



**Supplementary Figure S1. Expression of *dpr* genes.** RT-qPCR analysis of genes coding dehydrin-like proteins in WT,  $\Delta mbsA$ , and C' strains. The *eflA* gene as the endogenous control. Statistical differences between strains were evaluated with ANOVA test:  $**p < 0.01$ .

**Table S1.** Differentially expressed toxin related genes in *ΔmbsA* relative to WT strain.

<b>ID</b>	<b>Gene symbol</b>	<b>Annotation</b>	<b>Fold change</b>	<b>p-value</b>
8112	AFUA_6G09730	cytochrome P450 oxidoreductase GliF	168.13	0.015
8110	AFUA_6G09710	MFS gliotoxin efflux transporter GliA	109.36	0.005
8113	AFUA_6G09740	thioredoxin reductase GliT	60.74	0.005
8108	AFUA_6G09690	glutathione S-transferase GliG	26.02	0.024
8109	AFUA_6G09700	gliotoxin biosynthesis protein GliK	21.88	0.011
8107	AFUA_6G09680	O-methyltransferase GliM	17.57	0.020
4619	AFUA_3G14710	toxin biosynthesis protein (Fum3), putative	14.43	0.043
8114	AFUA_6G09745	conserved hypothetical protein	12.91	0.023
4710	AFUA_4G00400	O-methyltransferase, putative	12.31	0.003
108	AFUA_1G01450	toxin biosynthesis protein, putative	11.94	0.001
8111	AFUA_6G09720	methyltransferase GliN	9.83	0.094
4440	AFUA_3G12910	O-methyltransferase GliM-like, putative	7.75	0.040
8106	AFUA_6G09670	cytochrome P450 oxidoreductase GliC	7.12	0.003
6174	AFUA_5G02640	O-methyltransferase, putative	6.45	0
8105	AFUA_6G09660	nonribosomal peptide synthase GliP	6.43	0.006
8103	AFUA_6G09640	aminotransferase GliI	5.54	0.037
5867	AFUA_4G14240	O-methyltransferase, putative	3.33	0.011
6847	AFUA_5G10320	toxin biosynthesis protein (GliH), putative	3.25	0.010
3266	AFUA_2G17820	O-methyltransferase	2.59	0.010
6846	AFUA_5G10310	AflR-like C6 zinc cluster transcription factor, putative	2.44	0.266
4834	AFUA_4G02730	O-methylsterigmatocystin oxidoreductase, putative	1.68	0.001
5888	AFUA_4G14520	toxin biosynthesis protein, putative	1.35	0.043
5890	AFUA_4G14540	C6 transcription factor (AflR), putative	0.94	0.087
2071	AFUA_2G04380	LaeA-like methyltransferase, putative	0.70	0.085
1335	AFUA_1G14660	regulator of secondary metabolism LaeA	0.48	0.018

**Table S2.** Oligonucleotides used in this study.

<b>Name</b>	<b>Sequence (5'→3')a</b>	<b>Purpose</b>
oligo109	GCAATGTAAAGCTAACGTGCGTG	5' <i>AnipyrG</i> marker
oligo110	TGCCTTTAAGCTTCGGGTAGAG	3' <i>AnipyrG</i> marker
oligo386	TAGGCGGCTCCAGAGTCTTA	5' flanking region of <i>mbsA</i>
oligo1179	TTTGTAGGCTTTGGGCTGTTACAAAGCCGTGGAGGATGATAA	5' <i>mbsA</i> with <i>AnipyrG</i> tail
oligo1180	TTG	3' <i>mbsA</i> with <i>AnipyrG</i> tail
oligo389	CTGATCTACCCCTTGGAACGCAGCATTTTCATGTCTTTGCGCA	3' flanking region of <i>mbsA</i>
oligo390	TC	5' nested of <i>mbsA</i>
oligo391	GCATTCCGCAATTGAGACTT	3' nested of <i>mbsA</i>
oligo699	GCATTCCGCAATTGAGACTT	5' <i>eflA</i> for RT-qPCR normalization
oligo700	TGTTGCGACTCATGACCTGG	3' <i>eflA</i> for RT-qPCR normalization
oligo256	CCATGTGTGTCGAGTCCCTC	5' <i>brlA</i> for RT-qPCR
oligo257	GAACGTACAGCAACAGTCTGG	3' <i>brlA</i> for RT-qPCR
oligo303	TTCCAAGCAGAGCTTGTAC	5' <i>abaA</i> for RT-qPCR
oligo304	CCAGGTTCTTTGCACTTGAA	3' <i>abaA</i> for RT-qPCR
oligo305	GCTACCACTCTGCATCCTCA	5' <i>wetA</i> for RT-qPCR
oligo306	TACGAGCTCCAGCATGATTC	3' <i>wetA</i> for RT-qPCR
oligo689	ACGGCAGGAAGTTGTCTTCT	5' <i>gliP</i> for RT-qPCR
oligo690	CTGTCAGCGACTTGTTGGAT	3' <i>gliP</i> for RT-qPCR
oligo691	AAACCCCTGTGAATGCAGAC	5' <i>gliM</i> for RT-qPCR
oligo692	CCCCTTGAGATGAAAGGTGA	3' <i>gliM</i> for RT-qPCR
oligo693	CGATCTGTACCCCAACGAGT	5' <i>gliT</i> for RT-qPCR
oligo694	TTCTGGAACCTTGCCAGCTT	3' <i>gliT</i> for RT-qPCR
oligo1264	ACTCCACCATCCAGTTCCAG	5' <i>gliA</i> for RT-qPCR
oligo1265	TCCGAGTATCCCTCGATGTC	3' <i>gliA</i> for RT-qPCR
oligo1086	ACGGTGGCGGATATCGGGTGTA	5' <i>mbsA</i> for RT-qPCR
oligo1087	AAGACGAGGACGGCGGGAGAAAG	3' <i>mbsA</i> for RT-qPCR
oligo258	CTCGGAAGCGTATCAGGTCGTCT	5' <i>rodA</i> for RT-qPCR
oligo259	GGTTCCGTCGGGGTAGGCTCTT	3' <i>rodA</i> for RT-qPCR
oligo269	CTCTTCAACCAGTGCTCCAA	5' <i>rodB</i> for RT-qPCR
oligo270	GCAATGTTCTGCTTGCACTT	3' <i>rodB</i> for RT-qPCR
oligo1274	TGAAGTTCCTCGCTGTTGTC	5' <i>rodC</i> for RT-qPCR
oligo1275	GTGTTACCCGCACTTGTTCT	3' <i>rodC</i> for RT-qPCR
oligo418	GATGCGCAAGTCCCTGTGGTC	5' <i>mpkA</i> for RT-qPCR
oligo419	ACGCATCGCCGGGTTCTTCT	3' <i>mpkA</i> for RT-qPCR
oligo426	CGGCTACATGACCGAATATG	5' <i>rlmA</i> for RT-qPCR
oligo427	ACACGTCGATAGCTTTGGTG	3' <i>rlmA</i> for RT-qPCR

oligo508	CAGCTCCTGATATCAAGCCA	5' <i>sakA</i> for RT-qPCR
oligo509	CGCTTGGTATTTGCACCTTA	3' <i>sakA</i> for RT-qPCR
oligo1310	GAGAATACCCTGCGGTTTGT	5' <i>pbsB</i> for RT-qPCR
oligo1311	GGATCCTCTTCTTGGGATCA	3' <i>pbsB</i> for RT-qPCR
oligo1312	GGGCAAGAATCGGTTCGAGAAGTT	5' <i>sskB</i> for RT-qPCR
oligo1313	CGCAGGGATGGCACCGAAGTAAGA	3' <i>sskB</i> for RT-qPCR
oligo1182	CGCGGCGATACTTCCAGGTT	5' <i>chsC</i> for RT-qPCR
oligo1183	CATAATCGCCCACTCGTTGTCTA	3' <i>chsC</i> for RT-qPCR
oligo1184	GGCAACTTCCTCTCCTCCTT	5' <i>chsA</i> for RT-qPCR
oligo1185	CCAGGAACTGGTCAGGATGT	3' <i>chsA</i> for RT-qPCR
oligo1186	CCAACGTACATCAACGTGCT	5' <i>chsB</i> for RT-qPCR
oligo1187	TTGGCCAGTTCTGCCTCATA	3' <i>chsB</i> for RT-qPCR
oligo1262	CAAGGACTCTGAACGCACTG	5' <i>chsE</i> for RT-qPCR
oligo1263	CCCTTCTCTGCTCCCTTGAA	3' <i>chsE</i> for RT-qPCR
oligo1422	ATCGCTGCATTCCTGGGTCTGTCG	5' <i>hygB</i>
	CGCGCAAGCTCATCGGCATTTT	
oligo1423	CCGGCTCGGTAACAGAACTANNNNNNNNNNGCCNNN	3' <i>hygB</i>
	NNNNNNNCAGAACGGCGTAACCAAAAAGTCAC	
oligo1525	GTTGGAGCATATCGTTCAGAGCNNNNNNNNNNNTAGN	3' <i>mbsA</i> with <i>hygB</i> tail for
oligo1526	NNNNNNNNNTTCATCTTGACGACCGTTGATCTG	complementation
	<i>TAGTCTGTTACCGAGCCGGGCTGATGCGCAAAGACATG</i>	5' <i>mbsA</i> with <i>hygB</i> tail for
	<i>GCTCTGAACGATATGCTCCAACCATCTCTCGGAGTTGTCACA</i>	complementation

<sup>a</sup> Tail sequence is in italic.