

Supporting Information

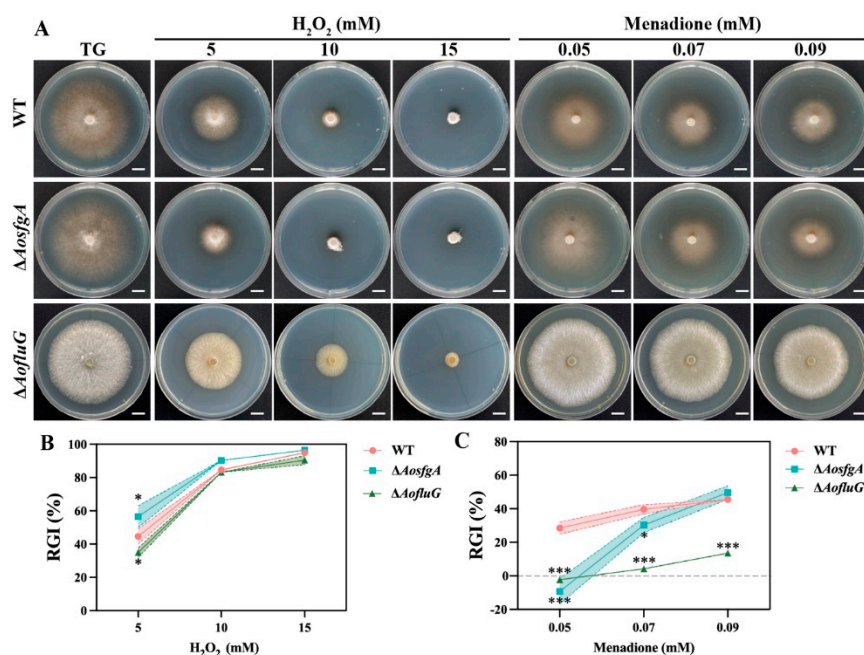


Figure S1. Comparison of stress response to oxidative reagents between WT, $\Delta AosfgA$ and $\Delta AofluG$ mutant strains. **(A)** Colony morphology on the medium supplemented with different oxidants. Bar = 1 cm. **(B, C)** Comparison of RGI values under H_2O_2 (B) and menadione (C). Asterisks indicate that the mutant strain significantly differs from the WT strain (Tukey's HSD, $*p < 0.05$, $***p < 0.001$).

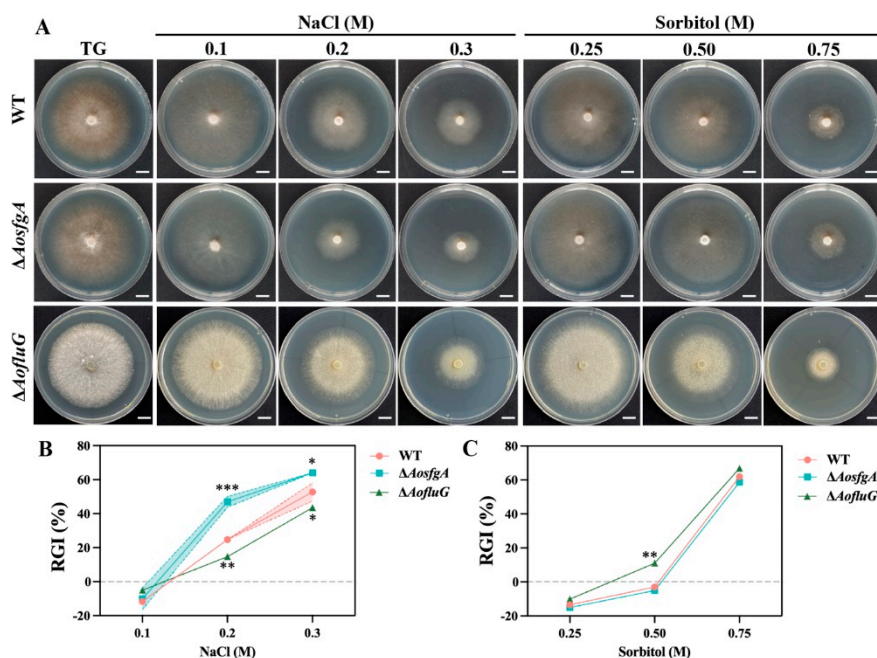


Figure S2. Comparison of stress response to osmotic reagents between WT, $\Delta AosfgA$ and $\Delta AofluG$ mutant strains. **(A)** Colony morphology on medium supplemented with different high osmotic chemical reagents. Bar = 1 cm. **(B, C)** Comparison of RGI values under NaCl (B) and sorbitol (C). Asterisks indicate that the mutant strain significantly differs from the WT strain (Tukey's HSD, $*p < 0.05$, $**p < 0.01$, $***p < 0.001$).

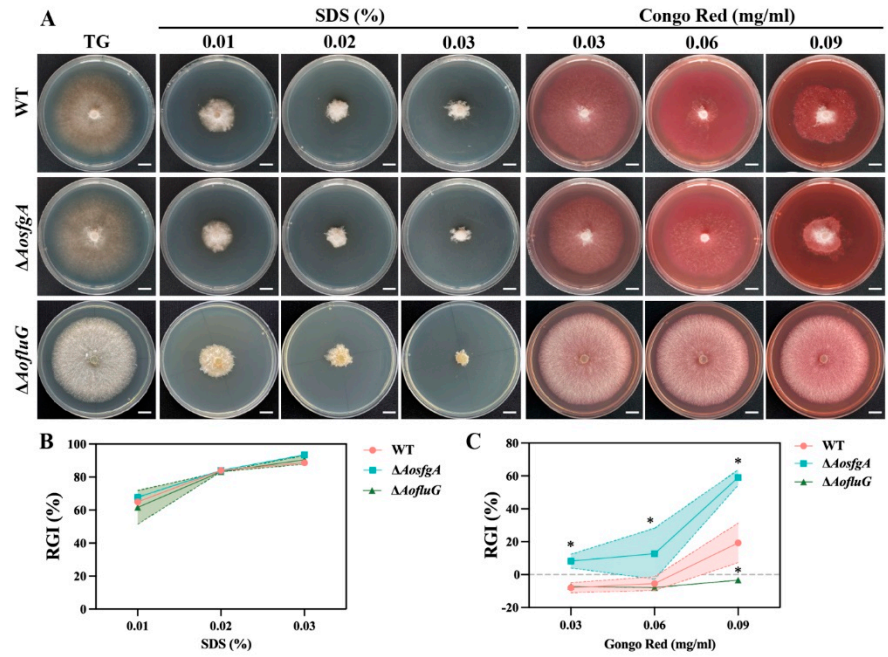


Figure S3. Comparison of stress response to cell wall synthesis-disturbing reagents between WT, $\Delta AofgA$ and $\Delta AofluG$ mutant strains. **(A)** Colony morphology on medium supplemented with different cell wall synthesis-disturbing reagents. Bar = 1 cm. **(B, C)** Comparison of RGI values under SDS (B) and congo red (C). Asterisks indicate that the mutant strain significantly differs from the WT strain (Tukey's HSD, $*p < 0.05$).

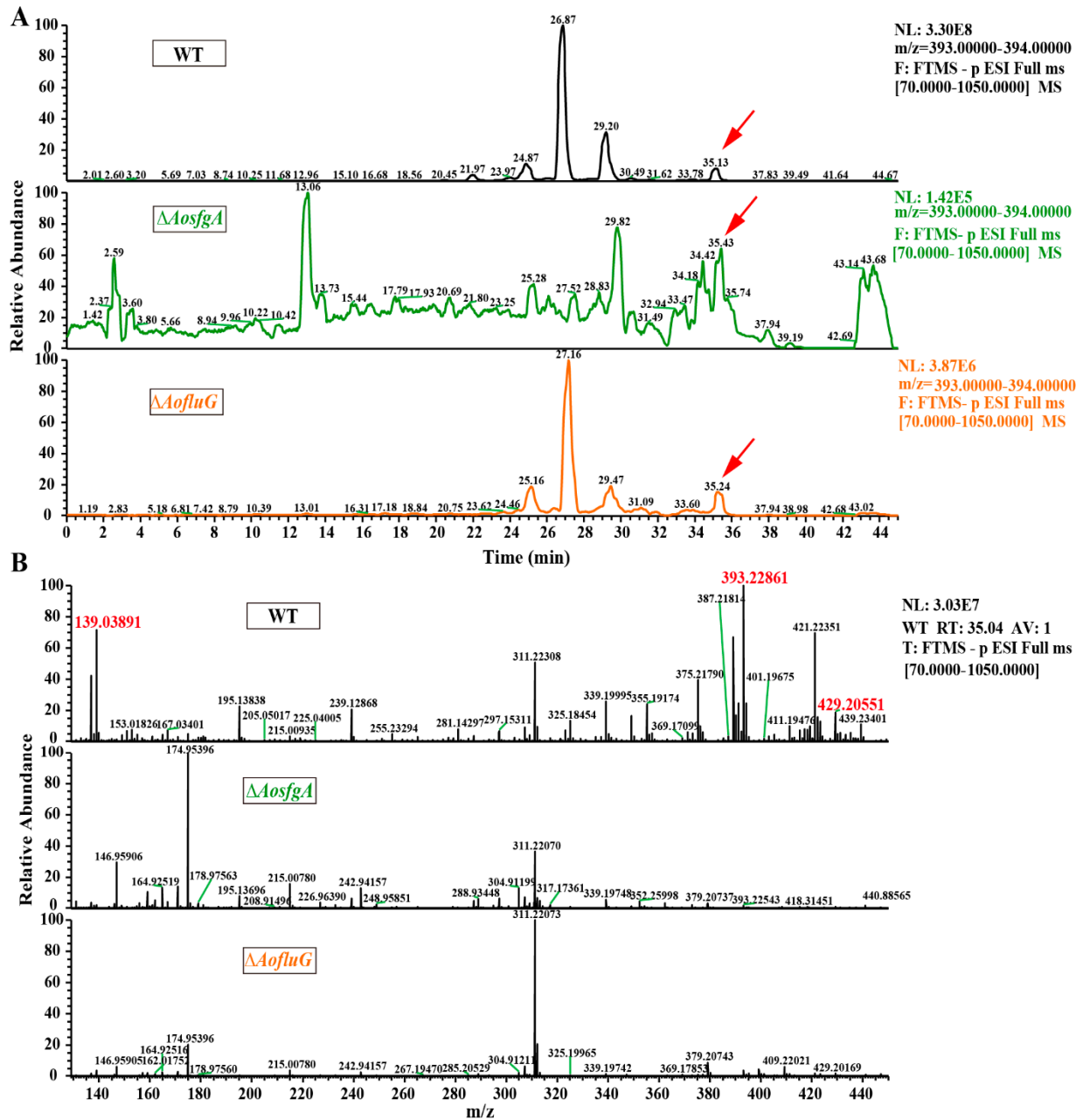


Figure S4. Detection of arthrobotrisins of WT, $\Delta AofluG$ and $\Delta AofluG$ mutant strains. **(A)** Chromatographic analysis of arthrobotrisins in WT, $\Delta AofluG$ and $\Delta AofluG$ mutant strains. **(B)** Mass spectrum analysis of arthrobotrisins in WT, $\Delta AofluG$ and $\Delta AofluG$ mutant strains. The diagnostic fragment ions (at m/z 139, 393, and 429) of arthrobotrisins was found in the WT strain.

Table S1. List of primers for RT-qPCR in this study.

Primers	Sequence (5'-3')	Sequence (3'-5')
Sporulation-related genes		
AOL_s00043g361 (<i>AofluG</i>)	GATTCCAGTCCCGTGAATTC	GCTAAGGAGAGGATGGGCAT
AOL_s00097g406 (<i>AosfgA</i>)	CTCCAACAATGAGGCCGAGA	GGGCTCGGACAAGGATAAA
AOL_s00215g516 (<i>AofluA</i>)	TTCAAACGCAGCTCCTTAC	AAGCGGTTGACAGATGAGA

AOL_s00078g317 (<i>AoflbB</i>)	AGCATATCCAGAACTTGTTCA	TAGAACCCCAATCAATATCCGG
AOL_s00007g157 (<i>AoflbC</i>)	CTCTCCGGCAAAGACAATCG	GTCGACTGAGGATAGTAGCT
AOL_s00097g46 (<i>AoflbD</i>)	TAAAAGGCAGAAAGTGACAATGC	CGATGGGATAAGAGTTGGATGA
AOL_s00215g48 (<i>AolphA</i>)	AATATCCTGCCATACTTACGGG	CTCTCAATATTTGCACTGCGG
AOL_s00054g700 (<i>AovosA</i>)	CAAACCACCCACCACCAAAT	GGATGGACAGGAGAAGGACC
AOL_s00054g811 (<i>AovelB</i>)	ATTCGCAACTTCTCCCTCA	GGCATGTTTGGATTCTGGGG
AOL_s00169g18 (<i>AoveA</i>)	AAGCTACACCAATCAACGC	TTGCGATGCTGACGATCTTG
AOL_s00075g211 (<i>AonsdD</i>)	ATTACGGCCGCCTAGTAGTC	CTCGTTTGGACCTGGTTGTG
AOL_s00006g570 (<i>Aohyp1</i>)	GCGGATCCAACATGAAGCTT	GGTTGACAACTGGGATGCTG
AOL_s00080g63 (<i>AoabaA</i>)	AACTTTATGCGCCTTGTCGT	TTGGCTAGGTGGTCTGTACG
AOL_s00079g294 (<i>Aoste12</i>)	GCTACACCTCGCTATGCCAA	ATTGTTTCAGTCGCAGCAGC
AOL_s00083g25 (<i>AostuA</i>)	AGTCCCGAAACGAGTCTAA	ATTGATCATGTGATTATCCT
AOL_s00097g514 (<i>AobrlA</i>)	TTGAGGCCTCGATCCGTAGA	AGGTAGATGGCGCTGTTACG
AOL_s00173g221 (<i>AowetA</i>)	TTACATGCCACCCAAGTCC	CAATTGCAACTGCGTCCACA
AOL_s00210g120 (<i>AomedA</i>)	TCCGGCCCAATGATTCAGAA	AGATCGCAGGAACATGGTGA
AOL_s00080g93 (<i>AolreB</i>)	CCAGGGTCGTCAGTATCTT	CAGCATCTTCCAGGTCAA
Internal control		
AOL_s00076g640 (<i>tub</i>)	CCACCTTCGTCGGTAACTC	TCGTCCATACCCTCACCAG

Table S2. List of primers for gene disruption in this study.

Primers	Sequence (5'-3')
Amplify the <i>AoSfgA</i> gene 5' flank	
<i>AoSfgA</i> -FF	GTAACGCCAGGGTTTTCCAGTCACGACGGCGCAAATTTGTCAGTTGGC
<i>AoSfgA</i> -FR	ATCCACTTAACGTTACTGAAATCTCCAACGAGCAGGGACGAAAACCTCTCA
Amplify the <i>AoSfgA</i> gene 3' flank	
<i>AoSfgA</i> -RF	CTCCTTCAATATCATCTTCTGTCTCCGACAATGAACTCGCTGAACTCGC
<i>AoSfgA</i> -RR	GCGGATAACAATTTACACAGGAAACAGCGAAAACCCGCCCTCTCGAA
Amplify the <i>AofluG</i> gene 5' flank	
<i>AofluG</i> -FF	GTAACGCCAGGGTTTTCCAGTCACGACGGTTAAGCGCTCTCATATTCTCC
<i>AofluG</i> -FR	ATCCACTTAACGTTACTGAAATCTCCAACAGATCCCGAACTATTTACCAGG
Amplify the <i>AofluG</i> gene 3' flank	
<i>AofluG</i> -FF	CTCCTTCAATATCATCTTCTGTCTCCGACCGAACCAGCTATGAGGAACG
<i>AofluG</i> -FR	GCGGATAACAATTTACACAGGAAACAGCTACCCGTAAACTGATTCATCG
Amplify the <i>hph</i> cassette	
Hph-F	GTCGGAGACAGAAGATGATATTGAAGGAGC
Hph-R	GTTGGAGATTTCAGTAACGTTAAGTGGAT
Verify the transformants	
<i>AoSfgA</i> -YZ-F	TGAGAGTTTTCGTCCCTGCTC
<i>AoSfgA</i> -YZ-R	GCGAGTTCAGCGAGTTCATT
<i>AofluG</i> -YZ-F	GTTAAGCGCTCTCATATTCTCC
<i>AofluG</i> -YZ-R	TACCCGTAAACTGATTCATCG
Make Southern blotting probe	
<i>AoSfgA</i> -TZ-F	CCCCCAAAGAGCAACCGTAA
<i>AoSfgA</i> -TZ-R	GAGCAGGGACGAAAACCTCTCA
<i>AofluG</i> -TZ-F	CTGCACCCGTTTCGATTTTCG

Table S3. The top twenty compounds with significant changes in $\Delta AofsgA$ mutant strain.

Name	Formula	Molecular Weight	RT (min)	Log2 Fold Change: $\Delta AofsgA/WT$	P-value: $\Delta AofsgA/WT$
Prednisone	C ₂₁ H ₂₆ O ₅	358.17724	35.799	-9.74	0.049952
Diamino-N-carbamoylmethaniminium	C ₂ H ₇ N ₄ O	103.06122	2.375	4.56	0.04994505
2'-(Ethylsulfanyl)-7',7'-dimethyl-5'-oxo-5',6',7',8'-tetrahydro-1'H-spiro[cyclohexane-1,4'-quinoline]-3'-carbonitrile	C ₁₉ H ₂₆ N ₂ O S	330.17787	34.543	2.11	0.04976551
2-hydroxy palmitic acid	C ₁₆ H ₃₂ O ₃	272.23472	41.169	-4.07	0.04974411
[FA (18:4)]6Z_9Z_12Z_15Z-octadecatetraenoic acid	C ₁₈ H ₂₈ O ₂	276.20826	37.006	-5.26	0.04956678
9-Keto heptadecylic acid	C ₁₇ H ₃₂ O ₃	284.23454	41.105	-7.22	0.04954504
3,4-Methylenedioxy-2',4'-dimethoxychalcone	C ₁₈ H ₁₆ O ₅	312.09903	34.003	-6.16	0.04954233
UNII:212]QJ15PS	C ₈ H ₁₂	108.09399	37.469	-3.21	0.04953087
N-arachidonylethanolamine	C ₂₂ H ₃ N O ₂	347.28166	41.441	-4.72	0.04944926
Cyclo(glycylprolylglycylprolylglycylprolyl)	C ₂₁ H ₃₀ N ₆ O ₆	462.22426	33.176	-3.41	0.04940738
Malyngic acid	C ₁₈ H ₃₂ O ₅	328.22431	33.425	-3.84	0.04925605
3-[(4-Chlorophenyl) sulfanyl]-6-methoxy-N-[3-(4-methyl-1-piperazinyl) propyl]-1H-indole-2-carboxamide	C ₂₄ H ₂₉ Cl N ₄ O ₂ S	472.16765	29.547	-5.69	0.04919087
Euchrenone a14	C ₃₀ H ₃₂ O ₅	472.22394	42.87	-3.67	0.04917107
2,6-DIMETHYLNAPHTHALENE	C ₁₂ H ₁₂	156.09361	36.165	-4.59	0.0491285
Î±-Calacorene	C ₁₅ H ₂₀	200.1561	31.246	-6.42	0.04907292
Panaxynol	C ₁₇ H ₂₄ O	244.18227	38.672	-7.64	0.04892482
4S-hydroperoxy-17S-HDHA	C ₂₂ H ₃₂ O ₅	376.2241	40.336	-9.83	0.04888879
6,3',4'-Trihydroxy-4-methoxy-5-methylaurone	C ₁₇ H ₁₄ O ₆	314.07835	33.917	-7.12	0.0488716
3,6,9,12,15-octadecapentaenoic acid	C ₁₈ H ₂₆ O ₂	274.19271	40.415	-5.74	0.04885755
Auricolic acid	C ₂₀ H ₃₆ O ₃	324.26583	40.792	-2.37	0.04885534

Table S4. The top twenty compounds with significant changes in $\Delta AofluG$ mutant strain.

Name	Formula	Molecular Weight	RT (min)	Log2 Fold Change: $\Delta AofluG/WT$	P-value: $\Delta AofluG/WT$
Trans-Non-2-en-(4,6,8)-trien-1-ol	C ₉ H ₆ O	130.04186	10.164	-3.84	0.04999131
3'-Angeloyloxy-2',4'-dihydroxy-6'-methoxychalcone	C ₂₁ H ₂₀ O ₆	368.12516	32.788	-4.81	0.04981307
Trichursin F	C ₂₅ H ₃₆ O ₇	448.24465	36.963	-6.84	0.04979714

12,13-dihydroxy-11-methoxy-9-octadecenoic acid	C ₁₉ H ₃₆ O ₅	344.25549	35.012	-8.84	0.0497816
DQ6125000	C ₁₄ H ₁₄ O	198.10416	31.429	-2.09	0.04975198
1H-Imidazole-4,5-dicarbohydrazide	C ₅ H ₈ N ₆ O ₂	184.07044	8.797	-4.16	0.04972341
CZ1330000	C ₁₂ H ₁₆	160.12498	10.392	-2.2	0.04963597
Callyspongenol C	C ₂₂ H ₂₄ O	304.18187	33.137	-5.72	0.04961497
Berkazaphilone A	C ₁₃ H ₁₆ O ₃	220.10954	40.575	-5.56	0.04958738
Grandiflorone	C ₁₉ H ₂₂ O ₄	314.15126	33.426	-2.64	0.04954353
12S-hydroxy-16-heptadecynoic acid	C ₁₇ H ₃₀ O ₃	282.21888	39.862	-8.47	0.04953914
naphthalen-1-ethanol	C ₁₂ H ₁₂ O	172.08855	17.434	-2.38	0.04952013
7,8,9,10-tetrahydro-9-hydroxy-4-methoxy-9-propyltetracene-6,11-dione	C ₂₂ H ₂₂ O ₄	350.15101	32.857	-5.93	0.04949931
Deoxycorticosterone Acetate	C ₂₃ H ₃₂ O ₄	372.2289	40.875	-8.03	0.04949851
2,2-Diphenylcyclopentanone	C ₁₇ H ₁₆ O	236.11963	18.766	-4.41	0.04936962
Brosimacutin G	C ₂₀ H ₂₀ O ₆	356.12553	24.165	-2.83	0.04920574
Dihydrochalcone	C ₁₅ H ₁₄ O	210.10388	31.847	-2.31	0.04917659
4'-O-Methylbavachalcone	C ₂₂ H ₂₄ O ₄	352.1668	24.108	-2.41	0.04911524
Benzoin	C ₁₄ H ₁₂ O ₂	212.08326	15.401	-2.55	0.04907194
3,5-anhydrogalacturonopyranosylbacteriohopanetetrol	C ₄₁ H ₆₈ O ₉	704.48475	38.647	-4.82	0.04906659