

Supplementary Information

Table S1. Bacterial strains used in this study.

Bacterial strains	Growth media ^a /Origin ^b
Marine sponge <i>Bacillus subtilis</i> : BD126-43	MA, MB/This work
BD230-19	MA, MB/This work
BD230-27	MA, MB/This work
BD230-29	MA, MB/This work
BD243-3	MA, MB/This work
CC15	MA, MB/This work
AF31	MA, MB/This work
MMA7	MA, MB/[1]
<i>Bacillus subtilis</i> NCDO 1769	LB/MDCC UCC
<i>Bacillus subtilis</i> NRRL B-23052 ^T	LB/BGSC
<i>Bacillus subtilis</i> 168	LB/BGSC
<i>Bacillus subtilis</i> DSM 347	LB/DSMZ
<i>Bacillus cereus</i> NCIMB 9373	LB/MDCC UCC
<i>Bacillus megaterium</i> ATCC 19213 (BGSC 7A2)	LB/BGSC
<i>Staphylococcus aureus</i> NCDO 949	BHI/MDCC UCC
MRSA ST 530	BHI/MDCC UCC
VISA22784	BHI/MDCC UCC
hVISA 35197	BHI/MDCC UCC
VRE EC725	BHI/MDCC UCC
<i>Enterococcus faecium</i> NCIMB 11508	BHI/MDCC UCC
<i>Listeria innocua</i> DPC 3567	BHI/MDCC UCC
<i>Listeria monocytogenes</i> EGDe	BHI/MDCCUCC
<i>Clostridium perfringens</i> NCDO 1799	TGB/MDCC UCC
<i>Clostridium sporogenes</i> NCDO 1791	TGB/MDCC UCC
<i>Clostridium difficile</i> 001	BHI/MDCC UCC
<i>Carnobacterium malteromaticum</i> LMG 9839	TSB/BCCM TM /LMG BC
<i>Lactococcus lactis</i> subsp. <i>cremoris</i> HP	GM17/MDCC UCC
<i>Escherichia coli</i> NCIMB 15943	LB/MDCC UCC
<i>Escherichia coli</i> MUH 103	LB/[2]
<i>Enterobacter aerogenes</i> NCIMB 10102	LB/MDCC UCC
<i>Salmonella</i> Typhimurium LT2	LB/MDCC UCC
<i>Pseudomonas aeruginosa</i> PAO1	LB/MDCC UCC
<i>Burkholderia cenocepacia</i> J2315	LB/[3]
<i>Stenotrophomonas maltophilia</i> K279A	LB/[4]
<i>Klebsiella pneumoniae</i> MUH 588	LB/[2]
<i>Serratia marcescens</i> MUH 436	LB/[2]
<i>Morganella morganii</i> MUH 988	LB/[2]
<i>Aeromonas hydrophila</i> LMG 2844	TSB(NA)/BCCM TM /LMG BC
<i>Listonella (Vibrio) anguillarum</i> LMG 4410	MB/DSMZ
<i>Candida glabrata</i>	YPD/MDCC UCC
<i>Candida albicans</i> SC5314	YPD/MDCC UCC
<i>Candida dubliniensis</i>	YPD/MDCC UCC
<i>Candida lusitanae</i>	YPD/MDCC UCC
<i>Candida parapsilosis</i>	YPD/MDCC UCC

^a Standard media were: LB, Luria Bertani; TGB, Thioglycolate broth (Merck); YPD, Yeast extract peptone dextrose media; BHI, Brain heart infusion (Merck); MA, Marine Agar; MB, Marine broth (Difco); TSB, Tryptic soya broth (Merck); NA, Nutrient agar (Difco); GM17, M17 broth (Merck) supplemented with

Glucose 0.5%; ^b Bacterial strains were obtained from the Microbiology Department Culture Collection, University College Cork (MDCC UCC), the *Bacillus* Genetic Stock Centre (BGSC), Belgium Coordinated Collections of Microorganisms (BCCMTM)/LGM Bacteria Collection and DSMZ, DSM Collection, Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH, Braunschweig, Germany. MRSA, methicillin resistant *Staphylococcus aureus*; VISA, vancomycin intermediate *Staphylococcus aureus*; hVISA, heterogeneous VISA, and VRE, vancomycin resistant enterococci.

Table S2. Oligonucleotide primers used in this study.

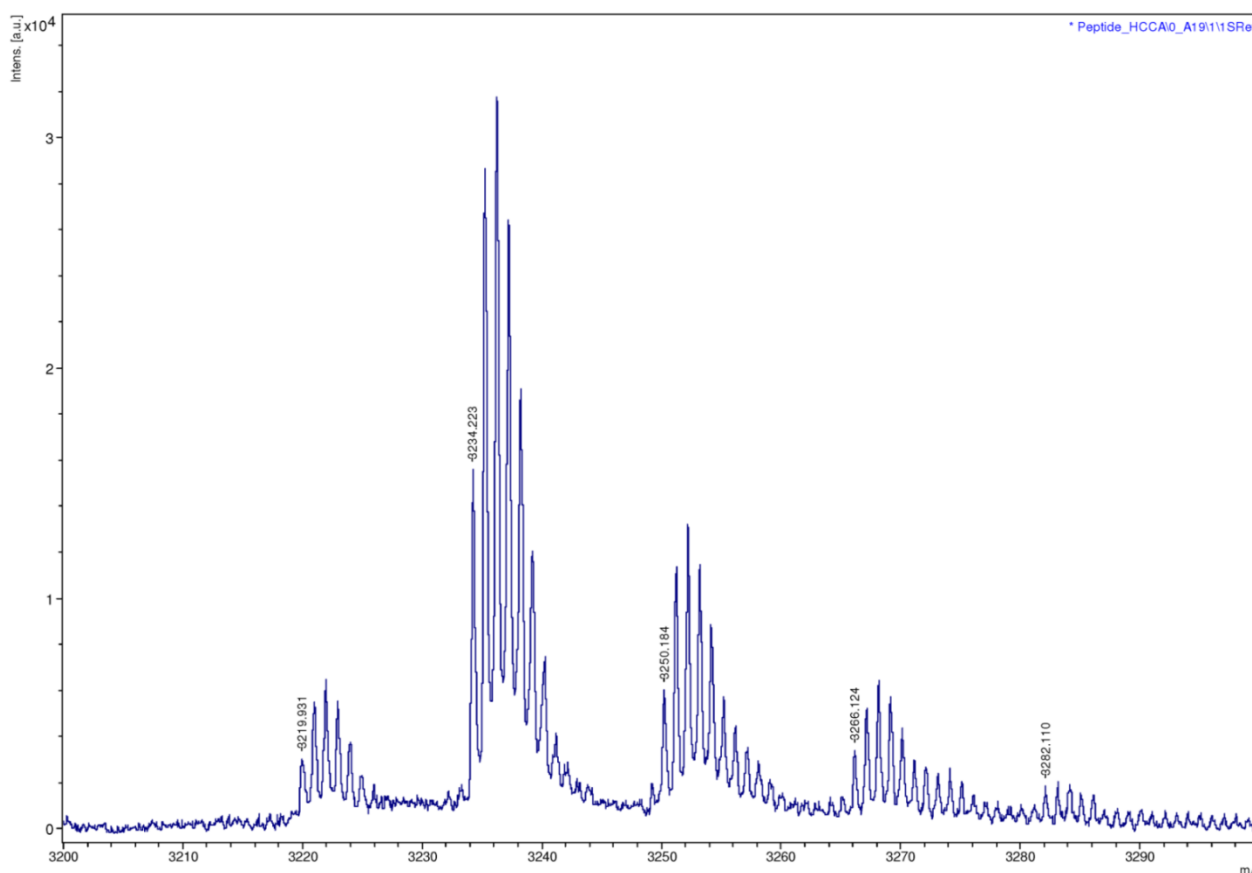
Primer	Sequence (5'-3') *	Annealing (°C)
<u>Construction of MMA7 Δsbo-albF::cat mutant</u>		
sboUp-F (HindIII)	CCCAAGCTTCCATCATTGCTCATCAGATTTGA	58
sbo-R (BamHI)	CGCGGATCCTCCGATCGAGCATGTTGCACAA	
albF-F (EcoRI)	CCGGAATTCCATCCTGCTTGATGCGTTATGGA	52
albF-R (XhoI)	CCGCTCGAGGTGTCTTCTGAGCCTCCGATCAA	
<u>Verification of MMA7 Δsbo-albF::cat mutant</u>		
ywiB-F	CACATGGAGTGTTATCGGTG	52
albFDown-R	CTGTAATCCGGTCCATGTGT	52
albA-R2	TGCCACAGTTTATGGACGAGAGG	52
albD-F	GCAGACAGAGCAGCAGCTCTGGA	52
cat255-R	CGTTTGTGAACTAATGGGTG	52
cat958-D [#]	GGGTAAGTAGCCTGCAGGCAATAGTTACCC	52
<u>Bacteriocins screening primers</u>		
<u>Subtilin</u>		
spaC-F	ACTATGAATCAATGGAAGG	48
spaS-R	TTGCAGTTACAAGTTAGTG	
<u>Sublancin</u>		
sublancin-F	GTGTGCTGCGTTGCTACAA	55
sublancin-R	TTGACGAGATACAAGCTAGTCC	
<u>Subtilosin</u>		
Sbo-F	GGTTGTGCAACATGCTCGAT	52
AlbA-R	CTCAGGAAGCTGGTGAAGTC	
<u>Subtilomycin</u>		
subA2569-F	TGCGGATGACAGATTCGTATTGC	60
subA2571-R	ACAGCTGTACCGTGCCCATATAGA	

* Introduced restriction sites are underlined; Cat, chloramphenicol resistance cassette; [#] [5].

Table S3. Sequence homology of the proteins encoded by the subtilomycin biosynthetic gene cluster *.

Protein	No. aa	Closest homologue	% Identity/ (Aligned region aa)	E Value [#]
SubA	56	<i>Bacillus thuringiensis</i> serovar <i>thuringiensis</i> str. T01001.	56% (28/50)	3E-07
SubP	324	<i>Bacillus amyloliquefaciens</i> DSM 7 subtilisin-type proteinase	34% (113/333)	6E-44
SubB	1045	<i>Paenibacillus polymyxa</i> E681 lantibiotic biosynthesis protein SpaB	31% (336/1075)	6E-144
SubC	440	<i>Bacillus thuringiensis</i> IBL 200 Lantibiotic biosynthesis protein	44% (185/424)	8E-109
SubI	80	<i>Lactococcus</i> phage BK5-T hypothetical protein	31% (16/51)	1.3
SubT	585	<i>Staphylococcus epidermidis</i> VCU121 ABC transporter, ATP-binding protein	45% (258/573)	0.0

* Results are from a BLASTp search of the GenBank protein database on 17/04/2013; [#] Expectation value.

Figure S1. Mass spectrometry analysis of RP-HPLC purified peptide showing a number of oxidised forms typical of the thioethers found in lantibiotics.

References

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