. and Brar, D.S. (2004) Rice genetics from Mendel to functional genomics. In: Khush, G.S., Brar, D.S. and Hardy, B. (eds) *Rice Genetics IV*. Proceedings of the Fourth International Rice Genetics Symposium, Los Baños, Laguna, Philippines, 22–27 October 2000. Science Publishers, New Delhi, India and International Rice Research Institute, Los Baños, Philippines, pp. 3–25.

Kiyosawa, S. (1980) The possible application of gene-for-gene concept in blast resistance. *Journal of Assisted Reproduction and Genetics* 14, 9–14.

Konate, G., Traore, O. and Coulibaly, M. (1997) Characterization of *Rice yellow mottle virus* isolates in Sudano-Sahelian areas. *Archives of Virology* 142, 1117–1124.

Konate, G., Sarra, S. and Traore, O. (2001) *Rice yellow mottle virus* is seedborne but not seed transmitted in rice. *European Journal of Plant Pathology* 107, 361–364.

Kouassi, N., N'Guessan, P., Albar, L., Fauquet, C. and Brugidou, C. (2005) Distribution and characterization of *Rice yellow mottle virus*: a threat to African farmers. *Plant Disease* 89, 124–133.

Kürschner, E., Bonman, J.M., Garrity, D.P., Tamisin, M.N., Pabale, D. and Estrada, B.A. (1992) Effects of nitrogen timing and split application on blast disease in upland rice. *Plant Disease* 76, 384–389.

Li, Z.Z., Zhao, H. and Ying, X.D. (1985) The weed carriers of bacterial leaf blight of rice. *Acta Phytopathologica Sinica* 15, 246–248.

Lin, F., Chen, S., Que, Z., Wang, L., Liu, X. and Pan, Q. (2007) The blast resistance gene *Pi37* encodes a nucleotide binding site leucine-rich repeat protein and is a member of a resistance gene cluster on rice chromosome 1. *Genetics* 177(3), 1871–1880.

Liu, G., Lu, G., Zeng, L. and Wang, G.L. (2002) Two broad-spectrum blast resistance genes, *Pi9(t)* and *Pi2(t)*, are physically linked on rice chromosome 6. *Molecular Genetics and Genomics* 267(4), 472–480.

Liu, H., Yang, W., Hu, B. and Liu, F. (2007) Virulence analysis and race classification of *Xanthomonas oryzae* pv. *oryzae* in China. *Journal of Phytopathology* 155, 129–135.

Mbodj, Y. (1989) La lutte intégrée contre les maladies du riz en Casamance, au Sénégal. DSc thesis, Université Catholique de Louvain, Louvain-la-Neuve, Belgium.

Mbodj, Y., Séré, Y., Sidibé, B. and Diallo, S. (1984) Les problèmes phytosanitaires du riz dans le Sahel. In: Compte rendus du seminaire international du Projet CILSS de Lutte Intégrée. Comité permanent Inter-Etats de Lutte contre la Sécheresse dans le Sahel, Ouagadougou, Burkina Faso, pp. 157–167.

Ndikumana, I., Gasoré, R., Issaka, S., Pinel-Galzi, A., Onasanya, A., Hassani-Mehraban, A., Fargette, D., Peters, D. and Séré, Y. (2011) *Rice yellow mottle virus* in rice in Rwanda: first report and evidence of strain circulation. *New Disease Reports* 23, 18.

Ndjiondjop, M.N., Albar, L., Fargette, D. and Ghesquière, A. (1999) The genetic basis of high resistance to *Rice yellow mottle virus* (RYMV) in cultivars of two cultivated rice species. *Plant Disease* 83, 931–935.

N'Guessan, P., Pinel, A., Caruana, M., Frutos, R., Sy, A., Ghesquière, A. and Fargette, D. (2000) Evidence of the presence of two serotypes of rice yellow mottle sobemovirus in Côte d'Ivoire. *European Journal of Plant Pathology* 106, 167–178.

Niño-Liu, D., Ronald, P. and Bogdanove, A. (2006) *Xanthomonas oryzae* pathovars: model pathogens of a model crop. *Molecular Plant Pathology* 7, 303–324.

Notteghem, J.L. and Baudin, P. (1981) *Principales maladies du riz en Afrique de l'ouest*. West Africa Rice Development Association, Monrovia, Liberia.

Nutsugah, S.K., Dogbe, J.K., Twumasi, J.K., Dartey, K., Chipilli, J., Sreenivasaprasad, S. and Séré, Y. (2004) Survey of rice blast and varietal screening in Ghana. In: Séré, Y., Sreenivasaprasad, S. and Nutsugah, S.K. (eds) *Rice Blast in West Africa: Characterisation of pathogen diversity, key screening sites and host resistance*. Africa Rice Center (WARDA), Cotonou, Benin, pp. 47–62.

Nutsugah, S.K., Twumasi, J.K., Chipili, J., Séré, Y. and Sreenivasaprasad, S. (2008) Diversity of the blast pathogen populations in Ghana and strategies for resistance management. *Plant Pathology Journal* 7(1), 109–113.

Nwillene, F. (1999) Current status and management of insect vectors of *Rice yellow mottle virus* in Africa. *Insect Science and its Application* 19, 179–185.

Onasanya, A., Ekperigin, M.M., Nwilene, F.E., Sere, Y. and Onasanya, R.O. (2009) Two pathotypes of *Xanthomonas oryzae* pv. *oryzae* virulence identified in West Africa. *Current Research in Bacteriology* 2, 22–35.

Ou, S.H. (1985) *Rice Diseases*, 2nd edn. CAB International, Wallingford, UK.

Ouedraogo, S.L., Somda, I., Wonni, I. and Seré, Y. (2007) Etude de la résistance au flétrissement bactérien de lignées inter- et intraspécifiques de riz de bas-fonds en conditions d'infestation artificielles. *African Crop Science Journal* 15(4), 191–199.

Pinel, A., N'Guessan, P., Bousalem, M. and Fargette, D. (2000) Molecular variability of geographically distinct isolates of *Rice yellow mottle virus* in Africa. *Archives of Virology* 145, 1621–1638.

Pinel-Galzi, A., Rakotomalala, M., Sangu, E., Sorho, F., Kanyeka, Z., Traoré, O., Sérémé, D., Poulicard, N., Rabenantoandro, Y., Séré, Y., Konaté, G., Ghesquière, A., Hébrard, E. and Fargette, D. (2007) Theme and variations in the evolutionary pathways to virulence of an RNA plant virus species. *PLoS Pathogens* 3, 1761–1770.

Poulicard, N., Pinel-Galzi, A., Hébrard, E. and Fargette, D. (2010) Why *Rice yellow mottle virus*, a rapidly evolving RNA plant virus, is not efficient at breaking *rymv1-2* resistance. *Molecular Plant Pathology* 11, 145–154.

Pressoir, G., Albar, L., Ahmadi, N., Rimbault, I., Lorieux, M., Fargette, D. and Ghesquière, A. (1998) Genetic basis and mapping of the resistance to *Rice yellow mottle virus*. II. Evidence of complementary epistasis between two QTLs. *Theoretical and Applied Genetics* 97, 1155–1161.

Rakotomalala, M., Pinel-Galzi, A., Albar, L., Ghesquière, A., Rabenantoandro, Y., Ramavovololona, P. and Fargette, D. (2008) Resistance to *Rice yellow mottle virus* in rice germplasm in Madagascar. *European Journal of Plant Pathology* 122, 277–286.

Reckhaus, P.M. (1983) Occurrence of bacterial blight of rice in Niger, West Africa. *Plant Disease* 67, 1039.

Roger, L. (1958) Les problèmes phytopathologiques dans les états de la communauté francaise en Afrique ainsi que dans les états du Cameroun, de Guinée et du Togo. *Rapport roneot ORSTOM* no. 4380. Office de la recherche scientifique et technique outre-mer, France.

Sallaud, C., Lorieux, M., Roumen, E., Tharreau, D., Berruyer, R., Svestasrani, P., Garsmeur, O., Ghesquiere, A. and Notteghem, J.L. (2003) Identification of five new blast resistance genes in the highly blast-resistant variety IR64 using a QTL mapping strategy. *Theoretical and Applied Genetics* 106, 794–803.

Savary, S., Teng, P.S., Willocquet, L. and Nutter, F.W. Jr (2006) Quantification and modeling of crop losses: a review of purposes. *Annual Review of Phytopathology* 44, 89–112.

Savary, S., Mila, A., Willocquet, L., Esker, P.D., Carisse, O. and McRoberts, N. (2011) Risk factors for crop health under global change and agricultural shifts: a framework of analyses using rice in tropical and subtropical Asia as a model. *Phytopathology* 101, 696–709.

Savary, S., Nelson, A., Willocquet, L., Pangga, I. and Aunario, J (2012) Modeling and mapping potential epidemics of rice diseases globally. *Crop Protection* 34, 6–17.

Seck, P.A., Diagne, A., Mohanty, S. and Wopereis, M.C.S. (2012) Crops that feed the world 7: rice. *Food Security* 4, 7–24.

Séré, Y. (1981) Rice blast prevention in Burkina Faso. In: *Proceedings of the Symposium on Rice Resistance to Blast*, Montpellier, France, 18–21 March. Service de Pathologie Végétale, Montpellier, France, pp. 51–65.

Séré, Y. (1988a) Une nouvelle maladie du riz au Burkina Faso. *Sahel PV Info* 4: 7–8.

Séré, Y. (1988b) La pyriculariose en riziculture irriguée : exemple de la Vallée du Kou (Burkina Faso). *Sahel PV Info* 4: 11–12.

Séré, Y. (1988c) Observations préliminaires sur *Corallocytostroma oryzae* Yu et Ziang responsable de symptômes curieux sur le riz au Burkina Faso. *Sahel PV Info* 5: 9–10.

Séré, Y. and Nacro, S. (1992) Les problèmes phytosanitaires du riz au Burkina Faso : bilan des recherches. Presentation at the Première réunion du groupe d'action sur la lutte intégrée contre les ennemis du riz, Bouaké, Côte d'Ivoire, February.

Séré, Y., Sy, A.A., Akator, S.K., Onasanya, A., Zai, K., Sreenivasaprasad, S., Nutsugah, S.K. and Twumasi, J.K. (2004) Analysis of *Magnaporthe grisea* population structure in Côte d'Ivoire as a prerequisite for the deployment of varieties with durable blast resistance. In: Séré, Y., Sreenivasaprasad, S. and Nutsugah, S.K. (eds) *Rice Blast in West Africa: Characterisation of pathogen diversity, key screening sites and host resistance*. Proceedings of a stakeholder workshop (Project R7552, UK Department for International Development Crop Protection Programme), Accra, Ghana, 5 March 2003. Africa Rice Center, Cotonou, Benin, pp. 72–102.

Séré, Y., Onasanya, A., Verdier, V., Akator, K., Ouédraogo, L.S., Segda, Z., Coulibaly, M.M., Sido, A.Y. and Basso, A. (2005) Rice bacterial leaf blight in West Africa: preliminary studies on disease in farmers' fields and screening released varieties for resistance to the bacteria. *Asian Journal of Plant Sciences* 4(6), 577–579.

Séré, Y., Onasanya, A., Afolabi, A., Mignouna, H.D. and Akator, K. (2007) Genetic diversity of the blast fungus, *Magnaporthe grisea* (Hebert) Barr, in Burkina Faso. *African Journal of Biotechnology* 6(22), 2568–2577.

Séré, Y., Onasanya, A., Nwilene, F.E., Abo, M.E. and Akator, K. (2008a) Potential of insect vector screening method for development of durable resistant cultivars to *Rice yellow mottle virus* disease. *International Journal of Virology* 4(2), 41–47.

Séré, Y., Sorho, F., Onasanya, A., Jobe, L., Darboe, S., Bojang, Y., Touray, M.L., Pinel-Galzi, A. and Fargette, D. (2008b) First report of *Rice yellow mottle virus* in rice in The Gambia. *Plant Disease* 93(2), 316.

Séré, Y., Sy, A.A., Sié, M., Onasanya, A., Akator, S.K., Kabore, B., Conde, C.K., Traore, M. and Kiepe, P. (2011) Importance of varietal improvement for blast disease control in Africa. In: Yanagihara, S. (ed.) Next Challenges in Rice Development for Africa: Workshop for New Collaboration between JIRCAS and AfricaRice. *JIRCAS Working Report* 70. Africa Rice Center, Cotonou, Benin and Japan International Research Center for Agricultural Sciences, Tsukuba, Japan, pp. 77–90.

Silué, D., Notteghem, J.L. and Tharreau, D. (1992) Evidence of a gene-for-gene relationship in the *Oryza sativa–Magnaporthe grisea* pathosystem. *Phytopathology* 82, 577–580.

Soko, D.F., Sere, Y. and Ake, S. (2010) Effet de l'âge de huit cultivars de riz sur l'expression génétique de la résistance au virus de la panachure jaune du riz / Effect of plant age on expression of genetic resistance to *Rice yellow mottle virus* (RYMV). *Journal of Applied Biosciences* 25, 1585–1593.

Song, W.-Y., Wang, G.-L., Chen, L.-L., Kim, H.-S., Pi, L.-Y., Holsten, T., Gardner, J., Wang, B., Zhai, W.-X., Zhu, L.-H., Fauquet, C. and Ronald, P.C. (1995) A receptor kinase-like protein encoded by the rice disease resistance gene, *Xa21. Science* 270, 1804–1806.

Sorho, F., Pinel, A., Traoré, O., Bersoult, A., Ghesquière, A., Hébrard, E., Konaté, G., Séré, Y. and Fargette, D. (2005) Durability of natural and transgenic resistance to *Rice yellow mottle virus*. *European Journal of Plant Pathology* 112, 349–359.

Suh, J.P., Roh, J.H., Cho, Y.C., Han, S.S., Kim, Y.G. and Jena, K.K. (2009) The *Pi40* gene for durable resistance to rice blast and molecular analysis of Pi40-advanced backcross breeding lines. *Phytopathology* 99, 243–250.

Sun, X., Cao, Y., Yang, Z., Xu, C., Li, X., Wang, P. and Zhana, Q. (2004) *Xa26*, a gene conferring resistance to *Xanthomonas oryzae* pv. *oryzae* in rice, encodes an LRR receptor kinase-like protein. *The Plant Journal* 37, 517–527.

Sy, A.A. and Séré, Y. (1996) *Manuel de Formation en Pathologie du Riz*. Association pour le développement de la riziculture en Afrique de l'ouest, Bouaké, Côte d'Ivoire.

Thiemélé, D., Boisnard, A., Ndjiondjop, M.-N., Chéron, S., Séré, Y., Aké, S., Ghesquière, A. and Albar, L. (2010) Identification of a second major resistance gene to *Rice yellow mottle virus*, *RYMV2*, in the African cultivated rice species, *O. glaberrima*. *Theoretical and Applied Genetics* 121, 169–179.

Thresh, J.M., Chancellor, T.C.B., Holt, J., Kimmins, F. and Zeigler, R.S. (2001) Comparative epidemiology of virus diseases of tropical rice. In: Sy, A.A., Hughes, J. and Diallo, A. (eds) *Rice Yellow Mottle Virus (RYMV): Economic importance, diagnosis and management strategies / La Panachure Jaune du Riz: Importance économique, diagnostic et stratégies de gestion.* West Africa Rice Development Association, Bouaké, Côte d'Ivoire, pp. 9–21.

Traoré, O., Pinel, A., Hébrard, E., Gumedzoé, M., Fargette, D., Traoré, A. and Konaté, G. (2006) Occurrence of resistance-breaking isolates of *Rice yellow mottle virus* in West and Central Africa. *Plant Disease* 90, 259–263.

Traoré, O., Pinel-Galzi, A., Sorho, F., Sarra, S., Rakotomalala, M., Sangu, E., Kanyeka, Z., Séré, Y., Konaté, G. and Fargette, D. (2009) A reassessment of the epidemiology of *Rice yellow mottle virus* following recent advances in field and molecular studies. *Virus Research* 141, 258–267.

Traoré, O., Pinel-Galzi, A., Issaka, S., Poulicard, N., Aribi, J., Aké, S., Ghesquière, A., Séré, Y., Konaté, G., Hébrard, E. and Fargette, D. (2010) The adaptation of *Rice yellow mottle virus* to the eIF(iso)4G-mediated rice resistance. *Virology* 408, 103–108.

Trinh, T.T. (1980) New rice diseases and insects in the Senegal River basin in 1978/79. *International Rice Commission Newsletter* 29, 37.

Valent, B. (1990) Rice blast as a model system for plant pathology. *Phytopathology* 80, 33–36.

Vera Cruz, C.M., Gossele, F., Kersters, K., Segers, P., Van Den Mooter, M., Swings, J. and De Ley, J. (1984) Differentiation between *Xanthomonas campestris* pv. *oryzae*, *Xanthomonas campestris* pv. *oryzicola* and the bacterial brown blotch pathogen on rice by numerical analysis of phenotypic features and protein gel electrophoregrams. *Journal of General Microbiology* 130, 2983–2999.

Vikal, Y., Das, A., Patra, B., Goel, R.K., Sidhu, J.S. and Singh, K. (2007) Identification of new sources of bacterial blight (*Xanthomonas oryzae* pv. *oryzae*) resistance in wild *Oryza* species and *O. glaberrima*. *Plant Genetic Resources: Characterization and Utilization* 5, 108–112.

Vodouhe, S.R., Ojegui, M. and Amadji, F. (1981) Impact of blast on rice cultivation in People's Republic of Benin. In: *Proceedings of the Symposium on Rice Resistance to Blast*, Montpellier, France, 18–21 March. Service de Pathologie Végétale, Montpellier, France, pp. 27–33.

Wang, Z., Mackill, D.J. and Bonman, J.M. (1989) Inheritance of partial resistance to blast in *indica* rice cultivars. *Crop Science* 29, 848–853.

Wang, G.L., Mackill, D.J., Bonman, J.M., McCouch, S.R., Champoux, M.C. and Nelson, R.J. (1994) RFLP mapping of genes confering complete and partial resistance to blast in a durably resistant rice cultivar. *Genetics* 136, 1421–1437.

WARDA (1999a) ROCARIZ Strategic Plan. A proposal submitted to the United States Agency for International Development. West Africa Rice Development Association, Bouaké, Côte d'Ivoire.

WARDA (1999b) *Program Report 1996–1997.* West Africa Rice Development Association, Bouaké, Côte d'Ivoire.

WARDA (2002) IPM Task Force report 2001–2002. Report submitted to the Second Regional Rice Research Review (4Rs), M'bé, Bouaké, Côte d'Ivoire, 9–12 April.

White, R.M., Notteghem, J.L. and Leach, J.E. (1995) Comparison of *Xanthomonas oryzae* pv. *oryzae* strains from Africa, North America, and Asia by restriction fragment length polymorphism analysis. *International Rice Research Notes* 20, 25–26.

Wolfe, M.S. (1985) The current status and prospects of multiline cultivars and variety mixtures for disease resistance. *Annual Review of Phytopathology* 23, 251–273.

Wu, X.M., Li, Y.R., Zou, L.F. and Chen, G.Y. (2007) Gene-for-gene relationships between rice and diverse *avrBs3/pthA* avirulence genes in *Xanthomonas oryzae* pv. *oryzae*. *Plant Pathology* 56, 26–34.

Xia, J.Q., Correll, J.C., Lee, F.N. and Ross, W.J. (2000) Regional population diversity of *Pyricularia grisea* in Arkansas and the influence of host selection. *Plant Disease* 84, 877–884.

Yoshimura, S., Yamanouchi, U., Katayose, Y., Toki, S., Wang, Z.X., Kono, I., Kurata, N., Yano, M., Iwata, N. and Sasaki, T. (1998) Expression of *Xa1*, a bacterial blight-resistance gene in rice, is induced by bacterial inoculation. *Proceedings of the National Academy of Sciences USA* 95, 1663–1668.

Zhu, Y., Chen, H., Fan, J., Wang, Y., Li, Y., Chen, J., Fan, J.X., Yang, S., Hu, L., Leungk, H., Mewk, T.W., Tengk, P.S., Wangk, Z. and Mundtk, C.C. (2000) Genetic diversity and disease control in rice. *Nature* 406, 718–722.

Zhu, Y.-Y., Fang, H., Wang, Y.-Y., Fan, J.X., Yang, S.-S., Mew, T.W. and Mundt, C.C. (2005) Panicle blast and canopy moisture in rice cultivar mixtures. *Phytopathology* 95, 433–438.