

## Supplementary Material

Table S1: Primer pairs used to screen for remnants of the *mcy* gene cluster

Fig. S1: Sequence alignment showing the sequences at the 5' end of the *mcy* gene cluster found in 25 non-toxic strains that had lost the *mcy* gene cluster

Fig. S2: Sequence alignment showing the sequence break point at the 3' end in 25 non-toxic strains that had lost the *mcy* gene cluster

**Table S1:** Oligonucleotides used to screen the non-toxic strains for remnants of the *mcy* gene cluster. Primers have been named according to the nucleotide position of the *mcy* gene cluster (AJ441056) (Christiansen *et al.*, 2003)

Forward Primers		Reverse primers		
Pos.	Sequence (5'-3')	Tm °C	Pos. Sequence(5'-3')	Tm °C
2	CAAGCGCGCCGCA	46	2 TCGCTATTGATCATTGATCAGGG	60
474	AATAGCGATTTTCCCAAGCATTC	57	474 TGGTCACAGTATGGGCGGAT	60
925	ATCCGCCATACTGTGACCA	59	925 TTCTTTAGGTCGTTAGGCTCCATT	58
1399	AATGGAGCCTAACGACCTAAAGAA	59	1399 AAAACACCTGTCTTGCCGATTC	59
1851	GAATCGGCAAGACAGGTGTTTT	58	1851 TCATTATTAAGTGTCTGTTCCCTCGAA	58
2308	AGGAACAGCAGTTAATAATGATGGC	59	2308 TTGGTTCCCGATGCTCCA	60
2761	TGGAGCATCGGGAACCAAT	60	2761 TTTAAGTGTCTTTGAAATAGGCGA	58
3208	TCGCCTATTTCAAAGCACTTAAA	58	3208 AATTTCTAGGAAGATTTGATACCCCA	58
3668	GGGTATCAAATCTTCTTAGAAATTGGA	60	3668 TTGTGTAGCAGCCAAAGCCA	59
4122	TGGCTTTGGCTGCTACACAA	59	4122 AGTTACCGATGATTCTTGCTTGAA	58
4571	TTCAAGCAAGAATCATCGGTAACCT	58	4571 TTGACCTAATTTGGGTTGCCA	59
5021	TGGCAACCCAAATTAGGTCAA	59	5021 AGTAGTGGCTCCTGTTCCGC	58
5472	GCGGAACAGGAGCCACTACT	58	5472 GGGTTGGCTGGGTTCAATAAT	59
5927	ATTATTGAACCCAGCCAACCC	58	5927 TCCTAATAGAGAAGATTGGGCGG	60
6378	CCGCCAATCTTCTCTATTAGGA	60	6378 CCGGATATTCTGAACGGCA	58
6830	TGCCGTTTCCAGAAATATCCGG	58	6830 AAGGAAAACGTTGCCAGTCAAT	59
7280	ATTGACTGGCAACGTTTTCTTAA	59	7280 TCGGATCTTCTTCTATTTGTGGTTT	58
7733	AAACCACAAATAGAAGAAGATCCGA	58	7733 AAGCCGACCGGAAACTACT	59
8192	AGTGTAGTTTCCGGTCGGCTT	59	8192 CGGTACCATGAGCTTCGATATAATCT	60
8650	AGATTATATCGAAGCTCATGGTACCG	60	8650 TGCCAGACCCATTCAAAGC	58
9125	GCTTTGAATGGGTCTGGCA	58	9125 CGCCAATACTATGTCCTAAAAGTGC	59
9576	CACTTTTAGGACATAGTATTGGCGAAT	59	9576 CGTACTCCTAAGATGATTAACCCAATAA	58
10036	GGTTAATCATCTTAGGAGTACGGTGC	59	10036AATCCTGTGCTGCGTGGAAATAAAACT	58
10498	AGTTTTATTTCCAGCGACAGGATT	58	10498AAAGGACAGGATGAAAACAATAACG	59
10952	CGTTATTGTTTTATCCTGTCTTT	59	10952AGAGTAGCATTGATAGTTGTTACCAATTTT	59
11408	GAAATTGGTAACAACATCAATGCTACTCT	59	11408ACAGTTTCCCTGACGTAAGCC	58
11857	GGCTTTACGTCAGGGAAACTGT	58	11857GGGCGAGTATAGTGATCTAATAATAAAGTTC	59
12316	ATTAGATCACTATACTCGCCCCCTATC	59	12316ACCCAGTAACTTCGCGTAATATCTGT	59
12790	ACAGATATTACGCGAAGTTACTGGG	59	12790CTAATTCGGTAATACGAGCCTGC	58
13240	GCAGGCTCGTATTACCGAATTAG	58	13240TCCTGTGCCAAAAAAGAGTCA	58
13693	TGACTCTTTTTTTTGGCACAGGA	58	13693TTCTAGCATCGGCAATGGC	58
14147	GCCATTGCCGATGCTAGAA	58	14147GCGGTTTTTGTATGAGCAGAAAT	58
14603	ATTTCTGCTCATAACAAAACCGC	58	14603GCAACGGCATATTCTAGGGC	58
15056	GCCCTAGAATATGCCGTTGCTA	59	15056TCCGTCAATTCCTGAAAAGTAACAG	58
15512	CTGTTACTTTTTCAGGAATTGACGGA	58	15512GATTTTCGAGTTGATGTTTTTGCAT	58
15978	AACATCAACTCGAAATCCGCC	60	15978CGAGTAACTAAAACCTGATATTTGGG	59
16432	CCAAAATATCAGGTTTTAGTTACTCGT	59	16432AAAAATGGAGATAATTCGCTAAAAGAAT	58
16884	ATTCTTTTAGCGAATTATCTCCATTTTT	58	16884ATATTTTTCAGCAGCAGCACAAGC	58
17338	TGCTGCTGCTGAAATATTACCG	59	17338TCCGAAAGTCAATGGTGGGT	59
17797	ACCCACCATGACTTTTCGGA	58	17797TCAAACAATTACATCTTCAACCATTTC	59
18246	GAATGGTTGAAGATGTAATTGTTTTGA	58	18246GAATGGTTGGACTTTGTTCTTTAAGATA	58
18707	CTTAAAGAACAAGTCCAACCATTCA	59	18707TGCTAATAACCAAAGCTGACGCT	59
19155	AGCGTCAGCTTTGGTTATTAGCA	59	19155CTGCATTGGGAATTCTAAAGGG	59

19616 TTAGAATTCCCAATGCAGTTTCG	59	19616 TTGATGTCTAAAAGCAGCGATGA	59
20070 TCATCGCTGCTTTTAGACATCAA	59	20070 GGGCATTGGGAGTCGAGTTA	59
20527 TAACTCGACTCCCAATGCC	59	20527 AGAGAGATGACGACCCATGACTC	58
20976 GAGTCATGGGTCGTCATCTCTCT	58	20976 GGTTATTATGGAAAACCTTGACCTAGGG	59
21438 CCCTAGGTCAAGTTTTCCATAATAACC	59	21438 ATAAAGTAACTAGGAATCATGTAAACTGGC	58
21880 GCCAGTTTACATGATTCCTAGTTACTTTAT	58	21880 CATTCCATAGGCATTATGATTTTGA	58
22341 ATAATGCCTATGGAATGCCAG	59	22341 TTGCCAGTCAGTATAATCTTTATAGTGAATT	58
22786 AATTCACTATAAAGATTATACTGACTGGCAA	58	22786 AAAGGATATTCTTGATTTTCATAAGCCT	58
23161 AGTCCTGCGGGATCAAATTAGA	59	23161 AAAATCTTCAGCGAATAAGTCGCT	59
23612 AGCGACTTATTCGCTGAAGATTTTAA	60	23612 AAGCCCATCTAAAATATTGAGAGCA	58
24003 CCCTATATTGAAAATGATGTAACCG	59	24003 TGCCAGAAGTAAATAGTAATAAGGCTTGA	60
24458 TCAAGCCTTATTACTATTTACTTCTGGCA	60	24458 AATGCTGGTTAATGGCTCTATCTG	59
24911 AGATAGAGCCATTAAACCAGCATTTG	60	24911 AATAAGTCAGTCTCTTGGATTTGATCAA	59
25341 GCATTCGCCCTCTTTGATCA	60	25341 CAGCTATAGGTAAGTACGATTAAAAAGTTT	59
25761 CGAGTACACAACCAACTAGAAAAACTTT	59	25761 ACATTCCCAACTCGATTGTAGGA	59
26209 TCCTACAATCGAGTTGGGAATGT	59	26209 AAAATAGTTCCTTGGGCTTGAGAA	58
26641 ATTGTCGTGCCTTTGATTCTCA	58	26641 GAGGATTGGGATTTTGGAAATG	58
27090 CATTTCCAAAATCCCAATCCTC	58	27090 GGCGGTTGCTTTTCATCAA	58
27544 TTGATGAAAAGCAACCGCC	58	27544 ATCCCTGATTTTGGCACTGTT	58
27994 AACAGTGCCAAAATCAGGGAA	58	27994 AAAATCCTGAGCGCAAACCTG	58
28444 CAAGTTTGCCTCAGGATTTT	58	28444 AGAACTCCTGTTAATGATGCGAA	58
28917 TTCGCATCATTAACAGGAGTTTCTT	59	28917 AGAGATACTCAGGTTGAGAACTTTTGC	59
29361 GCAAAAGTTCTCAACCTGAGTATCTCT	59	29361 TGATCATCGCTAAAACGCCAC	60
29813 GTGGCGTTT TAGCGATGATCA	60	29813 TTTGAATAGCTTGGAGAAGATTTAACAA	59
30292 TTCTCCAAGCTATTCAAAAAATCCC	60	30292 AGATTTTCCATGATTTTGGCAA	59
30766 CCAAAATCATGGAAAATCTCAGG	58	30766 TCATACCAATCTGTTAAGCCAATCT	58
31220 AGATTGGCTTAAACAGATTGGTATGA	58	31220 TAAAACCTGCTGAATCAGATAATCAAC	58
31691 TCAGCAGGTTTTAGGTTGGCA	59	31691 CCTGAATAATAACATCGACTAAATAGCG	59
32126 TTGTTAATCGCTATTTAGTCGATGTTATT	58	32126 GCCGTAAGCATAGTTAGCTTTAGATTC	58
32587 GAATCTAAAGCTAACTATGCTTACGGC	58	32587 TTGTAGGGTAACATCCTCAAAGTAATATG	59
33028 CATATTACTTTTGAGGATGTTACCCTACA	58	33028 TCCAAAGCACTGGTGGCTTC	60
33487 GAAGCCACCAGTGCTTTGGA	60	33487 TGAATAGCTGCTAGGTATAAAGCTAACTTG	59
33934 CAAGTTAGCTTTATACCTAGCAGCTATTCA	59	33934 TCTCAACTCCACATCGGGATT	58
34405 GTTGAGAGAAATAGATATCCTTACCCCTG	60	34405 TTGCAATGAGATCCCAATCACTA	58
34830 CGGCTAATCTAGCTAAAATTATCTGCTT	59	34830 AAGCCTCGCCACTACAAATCAC	59
35285 ATTTGTAGTGGCGAGGCTTTACC	60	35285 AGAATAGTTTCAATTTTCGCCCAAT	58
35749 ATTGGGCGAAATTGAAACTATTCT	58	35749 CCCCTAAGTGATGCCGAATC	58
36200 TTGATTCGGCATCACTTAGGG	59	36200 AACGACGTTATAGCGGAATTGG	59
36649 CCAATTCGGCTATAACGTCGTT	59	36649 TTTAATTGAGGTTGGAGCGGAT	59
37102 GCTCCAACCTCAATTAACCGT	58	37102 TGGGCCGCAGAAATTAGACT	58
37553 AGTCTAATTTCTGCGGCCA	58	37553 CACTCCAACCATCTAAAATAGAGTGG	58
38008 CCACTCTATTTTAGATGGTTGGAGTG	58	38008 AACCGCAGAGGCAAAGTATTG	58
38467 CAATACTTTGCCTCTGCGGTT	58	38467 TTTGAGTACGATTCCAGTCCCA	58
38921 TGGGACTGGAATCGTACTCAA	58	38921 CCGAGTTAGAGGAAGTACTGACT	58
39374 AGTCAAGTCAGTTCCTCTAACTCGG	58	39374 CAACTGAAGGTGGAATAGGAAGTGT	59
39828 AACTTCTATTCCACCTTCAGTTG	59	39828 ACGTAAGCCACTAATTTTGCCC	58
40278 GGGCAA AATTAGTGGCTTACGT	58	40278 CCTGGTGGGTTAAAGTCTAGAGA	59
40746 CCCACCAGGTTT TAGTCACG	59	40746 CATAAGTCTTCCAGTAAAACCTCCAGG	60
41190 CCTGGAGAGTTTTACTGGAAGACTTATG	60	41190 CACGGGAAAAGACTGGTAAACC	60
41664 CCGTGATTCTCCAACCTGCCT	59	41664 TTGATTTAAGTTGGCAACGGG	59
42126 CCGTTGCCAACTTAAATCAACAG	60	42126 TGTATTAATGGCAACGCATCAA	59
42578 TCCTTTGATGCGTTGCCA	58	42578 CGAAACGGTAATGCCAAAGAG	58
43041 CTCTTTGGCATTACCGTTTTCG	58	43041 GCTGAGGATTCTGGGCGAT	59
43500 ATCGCCAGAATCCTCAGC	59	43500 ACAGAATGATTCTATCTTCAAGGTGTCT	58

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43961 CACCTTGAAGATAGAATCATTCTGTTTAGA	60	43961AAGAGCTTCACCTCCACAAAAAA	58
44412 GTTTTTTGTGGAGGTGAAGCTCTT	59	44412GGGATGGCTGTCTAGAATTGTCTG	60
44854 AAATTCAGACAATTCTAGACAGCCATC	59	44854GGTGGGAAAAGACTTGTTAATAGCA	60
45305 TAAACAAGTCTTTTCCCACCCC	58	45305TAGCTCTGAGGTGATAATTGATAAAGAGAA	59
45758 TTCTCTTATCAATTATCACCTCAGAGC	59	45758TGTACCAATACTAATATCTTGCTGACCAC	59
46201 GTGGTCAGCAAGATATTAGTATTGGTACA	59	46201TGGCTAACATTGCTGTCAACAATT	60
46684 ATCCAGAGCAACCCATCGG	59	46684GGTTTTGCTAATACTAATAATCGAGGTTT	58
47127 AAACCTCGATTATTAGTATTAGCAAAACC	58	47127AAAAATAGACGCATTACCGATGGT	59
47559 AACTTACTGCATACCGTACCATCG	58	47559GGAGCAATCGTCCCAAGTCTC	60
48016 GAGACTTGGGACGATTGCTCC	60	48016TGCCTCCGAGTTCAAAAAATG	59
48475 CATTTTTTGAAGTCGGAGGCA	59	48475AATATTTCCAGCTATACTGGCAAAAAGT	58
48917 TTGCGGACTACTTTTGCCAGT	59	48917GGGAAGTCGGTGGGTAAGTTC	58
49372 GAACTTACCCACCGACTTCCC	58	49372TCAGGAATTTCCATCACTGTTTTG	59
49840 GGAAATTCCTGAAATTGAACATCA	58	49840TCAATAAAAATTCCCACCAATACTTCT	58
50243 AACCAATTAGCCCATTATCTACAAGAA	59	50243CCCAGACTGAAGGATCAAAACTAAA	59
50716 TAGTTTTGATCCTTCAGTCTGGGAA	59	50716GCTAAAGGCACACCCCAA	60
51148 CGTTGCTGGAGAACTACATATTGG	59	51148TGATCTTTGATCGGGTTTTGG	58
51608 CCAAAACCCGATCAAAGATCA	58	51608TGATCGATTAATTCTGCATATTGTTCTA	58
51990 TGGCTGATTATTTAACGGATTATACTATCT	58	51990GCTTGTATCCAATCATCTTCAACATC	59
52442 GATGTTGAAGATGATTGGATAACAAGC	59	52442GTAGTTTCTTCTTTCCAATAGCCAAAA	59
52889 TTGGCTATTGGAAAGAAGAACTACTT	58	52889AAGTATGCCGATCATATTGATTAACAA	58
53363 TTGTTAATCAATATGATCGGCATACTT	58	53363TGCGCCACAATTTGTCA	59
53843 TGACAAATTGTGGGCGCA	59	53843TAGCTTTGTTTCGATTTATATATTACCCC	59
54308 AAGCTACTATAAACTTTTTGACCAGGCA	60	54308AAAAATCATCAGGTTCTTTATCACCAT	58
54763 AAATAAATGGTGATAAAGAACCTGATGA	58	54763CCCCCTGAATTTTTACCGGA	60
55211 TGA CTCCGGTAAAAATTCAGGG	59	55211GCAAATCTTCCTGCTCCGAG	59

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## Supplementary figure legends

FIG. S1: Sequence alignment showing the 5' end flanking regions of *mcyT* found in 24 non-toxic strains (deletion types I-III). The functional *mcy* sequence is marked in bold, the translation stop site of *mcyT* is underlined (Pos. 449 of the *mcy* gene cluster of the toxic strain CYA126/8, AJ441056). One strain No252 (deletion type IV) did not contain *mcyT* but contained the same flanking region of the *mcy* gene cluster as the toxic strain directly linked to the remnant of the insertion element (see also Fig. 3). The stop translational site of *mcyT* (Pos. 449, AJ441056) is marked in bold and underlined.

FIG. S2: Sequence alignment showing the sequence break point at the 3' end of *mcyT* found in 24 non-toxic strains (deletion types I-III). For comparison the corresponding bi-directional promoter region located between the genes *mcyT* and *mcyD* of the *mcy* gene cluster sequence of the toxic strain CYA126/8 is shown in bold. The translation initiation site of *mcyT* (Pos. 1240, AJ441056) is marked in bold and underlined. The inverse repeats of the remnants of the transposable element that lead to the deletion of the *mcy* gene cluster are underlined. One strain No252 did not contain *mcyT* (deletion type IV) but contained the same remnant of an insertion element as well as the 3' end flanking region of the *mcy* gene cluster (1,406 bp downstream of *mcyJ* underlined).



