Rice BiP3 regulates immunity mediated by the PRRs XA3 and XA21 but not immunity mediated by the NB-LRR protein, Pi5

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Running title: The function of BiP3 in rice immune response

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List of abbreviations

ER, endoplasmic reticulum; BiP3, luminal-binding protein 3; BRI1, brassinosteroid-insensitive 1; EFR, elongation factor Tu receptor; FLS2, flagellin sensitive 2; HSP70, heat shock protein 70; M. oryzae, Magnaporthe oryzae; NB-LRR, nucleotide-binding domain and leucine-rich repeat; non-RD, non-arginine-aspartate; PRR, pattern recognition receptor; XA21, Xanthomonas resistance 21 receptor; Xoo, Xanthomonas oryzae pv. oryzae
ABSTRACT

Plant innate immunity is mediated by pattern recognition receptors (PRRs) and intracellular NB-LRR (nucleotide-binding domain and leucine-rich repeat) proteins. Overexpression of the endoplasmic reticulum (ER) chaperone, luminal-binding protein 3 (BiP3) compromises resistance to *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) mediated by the rice PRR XA21 (Park et al., PLoS ONE 5(2): e9262). Here we show that BiP3 overexpression also compromises resistance mediated by rice XA3, a PRR that provides broad-spectrum resistance to *Xoo*. In contrast, BiP3 overexpression has no effect on resistance mediated by rice Pi5, an NB-LRR protein that confers resistance to the fungal pathogen *Magnaporthe oryzae* (*M. oryzae*). Our results suggest that rice BiP3 regulates membrane-resident PRR-mediated immunity.
INTRODUCTION

Plants recognize conserved microbial signatures via pattern recognition receptors (PRRs) (Ronald and Beutler 2010). Well-characterized PRRs include the Arabidopsis flagellin sensitive 2 (FLS2) receptor, the Arabidopsis elongation factor Tu receptor (EFR), and the rice XA21 (Xanthomonas resistance 21) receptor (Gomez-Gomez and Boller 2000; Song et al. 1995; Zipfel et al. 2006). These proteins share a similar structure: an extracellular leucine-rich repeat (LRR) domain, a transmembrane (TM) domain, and an intracellular non-arginine-aspartate (non-RD) kinase domain. The non-RD kinase motif is a hallmark of kinases involved in the initial stages of PRR-mediated immunity. In contrast, RD kinases are associated with a function in developmental processes (Dardick and Ronald 2006). Rice XA3 (also known as XA26) also shares this LRR-TM-non-RD kinase domain structure (Sun et al. 2004; Xiang et al. 2006). XA3 also confers another important trait characteristic of PRRs: broad-spectrum resistance. For these reasons, XA3 is predicted to be a PRR (Chen and Ronald 2011; Ronald and Beutler 2010; Schwessinger and Ronald 2012).

Membrane-bound PRRs are synthesized in the endoplasmic reticulum (ER) where they are subject to ER-quality control (Li et al. 2009; Nekrasov et al. 2009; Park et al. 2010; Saijo 2010). The ER-quality control is a conserved process in eukaryotic cells responsible for monitoring correct folding and processing of membrane and secretory proteins (Kleizen and Braakman 2004). Many ER proteins, including HSP70 luminal-binding protein (BiP), HSP40 ERdj3B, stromal-derived factor 2 (SDF2), calreticulin3 (CRT3), UDP-glucose glycoprotein glucosyl transferase (UGGT), and ER retention defective 2B (ERD2B), are involved in ER-
quality control (Li et al. 2009; Liu and Howell 2010; Nekrasov et al. 2009). Recent research suggests that the ER-resident chaperone BiP, an integral protein of the ER quality control system, is one of the main chaperones regulating biogenesis and degradation of membrane-resident PRRs. For example, in BiP3-overexpressing rice plants, XA21-mediated immunity is compromised and accumulation/processing of XA21 after Xoo inoculation is significantly inhibited (Park et al. 2010). These results indicate that BiP3 regulates XA21 protein stability and processing and that this regulation is critical for resistance to Xoo. In Arabidopsis, a large ER chaperone complex BiP/ERdj3B/SDF2 is required for the proper accumulation of EFR, further supporting a role for ER-quality control in membrane-resident PRR-mediated function (Nekrasov et al. 2009).

In contrast to PRRs that recognize conserved microbial signatures, intracellular NB-LRR proteins, containing nucleotide-binding and leucine-rich repeat domains, perceive highly variable pathogen-derived effectors in the cytoplasm directly or indirectly. Many NB-LRR proteins, including Arabidopsis RPM1, RPS2, and RPS5, tobacco N and rice Pi-ta and Pi5, have been characterized (Bent et al. 1994; Grant et al. 1995; Jeon et al. 2003; Jia et al. 2000; Warren et al. 1998). In tobacco, a number of ER resident chaperones, including BiP, are up-regulated during the earlier stages of N immune receptor-mediated defense against Tobacco mosaic virus (Caplan et al. 2009). In Arabidopsis, BiP2 is also involved in folding and secretion of pathogenesis-related (PR) proteins (Wang et al. 2005). In a bip2 mutant, increased PR protein synthesis after benzothiadiazole S-methylester (BTH, salicylic acid analog) treatment is not accompanied by a concomitant increase in BiP protein accumulation, resulting in impaired BTH-induced resistance.
These results suggest that components of ER-quality control may also play a role in NB-LRR-mediated immunity (Padmanabhan and Dinesh-Kumar 2010).

A differential requirement for gene governing ER-quality control has been observed in structurally-related receptors. For example, Arabidopsis FLS2-mediated responses are not impaired in the mutants, sdf2, crt3, uggt, and erd2b (Li et al. 2009; Nekrasov et al. 2009). In contrast, these genes which encode ER proteins, are all required for EFR-mediated signal transduction. Similarly, overexpression of BiP3 in rice does not affect rice brassinosteroid-insensitive 1 (OsBRI1)-mediated signaling, even though OsBRI1 shows an overall structural similarity with XA21. In contrast to XA21, OsBRI1 carries the RD class of kinases and regulates growth and developmental responses. As observed for rice, Arabidopsis BiPs fail to interact with wild-type BRI1 (Hong et al. 2008). In animals, processing of Toll-like receptors (TLRs), which are key determinants of the innate immune response, also require specific ER chaperones. For example, despite of its role as a general housekeeping chaperone, mouse ER gp96 is specific for processing TLR2, 4, 5, 7, and 9 in macrophages (Liu et al. 2010; Takahashi et al. 2007; Yang et al. 2007). Although gp96-deficient macrophages fail to respond to flagellin, the ligand for TLR5, mutant macrophages display normal development and activation by interferon-c, tumor necrosis factor-a, and interleukin-1b (Yang et al. 2007).

Based on these results, we hypothesize that ER chaperones are specific to their substrates, differentially regulating plant responses. To test this hypothesis, we chose two different types of receptors, the membrane-resident PRR XA3 and the intracellular NB-LRR protein Pi5, and assessed if BiP3 overexpression affects these immune responses. We found that overexpression
of BiP3 compromises XA3-mediated immunity to *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) but not Pi5-mediated immunity to *Magnaporthe oryzae* (*M. oryzae*). These results indicate that BiP3 regulates PRRs and that BiP3 overexpression does not lead to a general ER stress response.
MATERIAL AND METHODS

Plant materials and growth conditions

The endoplasmic reticulum (ER) chaperone BiP3 overexpressing (BiP3ox) transgenic line 1A-6 (Park et al. 2010) and its background cultivar Kitaake, IRBB3 monogenic line carrying Xa3 (Xiang et al. 2006), and IRBL5-M monogenic line carrying Pi5 (Yi et al. 2004) were used in this study. The IRBB3 and IRBL5-M lines were crossed with BiP3ox 1A-6 to generate BiP3ox/XA3 and BiP3ox/Pi5 plants, respectively. Self-pollinated seeds (F2) were collected and were used in pathogen inoculations. Rice plants were grown in a greenhouse at 30°C during the day and at 20°C at night in a light/dark cycle of 14/10 hours.

Xanthomonas oryzae pv. oryzae inoculation and lesion length measurements

Rice plants were grown in the greenhouse normally until they were six-week-old and transferred to the growth chamber. Growth chambers were set on 14 hours light:10 hours dark photoperiod, 28/26°C temperature cycle, and 85/90% humidity. The Xoo strains PXO61 and PXO79 were used to inoculate rice by the scissors-dip method (Chern et al. 2005; Song et al. 1995). Xoo strains PXO61 and PXO79 were grown on PSA plate (Peptone Sucrose Agar, 10 g/L peptone, 10 g/L sucrose, 1 g/L glutamic acid, 16 g/L agar, and pH 7.0) containing cephalexin (100 µg/L) for three days and suspended with water at OD=0.5 (600 nm) for inoculation. Only the top two to three expanded leaves of each tiller were inoculated.

Magnaporthe oryzae inoculation and disease evaluation

M. oryzae R01-1, which is incompatible with the Pi5-carrying line (Lee et al. 2009) and
compatible with the cultivar Kitaake, has been commonly used to evaluate disease resistance. *M. oryzae* R01-1 was grown on rice flour medium containing 20 g/L rice flour powder, 10 g/L dextrose, and 12 g/L agar in the dark for 2 weeks at 22°C (Lee *et al.* 2009). Conidia were induced for 5 days by scratching the plate surface with a sterilized loop. Agar blocks covered with spores were placed on the injured spot of 2.0 mm diameter according to the leaf punch inoculation (Takahashi *et al.* 1999). The second fully expanded leaves from the top of five-week-old plants were used for *M. oryzae* inoculation. The inoculated plants were placed in sealed containers to maintain humidity in the dark for 24 hours at 24°C and then incubated at the same relative humidity under a 14/10 hours (light/dark) photoperiod. For disease evaluation, blast lesion lengths were measured 10 days after inoculation.

**Genomic DNA isolation and PCR analysis**

Genomic DNAs were extracted from leaves of individual plants following the protocol described previously (Chen and Ronald 1999). The gene-specific primers for PCR were as follows: for *BiP3*, 5´-GCTGCTGCTATTGCGTACGGTTTGGACA-3´ and 5´-AATCATCGCAAGACCGGCAACAGG-3´; for *Pi5-1*, 5´-TTATGAGATTAGGAGTGTAT-3´ and 5´-ATGTAAAGGCAAAAGCTGAT-3´; and for *Pi5-2*, 5´-CTCTTGATTAGGAGTGTAT-3´ and 5´-GGATGATGTGATCTCGAGAG-3´; and for *Xa3*, 5´-CACCCCACGCAAGCCTCTCA-3´ and 5´-CTCCGTCATCAGCCATAACTC-3´. We carried out PCR experiments. PCR conditions were pre-denaturation for 3 min at 94°C, followed by 35 cycles of polymerization, each consisting of 30 s of denaturation at 94°C, annealing for 30 s at 58°C, and an extension step of 30 s at 72°C. The PCR product was separated on a 1.5%
agarose gel and stained with ethidium bromide to detect the amplicons.
RESULTS

Overexpression of BiP3 compromises membrane-resident PRR XA3-mediated immunity

As is typical of PRRs, XA3 confers broad-spectrum resistance to Xoo strains including PXO61 and PXO79 (Cao et al. 2007). To explore the biological role of BiP3 in XA3-mediated immunity, we first investigated the presence of a functional Xa3 gene in the genome of rice cultivar Kitaake. Using the scissors-dip-method, we inoculated Kitaake plants with Xoo strains PXO61 and PXO79. Figure 1A shows typical leaves from Kitaake wild type and Xa3-possessing IRBB3 plants 14 days after inoculation with Xoo strains. While IRBB3 was highly resistant, showing short lesions (approximately 4 to 5 cm), the inoculated leaves of Kitaake plants developed long water-soaked lesions (approximately 17 to 20 cm) typical of bacterial blight disease (Fig. 1B). These results indicate that Kitaake plants do not possess a functional Xa3 gene.

To generate XA3 plants overexpressing BiP3, we first crossed IRBB3 (XA3, pollen donor) with transgenic Kitaake overexpressing BiP3 (BiP3ox 1A-6, pollen recipient) (Park et al. 2010). The presence of the BiP3ox and/or Xa3 genes in the resulting F1 was confirmed by PCR analysis with primers specific for BiP3ox or Xa3 (data not shown). The F2 segregating progenies (a total of 41 segregating progeny) were inoculated with Xoo strain PXO61, and examined for cosegregation of the genotype with lesion length developments (Fig. 2A). XA3 plants lacking BiP3ox (BiP3ox/XA3, -/+ ) developed short lesion lengths (approximately 2 to 3 cm), indicating that Xa3 confers resistance to Xoo strain PXO61. In contrast, all XA3 plants carrying BiP3ox (BiP3ox/XA3, +/+ ) displayed significantly compromised resistance to Xoo strain PXO61. The long lesions formed (approximately 15 cm) are similar to those of the segregants lacking Xa3
Bacterial growth was also monitored over time (Fig. 2B). Xoo strain PXO61 populations in XA3 plants (BiP3ox/XA3, -/- and +/-) reached approximately $5.5 \times 10^7$ colony-forming units per leaf (cfu/leaf), whereas the population in the segregants lacking Xa3 (BiP3ox/XA3, -/- and +/-) reached to more than $9.1 \times 10^8$ cfu/leaf. In plants carrying both Xa3 and BiP3ox (BiP3ox/XA3, +/-), the bacterial populations grew to $8.3 \times 10^8$ cfu/leaf, a greater than fifteen-fold increase compared to the XA3 plants. The F2 progenies inoculated with another Xoo strain PXO79 showed similar results with increased lesion length developments and bacterial populations (Fig. 2C and D). These results demonstrate that overexpression of BiP3 compromises XA3-mediated immunity against Xoo.

**Overexpressed BiP3 does not affect Pi5-mediated immunity**

We have previously shown that Kitaake plants overexpressing BiP3, lacking Xa21, do not show alterations in resistance to Xoo strain PXO99, suggesting that an increased level of BiP3 does not affect the general defense response to bacterial pathogen Xoo (Park et al. 2010). To determine if enhanced expression of BiP3 can affect the resistance level to fungal pathogen, we inoculated the BiP3ox and the Kitaake wild type plants with *M. oryzae* R01-1. Figure 3A shows a typical leaf from each of the inoculated rice plants 10 days after *M. oryzae* inoculation. We found both BiP3ox and Kitaake plants displayed similar blast lesions of approximately 1.0 to 1.2 cm (Fig. 3B), indicating that BiP3 overexpression does not affect general resistance to *M. oryzae*.

To further determine if enhanced expression of BiP3 can affect NB-LRR-mediated resistance to *M. oryzae*, we examined the effect of BiP3 overexpression on Pi5-mediated resistance to *M. oryzae*. Pi5 resistance is controlled by two genes, Pi5-1 and Pi5-2, which encode
coiled-coil (CC)-NB-LRR proteins (Lee et al. 2009). We produced double transgenic plants carrying both *Pi5* and *BiP3ox* by crossing the IRBL5-M carrying *Pi5* (pollen donor) and *BiP3ox* 1A-6 lines (pollen recipient). The presence of the *BiP3ox* and/or *Pi5* in the resulting F₁ was confirmed by the PCR analysis with primers specific for *BiP3ox* or *Pi5* (data not shown). The F₂ segregating individual plants (a total of 64 segregating progeny) from 5 F₁ lines (*BiP3ox/Pi5*, +/-) were then inoculated with *M. oryzae* R01-1 (Fig. 4A and B). We found that all *BiP3ox/Pi5* plants carrying both genes (+/++; #2, 4, 5, 6, 7, 8, and 10 in Fig. 4A) remained completely resistant to the *M. oryzae* strain comparable to the parental line IRBL5-M or segregants carrying *Pi5* but lacking *BiP3ox* (*BiP3ox/Pi5*, -/+; #9 in Fig. 4A). In contrast, the parental *BiP3ox* line or segregants carrying *BiP3ox* but lacking *Pi5* (*BiP3ox/Pi5*, +/-; #1 and 3 in Fig. 4A) were all susceptible to the *M. oryzae*. These results indicate that overexpression of *BiP3* does not interfere with either general or *Pi5*-mediated resistance to *M. oryzae.*
DISCUSSION

After PRRs are synthesized in the ER, the folding states of the PRRs are monitored by ER chaperones. BiP is one of the most abundant chaperones, functioning in the ER-quality control (Liu and Howell 2010; Otero et al. 2010). In Arabidopsis, the ER quality control complex SDF2/ERdj3B/BiP is required for EFR accumulation and the EFR-mediated immune response (Li et al. 2009; Saijo 2010). In contrast, in rice, BiP3 overexpression significantly inhibits XA21 accumulation. These results suggest that overexpression of BiP3 results in XA21 degradation possibly via ER-associated degradation as an ER-quality control mechanism (Park et al. 2010).

The genetic requirement for BiP in Arabidopsis PRR-mediated immune responses has been difficult to elucidate because single mutants (bip1, bip2, or bip3) and a double mutant (bip1 bip2) all display normal EFR-mediated immune response (Nekrasov et al. 2009). Silencing of all three Arabidopsis BiP genes caused lethality (Hong et al. 2008). Therefore, the direct involvement of Arabidopsis BiPs in the biogenesis of EFR has not been demonstrated (Li et al. 2009). Similarly in rice, mutants silenced for BiP3, display no obvious phenotypes (Park et al. 2010). However, we have demonstrated that BiP3 directly interacts with XA21 in the ER and that transgenic plants overexpressing BiP3 are compromised in XA21-mediated immune responses to Xoo, highlighting the important role of BiP3 in the XA21-mediated immune response (Park et al. 2010). Here, we also show that overexpression of BiP3 compromises resistance mediated by the PRR XA3.

The rapid transcriptional induction and protein accumulation of ER chaperones including BiP in response to various pathogens and/or effector treatments (Caplan et al. 2009; Foster-
Hartnett et al. 2007; Fujiwara et al. 2006; Jelitto-Van Dooren et al. 1999; Zulak et al. 2009) suggests that BiP may also play a role in NB-LRR protein-mediated resistance. Supporting this hypothesis, confocal microscopy experiments examining Arabidopsis NB-LRR proteins found many of NB-LRRs to be localized to the ER (Caplan et al. 2009). Thus, the ER-resident NB-LRR proteins likely require ER chaperones for maturation (Caplan et al. 2009). Here we show that rice BiP3 overexpression does not affect Pi5-mediated resistance to M. oryzae. These results suggest that overexpressed BiP3 does not have a role in the biogenesis of Pi5 itself or in Pi5-mediated signaling. These data also indicate that BiP3 overexpression does not lead to a general ER stress response affecting resistance. Thus it is likely that other ER chaperones are involved in the Pi5-mediated immune response to M. oryzae.

This research has focused on BiP’s involvement in immunity mediated by the PRR XA3 and the NB-LRR Pi5 protein. Rice plants overexpressing BiP3 are compromised in membrane-resident PRR XA3-mediated immunity to Xoo but not intracellular NB-LRR Pi5-mediated immunity to M. oryzae. These results suggest that BiP3 is involved in the biogenesis of other PRRs, rather than a general role in the resistance caused by non-specific ER stress.
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Competing interests

The authors declare no competing financial interests.

Authors’ contributions

C.J.P., J.S.J., and P.C.R. contributed to project design. C.J.P., M.Y.S., and C.Y.K. performed experiments. C. J. P., J.S.J., and P.C.R. wrote the paper. All authors discussed the results and commented on the manuscript.
REFERENCES


FIGURE LEGENDS

**Fig. 1.** Rice cultivar Kitaake does not carry a functional Xa3. (A) Kitaake plants were susceptible to *Xoo* strains PXO61 and PXO79. Kitaake and IRBB3 plants were inoculated with *Xoo* strains PXO61 or PXO79 at six-week-old age and a representative leaf was harvested 14 days after inoculation for photograph. (B) Kitaake plants developed long lesion lengths after inoculation with *Xoo* strains PXO61 or PXO79. Lesion lengths of Kitaake and IRBB3 plants were measured 14 days after inoculation. Each data point represents the average and standard deviation of at least three samples.

**Fig. 2.** Overexpression of *BiP3* compromises XA3-mediated resistance. (A) Lesion length developments of *Xoo* PXO61-inoculated segregants (F²) of BiP3ox/XA3. Each data point represents the average and standard deviation of at least three samples. BiP3ox/XA3 (*BiP3ox/Xa3, +/+*); BiP3ox (*BiP3ox/Xa3, +/-*); XA3 (*BiP3ox/Xa3, -/+*); Null segregants (*BiP3ox/Xa3, -/-*). (B) *Xoo* PXO61 populations in segregants (F²) of BiP3ox/XA3. For each time point, the bacterial populations were separately determined for three leaves. Capped, vertical bars represent standard deviation of values (cfu/leaf) from three samples. Experiments were repeated over two times with similar results. BiP3ox/XA3 (*BiP3ox/Xa3, +/+*); BiP3ox (*BiP3ox/Xa3, +/-*); XA3 (*BiP3ox/Xa3, -/+*); Null segregants (*BiP3ox/Xa3, -/-*). (C) and (D) Lesion length developments and bacterial populations after *Xoo* strain PXO79 inoculation.

**Fig. 3.** BiP3 overexpression does not affect the general defense response to *M. oryzae*. (A) Image of disease lesions on one leaf from Kitaake and BiP3ox 10 days after *M. oryzae* R01-1 inoculation. Plants were inoculated at five-week-old age and harvested for photograph. (B)
Lesion lengths of Kitaake and BiP3ox were measured 10 days after inoculation. Each data point represents the average and standard deviation of at least 30 samples.

**Fig. 4.** Overexpression of BiP3 does not compromise Pi5-mediated resistance. (A) Phenotype/genotype cosegregation analysis of a total of 64 segregating F₂ progeny \( [BiP3ox/Pi5; 43 (+/+), 6 (-/+), 13 (+/-), 2 (-/-)] \) derived from BiP3ox/Pi5 F₁ line in response to *M. oryzae* R01-1 inoculation. Detailed inoculation and genotyping methods are described in the materials and methods. (B) Lesion lengths of F₂ progeny derived from BiP3ox/Pi5 F₁ line in response to *M. oryzae* R01-1 inoculation. Each data point represents the average and standard deviation of at least 30 samples. BiP3ox \( (BiP3ox/Pi5, +/-) \); BiP3ox/Pi5 \( (BiP3ox/Pi5, +/+); Pi5 (BiP3ox/Pi5, -/+).
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