

## **UC Davis**

### **UC Davis Previously Published Works**

#### **Title**

Characterization of four rice mutants with alterations in the defence response pathway.

#### **Permalink**

<https://escholarship.org/uc/item/6g33j04f>

#### **Journal**

Molecular plant pathology, 6(1)

#### **ISSN**

1364-3703

#### **Authors**

Campbell, M A

Ronald, P C

#### **Publication Date**

2005

Peer reviewed

# Characterization of four rice mutants with alterations in the defence response pathway

M. A. CAMPBELL AND P. C. RONALD\*

Department of Plant Pathology, One Shields Avenue, UC-Davis, Davis, CA 95616, USA

## SUMMARY

A fast-neutron mutagenized population of rice seedlings was screened with *Magnaporthe grisea*, the causal agent of rice blast disease, to identify mutants with alterations in the defence response. Three mutant lines, *ebr1*, *ebr2* and *ebr3* (enhanced blast resistance) were identified that display enhanced resistance to *M. grisea*. *ebr1* and *ebr3* also confer enhanced resistance to the bacterial pathogen *Xanthomonas oryzae* pv. *oryzae* (*Xoo*). *ebr3* develops a lesion mimic (LM) phenotype upon inoculation with *M. grisea*, and the phenotype is also induced by a shift in environmental conditions. The fourth mutant line, *ncr1* (necrosis in rice), has an LM phenotype under all conditions tested and lacks enhanced resistance to either *M. grisea* or *Xoo*. Complementation testing using the mutant lines *ebr3* and *ncr1* indicates that the *ebr3* and *ncr1* loci are nonallelic and recessive. *ebr1* and *ebr2* display no alterations in expression of the rice pathogenesis-related (PR) genes *PBZ1* and *PR1*, compared to wild-type CO39. *ebr3* has an elevated expression of *PBZ1* and *PR1* only in tissue displaying the LM phenotype. *ncr1* strongly expresses *PBZ1* in tissue displaying the LM phenotype, whereas *PR1* expression in this tissue is similar to wild-type CO39.

## INTRODUCTION

Plants defend themselves against pathogen challenge by the activation of defence response pathways that result in coordinated defence gene expression and the subsequent containment of the pathogen (Staskawicz *et al.*, 1997). One feature of a host resistance reaction is the hypersensitive response (HR), which is characterized by rapid plant cell death immediately at the point of pathogen ingress (Dangl *et al.*, 1996). This localized HR response is a specialized version of programmed cell death (PCD)

(Greenberg, 1996). The HR is correlated with a transient burst of active oxygen species, activation of specific defence related genes, accumulation of antimicrobial compounds, and alterations in of the cell wall (Yin *et al.*, 2000). In some plant species, the HR leads to a systemic response that confers enhanced resistance to subsequent pathogen infections (Ryals *et al.*, 1996). This secondary response has been termed systemic acquired resistance (SAR) and is accompanied by an elevated expression of pathogenesis-related (PR) genes (Uknes *et al.*, 1992).

Genetic screens have led to the isolation of mutants that develop an HR-like response in the absence of pathogen challenge (Dangl *et al.*, 1996; Greenberg *et al.*, 1994; Walbot *et al.*, 1983; Wolter *et al.*, 1993; Yin *et al.*, 2000). It has been proposed that these mutants carry defects in PCD pathways, making them unable to contain the boundaries of cell death once an HR has been initiated (Dangl *et al.*, 1996). This mutant class is commonly termed 'lesion mimics' (LM) (Walbot, 1983). The LM phenotype may occur in response to various stimuli that include alterations in light regimens or temperature or pathogen challenge (Dietrich *et al.*, 1994; Yamanouchi *et al.*, 2002; Yin *et al.*, 2000). Mutations in key steps of metabolism have also been identified in maize LM mutants that lead to the toxic or deleterious accumulation of intermediates (Gray *et al.*, 1997; Hu *et al.*, 1998; Mach *et al.*, 2001). The plethora of LM mutants identified in a broad range of plant species suggests that multiple and independent pathways are required for the proper initiation and containment of the HR (Lorrain *et al.*, 2003).

The appearance of the LM phenotype can occur with a simultaneous activation of the defence response (Dangl *et al.*, 1996). Defence response activation phenotypically manifests itself as enhanced resistance to pathogens, the induction of SAR, and the elevated expression of PR genes (Ryals *et al.*, 1996). Enhanced resistance LM mutants have been shown for either a single pathogen species or broad spectrum, non-species specific resistance, similar to SAR (Buschges *et al.*, 1997; Dietrich *et al.*, 1994; Takahashi *et al.*, 1999). Conversely, LM mutants have been identified that have elevated PR gene expression without the concomitant enhanced resistance to pathogens (Greenberg *et al.*, 1994; Yin *et al.*, 2000). This uncoupling of defence response

\*Correspondence: Pamela Ronald, Department of Plant Pathology, One Shields Avenue, UC-Davis, Davis, CA 95616, USA. Tel.: +1 530 752 1654, Fax: +1 530 752 5674, E-mail: pcronald@ucdavis.edu

activation and PCD suggests that there exist PCD signalling pathways that are independent of the defence response (Lorrain *et al.*, 2003). Further characterization of the LM mutant class will highlight their unique role in the defence response as well as the regulatory and metabolic steps essential for initiation and containment of PCD.

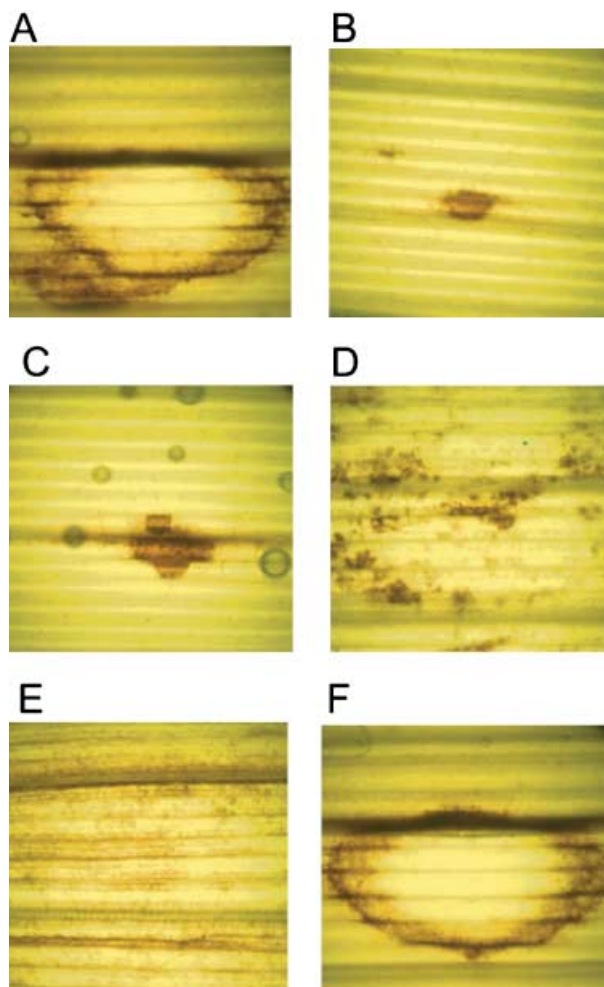
Three collections of LM mutants have recently been identified and characterized in rice. The 13 *spl* (*spotted leaf*) and three *cdr* (*cell death and resistance*) LM mutants were all found to spontaneously develop HR-like lesions and all had an elevated expression of the rice PR genes *PBZ1* and *PR1* in tissue displaying the LM phenotype (Misobuchi *et al.* 2002a; Takahashi *et al.*, 1999; Yin *et al.*, 2000). Eight *spl* mutants and all three *cdr* mutants display enhanced resistance to the fungal pathogen *Magnaporthe grisea* (*M. grisea*), which is the causal agent of rice blast disease (Ou, 1985; Takahashi *et al.*, 1999; Yin *et al.*, 2000; Mizobouchi *et al.*, 2002b). The five remaining *spl* mutants have no enhanced resistance to *M. grisea*, even though they have an elevated expression of *PBZ1* and *PR1* (Yin *et al.*, 2000). Further characterization of these mutants will be critical to the identification of the stimuli that initiate the HR, the mechanisms by which rice maintains the boundaries of an HR, and the relationship between the pathways for defence response activation and PCD.

In order to identify new loci involved in the defence response of rice, a genetic screen of the rice cultivar CO39 was performed using *M. grisea*. CO39 is partially susceptible to the CA-1 isolate of *M. grisea* that was used in this screen (Greer and Webster, 2001). Three mutant lines were identified as having an enhanced resistance phenotype to *M. grisea*. These lines are designated as *ebr1* (enhanced blast resistance 1), *ebr2* and *ebr3*. *ebr1* and *ebr3* also have enhanced resistance to the bacterial pathogen *Xanthomonas oryzae* pv. *oryzae* (*Xoo*). *ebr3* has an LM phenotype that resembles an HR and is induced by *M. grisea* and *Xoo* inoculation. This LM phenotype can also be induced in the growth chamber in the absence of pathogen inoculation. The *ebr1* and *ebr2* mutant lines do not display an LM phenotype and therefore belong to a newly identified class of enhanced resistance rice mutants (Zhang *et al.*, 2003). A fourth mutant line, *ncr1* (necrosis in rice 1) has an LM phenotype that spontaneously appears on seedlings at 2 weeks post-germination. In *ncr1*, the lesions appear as patches that spread across the leaf as it emerges. *ncr1* mutants have no resistance to *M. grisea* on leaves lacking the LM phenotype, and *ncr1* lacks enhanced resistance to *Xoo*.

## RESULTS

### Initial characterization of *ebr1*, *ebr2*, *ebr3* and *ncr1* with the CA-1 isolate of *M. grisea*

Three putative mutant lines were found to have enhanced resistance to *M. grisea* and were grouped as *ebr* lines. Wild-type CO39



**Fig. 1** Brightfield microscopy (40× magnification) of inoculated tissue observed 7 days post-inoculation with the CA-1 isolate of *M. grisea* for the four mutants and wild-type CO39. All images utilize cleared leaf tissue. Seedlings were inoculated at 3 weeks. (A) Wild-type CO39 cultivar displaying a type 3 lesion. (B) *ebr1* leaf tissue displaying a type 1 lesion. (C) *ebr2* leaf tissue displaying a type 2 lesion. (D) *ebr3* leaf tissue displaying the LM phenotype. (E) *ncr1* leaf tissue displaying the necrotic LM phenotype. (F) *ncr1* leaf tissue lacking the LM phenotype displaying a type 3 *M. grisea* lesion. The size marker (black bar) represents 0.5 mm.

develops type 3 lesions at 7-days post-inoculation with the CA-1 isolate of *M. grisea* (Fig. 1A). *ebr1* develops type 0 and 1 lesions at 7-days post-inoculation, with CA-1 reflecting a complete resistance phenotype (Fig. 1B) whereas the *ebr2* mutant develops type 1 and 2 lesions at 7 days post-inoculation reflecting an enhanced resistance phenotype (Fig. 1C). The degree of enhanced resistance in *ebr2* is less than that of *ebr1*, but this mutant has a noticeable reduction in size and frequency of CA-1 lesions when compared with CO39. *ebr3* does not develop characteristic *M. grisea* lesions at 7 days post-inoculation. In contrast, *ebr3* displays an LM phenotype on all leaves at 7 days post-inoculation

**Table 1** *M. grisea* reaction scores over 10 days post-inoculation using the CA-1 isolate\*

Mutant line	Day 0	Day 2	Day 3	Day 4	Day 5	Day 7	Day 10
CO39	0	1	1 & 2	1 & 2	2	2 & 3	3
<i>ebr1</i>	0	0	0	0 & 1	0 & 1	0 & 1	1
<i>ebr2</i>	0	0	0 & 1	0 & 1	1	1 & 2	1 & 2
<i>ebr3</i>	0	0	1	LM <sup>b</sup>	LM <sup>b</sup>	LM <sup>†</sup>	Dead
<i>ncr1</i> ‡	0	0	1	1 & 2	2	2 & 3	3

\*Reaction scores follow a 0–5 numerical rating described in the Experimental procedures (Mackill and Bonman, 1992).

†Indicates the appearance of a LM phenotype. These observed lesions are not characteristic of *M. grisea* infection.

‡The lesion scores for the *ncr1* line are for leaf 5 only.

(Fig. 1D). *ebr3* seedlings grown under MI conditions also develop the LM phenotype on older leaves (see below). The fourth mutant line, *ncr1*, develops a necrotic LM phenotype at 2 weeks post-germination on leaves 1 and 2. By 4 weeks, the LM phenotype is present on leaves 1–4 on 4 week-old *ncr1* seedlings (Fig. 1E). No *M. grisea* lesions were observed on tissue displaying the *ncr1* LM phenotype, suggesting that the LM phenotype triggers enhanced resistance to *M. grisea*. On leaf 5 of 4 week-old inoculated *ncr1* seedlings, type 3 *M. grisea* lesions develop (Fig. 1F). The *ebr3* LM phenotype has clusters of necrosis that are distinct from the *ncr1* necrotic LM phenotype that spreads along the parallel vascular bundles (Fig. 1D,F).

#### Characterization of *ebr1*, *ebr2*, *ebr3* and *ncr1* over a 10 day span post-inoculation with the *M. grisea* isolate CA-1

A 10-day evaluation of *M. grisea* lesion development was made for each of the mutants and wild-type CO39 using the CA-1 isolate on 4-week-old seedlings (Table 1). CO39 wild-type seedlings developed type 2 and 3 lesions by 7 days post-inoculation. At 10 days post-inoculation, all lesions developed as type 3. *ebr1* had lesion scores of 0 and 1 over the 10 days post-inoculation indicating complete resistance. *ebr2* had delayed development of *M. grisea* lesions and a reduction in lesion size (types 1 and 2) and frequency. *ebr3* appears phenotypically normal during the first 3 days post-inoculation when compared with CO39. However, on the fourth day post-inoculation, the *ebr3* LM phenotype appears in patches across all leaves. On the seventh day post-inoculation, the *ebr3* LM phenotype has spread across the leaves. On the tenth day post-inoculation, the inoculated leaves are covered with the LM phenotype and have died. *ncr1* develops type 3 *M. grisea* lesions by day 7 only on the leaf 5 (not displaying the necrotic LM phenotype). *ncr1* leaves 1 through 4 display the necrotic LM phenotype and lack observable *M. grisea* lesions. Inoculation with CA-1 did not induce the necrotic LM phenotype for *ncr1*.

**Table 2** Leaf phenotype of *ebr3* seedlings over 10 days under mock-inoculation conditions\*

Leaf†	Day 0	Day 2	Day 3	Day 4	Day 5	Day 7	Day 10
1	WT‡	WT	WT	LM§	LM	LM	LM
2	WT	WT	WT	WT	LM	LM	LM
3	WT	WT	WT	WT	WT	LM	LM
4	WT	WT	WT	WT	WT	WT	WT
5	WT	WT	WT	WT	WT	WT	WT

\*Mock-inoculation conditions are described in the Experimental procedures.

†Leaf stage is from 1 (basal, oldest) to 5 (apical, youngest) (Century *et al.*, 1999).

‡WT indicates a wild-type phenotype.

§LM indicates the appearance of LM phenotype.

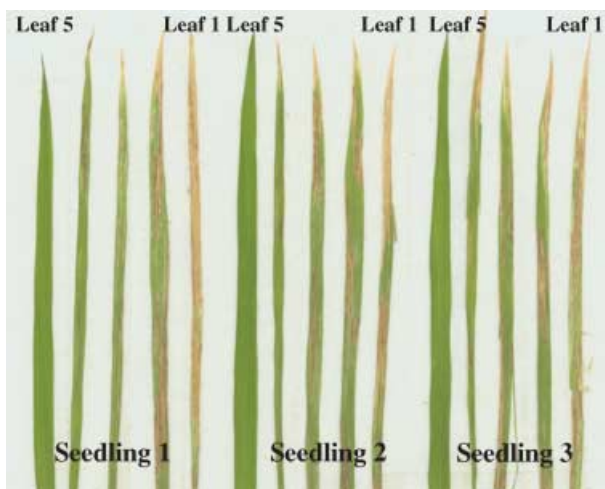
#### The LM phenotype was observed on *ebr3* mutants under mock-inoculated, but not greenhouse, conditions

The four mutants and CO39 3-week-old seedlings were subjected to mock-inoculation (MI) conditions and were evaluated over a 10-day period. *ebr1* and *ebr2* MI seedlings were phenotypically identical when compared with the CO39 wild-type seedlings. The *ebr3* MI seedlings developed the LM phenotype on leaves 1, 2 and 3 (Table 2). The MI *ebr3* LM phenotype appeared in an age-dependent fashion, with leaf 1 developing the phenotype at day 4. Leaves 2 and 3 developed the LM phenotype at days 5 and 7, respectively, and *ebr3* leaf 5 did not display the LM phenotype after 10 days under MI conditions. In contrast, *M. grisea*-inoculated *ebr3* mutants develop the LM phenotype on all five leaves of the seedling by day 4 post-inoculation. Greenhouse grown *ebr3* 4-week-old seedlings never developed the LM phenotype in repeated assays.

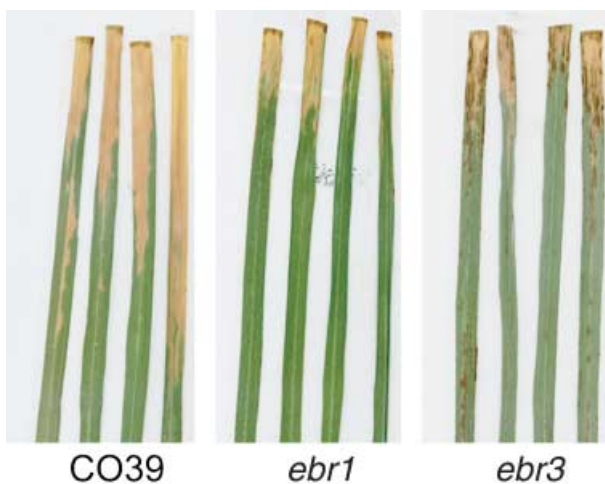
Unlike the inducible *ebr3* LM phenotype, *ncr1* mutants under MI conditions are not phenotypically different from greenhouse grown *ncr1* mutants of the same age, indicating that a shift in environmental conditions neither exacerbated nor reduced the necrotic LM phenotype (data not shown). Figure 2 shows the age-dependent progression of the *ncr1* LM phenotype on leaves 1–5 of 4-week-old seedlings.

#### *ebr1* and *ebr3* confer enhanced resistance to the PX099 isolate of *Xoo*

To assess if the *ebr1*, *ebr2* and *ebr3* mutants also conferred resistance to a bacterial pathogen, these mutants were inoculated with the PX099 isolate of *Xoo* (Hopkins *et al.* 1992). Compared to the CO39 control, *ebr1* and *ebr3* restrict the progression of the *Xoo*-induced water soaked lesions (Fig. 3). Inoculation with *Xoo* induces the *ebr3* LM phenotype at the point of inoculation (Fig. 3). All plants were grown in the greenhouse prior to inoculation (greenhouse grown *ebr3* mutant lines do not display the



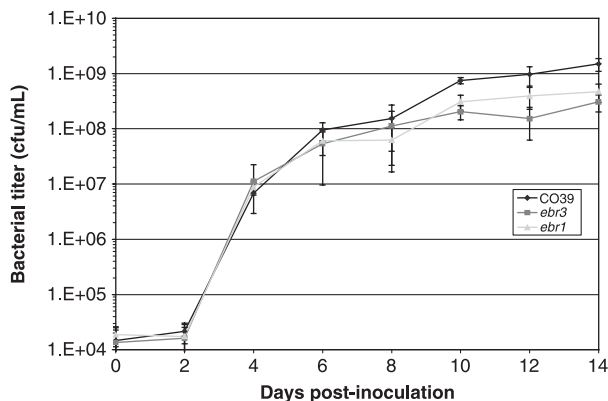
**Fig. 2** Macroscopic visualization of the necrotic LM phenotype of *ncr1* greenhouse-grown seedlings at 4 weeks old. Five leaves are shown from three separate seedlings. For each seedling leaf series, the leftmost leaf is leaf 5 and the rightmost leaf is leaf 1.



**Fig. 3** Lesion length analysis for the PXO99 isolate of *Xoo* on 6-week-old plants. Representative leaves displaying water-soaked lesions at are shown at 14-days post-inoculation for wild-type CO39 and the *ebr1* and *ebr3* lines.

LM phenotype). A quantitative *Xoo* growth curve analysis was performed for *ebr1* and *ebr3* using PXO99, with the wild-type CO39 as a control. The 14-day growth curve analysis indicated that both *ebr1* and *ebr3* have a nearly 10-fold reduction of bacterial titre at 10-, 12-, and 14-days post-inoculation when compared with wild-type CO39 (Fig. 4). PXO99 lesion length analysis for *ebr2* showed no significant reduction in lesion lengths, and a bacterial growth curve analysis did not show a significant difference in bacterial titre when compared with CO39 (data not shown).

At 6 weeks, all expanded leaves of *ncr1* displayed an LM phenotype that obscured the progression of *Xoo*-induced water

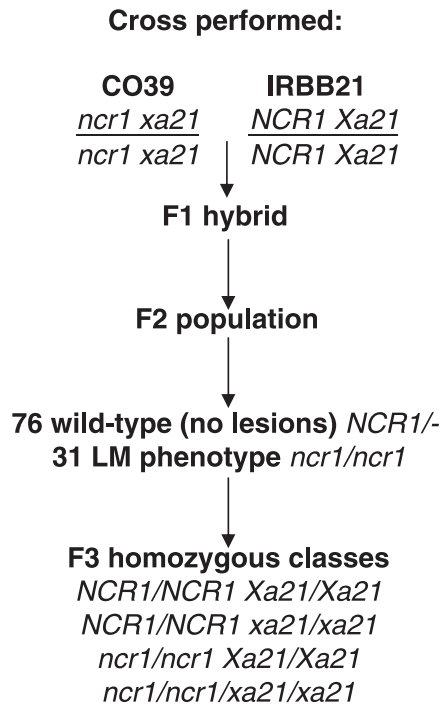


**Fig. 4** Growth curve analysis for CO39 and the *ebr1* and *ebr3* lines using the PXO99 isolate of *Xoo*. All data points over the 14 day assay period are the average of the titre of five independently inoculated leaves. Error bars indicate the standard deviation of the average.

soaked lesions; therefore lesion length analysis could not be performed on the *ncr1* mutants. Instead, a growth curve assay was performed using the IRBB21 line carrying the dominant *Xa21* resistance gene as a resistant control. *Xa21* confers complete resistance to the PXO99 isolate of *Xoo* (Song *et al.*, 1995). CO39, having the *xa21* allele, is fully susceptible to PXO99. If *ncr1* has enhanced resistance in leaves displaying the LM phenotype, the reduction in bacterial titre can be compared with the complete resistance conferred by *Xa21*. An F<sub>2</sub> population was developed from a cross between *ncr1* and the Indica cultivar IRBB21. F<sub>3</sub> families representing the four possible homozygous combinations were identified (Fig. 5). From this cross, the *ncr1* locus was found to have a recessive mode of inheritance (see 'Mode of inheritance' below). The two homozygous F<sub>3</sub> families with the *xa21* susceptibility allele, i.e. *NCR1/NCR1 xa21/xa21* (no LM phenotype) and *ncr1/ncr1 xa21/xa21* (LM phenotype), had similar bacterial titres ( $\sim 1 \times 10^9$  cfu/mL) at 14-days post-inoculation (Fig. 6). By contrast, both F<sub>3</sub> families with the dominant *Xa21* resistance gene, i.e. *NCR1/NCR1 Xa21/Xa21* (no LM phenotype) and *ncr1/ncr1 Xa21/Xa21* (LM phenotype), had a 10-fold reduction in the bacterial titre ( $\sim 1 \times 10^8$  cfu/mL). These results indicate that the *ncr1* LM phenotype conferred by the *ncr1/ncr1* genotype did not restrict bacterial growth. Furthermore, *Xa21*-mediated signalling was not affected in plants having the *ncr1/ncr1* genotype, indicating that these loci do not interact epistatically.

### The *ncr1* and *ebr1* mutants display a short stature

During characterization of the mutants with *Xoo*, both the *ebr1* and *ncr1* lines were observed to have a reduction in stature. To further investigate this phenotype, 30 six week-old CO39 were evaluated for their height. All 150 plants were measured at the same time and were grown under identical greenhouse

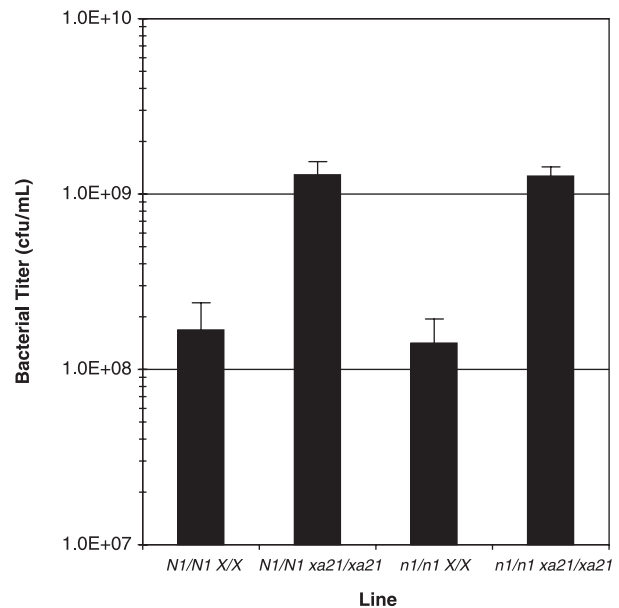


**Fig. 5** Scheme for developing the four F<sub>3</sub> homozygous lines from a cross between IRBB21 and the *ncr1/ncr1* genotype.

conditions for 6 weeks. The height was measured after extending the youngest, emerging leaf vertically. CO39 was found to have an average height of 75 cm ( $\pm$  4.1 cm). Both *ebr2* (77 cm ( $\pm$  4.0 cm)) and *ebr3* (81 cm ( $\pm$  3.9 cm)) were not significantly different from CO39. In contrast, both the *ebr1* and *ncr1* lines displayed significant reductions in stature with measured heights of 63 cm ( $\pm$  5.2 cm) and 64 cm ( $\pm$  3.1 cm), respectively.

#### PR gene expression analysis of the four mutants

The four mutants were analysed for their expression of the rice PR genes *PR1* and *PBZ1*. All analyses took place on 4-week-old seedlings. For the CO39, *ebr1*, *ebr2* and *ebr3* seedlings grown under GH conditions, no expression of *PR1* and *PBZ1* was detected (data not shown). When grown under MI conditions, *ebr1* and *ebr2* and CO39 had a very low expression of both *PR1* and *PBZ1*, whereas *ebr3* seedlings had an elevated expression of both PR genes (Fig. 7A). *ebr3* shows the LM phenotype under these conditions (Table 2). Next, leaves 1, 2 and 3 of *ebr3* showing the LM phenotype were sampled separately from leaves 4 and 5 that displayed no lesions. As a control, the same leaves were sampled from 4-week-old *ebr3* seedlings grown under GH conditions that do not display the LM phenotype. *PR1* and *PBZ1* only have elevated expression in leaves 1, 2, and 3 displaying the LM phenotype that is induced by MI conditions (Fig. 7B). When



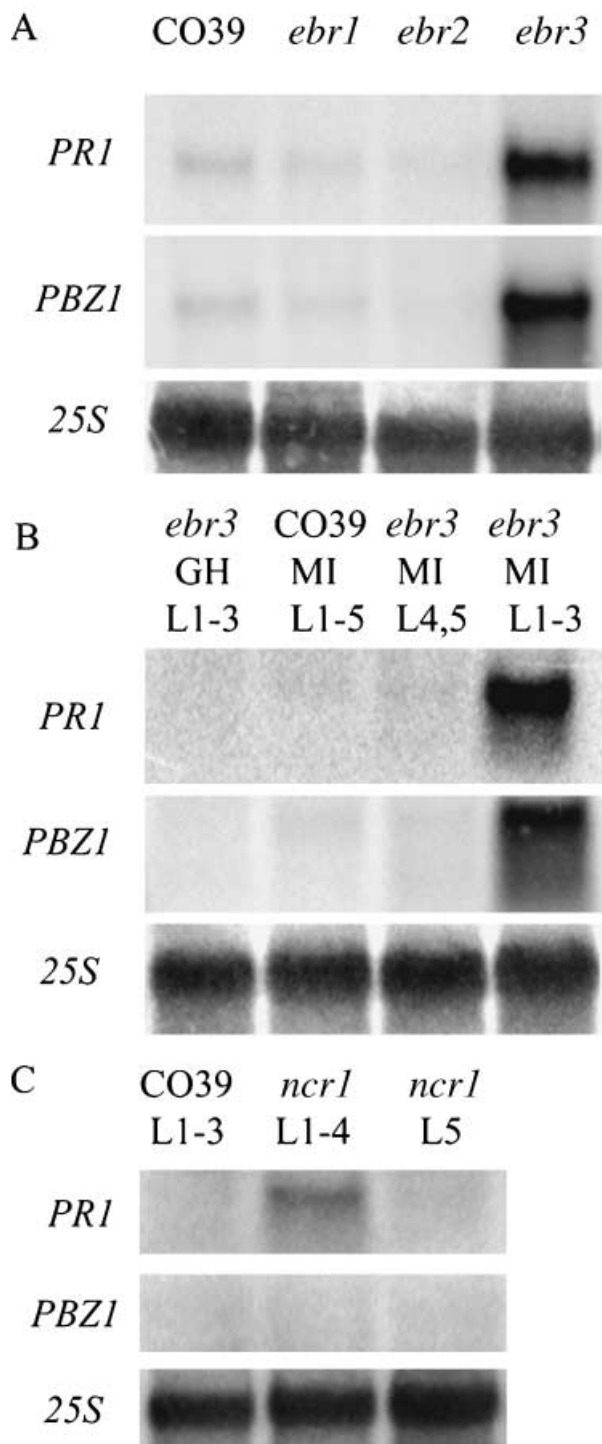
**Fig. 6** Bacterial titres at 14 days post-inoculation for the four F<sub>3</sub> homozygous lines using the PXO99 isolate of *Xoo*. Each bar represents the average of five independent inoculations. The error bars are the standard deviation of the mean. *N1* = *NCR1* (from IRBB21), *n1* = *ncr1*, *X* = *Xa21* (PXO99 resistance gene), and *xa21* = CO39 susceptibility allele.

grown under GH conditions, these same leaves from *ebr3* do not display an elevated expression (or the LM phenotype)

The *ncr1* LM phenotype is apparent on leaves 1–4 but not on leaf 5 for 4-week-old seedlings. These leaves were sampled separately for RNA expression analysis. In the *ncr1* line, an elevated expression of *PBZ1* was observed for leaves 1–4 with the necrotic LM phenotype and no *PBZ1* expression was observed in leaf 5, which is similar to wild-type CO39 (Fig. 7C). In contrast to *PBZ1*, *PR1* did not have an elevated expression in either set of *ncr1* leaves (Fig. 7C).

#### Mode of inheritance for *ncr1* and *ebr3*

The segregation analysis of an F<sub>2</sub> population derived from the *ncr1* mutant line and IRBB21 cross support the hypothesis that the *ncr1* locus has a recessive Mendelian mode of inheritance (Table 3). Chi-square analysis of the F<sub>2</sub> phenotypic segregation data supports this hypothesis. For the F<sub>2</sub> populations derived from reciprocal crosses of the *ebr3* and *ncr1* mutant lines, segregation data and  $\chi^2$  analysis support the hypothesis that both the *ebr3* and *ncr1* mutants have a recessive mode of inheritance (Table 4). A cross between two recessive mutants should phenotypically segregate 9 : 3 : 3 : 1 by Mendelian laws of inheritance. In the phenotypic score of the F<sub>2</sub> populations, all lines displaying the *ncr1* LM phenotype were identified visually in 3-week-old greenhouse grown seedlings and were tagged. The F<sub>2</sub> populations were



**Fig. 7** Expression analysis for *PBZ1* and *PR1* in 4-week-old *ebr1*, *ebr2*, *ebr3*, and *ncr1* seedlings. (A) *PR1* and *PBZ1* expression analysis for *ebr1*, *ebr2* and *ebr3* lines. RNA was isolated from whole seedling samples grown under mock-inoculation (MI) conditions. A *25S* rDNA probe was used as a control to evaluate equal transfer. (B) Expression analysis of *PR1* and *PBZ1* in 4-week-old *ebr3* seedlings. Lane 1 has *ebr3* tissue that was grown under greenhouse conditions (GH) and lacks the LM phenotype (L1–3). Lane 2 is wild-type CO39

then subjected to MI conditions to induce the *ebr3* HR-like phenotype. After 7 days, the *ebr3* LM phenotype was readily apparent on leaves 1 and 2 of the  $F_2$  seedlings. Any tagged individual displaying both the *ncr1* necrotic LM phenotype with the *ebr3* HR-like LM phenotype was scored as a double mutant. For these double mutants, the *ncr1* necrotic LM phenotype was not sufficient to induce the *ebr3* HR-like LM phenotype under greenhouse conditions. The *ebr3* LM phenotype was only induced in the double mutants in response to the shift to MI conditions. The double mutants with the *ebr3/ebr3 ncr1/ncr1* genotype displayed both of their respective LM phenotypes simultaneously. The *ncr1* and *ebr3* loci do not interact epistatically since the  $\chi^2$  analysis supports the 9 : 3 : 3 : 1 segregation ratio. The mode of inheritance for the mutant loci in the *ebr1* and *ebr2* lines has not yet been determined.

## DISCUSSION

This genetic screen successfully identified four mutant lines having disparate phenotypes in response to inoculation with the CA-1 isolate of *M. grisea*. The lines include two with enhanced resistance to CA-1 (*ebr1* and *ebr2*), one with enhanced resistance to CA-1 and an inducible lesion mimic phenotype (*ebr3*), and a lesion mimic mutant (*ncr1*) that spontaneously developed necrotic patches. These mutants were further characterized with the bacterial pathogen *Xoo* for variation in stature and for expression of the rice PR genes *PBZ1* and *PR1*. In addition, the mode of inheritance was determined for the *ebr3* and *ncr1* mutations that cause lesion mimic phenotypes.

The *ebr1* line displays complete resistance to the CA-1 phenotype and also confers enhanced resistance to the bacterial pathogen *Xoo*. A lesion length assay with PXO99 showed a reduction in water-soaked lesion symptoms that was verified with the quantitative growth curve assay. Average PXO99 titres were significantly reduced at the 10-, 12- and 14-day time points with a nearly 10-fold reduction at the 14-day time point. This reduction in average titre is comparable to the complete resistance affected by the *Xa21* resistance gene. Expression analysis indicated that *ebr1* does not display an elevated expression of rice PR genes. In addition, a lesion mimic phenotype was not observed under any of the described environmental conditions

grown under MI conditions. Lane 3 is *ebr3* tissue collected from leaves 4 and 5 (L4,5) grown under MI conditions and lacks the LM phenotype. Lane 4 is *ebr3* tissue collected from leaves 1, 2 and 3 (L1–3) grown under MI conditions and display the LM phenotype. *25S* rDNA probe was used as a control to evaluate equal transfer. (C) Expression analysis of *PR1* and *PBZ1* in four week-old *ncr1* seedlings. All tissue sampled was grown under greenhouse conditions. Lane 1 is tissue sampled from leaves 1 through 5 for CO39. Lane 2 is *ncr1* tissue sampled from leaves 1, 2, 3 and 4 that display the LM phenotype. Lane 3 is *ncr1* tissue sampled from leaf 5 that lacks the necrotic LM phenotype. *25S* rDNA probe was used as a control to evaluate equal transfer.

**Table 3** F<sub>2</sub> segregation analysis to determine the mode of inheritance for *ncr1*

Genotype	F <sub>1</sub> phenotype	F <sub>2</sub> total	Phenotype		Ratio*	$\chi^2$
			Wild-type	<i>ncr1</i>		
<i>ncr1ncr1</i> × <i>NCR1NCR1</i>	Wild-type	107	76	31	3 : 1	0.9 ( $P > 0.34$ )

\*Indicates the expected F<sub>2</sub> Mendelian ratio for a single recessive trait.

**Table 4** F<sub>2</sub> segregation analysis to determine the mode of inheritance for *ebr3* and *ncr1*

Genotype	F <sub>1</sub> *	F <sub>2</sub> total	Phenotype				Ratio‡	$\chi^2$
			WT	<i>ncr1</i>	<i>ebr3</i>	<i>ncr1</i> & <i>ebr3</i> †		
<i>ebr3ebr3</i> × <i>ncr1ncr1</i>	WT	165	95	27	37	6	9 : 3 : 3 : 1	3.54 ( $P > 0.34$ )
<i>ncr1ncr1</i> × <i>ebr3ebr3</i>	WT	392	217	82	75	18	9 : 3 : 3 : 1	2.79 ( $P > 0.42$ )

\*WT = lack of LM phenotype for either *ncr1* or *ebr3*.

†The phenotype of the double mutants has both the patches of necrosis for *ncr1* and the brown, speckling lesions characteristic of *ebr3*.

‡The expected F<sub>2</sub> Mendelian ratio for a cross between two recessive, non-allelic, and unlinked loci.

for *ebr1*. Based upon this characterization, *ebr1* is a novel addition to the collection of rice enhanced resistance mutants and mutant lines (Zhang *et al.*, 2003).

The rice *ebr1* mutant shares many characteristics with *Arabidopsis* lines carrying the *edr1* mutation. *edr1* was identified from a genetic screen using the bacterial pathogen *Pseudomonas syringae* and was subsequently determined to have enhanced resistance to the fungal pathogen *Erysiphe cichoracearum* (Frye and Innes, 1998). Similar to rice *ebr1*, *Arabidopsis edr1* does not display an elevated expression of the *Arabidopsis* PR genes *PR1*, *PR2* and *PR5*, and does not display a lesion mimic phenotype (Frye and Innes, 1998). *EDR1* encodes a MAPKK kinase and is postulated to negatively regulate the inducible expression of the defence response (Frye *et al.*, 2001). A putative orthologue of *EDR1* is present in rice in the dbEST database (accession no. D41138). Subsequent analysis will be needed to determine if the *ebr1* carries a genomic alteration in this *EDR1* orthologue.

The *ebr2* has enhanced resistance to the CA-1 isolate when compared to wild-type CO39. The 10-day CA-1 inoculation assay revealed that *ebr2*, with type 1 and 2 lesions, has a reduction in lesion severity. This mutant, unlike *ebr1*, has no enhanced resistance to *Xoo*. Rice PR gene expression analysis indicates that the *ebr2* line does not constitutively express *PR1* or *PBZ1*, nor does it display a lesion mimic phenotype under any of the environmental conditions tested.

Because *ebr1* and *ebr2* both display enhanced resistance to the CA-1 isolate, they may also confer resistance to other *M. grisea* strains. Previous research has shown that CO39 is highly susceptible to a wide range of *M. grisea* isolates, and these strains would therefore be logical candidates for testing on *ebr1* and *ebr2* (Inukai *et al.*, 1994; Mackill and Bonman, 1992). However, USDA restrictions prevent the import of these isolates into California, so these tests will need to be conducted at other locations.

Recently, the *pmr* class of mutants from *Arabidopsis* has been characterized for resistance to the obligate biotroph *Erysiphe cichoracearum* (powdery mildew) (Vogel and Sommerville, 2000; Vogel *et al.*, 2002). The enhanced resistance in these mutants was not broad spectrum. All *pmr* mutants were susceptible to the bacterial pathogen *Pseudomonas syringae*. The loci identified in this *Arabidopsis* screen are postulated to encode susceptibility factors resulting from fungal species evolving the ability to utilize host genes for its own needs. This adaptation is further supported by the narrow spectrum of enhanced resistance in the *pmr* mutants (Vogel and Sommerville, 2000; Vogel *et al.*, 2002). The *ebr2* line, having enhanced resistance to only CA-1, may represent a mutation in a susceptibility factor for *M. grisea*, whereas the *ebr1* line, having broad-spectrum resistance *M. grisea* and *Xoo*, does not fit the phenotypic characteristics for a susceptibility factor. An import restriction for *M. grisea* into California has prevented a comprehensive screening of *ebr1* and *ebr2* with a broad range of isolates. Subsequent BLAST screening elsewhere will reveal more phenotypic data on the type and degree of *M. grisea* resistance, and will be of particular use in the further characterization of *ebr2*.

The *M. grisea* enhanced resistance in the *ebr3* mutant line is quite different from either *ebr1* or *ebr2*. Inoculation with CA-1 induced a LM phenotype that eventually led to the death of the leaf over the course of a 10-day inoculation assay. The LM phenotype was also induced by MI and *Xoo* inoculation. *ebr3* confers enhanced resistance to *Xoo* in both lesion length and growth curve analyses, and the resistance is similar to that conferred by *Xa21*. Expression of *PR1* and *PBZ1* are elevated in leaves that display the LM phenotype but not in CO39 or *ebr3* leaves lacking the LM phenotype. This broad-spectrum resistance to both a fungal and bacterial pathogens share features with plants that are undergoing SAR. For example, *ebr3* shares many similarities with



the *Arabidopsis lsd1* (*lesions simulating disease 1*) mutant (Dietrich *et al.*, 1994). The *lsd1* lesion mimic phenotype is induced by both a shift in lighting regimen and pathogen challenge. Similar to *ebr3*, the pathogen-induced LM phenotype spreads to consume the leaf. *Arabidopsis* PR genes are strongly expressed in leaves displaying the lesion mimic phenotype, and *lsd1* has enhanced resistance to both bacterial and oomycete pathogens (Dietrich *et al.*, 1994; Dietrich *et al.*, 1997). Similarly, a rice lesion mimic mutant, *spl11*, shares many of the phenotypic characteristics with the *ebr3* line and *lsd1*, including enhanced resistance to both fungal and bacterial pathogens, elevated PR gene expression in lesion mimic affected tissue, and induction of the lesion mimic phenotype by pathogen inoculation. Unlike either *ebr3* or *lsd1*, the *spl11* mutant has not been reported to have induction of the lesion mimic phenotype under an alteration of environmental conditions. In contrast to all rice lesion mimic mutants reported to date, the *ebr3* line develops the HR-like lesion mimic phenotypes spontaneously under greenhouse conditions (Takahashi *et al.*, 1999; Yin *et al.*, 2000). Therefore, *ebr3*, with the inducible LM phenotype, represents a new class of rice lesion mimic mutants.

The *ncr1* mutant line develops a patchy LM phenotype at 2 weeks post-germination. Leaves lacking the LM phenotype display type 3 lesions in response to *M. grisea*. LM unaffected tissue did not display obvious *M. grisea* lesions although the susceptible phenotype may have been obscured by the LM phenotype. Unlike *ebr3*, the LM phenotype conferred by the *ncr1/ncr1* genotype has neither enhanced resistance to *Xoo* nor was the LM phenotype induced by *M. grisea*. Similarly, five previously described *spl* mutants, *spl2*, *spl3*, *spl4*, *spl6* and *spl7*, have no enhanced resistance to four different isolates of *M. grisea*. Moreover, inoculation with these isolates did not induce the LM phenotype on any of the five mutants in a way that was consistent with the *ncr1* mutant (Yin *et al.*, 2000). The *ncr1* mutation does not confer resistance to *Xoo*. The *ncr1/ncr1 xa21/xa21* and *NCR1/NCR1 xa21/xa21* F<sub>3</sub> lines had similar bacterial titres of  $\sim 1 \times 10^9$  cfu/mL. By comparison, the presence of the *Xoo* resistance gene *Xa21* reduced bacterial titre 10-fold in both the *NCR1/NCR1 Xa21/Xa21* and *ncr1/ncr1 Xa21/Xa21* genotypes. For these five *spl* mutants, no characterizations with *Xoo* were described (Yin *et al.*, 2000). The *ncr1* mutant line has a differential expression of PR genes, in contrast to the *spl* mutants that strongly express both *PBZ1* and *PR1* in LM affected tissue. Given that the *ncr1* line only expresses *PBZ1* in LM affected tissue, this mutant is unusual among rice LM mutants in its differential expression of *PR1*. This mutant will need to undergo complementation analysis testing with the *cdr* and *spl* mutants in order evaluate if these mutants are allelic

Two mutants having an LM phenotype were identified in this screen. These two additions bring the total number of LM mutants characterized for alterations in the defence response to 14 (Takahashi *et al.*, 1999; Yin *et al.*, 2000). Only one of these LM mutants, *spl7*, has been cloned and was found to share sequence

similarity with heat stress transcription factors (Yamanouchi *et al.*, 2002). Subsequent mapping and identification of the mutant alleles for the *ebr3*, *ncr1*, *spl* and *cdr* mutants will prove useful in uncovering the components involved in the regulation and control of the HR. As with *Arabidopsis* and maize, the large number of rice LM mutants obtained thus far indicate that multiple, independent pathways are involved in PCD, and only a subset of these are also involved in the defence response. Subsequent genetic analysis of these rice LM mutants will uncover the degree of conservation among PCD pathways in higher plants.

## EXPERIMENTAL PROCEDURES

### *M. grisea* inoculum preparation

The *M. grisea* CA-1 isolate was obtained from R. Webster at UC-Davis and maintained at  $-20$  °C (Greer and Webster, 2001). Cultures were grown at RT on oatmeal agar (OA). OA was prepared by mixing 100 g of rolled oats in 1 L of water and holding the mixture at 70 °C for 1-h. The oats were filtered out and the solution was brought to 2 L with water. Bacto Agar (13.5 g/L) was added and the solution was autoclaved. The oatmeal agar was then cooled to 60 °C and ampicillin was added to a final concentration of 25 µg/L. The plates were then poured. Plate cultures were seeded from the master culture and were grown for 14 days in darkness at RT. Conidiation was induced by scraping the mycelia with a sterile spoon and continuously illuminating the scraped plate cultures for 5 days at RT. Ten millilitres of water was then added to the plate and the surface scraped to harvest the conidia. The conidial suspension was filtered through Miracloth and adjusted to  $5 \times 10^4$  conidia/mL using a haemocytometer.

### *M. grisea* disease evaluation

Seedlings were grown for 3 weeks in the greenhouse. Seedlings were then moved to the dew chamber (100% r.h.) for spray inoculation. Seedlings remained in the dew chamber for 16 h in complete darkness. Inoculated seedlings were then removed from the dew chamber and grown in a controlled environmental chamber for 6 days under 12 h light at 28 °C and 12 h darkness at 20 °C. The relative humidity was maintained at 85%. The chamber was equipped with metal halide and incandescent lights providing a PAR of 103 µmol photons/m<sup>2</sup>/s<sup>1</sup>. PAR reflects the total light intensity between 400 nm and 700 nm. By comparison, PAR for a sunny day in the greenhouse is  $\sim 670$  µmol photon/m<sup>2</sup>/s (Fitzgerald *et al.*, 2004). Total light abundance and quality were monitored using a LiCor 1800 spectroradiometer. Disease reactions were scored at 7 days post-inoculation according to a standardized protocol (Mackill and Bonman, 1992). The lesions were scored from 0 to 5 as follows: 0 = no evidence of infection, 1 = brown specking indicative of an HR response

(< 0.5 mm in diameter), 2 = brown lesions having a 0.5–1 mm diameter, 3 = round to elliptical lesion 1–3 mm in diameter (or length) with a grey centre, 4 = spindle shaped lesions with a grey centre, and 5 = coalesced type 4 lesions across the majority of the leaf. Plants with lesion scores of 0–2 are resistant, 3 are partially susceptible, and 4–5 are susceptible.

### Creation of the mutant population and initial screening

Three thousand wild-type CO39 seeds were irradiated with 15 Gy of fast-neutron irradiation at the International Atomic Energy Commission in Austria. The M<sub>1</sub> plants were grown in the greenhouse. M<sub>2</sub> seeds from 2700 M<sub>1</sub> parents were harvested and maintained separately. M<sub>2</sub> seeds from each M<sub>1</sub> parent were sterilized in a 10% bleach solution for 30 min at room temperature (RT). The sterilized M<sub>2</sub> seeds were washed three times in sterile water. Twenty to 40 M<sub>2</sub> seeds from each M<sub>1</sub> parent were germinated in Petri dishes with 10 mL distilled water at RT until both the radicle and epicotyl had emerged. All germinated seeds were grown in the greenhouse for 3 weeks. Aberrations in chlorophyll deposition (i.e. zebra mutants (Kinoshita, 1998)), albinos, seedling lethals, and morphological variants were scored for the first 20 000 M<sub>2</sub> seedlings representing progeny from 800 M<sub>1</sub> parents. A mutational rate of 1.2% was collectively observed for these phenotypes. The seedlings were then moved to the dew chamber for inoculation as described above.

### Definition of leaf stages

Four-week-old greenhouse grown CO39 seedlings have five leaves. These leaves are numbered according to the order of emergence (Century *et al.*, 1999). Leaf 1 is basal and is the oldest leaf and leaf 5 is apical and is the youngest leaf.

### Putative mutant identification

Over 70 000 M<sub>2</sub> individuals were scored for their reaction with CA-1. One hundred and twenty-one individuals displayed alterations in the defence response. These 121 M<sub>2</sub> individuals were derived from 54 separate M<sub>1</sub> parents. These 121 M<sub>2</sub> individuals were isolated and selfed to generate M<sub>3</sub> progeny. The M<sub>1</sub> line 1902 gave rise to three M<sub>2</sub> progeny with complete resistance to CA-1 and 22 partially susceptible progeny. The three M<sub>2</sub> individuals from line 1902 with complete resistance were selfed. Twenty M<sub>3</sub> seedlings from each of the three M<sub>2</sub> parents with complete resistance were re-screened with *M. grisea*. All M<sub>3</sub> progeny also displayed complete resistance. These M<sub>3</sub> progeny with enhanced resistance were pooled, and the line renamed ebr1. The M<sub>1</sub> line 1946 gave rise to two M<sub>2</sub> progeny with enhanced resistance to CA-1 and 22 partially susceptible progeny. The two enhanced resistance M<sub>2</sub> individuals were selfed. Twenty M<sub>3</sub> seedlings from

the two enhanced resistance M<sub>2</sub> parents were re-screened with *M. grisea*. All M<sub>3</sub> progeny displayed enhanced resistance. These M<sub>3</sub> progeny were pooled and the line renamed ebr2. The M<sub>1</sub> line 803 gave rise to one M<sub>2</sub> progeny with a LM phenotype and enhanced resistance to CA-1 and 24 partially susceptible progeny. The M<sub>2</sub> parent with the LM phenotype and enhanced resistance was selfed. Twenty M<sub>3</sub> progeny all displayed the LM phenotype and enhanced resistance to *M. grisea*. These M<sub>3</sub> progeny were pooled and the line was renamed ebr3. The M<sub>1</sub> line 2099 gave rise to two M<sub>2</sub> progeny that displayed an LM phenotype at 2 weeks post-germination and 23 wild-type progeny. The two M<sub>2</sub> parents with the LM phenotype were selfed. Twenty M<sub>3</sub> progeny from both M<sub>2</sub> parents all displayed the LM phenotype. These M<sub>3</sub> progeny were pooled and the line renamed ncr1.

For the four lines (1902, 1946, 803 and 2099), the M<sub>2</sub> siblings that displayed the partially susceptible phenotype were also selfed and the resulting M<sub>3</sub> progeny were re-screened. These M<sub>3</sub> progeny all displayed the wild-type phenotype.

### Histochemical analysis

Leaves were cleared using a lactophenol solution (50% of 95% ethanol and 5% water solution, 25% water-saturated phenol, 25% lactic acid). Detached leaves were immersed in lactophenol and incubated at 65 °C overnight. The lactophenol solution was replaced and leaves were cleared for an additional 24-h at 65 °C. The leaves were then equilibrated in 70% glycerol solution for microscopy.

### *Xoo* inoculum preparation, inoculation and growth curve protocol

Lesion length assays on 6-week-old plants were performed as described previously (Song *et al.*, 1995). A 14-day growth curve analysis on 6-week-old plants was performed as described previously using the PXO99 isolate of *Xoo* (Song *et al.*, 1995). All plants were grown for 6 weeks in the greenhouse and moved to the controlled environmental chamber for the 14-day inoculation assays with *Xoo*. Inoculations were performed using a *Xoo* suspension of OD = 600 nm. *Xoo in vitro* culture methods have been previously described (Song *et al.*, 1995).

### Rice crosses

The ncr1 mutant line was crossed with IRBB21 (pollen donor) in the greenhouse. F1 hybrid seed was dehusked and surface sterilized with 10% bleach before germination. True F<sub>1</sub> hybrids were verified by scoring for the presence of the *Xa21* resistance gene using a primer set derived from the *Xa21* genomic sequence (GENBANK no. U72723). The forward primer was 5'-ATAGCAACTGATTGCTTGG and the reverse primer 5'-CGATCGGTATAACAGCAAAC. The conditions for PCR amplification were 94 °C for 30 s, 55 °C for

45 s, and 72 °C for 90 s for 35 cycles. This primer set detects a 1377 bp amplicon from the IRBB21 *Xa21* allele and an ~1300 bp amplicon from the CO39 *xa21* allele that were resolved on a 1% agarose gel. Three true F<sub>1</sub> hybrids were identified, and F<sub>2</sub> seed was collected. F<sub>2</sub> individuals homozygous for the *Xa21* resistance gene were determined by PCR. Based upon phenotypic screening of the segregating F<sub>2</sub> population, *ncr1* was found to have a recessive mode of inheritance (see 'Mode of inheritance' below). The F<sub>3</sub> progeny were screened with the *Xa21* primer set to identify the presence of the alleles and were also visually screened for the *ncr1* LM phenotype. Reciprocal crosses were performed for the *ebr3* and *ncr1* lines. All crosses were performed in the greenhouse.

### Tissue collection protocols for RNA gel blot analysis

Tissue was collected from 4-week-old *ebr1*, *ebr2*, *ebr3* and CO39 seedlings under two separate environmental conditions for RNA gel blot analysis. Greenhouse conditions (GH) were seedlings grown for 4 weeks in the greenhouse. For mock inoculation (MI) conditions, the seedlings were grown for 3 weeks in the greenhouse, moved to the dew chamber for 16 h, and then grown under controlled environmental conditions (in the same chamber used for inoculations) for 7 days. Whole seedlings were taken for tissue sampling. For *ebr3*, MI conditions were sufficient to induce the LM phenotype on leaves 1, 2 and 3. *ebr3* tissue showing the LM phenotype (leaves 1, 2 and 3) was sampled separately from *ebr3* tissue lacking the LM phenotype (leaves 4 and 5) for subsequent RNA gel blot analysis. *ncr1* mutants were grown under GH conditions for 4 weeks. Leaves 1, 2, 3 and 4 displayed the LM phenotype and were sampled separately from leaf 5 lacking the LM phenotype.

### RNA gel blot analysis

Total RNA was isolated with TRIZOL Reagent (Life Technologies, Gaithersburg, MD). Ten to 15 µg of RNA per lane was separated on 1% formaldehyde-agarose gels and transferred to Hybond-N+ membranes (Amersham Pharmacia Biotech, Buckinghamshire, UK) using capillary transfer with 20× SSPE. <sup>32</sup>P-labelled DNA probes were generated using Ready-to-Go DNA Labeling Beads (Amersham Biosciences, Piscataway, NJ). The hybridization solution was (per 100 mL): 50 mL of formamide, 30 mL 20× SSPE, 10 mL 50× Denhardt's solution, 5 mL 10% SDS and 5 mL of water. Ten grams of dextran sulphate were dissolved in 100 mL of hybridization solution prior to use. All hybridizations took place at 42 °C. All hybridized blots were washed with 2× SSPE, 0.1% SDS twice and then washed once with 1× SSPE, 0.2% SDS. All washing steps were 15 min in duration at 42 °C. Membranes were stripped using boiling 0.5% SDS and left to cool for 3 h. All RNA blots were re-probed with a rice 25S rDNA probe as a control to evaluate equal transfer. *PR1* was obtained from M. Yoshikawa

(Department of Biology, San Francisco State University) as a 174 bp insert in the plasmid pCRII (Invitrogen, Carlsbad, CA) (unpublished data). *PR1* probe DNA was obtained by PCR amplification using the M13 forward and reverse primers. *PBZ1* (GENBANK accession no. D31870) was isolated by PCR amplification using the sequence specific primers PBZ1-5 and PBZ1-6 (PBZ1-5 = 5'CATGCTACTGCTCACCTTTGA and PBZ1-6 = 5'TCATCTAGGTGGGATATACT). PCR products were purified from agarose gels using the GeneClean Spin Kit (Bio101, Carlsbad, CA).

### ACKNOWLEDGEMENTS

We thank John Emery for coordinating the mutagenesis of the CO39 seed. This work was supported by the NIH, grant no. GM55962, and Pioneer. We thank R. Webster for providing the CA-1 isolate of *M. grisea*. Generous thanks are given to both Steve Silva and Lance Benson for their diligence in maintaining supplies at the greenhouse and growth chamber facilities.

### REFERENCES

- Buschges, R., Hollricher, K., Panstruga, R., Simons, G., Wolte, R.M., Frijters, A., van Daelen, R., van der Lee, T., Diergaarde, P., Groenendijk, J., Topsch, S., Vos, P., Salamini, F. and Schulze-Lefert, P. (1997) The barley Mlo gene: a novel control element of plant pathogen resistance. *Cell*, **88**, 695–705.
- Century, K.S., Lagman, R.A., Adkisson, M., Morlan, J., Tobias, R., Schwartz, K. and Smith, A. (1999) Short communication: developmental control of *Xa21*-mediated disease resistance in rice. *Plant. J.* **20**, 231–236.
- Dangl, J.L., Dietrich, R.A. and Richberg, M.H. (1996) Death don't have no mercy. *Plant Cell*, **8**, 1793–1807.
- Dietrich, R.A., Delaney, T.P., Uknes, S.J., Ward, E.R., Ryals, J.A. and Dangl, J.L. (1994) *Arabidopsis* mutants simulating disease resistance response. *Cell*, **77**, 565–577.
- Dietrich, R.A., Richberg, M.H., Schmidt, R., Dean, C. and Dangl, J.L. (1997) A novel zinc finger protein is encoded by the *Arabidopsis* *LSD1* gene and functions as a negative regulator of plant cell death. *Cell*, **88**, 685–694.
- Fitzgerald, H.A., Chern, M.S., Navarre, R. and Ronald, P.C. (2004) Overexpression of (At) NPR1 in rice leads to a BTH- and environment-induced lesion mimic/cell death phenotype. *Mol. Plant-Microbe Interact.* **17**, 140–151.
- Frye, C.A. and Innes, R.W. (1998) An *Arabidopsis* mutant with enhanced resistance to powdery mildew. *Plant Cell*, **10**, 947–956.
- Frye, C.A., Tang, D. and Innes, R.W. (2001) Negative regulation of defenses response in plants by a conserved MAPKK kinase. *Proc. Natl Acad. Sci. USA*, **98**, 784–786.
- Gray, J., Close, P.S., Briggs, S.P. and Johal, G.S. (1997) A novel suppressor of cell death in plants encoded by the *Ls1* gene of maize. *Cell*, **89**, 25–31.
- Greenberg, J.T. (1996) Programmed cell death: a way of life for plants. *Proc. Natl Acad. Sci. USA*, **93**, 12094–12097.
- Greenberg, J.T., Guo, A., Klessig, D.F. and Ausubel, F.M. (1994) Programmed cell death in plants: a pathogen-triggered response activated coordinately with multiple defense functions. *Cell*, **77**, 551–563.

- Greer, C.A. and Webster, R.K. (2001) Occurrence, distribution, epidemiology, cultivar reaction, and management of rice blast disease in California. *Plant Dis.* **85**, 1096–1102.
- Hopkins, C.M., White, F.F., Choi, S.-H., Guo, A. and Leach, J. (1992) Identification of a family of avirulence genes from *Xanthomonas oryzae* pv. *Oryzae*. *Mol. Plant-Microbe Interact.* **5**, 451–459.
- Hu, G., Yalpani, N., Briggs, S.P. and Johal, G.S. (1998) A porphyrin pathway impairment is responsible for the phenotype of a dominant disease lesion mimic mutant of maize. *Plant Cell*, **10**, 1095–1105.
- Inukai, T., Nelson, R.J., Zeigler, R.S., Sarkarung, S., Mackill, D.J., Bonman, M., Takamura, I. and Kinoshita, T. (1994) Allelism of blast resistance genes in near-isogenic lines of rice. *Phytopathology*, **84**, 1278–1283.
- Kinoshita, T. (1998) Linkage map using mutant genes in rice. *Rice Genet. Newsletter*, **15**, 13–74.
- Lorrain, S., Vailleau, F., Balagué, C. and Roby, D. (2003) Lesion mimic mutants: keys for deciphering cell death and defense pathways in plants? *Trends Pl. Sci.* **8**, 263–271.
- Mach, J.M., Castillo, A.R., Hoogstraten, R. and Greenberg, J.T. (2001) The *Arabidopsis*-accelerated cell death gene *ACD2* encodes red chlorophyll catabolite reductase and suppresses the spread of disease symptoms. *Proc. Natl Acad. Sci. USA*, **98**, 771–776.
- Mackill, D.J. and Bonman, M. (1992) Inheritance of blast resistance in near-isogenic lines of rice. *Phytopathology*, **82**, 746–749.
- Mizobuchi, R., Hirabayashi, H., Kaji, R., Nishizawa, Y., Satoh, H., Ogawa, T. and Okamoto, M. (2002a) Differential expression of disease resistance in rice lesion-mimic mutants. *Plant Cell Rep.* **21**, 390–396.
- Mizobuchi, R., Hirabayashi, H., Kaji, R., Nishizawa, Y., Yoshimura, A., Satoh, H., Ogawa, T. and Okamoto, M. (2002b) Isolation and characterization of rice lesion-mimic mutants with enhanced resistance to rice blast and bacterial blight. *Plant Sci.* **163**, 345–353.
- Ou, S.H. (1985) *Rice Diseases*. Wallingford, UK: Commonwealth Agricultural Bureaux.
- Ryals, J.A., Neuenschwander, U.H., Willits, M.G., Molina, A., Steiner, H.Y. and Hunt, M.D. (1996) Systemic acquired resistance. *Plant Cell*, **8**, 1809–1819.
- Song, W.Y., Wang, G.L., Chen, L.L., Kim, H.K., Pi, Y.P., 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**, 1824–1827.
- Staskawicz, B.J., Ausubel, F.M., Baker, B.J., Ellis, J.G. and Jones, J.D.G. (1997) Molecular genetics of plant disease resistance. *Science*, **268**, 661–667.
- Takahashi, A., Kawasaki, T., Henmi, K., Shi, K., Kodama, O., Satoh, H. and Shimamoto, K. (1999) Lesion mimic mutants of rice with alterations in early signaling events of defense. *Plant J.* **17**, 535–545.
- Uknes, S., Mauch-Mani, B., Moyer, M., Potter, S., Williams, S., Dincher, S., Chandler, D., Slusarenko, A., Ward, E. and Ryals, J. (1992) Acquired resistance in *Arabidopsis*. *Plant Cell*, **4**, 645–656.
- Vogel, J.P., Raab, T.K., Schiff, C. and Somerville, S.C. (2002) *PMR6*, a pectate lyase-like gene required for powdery mildew susceptibility in *Arabidopsis*. *Plant Cell*, **14**, 2095–2106.
- Vogel, J. and Somerville, S. (2000) Isolation and characterization of powdery mildew-resistant *Arabidopsis* mutants. *Proc. Natl Acad. Sci. USA*, **97**, 1897–1902.
- Walbot, V., Hosington, D.A. and Neuffer, M.G. (1983) Disease lesion mimic mutants. In: *Genetic Engineering of Plants* (Kosuge, T., Meredith, C.P. and Hollaender, A., eds), pp. 431–442. New York: Plenum Press.
- Wolter, M., Hollricher, K., Salamini, F. and Schulze-Lefert, P. (1993) The *mlo* resistance alleles to powdery mildew infection in barley trigger a developmentally controlled defence mimic phenotype. *Mol. General Genet.* **239**, 122–128.
- Yamanouchi, U., Yano, M., Lin, H., Ashikari, M. and Yamada, K. (2002) A rice spotted leaf gene, *Spl7*, encodes a heat stress transcription factor protein. *Proc. Natl Acad. Sci. USA*, **99**, 7530–7535.
- Yin, Z., Chen, J., Zeng, L., Goh, M., Leung, H., Khush, G.S. and Wang, G.L. (2000) Characterizing rice lesion mimic mutants and identifying a mutant with broad-spectrum resistance to rice blast and bacterial blight. *Mol. Plant-Microbe Interact.* **13**, 869–876.
- Zhang, M.X., Xu, J.L., Luo, R.T., Shi, D. and Li, Z.K. (2003) Genetic analysis and breeding use of blast resistance in a japonica rice mutant R917. *Euphytica*, **130**, 71–76.