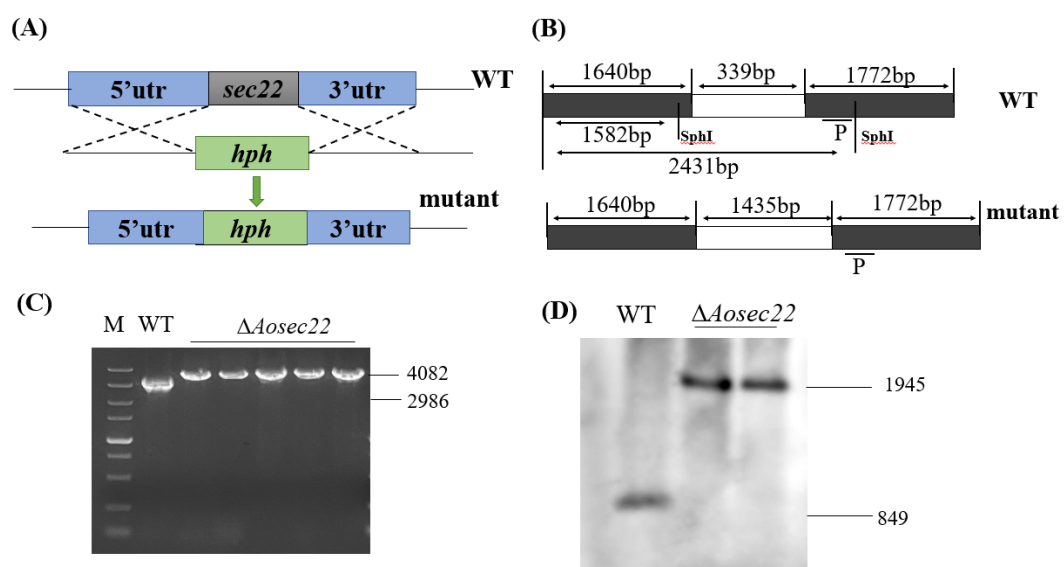
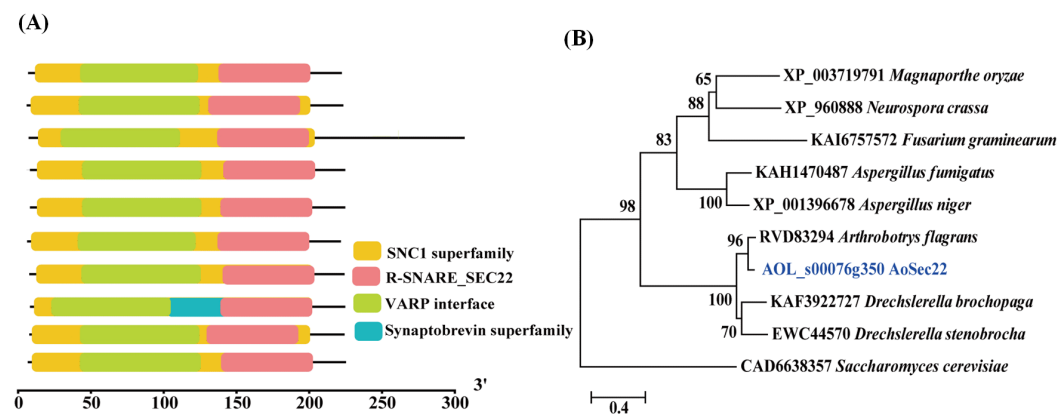


Supporting Information



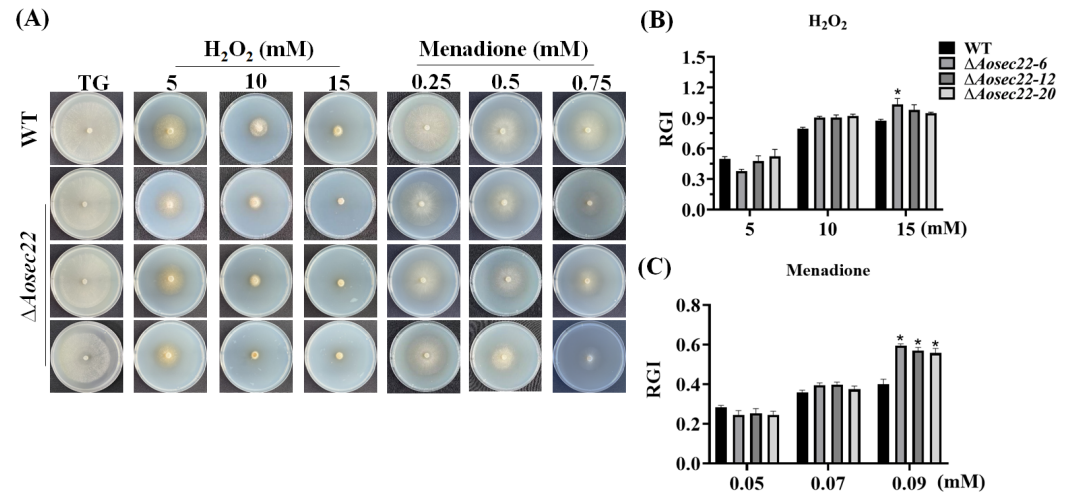


Figure S3. Comparison of oxidative stress responses between WT and $\Delta Aosec22$ mutant strains. (A) Colonial morphology of fungal strains under oxidative stress. (B) Relative growth inhibition (RGI) of fungal colonies after being grown for 6 days at 28 °C on TG plates supplemented with different concentrations of H₂O₂ and menadione. An asterisk indicates a significant difference between $\Delta Aosec22$ mutant and the WT strain (Tukey's HSD, $p < 0.05$).

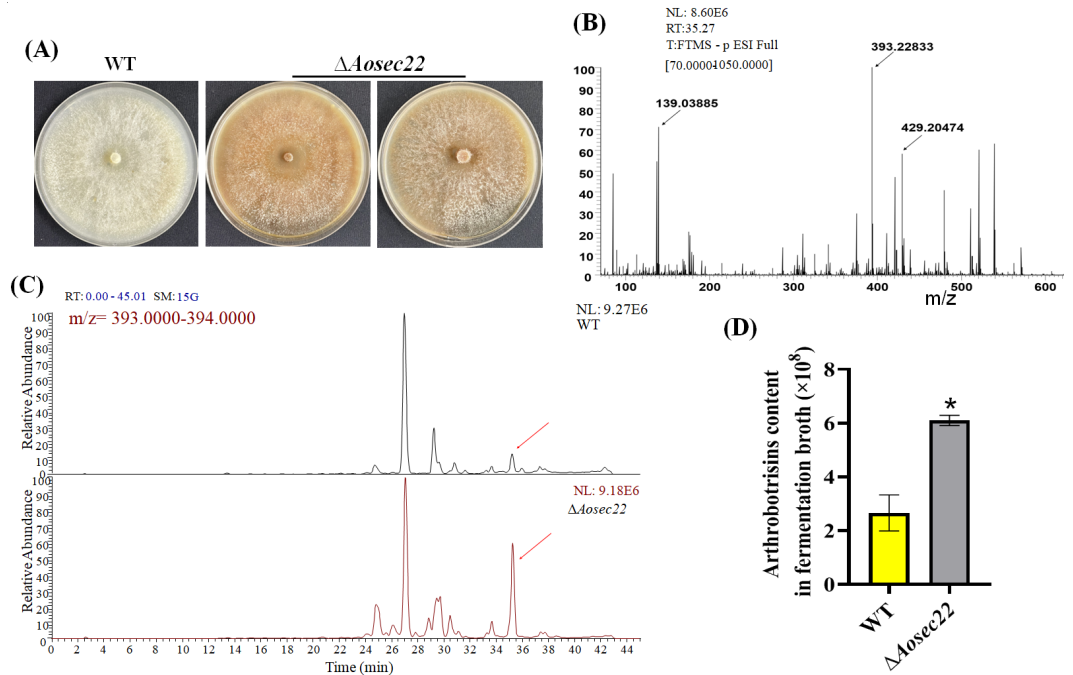


Figure S4. Comparison of the color of colony and the content of arthrobotrisins. (A) The WT and mutant were incubated on PDA medium for 10 days. (B) Mass spectrogram of arthrobotrisins in the WT strain (diagnostic fragments ion at m/z 139, 393, and 429). (C) Mass spectrogram of arthrobotrisins in the WT and $\Delta Aosec22$ strains (diagnostic fragments ion at m/z 393.0000-394.0000). RT = 35.12 min. (D) The quantification data for arthrobotrisins.

Table S1. List of primers used for gene manipulation in this study.

AoSec22-5F	GTAACGCCAGGGTTTTCCAGTCACGACGACTCCTGCTGATTGTCCT	Amplify the <i>AoSec22</i>
AoSec22-5R	ATCCACTTAACGTTACTGAAATCTCCAACCTTTGTACTGCTGGAGAT	gene 5' flank
AoSec22-3F	CTCCTTCAATATCATCTTCTGTCTCCGACCAAGGGTTATGACGAAGA	Amplify the <i>AoSec22</i>
AoSec22-3R	GCGGATAACAATTCACACAGGAAACAGCTCCGAAGTTTGCGTGTCT	gene 3' flank
Hph-f	GTCGGAGACAGAAGATGATATTGAAGGAGC	Amplify the <i>hph</i>
Hph-r	GTTGGAGATTTCAGTAACGTTAAGTGGAT	cassette
YZ-Sec22-F	GCACTCCAGACACCACCT	Verify the
YZ-Sec22-R	CAGCCACATAACCGTCCC	transformants
Probe-Sec22-F	CAAGGGTTATGACGAAGA	Make Southern
Probe-Sec22-R	CTGAGTCAGATCCGTTCC	blotting probe

Table S2. Paired primers for RT-qPCR analysis of genes associated with phenotypes such as conidiation and fatty acid oxidation in *A. oligospora*.

Description	Gene name	Sequence (5'-3')
Sporulation-related genes	AOL_s00007g157 (<i>flbC</i>)	flbC-5F-CTCTCCGGCAAAGACAATCG flbC-3R-GTCGACTGAGGATAGTAGCT
	AOL_s00043g361 (<i>fluG</i>)	fluG-5F-GATTCCAGTCCCGTGAATTC fluG-3R-GCTAAGGAGAGGATGGGCAT
	AOL_s00080g63 (<i>abaA</i>)	abaA-5F-AACTTTATGCGCCTTGTCGT abaA-3R-TTGGCTAGGTGGTCTGTACG
	AOL_s00054g811 (<i>velB</i>)	velB-5F-ATTCGCAACTTCTCCCTCA velB-3R-GGCATGTTTGGATTCTGGGG
	AOL_s00097g514 (<i>brlA</i>)	brlA-5F-AACTCCATCACCATCCGTAA brlA-5R-CAGGATATTCGGCACTCA
	AOL_s00173g221 (<i>wetA</i>)	wetA-5F-CCCTGTGCTACTATTGTAC wetA-5R-CCGTTGCGAGCATTCTT
β-tubulin gene	AOL_s00076g640 (<i>tub</i>)	tubA-F-CCACCTTCGTCGGTAACTC tubA-R-TCGTCCATACCCTCACCAG
Genes related to fatty acid oxidation	AOL_s00004g288	288-5F-AAGAAATCCCACTTCAGAGAGG 288-3R-TACGTGTCCAGTAACATAGCTC
	AOL_s00081g51	51-5F-GCCGATCCTTACCAAATCATTC 51-3R-CCAATTCTTTCCGTAGCTGAG
	AOL_s00210g122	122-5F-GCCGCACATATTGTTAACAGAT 122-3R-TGATCTTGCTGTCTCAGTCAT
	AOL_s00110g113	113-5F-CTAACAGAACTCAAGCATCGG 113-3R-GGAACCGGATTCATGAAATGAG
	AOL_s00079g276	276-5F-AACAATCCGTCGTTATTGTTC 276-3R-GCGATCATGTAGTCTAGTCCTC
	AOL_s00054g29	29-5F-GGTATCTACGAAATTTTGCC 29-3R-GTGCAATATAATCGGGCTTGAG
	AOL_s00004g606	606-5F-TTCGGATTGTTATTACCTCCC 606-3R-TAACATGAGTCGCTTGTGTTG