

FIG S1 Phylogenetic relationships of Rad23 orthologs found in *B. bassiana* and other entomopathogenic or non-entomopathogenic fungi. The NCBI accession code of each protein and the identity of its sequence to the *B. bassiana* Rad23 are shown in the parentheses following each fungal name. The bootstrap values of 1000 replications are given at nodes. Scale: branch length proportional to genetic distance assessed with the neighbor-joining method in MEGA7 software at <http://www.megasoftware.net/>.

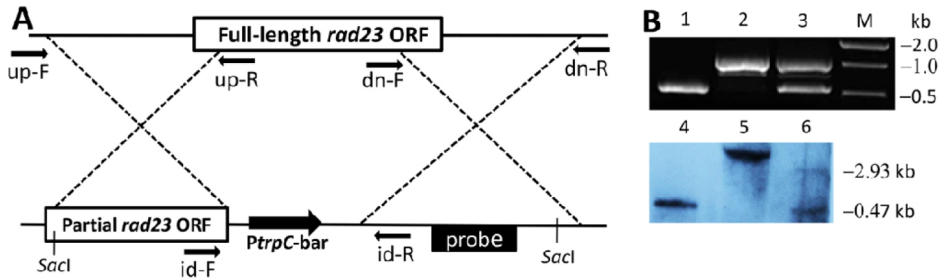


FIG S2 Generation and identification of *rad23* mutants. **(A)** Schematic diagram for the deletion strategy of *rad23* in *B. bassiana*. **(B)** The *rad23* mutants identified through PCR (lanes 1–3) and Southern blot (lanes 4–6) analyses with paired primers and amplified probe (Table S1). Lanes 1 and 4: wild-type. Lanes 2 and 5: $\Delta rad23$ mutant. Lanes 3 and 6: $\Delta rad23::rad23$ mutant. Genomic DNA of each strain was digested with *SacI* at the marked sites to probe *rad23* through Southern hybridization.

TABLE S1 Paired primers used for manipulation of *rad23* in *B. bassiana*.

Primers	Paired sequences (5'–3')*	Purpose
Rad23-F/R	<u>ATTCAATCACAAACACCTTCAAATGAAGGTCACCTTCAGAGATCTCA</u> / <u>TCCTCGCCC</u> <u>TTGCTCACCA</u> TTGGCTCGCAGGCGGCTGCTCGTCC	Cloning <i>rad23</i> cDNA (1134 bp) for fusion to <i>mCherry</i>
Rad23up-F/R	<u>TGGGCCCGCGCGCC</u> <i>GAATTC</i> CAAGCGTAGCCGAAGCC / <u>TGGCTGCAGGTCGACGG</u> <i>ATCC</i> TGCGTGGTTGATTGAGTA	Cloning <i>rad23</i> 5' fragment (1355 bp) for <i>rad23</i> deletion
Rad23dn-F/R	<u>GACCCATGGCTCGAG</u> <i>TCTAGA</i> AAGGAACGCATTTCTACCG / <u>GGTGGTGGTGGCTAG</u> <i>CGTTAACT</i> CCCCGATTACTCGTTGTGC	Cloning <i>rad23</i> 3' fragment (1552 bp) for <i>rad23</i> deletion
Rad23fl-F/R	<u>GGGGACAAGTTTGTACAAAAAAGCAGGCTCACCACCACAAGAAACAGC</u> / <u>GGGGA</u> <u>CCACTTTGTACAAGAAAGCTGGGTGCATAGGATTCGGCGTAG</u>	Cloning full-length <i>rad23</i> (4767 bp) for complementation
pRad23-F/R	CCATCAAACGCCAACCC / TGTTTCGTCCGCACCTGA	PCR detecting <i>rad23</i> (565/1090 bp)
sbRad23-F/R	CCCGCAGTGAATCACATTTTGGC / TGTGGAGGCGTTTCGATTTGACTT	Southern probe of <i>rad23</i> (283 bp)
cPhr1-F/R	CAATCACAAACACCTTCAAATGGCGCCTCGTCAACGAAGCG / CTTGCTCACCATG AATTC_GATATCCTACGCCACAGCCGCTTGTACGCA	Cloning <i>phr1</i> cDNA (1764 bp) for yeast hybrid
cPhr2-F/R	CAATCACAAACACCTTCAAATGACAAAGCCCAGAGTCATTTATT / CTTGCTCACCAT GAATTC GATATCTCACGTTTTCTGCTTCTTCGCTGAC	Cloning <i>phr2</i> cDNA (1872 bp) for yeast hybrid and overexpression

* Bold regions in italics denote the restriction enzyme sites for deletion of *rad23* (*EcoRI/BamHI* and *XbaI/SpeI*).

Underlined regions denote the fragments for *rad23* fusion to *mCherry*, homogenous recombination of *bar*-separated 5' and 3' fragments for targeted gene deletion or the gateway exchange fragments for targeted gene complementation.

TANLE S2. Paired primers used for transcriptional profiling of phenotype-related genes via qPCR.

Gene	Tag locus*	Annotation	Sequences (5'–3') of paired primers
Used as internal standard			
<i>actin</i>	BBA_04860	β-actin	GGCAACATTGTCATGTCTGG / TTTGCTGGAAGGTGGATAGG
<i>tef</i>	BBA_02388	translation elongation factor 1 alpha	TGAGGCTTTCACCGACTACC / TTATTCTTGGTGGCCTGG
Involved in photoreactivation			
<i>rad23</i>	BBA_01030	UV excision repair protein Rad23	AGCAGAAATTCACCTCGAA / ACGAAGCCCTTTCTCTCAAT
<i>phr1</i>	BBA_01664	CPD photolyase	AAAAAGAGAATCCGCTTCTCACTTACA / AAAAAGCCAGTAGCCTTATTATCTTG
<i>phr2</i>	BBA_01034	6-4 PP photolyase	AAAAAGTTCACATCATTTCTCCACCAC / AAAAAGCTTCGACCCGACGATCT
Involved in response to oxidative stress			
<i>sod1</i>	BBA_02311	Cytosolic Cu/ZnSOD	GCGGCTTCCACATCCACACCTTTG / GGTCCAGCGTTGCCAGTCTTGAG
<i>sod2</i>	BBA_09706	Cytosolic MnSOD	CCAGTGTTTGGCATTGACATG / TCAGCCGCTTCCAGTTGATG
<i>sod3</i>	BBA_09382	Mitochondrial MnSOD	TCTCCGGCAAGATTATGGAGC / TTGGCGTCATTCTTGGCCT
<i>sod4</i>	BBA_04317	Mitochondrial FeSOD	CGAGATGGTCTTACGGCTTACG / GCTCCAGGTGTTGAGGCATAG
<i>sod5</i>	BBA_01984	Cell wall-anchored Cu/ZnSOD	CGGCGACCTCAGCGGCAAGTAC / GCCAGCAACAACAGGGACCGTAGG
<i>cat1</i>	BBA_06186	Catalase A	CCGTCTGGGCATCAACTGGGAAG / GCTGGGCGTGGTCTGGTAG
<i>cat2</i>	BBA_05603	Catalase B	CCTCTGACGTTGGCGGCCCTTTC / CCGTGTCCGTGCTGCCTCGTG
<i>cat3</i>	BBA_09109	Catalase C	GAGGAGCCACAGCAACGCACAAGAG / TGAGGACGACAAGGCCGCCATTC
<i>cat4</i>	BBA_09760	Catalase D	CGGCTGCGGTGTCTTGTCCATAC / CCTTGTGCGCGTTCTGGCGAAG
<i>cat5</i>	BBA_09338	Catalase P	GCTGGGCTGATCTGCTGGTCTTG / TCCTTGCTGTAACGGTGGCTGTGCG
<i>cat6</i>	BBA_06567	Catalase-like protein	TCAAGTCGGTTCAGGAGATGGAG / TTGTTGCGTCTTCAATCGGAGTG
Involved in hog pathway			
<i>ssk2</i>	BBA_00937	MAP kinase kinase kinase Ssk2	TCAGACCTGCTTCGTGTTTG / GAATGTGTCGTCCACGTGTC
<i>pbs2</i>	BBA_02330	MAP kinase kinase Pbs2	ATTTGCGACTTTGGCGTTAG / AAGACTCCACACGTGCTCT
<i>hog1</i>	BBA_05209	MAP kinase Hog1	ATACTACCGCGCTCCTGAGA / CTGGCAATGGTGTGATGAC
Involved in asexual development			
<i>brlA</i>	BBA_07544	Development activator BrlA	GACCCAGTTCACAGACAAG / CAGTAATCTTCGTGCTTCTC
<i>abaA</i>	BBA_00300	Conidiation factor AbaA	GCAAGTCTCCAGCCATAT / CTCCTCTTCGTATAGTAGTC
<i>wetA</i>	BBA_06126	Conidial maturation factor WetA	CGCAGACGAATTTGACTT / GCTGGTGGTTGAATACAT
<i>fluG</i>	BBA_04942	Developmental protein FluG	CCATCAGGATACATCGTCTT / AGATTCATAGTCTCCGCTAA
Involved in DNA damage repair			
<i>asf</i>	BBA_01428	ASF1-like histone chaperone	TAAGTGTGGTCTTCTGA / GAGTCGATTCTGTGTTTC
<i>chk2</i>	BBA_06016	Checkpoint kinase 2	CGAATCGTCACTGCTTAA / GTTCCGTTGCTGGATAAG
<i>mec1</i>	BBA_02334	Putative protein kinase MEC1	AGGCACGACAAGAGAATA / TGAGAAGTGACAGGATGG
<i>PCNA</i>	BBA_00352	Proliferating cell nuclear antigen	GGTCAAGATTTGCTGTC / GTAGAAGTGACAGGATGG
<i>rad4A</i>	BBA_02814	Rad4 transglutaminase-like protein	CCTAGTGAGGAGCCACAAGC / GACGTCCTGGAACCAAGT
<i>rad4B</i>	BBA_02963	Rad4 transglutaminase-like protein	CGGACAAACCCGAGATAAAA / GAGCTCTTCCCTGTTTGTGTC
<i>rad52</i>	BBA_06117	Putative recombinase RAD52	AAGTCTTGCGTCGTTATC / GCTATCAGTGTTCCTTCA
<i>rad53</i>	BBA_00126	Putative protein kinase RAD53	AACATCCTCATCAACTCTC / ATCGCTGTAATCATCTT
<i>tell</i>	BBA_02241	PDNA-binding protein kinase TEL1	AATATGATTGATGAGTGGGAAG / AAGAATGATGCGGTAGAA
<i>top1</i>	BBA_00975	Topoisomerase I	AATACGAGCACATAACTT / GTCTCATTGTAGCGAATA
<i>yku70</i>	BBA_06892	DNA helicase YKU70	CGGTCGCTATTCTCTAAT / GCTTGTCTGTAATGATG

* Gene accession codes of *B. bassiana* genome under the NCBI accession NL_ADAH00000000.