

Table S1 Primers used in this study.

Primers	Paired sequences (5'–3')*	Purpose
P1/P2	<u>ACGAGCTGTACAAGTAACCCGGAAGTAAAGCCG</u> AAGAGTG/ <u>CTCGGTACCAAGCTTGGCTGCAGTTTGTCTTGGG</u> TATGGG	Amplifying 5'-fragment of <i>BbSdhC1</i>
P3/P4	<u>ACCCATGGCTCGAGTCTAGACTGTCTGGCGTGGC</u> GTAT / <u>GTGGCTAGCGTTAACTAGT</u> TCCGAGAATGAAGTCCGC	Amplifying 3'-fragment of <i>BbSdhC1</i>
P5/P6	<u>ATCCGTCGACCTGCAGCCAAGCTTTCGAGTAAG</u> TAATGCTTTCTATG / <u>ACACTAGTCAGATCTTCTAGTGTCCATAACGGAA</u> CGACTACAATA	Cloning the <i>BbSdhC1</i> full ORF for gene complementation
P7/P8	GCATCGTGTCCACCTACC / AAGCCCCTTTCGCTCCAT	Screening transformants
P9/P10	TCGGTCGTATGATAGGATGATTT/TTAACGTGCAT AGCGAGTGGAAC	Preparing <i>BbSdhC1</i> probe
P11/P12	<u>AAGCTTGAATTCGAGCTCGGTAATCTCGCTCGGCT</u> GTCCT / <u>ACACTAGTCAGATCTTCTAGTGTGCTTGTAGTTCG</u> CATTCC <u>TGGGCCCGGCGCGCCGAATTC</u> CCCCCTTACAACA	Amplifying the promoter of <i>BbSdhC1</i> for Y1H test
PL _{BbSdhC1} F/R	ACCAT/ <u>TGGCTGCAGGTCGACGGATCCTTGATAGCCTGGT</u> CCTGA	Amplifying <i>BbSdhC1</i> cDNA
P BbSdhC2 ^F / R	<u>GACCCATGGCTCGAGTCTAGAGCACCGACCTCGC</u> TGAAA/ <u>GTGGCTAGCGTTAACTAGTGTCCGTCGCCATCC</u> TCTT	Amplifying <i>BbSdhC2</i> cDNA
P13/P14	TCAGGCGTCTCCGTCTTGAG/CAGTGATGAGCAGA TGGA	qRT-PCR for <i>BbSdhC1</i>
ActinF/ R	GGCAACATTGTCATGTCTGG/TTTGCTGGAAGGTG GATAGG	Reference in qRT-PCR

*: The underlined region is required for homologous recombination during plasmid construction.

Fig. S1 Sequence alignment of the SdhC homologs. Multiple sequence alignment was performed by ClustalW software. Abbreviations for fungal species are shown as follows, Sc: *Saccharomyces cerevisiae* S288C; Ca: *Candida albicans* 12C; Sp: *Schizosaccharomyces pombe*; Af: *Aspergillus fumigatus* Af293; Po: *Pyricularia oryzae* Y34; Nc: *Neurospora crassa* OR74A; Bb: *Beauveria bassiana* ARSEF 2860; Cm: *Cordyceps militaris* CM01; Bbr: *Beauveria brongniartii* RCEF 3172; Mr: *Metarhizium robertsii* ARSEF 23; Ma: *Metarhizium acridum* CQMa 102.

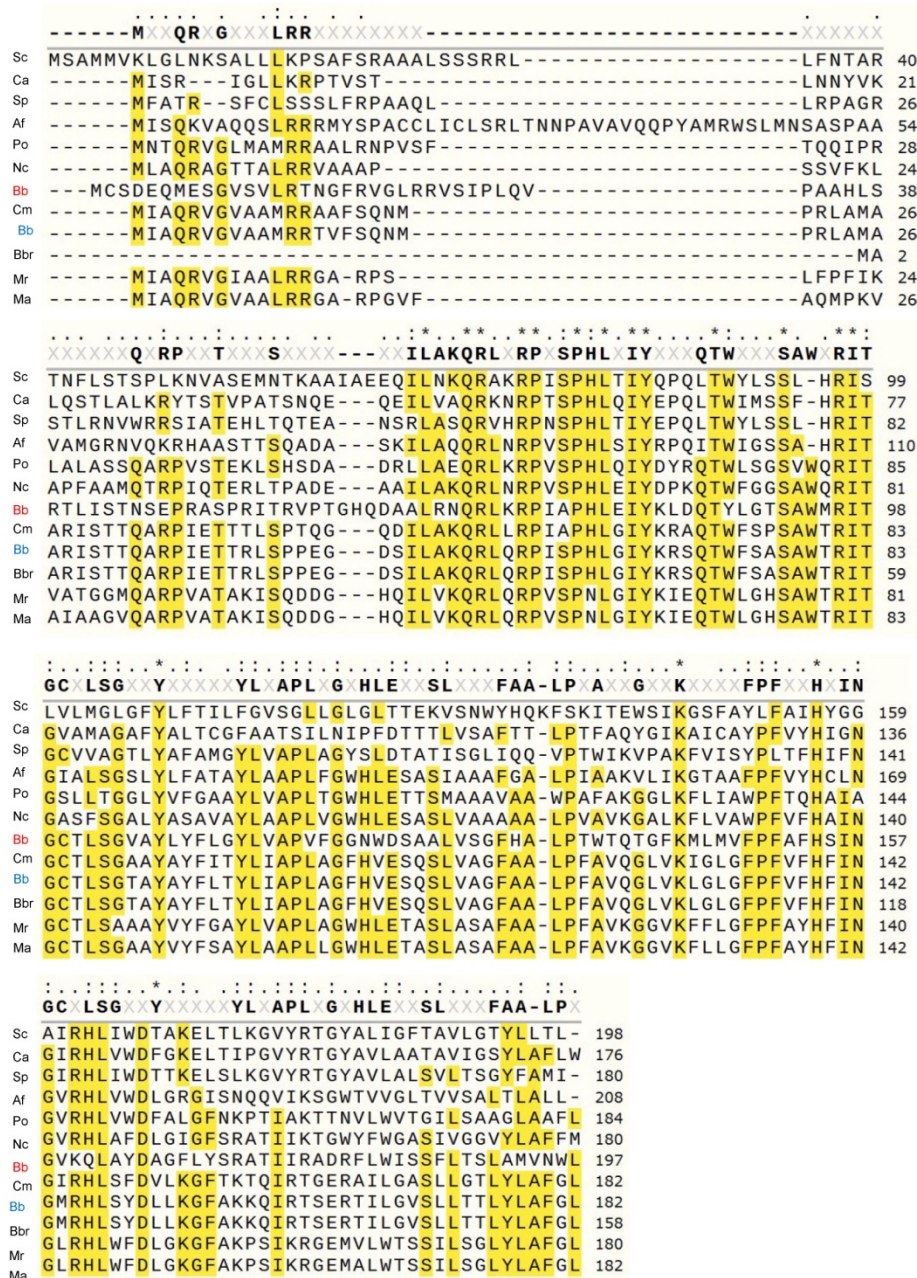


Fig.S2 Gene disruption and complementation in *B. bassiana*

(A) Schematic diagram deciphering the homologous recombination for gene disruption in fungal genome. The correct gene disruption and complemented mutants were screened by PCR reaction (B) and further confirmed by Southern blotting (C). In panel (B), lane 1, 2 and 3 are the wild-type, $\Delta Bbsdhc1$, and complementation stains. Lane M: DNA marker. In panel (C), lane 1, 2 and 3 are the $\Delta Bbsdhc1$, wild-type, and complementation stains. The electrophoretic positions and sizes of the DNA bands are indicated.

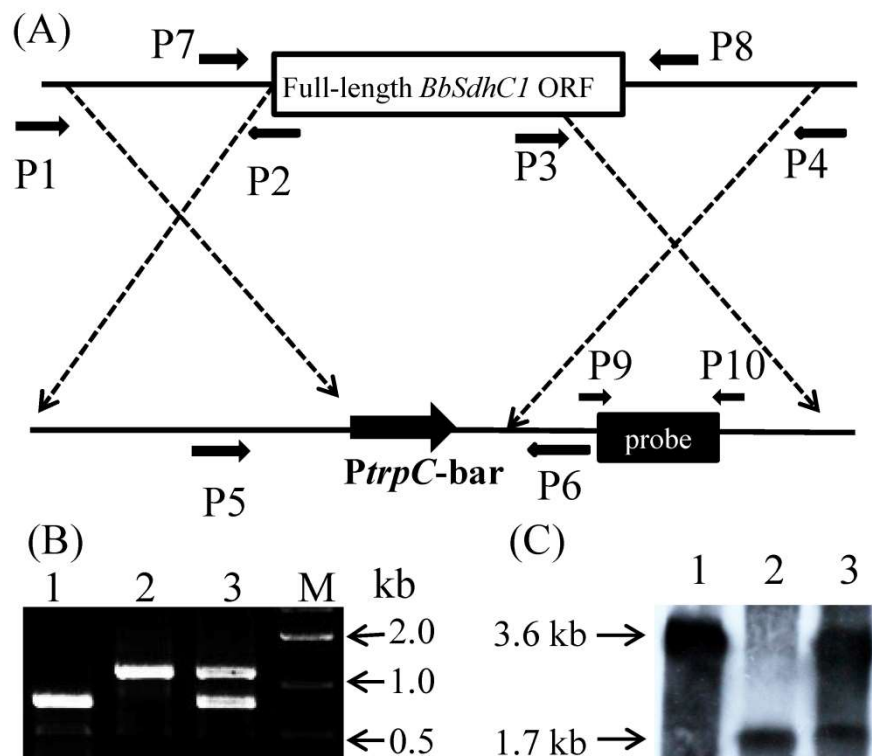


Fig. S3 ROS content in aerial mycelia of *B. bassiana*

(A) After cultured on SDAY medium for 4 days, the hyphae of $\Delta Bbsdhc1$ mutant, the wild-type and complemented strain were collected and stained with DHE. Green fluorescence signals of each strain were observed under laser scanning confocal microscope. (B) The fluorescence intensity among strains was subjected to Mann-Whitney analysis and significance (indicated with an asterisk) was determined when p value is less than 0.05.

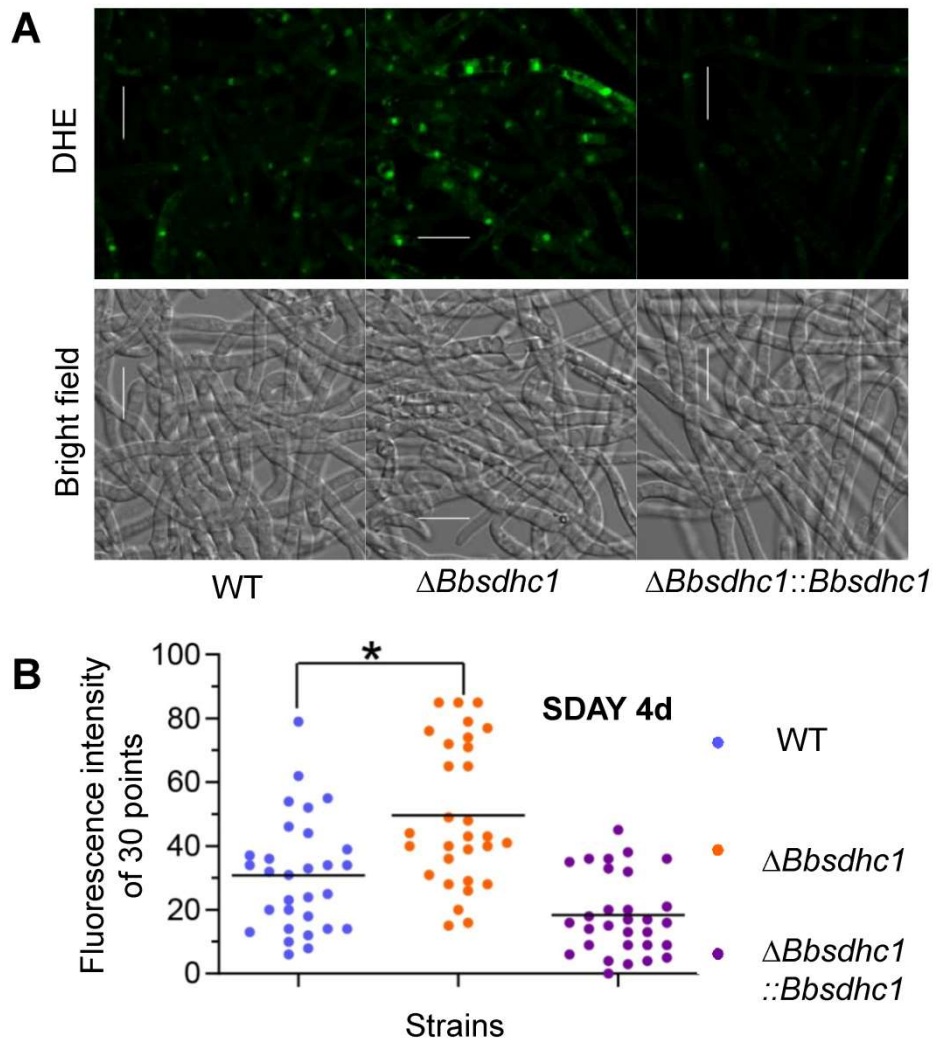


Fig. S4 Analyses of the promoter region of *BbSdhC1*. No typical *MluI* sites in the promoter of *BbSdhC1*, but the similar sites are present.

ATCTCGCTCGGCTGTCCTGGCCGTCCAAGCTGCGACTTCTTTCAAACCCCTCCATCTGCTCTGGCGGGC
GTGACGCAGGCTGCAGTGGCGTGTGGACTGGACCAGGCGCCACAGCATTGACGCGAATGCCCTTTGG
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TTTCGTAATGGCAAACATTTGCAAAATGTTGCTCCTGAATGTGCTCTCAACATCGTCGAGGTTTATTTCA
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ACATGCTTTTCGACAGCCTGGAGACAGGTTTTGTTGTCCATTAGATCACCCGCAACCAAGAGGCACCTTTC
CGCCCTCCTTTCCACCATTTCTTCGTATCGTTGGCGTCTTGCTCCTCCTCTGGCAGGTACACAATCGTC
ACGTCGGAGCCTTCTCTGGCAAACAAGACGGCAATTGAGCGACCGATGCCAGAGCTGTAAAGTCAATC
AATAATTGCTAACCCAGAACGAGCAAGGGGAAGAACTGAGCTACTCACTCGCCACCTGTAATGAGAG
CCTTGTTCCTTTCAATTTGCCCGCAGCAAGATATTCATGGTGTCTTTGCCCTCGAGCTTAGTAGA
CTCGCTGGACGGCGCCATGTCCCTTCGGACCTAGAAAAAAAAAACAGTTAGTGTGCTGCTCTCATGT
ATGCATCGTGTCCACCTACC CGGGGAGATTCTGGGCTTGAGCCTGAGGAACAGGCTTGAAGCCACCAC
CTTCGGACTTGGACATGGAGAATGGTACGATAGAAAAATAGCGTGAATAATTCTTGATGAGAATTGA
GTGTGTAACCCGGCACGGAAATTGCAAATTGATAGCCTGGTCCTGATGTGACTAGCTGGGAGTTTGAT
GAGATTGATACGTGATGGGTGCATGGCGGGCTTTTGTAGTAGACTGAGCAGACCTGGCCCATACCCAA
GACAAACAGTTTTATCCTGATTTTAACAAGTCAAATAGGCCAATGAATTCAGGGAATGCGAACTACAAG
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