Supplemental Materials

Supplemental figure legends

Supplemental Figure 1. Inserts in four isolated plasmids (MST5-4, MST5-5, MST15-13 and MST15-34) conferring RNA tolerance.

Open box, ORF positions; Blank regions within boxes, introns.

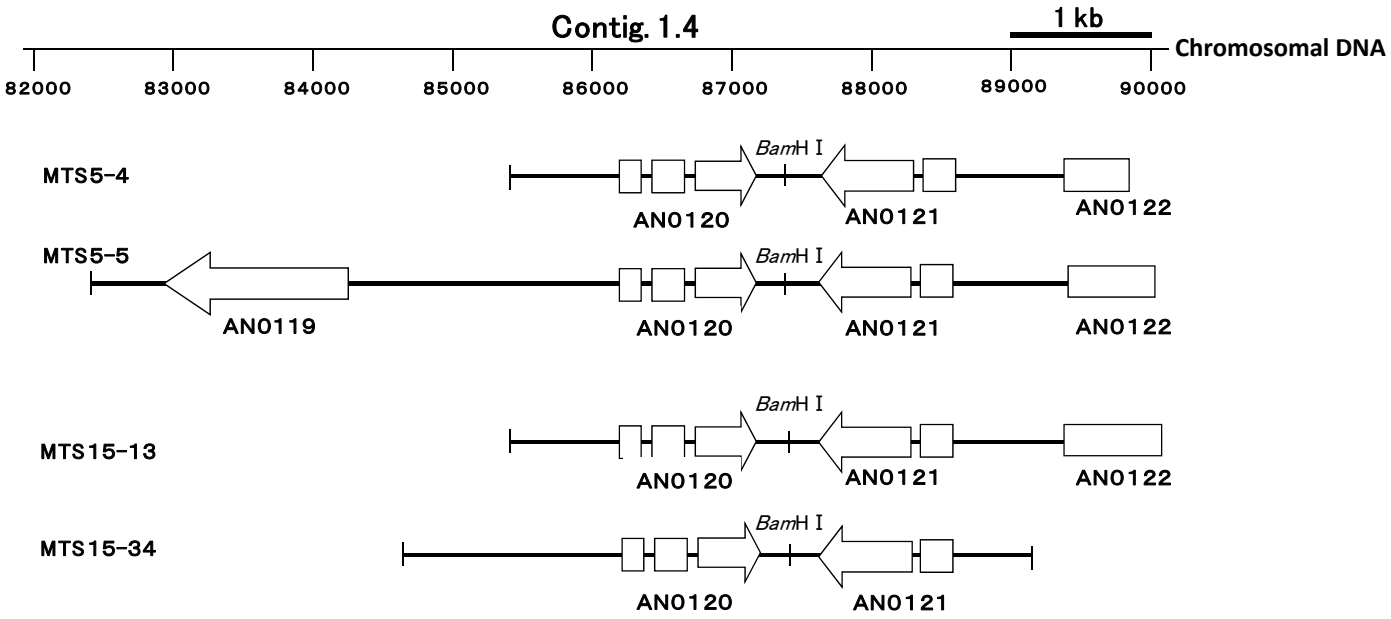
Supplemental Figure 2. Deduced amino acid sequence alignment of PBG-D from *A. nidulans* (A.n.PBG-D), *S. cerevisiae* (S.c.PBG-D) and *E. coli* (E.c.PBG-D).

Sequences were aligned using ClustalW. Black and white boxes, identical and similar amino acids, respectively.

Supplemental Figure 3. Southern blot analysis of ALC and Δ*fhb* gene disruptants. Restriction enzymes used to digest the genomic DNAs from parent and mutant strains are indicated. PalcA indicates the gene promoter of *alcA*. Black bars represent position of hybridization probes. P, parental strains; R, recombinant strains. Predicted size shifts are indicated in corresponding Southern blots.

Supplemental Figure 4. Growth of WT and ALC strains.

Colonies appeared on MM agar medium (pH 5.5) containing 25 mM $NaNO_2$ after incubating WT and ALC conidia at 37˚C for 48 h. Proline (Pro), methionine (Met) and ergosterol (Erg) were added to the medium at final concentrations of 5 mM, 10 mM, 10 mM, and 10 μg mL^{-1}, respectively.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MTS15-13
MTS15-34

Fig. S1

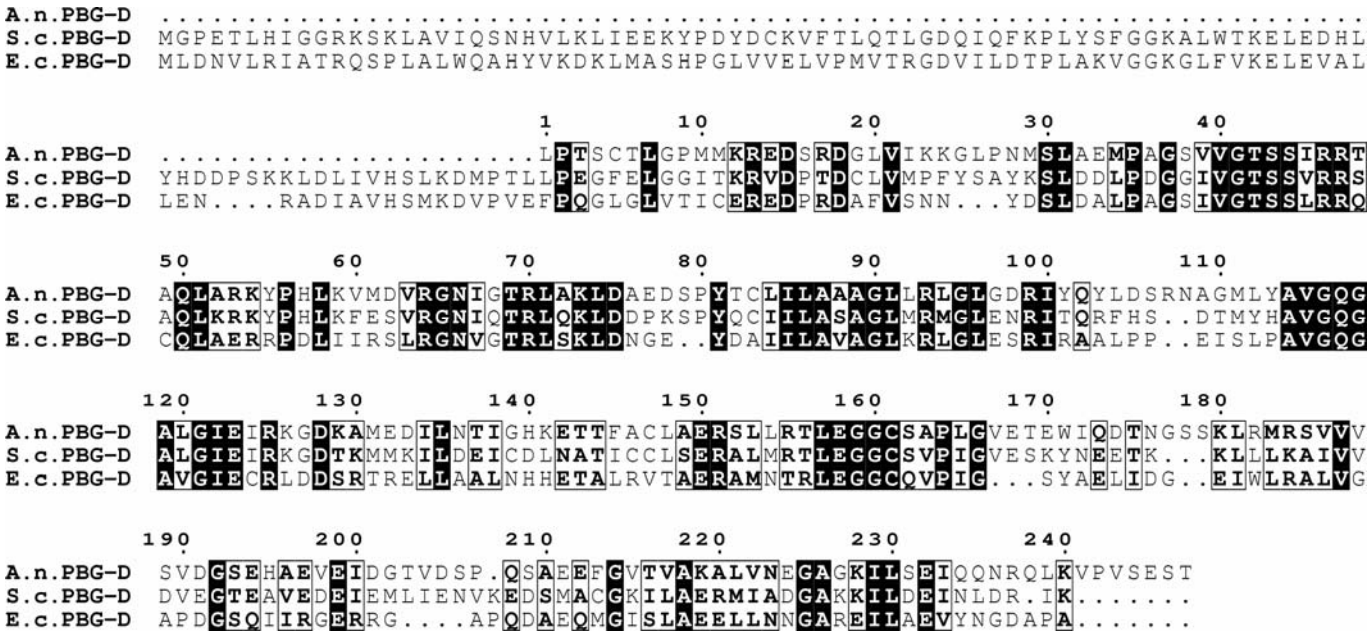
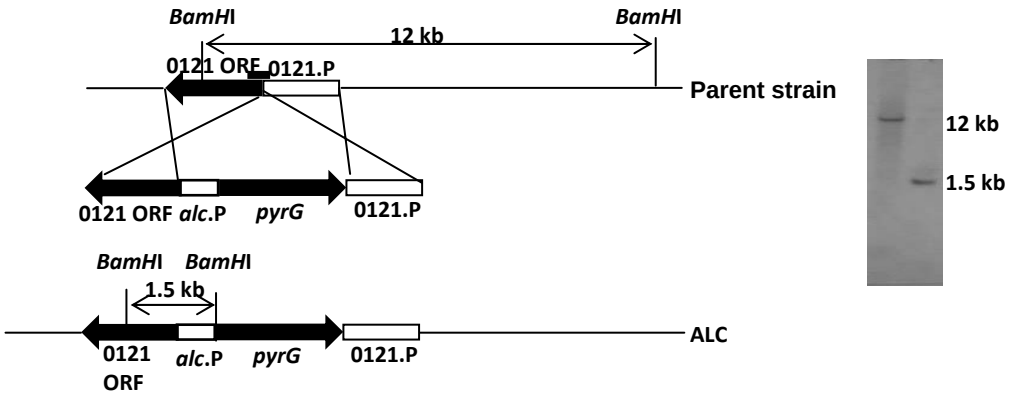


Fig. S2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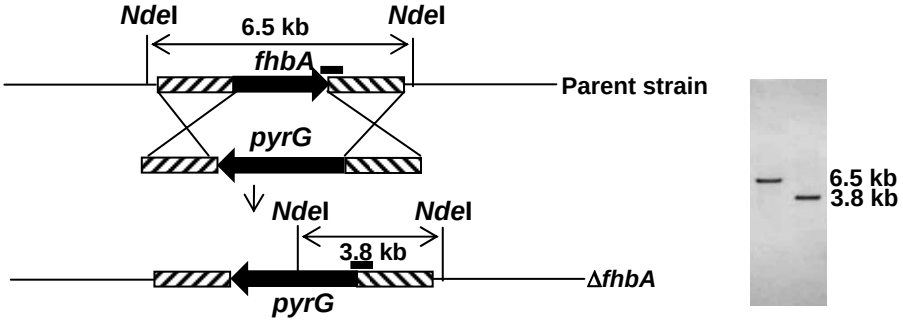
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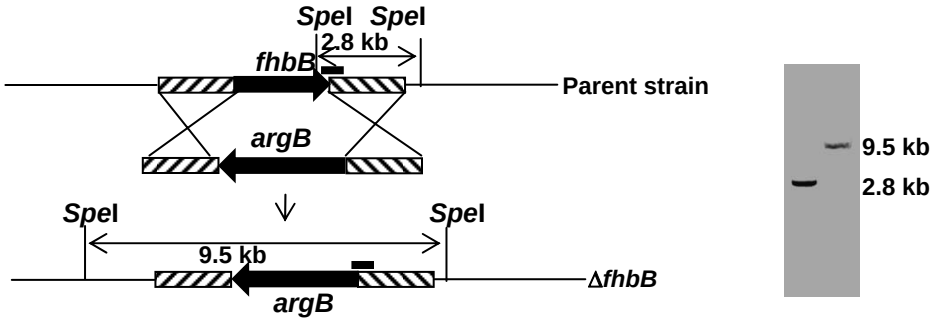
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Fig. S3

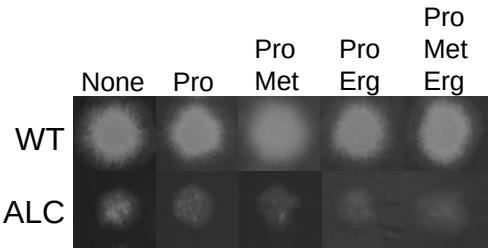

Fig. S4

Supplemental Table S1. Primers used in this study.

Primer name	Sequence (5′→3′)	Restriction enzyme
pyrG-F	TATCCCGGGGAATTCGATACCTGTCGAAAG	*Sma*I
pyrG-R	CATACCCGGGTCAGTGCTTGTCTACCAG	*Sma*I
argB-F	CCGGGGATCCAAGCTTTATTTCGCGGTTTTTTGG	*BamH*I
argB-R	ATTAGCATGCGTCGACCTACAGCCATTGC	*Sph*I
Δ*hemC*-1	GGCTGCAGCGGGATTTCATGCGATA	*Pst*I
Δ*hemC*-2	GGGATATCGTTGAGAGGCGTTTCT	*EcoR*V
Δ*hemC*-3	GGCCGCGGGGCAGCCTTCGATTTTAA	*Sac*II
Δ*hemC*-4	GGGCGGCCGCCTCTTGGGTTTGCTTCTT	*Not*I
Δ*fhbA*-1	GGGATATCATCTCCGTCACGAAGAAA	*EcoR*V
Δ*fhbA*-2	GCTGCAGCAACCTTATCAGCG	*Pst*I
Δ*fhbA*-3	CCTCTAGATTTCATCCACGGCGC	*Xba*I
Δ*fhbA*-4	GGGCGGCCGCGGTCGCAAACAAGTTGT	*Not*I
Δ*fhbB*-1	CTCGGAATTCCCAGGAACAGATTAAAACC	*EcoR*I
Δ*fhbB*-2	TGACTGTCGACATTAATCAGCGGAGCTGGGC	*Sal*I
Δ*fhbB*-3	TAGAGCATGCGCCCTTTGGTGATTTTGTGC	*Sph*I
Δ*fhbB*-4	GGCCCTGCAGTGTTCCGAATTACCTCGAAC	*Pst*I
alcA-F	GGGCGGCCGCGGGGCGGAAATTGACA	*Not*I
alcA-R	GCGGGGTTTGAGTTGTCATTTTGAGGCGAGGTGATAGGAT	
hemC-F	ATGACAACTCAAACCCCGC	
hemC-R	GGCCGCGGAAGAAACAAATGACGTTGTC	*Sac*II
ALC-probe-F	TTCTACAGCGGAACCGCCTC	
ALC-probe-R	AAGGTTGTCTCCTTATGACC	
Δ*fhbA*-probe-F	GAGCTGTCCATCACGGGAGC	
Δ*fhbA*-probe-R	GTTGATCGGTCGGTTCCCAC	
Δ*fhbB*-probe-F	CAGCCGCGACAGTACAGTCTG	
Δ*fhbB*-probe-R	TCAACGGCCCGCCTTCGGCG	
q-RT-*hemC*-F	CCAGTACTTGGACTCAAGGAAC	
q-RT-*hemC*-R	CTCAGCATGTTCACTACCATC	
q-RT-*fhbA*-F	CATGGCACCACCATCACCAAGG	
q-RT-*fhbA*-R	GGTTGTCGATATAGCTCGCG	
q-RT-*fhbB*-F	TATGCGACCAGTGCTCTC	
q-RT-*fhbB*-R	CGCTTGGTGCGAGGAGTTG	
q-RT-*niiA*-F	AACAGGCGGCAGAAGATCG	
q-RT-*niiA*-R	TGCGGTGCTCGAAGTACGAC	
q-RT-hemC-F	CCAGTACTTGGACTCAAGGAAC	
q-RT-hemC-R	CTCAGCATGTTCACTACCATC	
q-RT-*actA*-F	GAAGTCCTACGAACTGCCTGATG	
q-RT-*actA*-R	AAGAACGCTGGGCTGGAA	

Sequences corresponding to restriction enzymes are underlined.