



Supplementary Materials: Micellar Antibiotics of *Bacillus*

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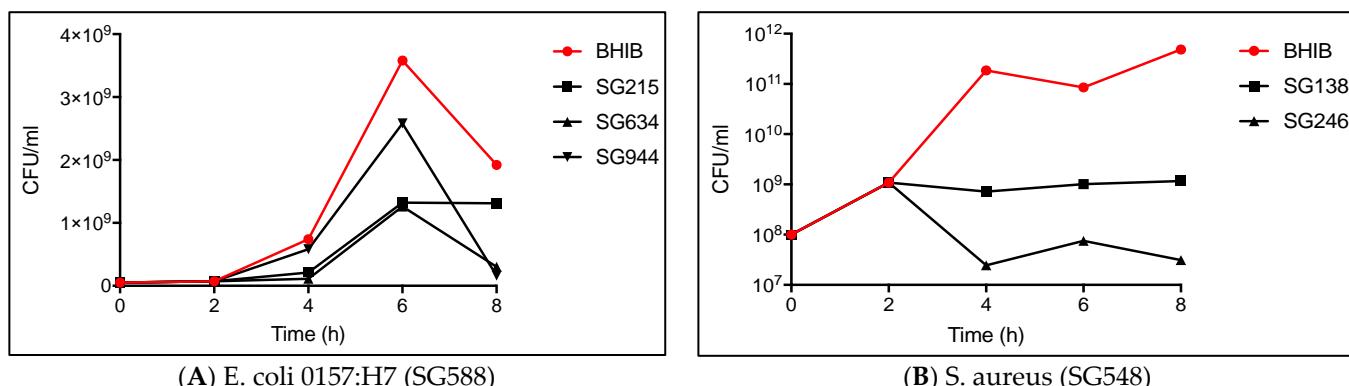


Figure S1. Pathogen growth kinetics using CFU counts. Cell free supernatants from *Bacillus* strain cultures (SGx) were added (1:10 v/v, indicated by red arrow) to mid-logarithmic cultures of Gram negative and Gram-positive pathogens. Growth was monitored by determination of CFU/ml in cultures with or without (untreated) addition of supernatants.

Table S1. Genome analysis of lipopeptide, polyketide and bacilysin genes present in *B. velezensis* 'active' strains. Operons identified from genome sequencing of *B. velezensis* strains with activity to *C. difficile*. Activities determined to CD630 using a microdilution assay are shown as the dilution factor. ANI values (two-way) compared to *B. velezensis* (NCBI: NZ_CP018133.1) are given as a % and were determined using the Enveomics program [1]. The order of ORFs in the fengycin operon differs between strains as indicated.

Antimicrobial	SG57	SG137	SG185	SG277	SG297
a-CD630 activity	1:80	1:80	1:80	1:160	1:160
ANI value	97.25	98.00	97.99	97.59	98.90
surfactin	<i>srfAA-D</i>	<i>srfAA-D</i>	<i>srfAA-D</i>	<i>srfAA-D</i>	<i>srfAA-D</i>
fengycin	<i>yng-fenBAEDC</i>	<i>yng-fenBAEDC</i>	<i>yng-fenBAEDC</i>	<i>yng-fenED-/-CBA</i>	<i>yng-EDCBA</i>
iturins	<i>fenF, mycA-C</i>	<i>fenF, mycA-C</i>	<i>fenF, mycA-C</i>	<i>fenF, mycA-C</i>	<i>fenF, mycA-C</i>
bacilysin	<i>bacA-E</i>	<i>bacA-E</i>	<i>bacA-E</i>	<i>bacA-E</i>	<i>bacA-E</i>
bacillaene (<i>pks1</i>)	<i>pksA-S</i>	<i>pksA-S</i>	<i>pksA-S</i>	<i>pksA-S</i>	<i>pksA-S</i>
macrolactin (<i>pks2</i>)	<i>mlnA-H</i>	<i>mlnA-H</i>	<i>mlnA-H</i>	<i>mlnA-H</i>	<i>mlnA-H</i>
difficidin (<i>pks3</i>)	<i>dfnA-O</i>	<i>dfnA-O</i>	<i>dfnA-O</i>	<i>dfnA-O</i>	<i>dfnA-O</i>

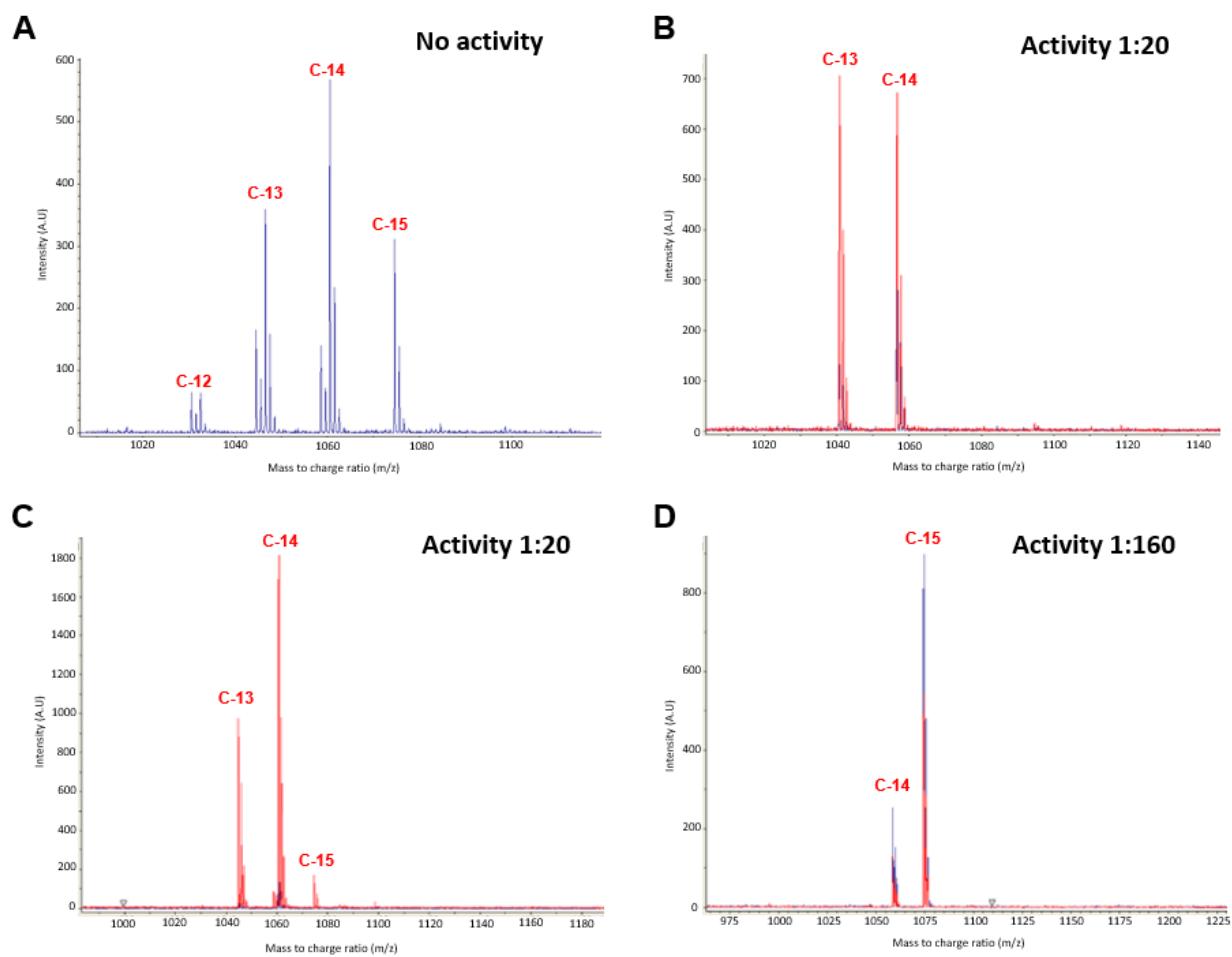


Figure S2. MALDI-TOF analysis of commercial vs *Bacillus* surfactins. MALDI-TOF analysis of commercially acquired surfactin (Sigma S3523) (A) and surfactin from three distinct ‘active’ fractions collected after RP-HPLC separation of the SG277 SEC material; active fraction exhibiting activity against CD630 of 1:20 (B), active fraction exhibiting activity against CD630 of 1:20 (C), active fraction exhibiting activity against CD630 of 1:160 (D). Activity against CD630 (1/dilution factor) and surfactin species are indicated in the figures. Activity was greatest in the fraction containing C-15 surfactin (D).

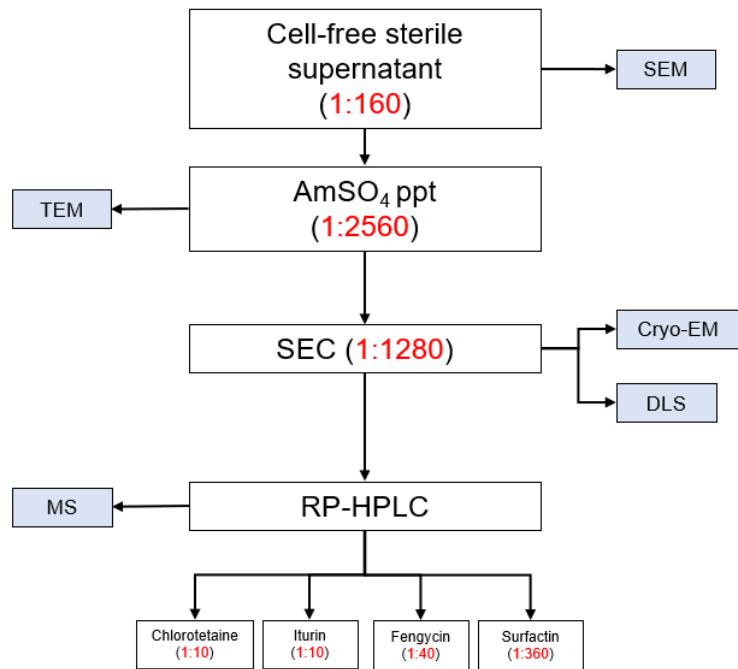


Figure S3. Purification steps. Flow diagram showing purification steps of culture supernatants and analyses performed. TEM: transmission electron microscopy, MS: MALDI-TOF analysis, DLS: dynamic light scattering, SEC: size exclusion chromatography, RP-HPLC: Reversed-phase high performance liquid chromatography. Activity against CD630 using a microdilution assay is indicated in brackets.

Table S2. Antimicrobial screening^a.

Group ^b	Strain No.	Species ^c	Biosurfactant activity ^d	Gram-negative					Gram-positive				
				Heat resistance ^e	Salmonella				<i>B. cereus</i> (SG584)	<i>C. difficile</i> (630)	<i>S. hominis</i> (ATCC 27844)	<i>S. aureus</i> (SG548)	<i>L. monocytogenes</i> (NCTC 19115)
					<i>E. coli</i> (O157:H7; 078:K80)	<i>E. enterica</i> (NCTC 13349:SG576)	<i>K. aerogenes</i> (NCTC 1006))					
	SG634	<i>B. velezensis</i>	+++	+	BS							BS	
	SG113	<i>B. velezensis</i>	+	+	BS								
	SG661	<i>B. velezensis</i>	+++	+	BS								
	SG630	<i>B. velezensis</i>	+	+				BS					
	SG184	<i>B. velezensis</i>	+++	+			BS					BS	
	SG545	<i>B. velezensis</i>	+	+								BC	
	SG91	<i>B. velezensis</i>	++	+					BC		BS	BC	BC
	SG309	<i>B. velezensis</i>	+	+								BC	
	SG541	<i>B. velezensis</i>	+	+				BC					
	SG944	<i>B. velezensis</i>		+	BS						BS		
	SG71	<i>B. velezensis</i>	+	+			BS				BS		
	SG660	<i>B. velezensis</i>	++	+			BS				BS		
	SG677	<i>B. velezensis</i>	+++	+							BS		
	SG57	<i>B. velezensis</i>	++	+					BL				
	SG137	<i>B. velezensis</i>	++	+					BL				
" <i>B. subtilis</i> "	SG185	<i>B. velezensis</i>	++	+					BL				
	SG277	<i>B. velezensis</i>	+++	+					BL				
	SG297	<i>B. velezensis</i>	+++	+					BL		BC		
	SG202	<i>B. velezensis</i>	+	+		BS					BC		
	SG943	<i>B. velezensis</i>		+							BS	BS	
	SG633	<i>B. velezensis</i>	+	+							BC		
	SG629	<i>B. velezensis</i>	+	+		BS					BC		
	SG695	<i>B. velezensis</i>	+	+							BC		
	SG138	<i>B. velezensis</i>	++	+							BS		
	SG18	<i>B. amyloliquefaciens</i>	+	+	BS								
	SG246	<i>B. amyloliquefaciens</i>	+	+		BS				BC		BS	
	SG531	<i>B. subtilis</i>	+	+				BS					
	SG308	<i>B. subtilis</i>	++	+			BS						
	SG281	<i>B. subtilis</i>	+	+			BS						
	SG691	<i>B. subtilis</i>	+++	+	BS								
	SG3	<i>B. subtilis</i>	++	+	BS								
	SG310	<i>B. mojavensis</i>	+++	+			BS						
	SG215	<i>B. infantis</i>	+	+	BS								
	SG836	<i>B. pseudomycoides</i>	-	+			BS						
Other	SG655	<i>Viridibacillus arvi</i>	++	+			BS						
	SG224	<i>Mesobacillus subterraneus</i>	++	+							BS		

^a cultures from strains were tested for inhibitory activity to a panel of Gram negative and Gram positive pathogens. Initial screening was by well diffusion and secondary screening using co-culture where activity is defined as BS, bacteriostatic, BC, bactericidal or BL, bacteriolytic. Strains were obtained from strain collections or were lab stocks.^b operational group of related species, [2].^c species assigned by *gyrA* sequence analysis [3] for members of the *B. subtilis* group and 16S rRNA [4,5] for remaining strains. ^d biosurfactant activity defined as zone of oil displacement; +, <10mm; ++, 10–20mm; +++, >20mm.^e inhibitory activity present after heating of cell-free supernatant for 15 min. at 90°C.

References:

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