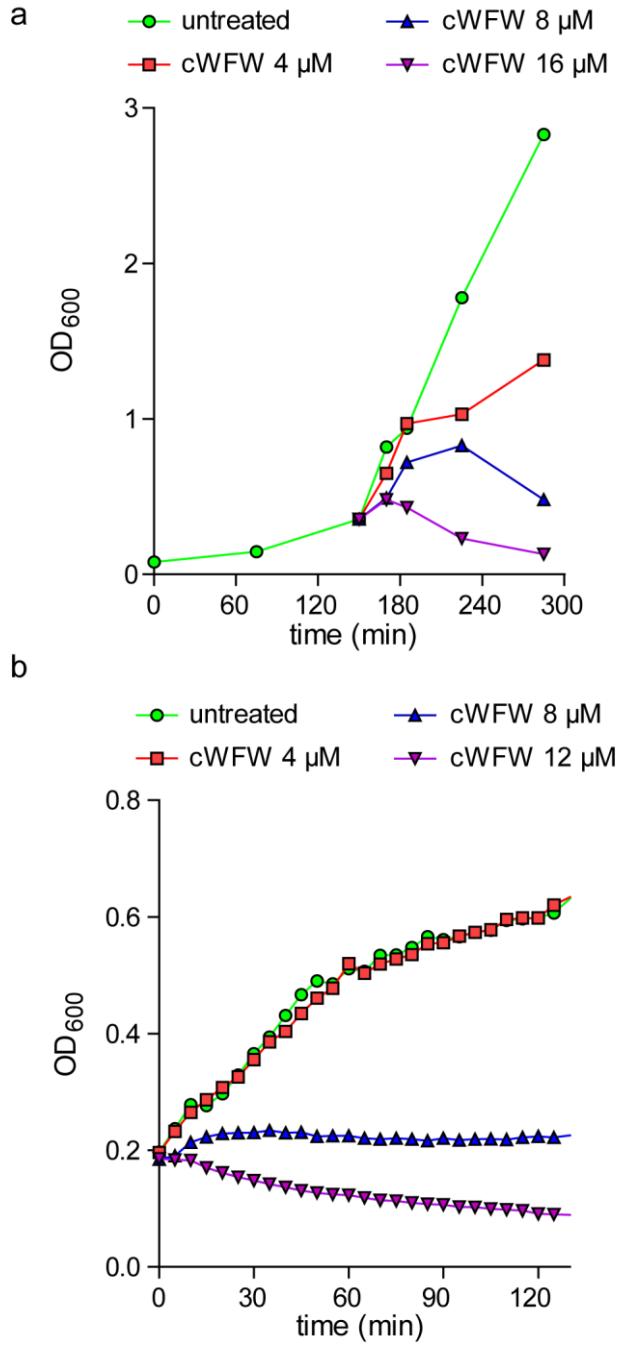


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8 **Antimicrobial peptide cWFW kills by combining lipid phase separation with autolysis**
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10 Supplementary Information
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13 Kathi Scheinpflug, Michaela Wenzel, Oxana Krylova, Julia E. Bandow, Margitta Dathe, and
14 Henrik Strahl
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19 Content:
20 Supplementary Figures 1-3
21 Supplementary Tables 1-5
22 Supplementary Movie 1
23 Supplementary References

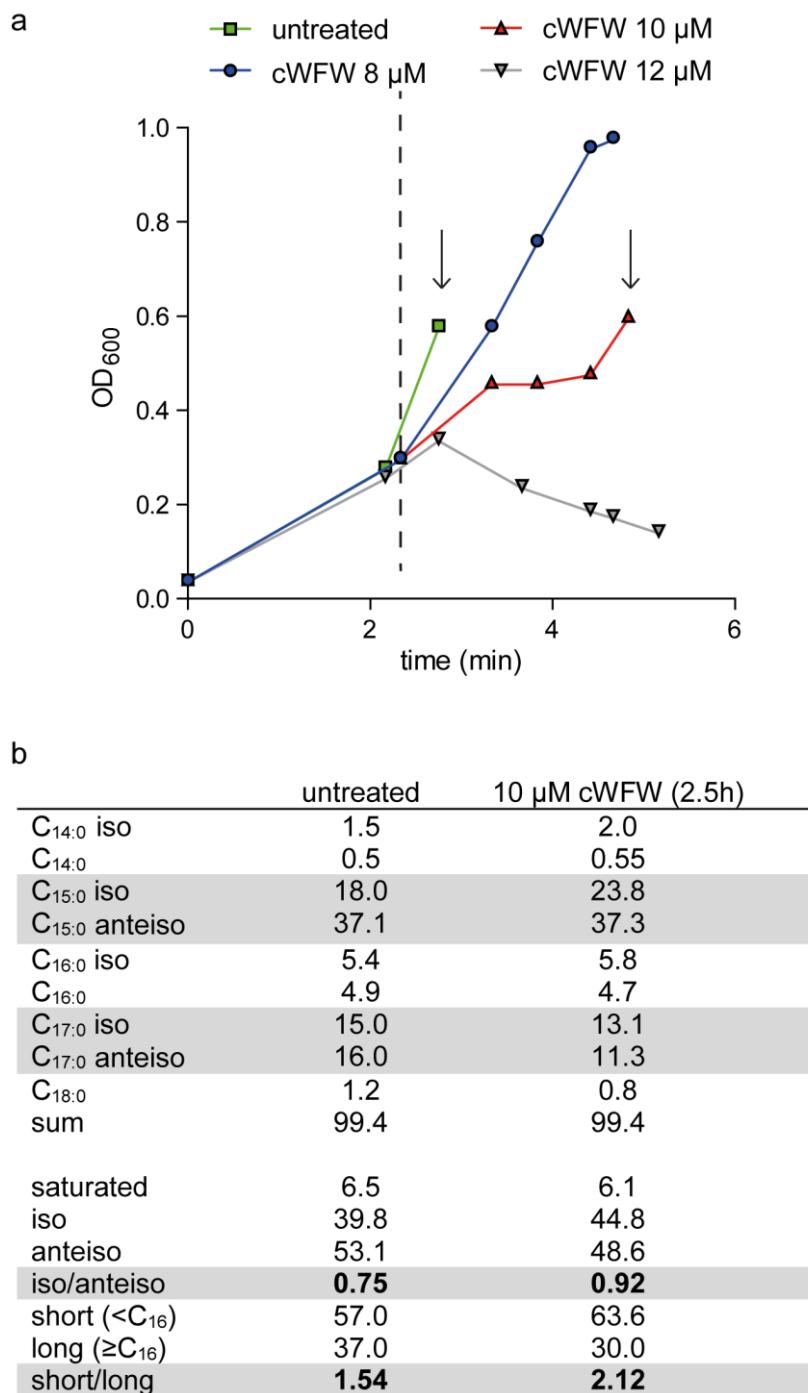


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25 **Supplementary Fig. 1: Concentration-dependent growth inhibition of *B. subtilis* in the**
 26 **different growth media used in this study**

27 (a) Growth curves of *B. subtilis* 168/DSM402 at 37 °C in BMM upon addition of different
 28 concentrations of cWFW. The time point of cWFW addition is indicated with a dashed line.
 29 The selected inhibitory concentration (8 µM) was used for proteome and ion content analysis.
 30 (b) Growth curves of *B. subtilis* 168 at 37 °C in LB-medium in the presence of different

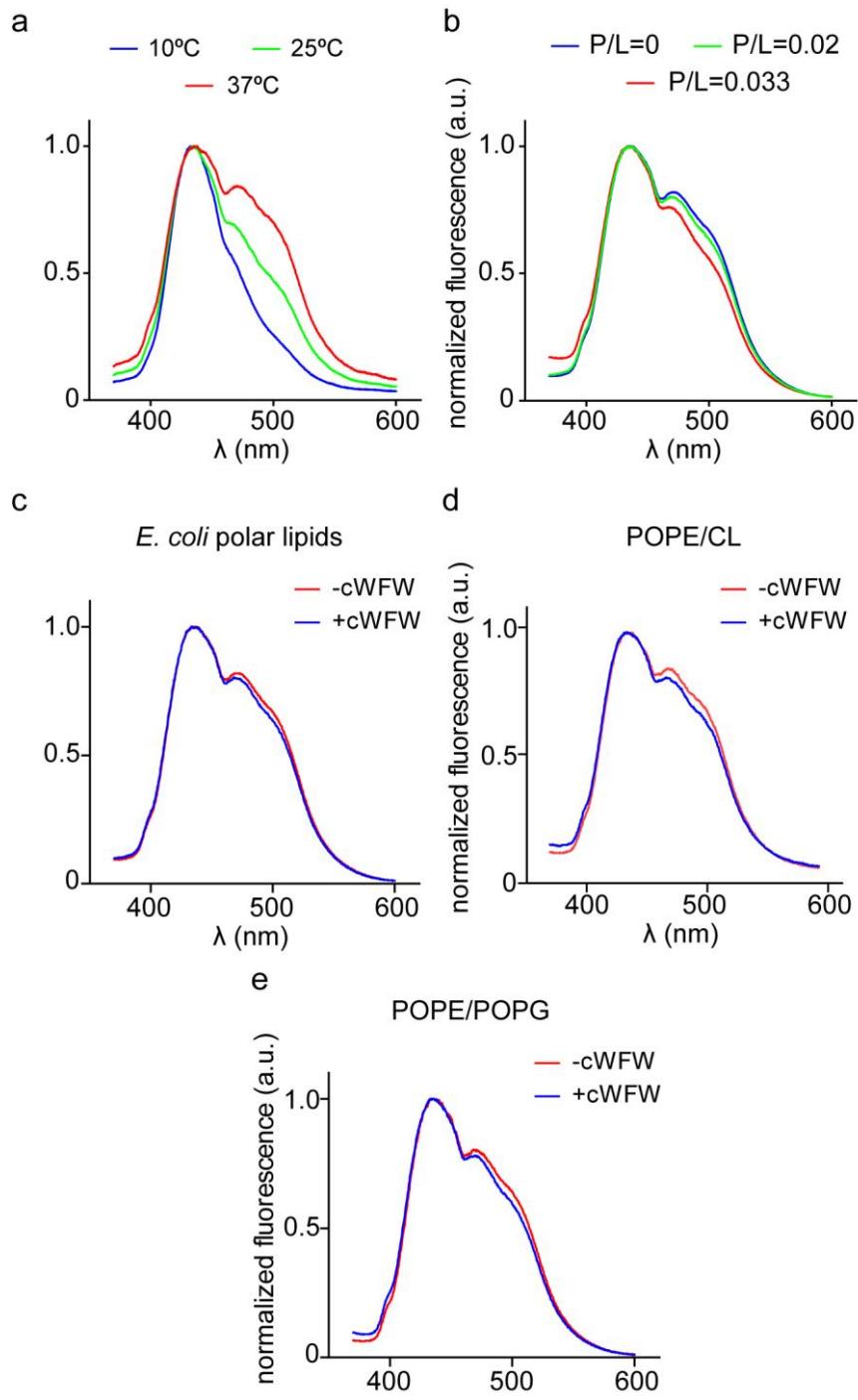
31 concentrations of cWFW as measured on microtiter plates. The growth inhibition upon peptide
32 addition to a logarithmically growing culture at $OD_{600}=0.2$ is shown. The graphs depict a
33 representative of three independent measurements.



34

35 **Supplementary Fig. 2: Membrane fatty acid adaptation in response to cWFW**

36 (a) Growth curves of *B. subtilis* 168 at 37 °C in LB medium upon addition of different
 37 concentrations of cWFW. The time points of cell harvest for fatty acid analysis are indicated
 38 with arrows. The graphs depict a representative of two independent measurements. (b) The
 39 cellular fatty acid profile in the absence of cWFW and after 2.5 h incubation with 10 μ M
 40 cWFW. Strain used: *B. subtilis* 168 (wild type).



41

42 **Supplementary Fig. 3: cWFW-dependent laurdan fluorescence emission spectra in LUVs**

43 **of varying lipid composition**

44 (a) Fluorescence emission spectrum of laurdan incorporated into large unilamellar vesicles

45 (LUVs) formed of *E. coli* polar lipid extract at different temperatures. Note the spectral shift

46 caused by reduced membrane fluidity at lower temperatures. (b) Fluorescence emission

47 spectrum of laurdan stained LUVs formed of *E. coli* polar lipids at 37 °C in the presence of

48 different concentrations of cWFW. P/L indicates peptide-to-lipid molar ratio. (C-D)
49 Fluorescence emission spectrum of laurdan stained LUVs formed of *E. coli* polar lipids, a
50 binary mixture of POPE and cardiolipin (POPE/CL) and a binary mixture of POPE and POPG,
51 respectively, in the absence and presence of cWFW (P/L=0.02). The spectra depict a
52 representative of two independent measurements.

53 **Supplementary Table 1: Comparison of cWFW with proteome response library**

protein	cWFW	MP196	vancomycin	mersacidin	gallidermin	nisin	gramicidin S	valinomycin	gramicidin A	ionomycin	triton X-100
YceC*	x	x	x	x	x		x			x	x
FosB	x	x									
YfhM	x	x								x	x
YthP	x	x									
YvlB	x	x			x		x	x		x	x
LiaH#	x	x		x	x	x	x				
RacX	x	x					x	x			
YpuA#	x			x	x	x	x				
DltA	x	x			x						
PspA°	x	x			x	x	x	x	x		x
YjdA	x	x					x	x			
YoxD	x	x	x				x		x		
NadE°	x	x			x	x	x	x	x		x
NfrA	x	x			x		x	x			
YwrO	x	x					x				x
CitZ	x	x						x		x	
GsiB	x	x					x	x			
YdaG	x	x									
Dps	x	x						x			
ClpP	x					x					
Tpx	x									x	
YqiW	x									x	
YdbD	x	x				x					
SpoVG	x	x					x			x	
total markers	52	36	5	13	25	8	21	22	5	38	26

54 *specific marker for cell envelope stress, °specific marker for membrane stress, #specific marker for
 55 inhibition of membrane-bound cell wall biosynthesis steps ¹.

56 **Supplementary Table 2: Details of mass spectrometric protein spot identification (nLC-**
 57 **ESI-MS)**

protein	mass weight [Da]	pl	PGLS score	number of matching proteins	coverage [%]	number of peptides with fragment data	precursor mass error [ppm]	product mass error [ppm]
AcsA	64850	5.54	4431	48	36	48	1.38	4.08
ClpC	90063	5.75	22605	182	60	159	1.55	4.88
FosB	17161	6.14	754	4	17	4	1.57	2.17
NfrA	28302	5.73	9602	24	33	20	1.58	4.45
SalA	38614	5.23	6829	18	44	33	1.42	3.67
YfhM	32737	6.07	7499	22	46	20	1.23	3.88
YpuA	31275	4.51	20679	38	53	30	1.75	4.39
GroEL	57388	4.53	35524	178	90	178	2.80	7.77
OhrB	14591	4.73	7866	23	94	23	2.07	9.24
GtaB	33049	4.91	36499	111	96	111	2.18	7.66
TpiA	27012	4.79	1709	10	32	10	2.21	10.05
PepF	77024	5.49	15612	116	63	116	1.63	7.80
PurH	55719	5.13	4098	60	51	60	3.24	8.39
Ywjl	33929	5.06	15972	43	74	43	2.01	7.46
FbaA	30381	5.02	12444	63	85	63	2.06	8.03
MinD	29388	4.98	16778	43	62	43	1.68	7.57
YkaA	23829	4.90	7090	27	63	27	1.86	9.71

59 **Supplementary Table 3: Details of mass spectrometric protein spot identification**
 60 **(MALDI-ToF/ToF)**

protein	mass weight [Da]	pl	mascot protein score	mascot protein score % C.I.	number of peptides used for identification
CitZ	41702	5.55	444	100	16
ClpP	21668	5.19	353	100	12
DltA	55773	5.10	276	100	13
Dps	16583	4.64	168	100	8
GlpK	55045	5.16	96	100	11
GroEL	57388	4.53	146	100	11
GsiB	13789	5.31	122	100	5
IspH	34902	5.68	91	100	2
LiaH	25682	6.20	112	100	13
LuxS	17703	5.29	301	100	5
NadE	30376	5.07	459	100	16
PspA	25125	5.87	91	100	11
RacX	25270	5.46	73	100	3
SodA	22561	5.33	414	100	8
SpoVG	10886	5.25	348	100	10
Tpx	18204	4.89	403	100	15
YceC	21810	5.46	224	100	14
YdaG	15867	5.33	111	100	5
YdbD	30238	5.06	103	100	10
YjdA	27432	5.74	55	99	5
YoxD	25283	5.48	434	100	20
YqiW	16186	5.00	137	100	7
YqkF	34695	5.30	535	100	14
YthP	26490	5.39	195	100	5
YvIB	41056	5.50	156	100	10
YvyD	21966	5.36	393	100	11
YwrO	19942	5.33	166	100	7
YxaB	39738	4.72	452	100	18

62 **Supplementary Table 4: Strains used in this study**

Strain	Relevant Genotype	Induction	MIC	Source
<i>B. subtilis</i> 168	wild type	-	6*	2
<i>B. subtilis</i> 168/DSM402	wild type	-	8#	3
<i>B. subtilis</i> KS69	<i>amyE::spc Pxyl-msfgfp-mreB</i>	0.3% xyl	nd	this work
<i>B. subtilis</i> KS70	<i>amyE::spc Pxyl-msfgfp-mbl</i>	0.3% xyl	nd	this work
<i>B. subtilis</i> TNVS175	<i>amyE::spc Pxyl-murG-msfgfp</i>	0.05% xyl	nd	4
<i>B. subtilis</i> KS19	<i>lytABC::neo lytD::tet lytE::cat lytF::spc</i>	-		this work
<i>B. subtilis</i> L16648	<i>lytABC::neo lytD::tet lytE::cat lytF::spc</i>	-	nd	5
<i>B. subtilis</i> HB5343	<i>psd::ery</i>	-	6*	6
<i>B. subtilis</i> SDB206	<i>ywiE::neo clsB::spc clsA::ery</i>	-	6*	7
<i>B. subtilis</i> BS23	<i>cat atpA-gfp:Pxyl-'atpA</i>	0.5% xyl	nd	8
<i>B. subtilis</i> HS41	<i>amyE::tet Pxyl-yhaP-gfp</i>	1% xyl	nd	9
<i>B. subtilis</i> HS64	<i>amyE::spc Pxyl-WALP23-gfp</i>	1% xyl	nd	this work
<i>B. subtilis</i> KR318	<i>amyE::psc Phyperspank -spoVM-gfp</i>	1 mM IPTG	nd	10
<i>B. subtilis</i> HS65	<i>amyE::spc Pxyl-gfp-junLZ-MTS_{MinD}</i>	1% xyl	nd	this work
<i>B. subtilis</i> HS208	<i>amyE::spc Pxyl-MTS_{SepF}-junLZ-gfp</i>	1% xyl	nd	11

63 *determined in LB, #determined in BMM

64

65 **Supplementary Table 5: Oligonucleotides**

Oligonucleotide	Sequence
JunLZ-for	gcgcgGGATCCTTGGTGGTCGTACGCTCGTCC
MTS-rev	gcgcgAAGCTTAAGATCTTACTCCGAAAAATGA
pSG1154-for	ATGAGTAAAGGAGAAGAACCTTTCAC
pSG154-rev	CATCCTAGGAATCTCCTTCTAG
WALP23-for	ATGGCTTGGTGGTAGCCTTGGCATTGGCGCTTGCTCTGCCCTGGC
WALP23-rev	CGCCCACCACAGGGCTAACGCCAATGCCAGGGCGAGAGCAAGCGCC
WALP23-IFfor	GAGATTCTAGGATGGCTTGGTGGTTAGCCTG
WALP23-IFrev	TCTCCTTACTCATTCTGAGCCGCTTGCACGCCACCACAGGGCTAAC

66

67 **Supplementary Movie 1: cWFW-dependent cell lysis**

68 Growth and lysis of *B. subtilis* 168 at 37 °C in solid LB medium in the absence and presence
69 of cWFW (25 µM). Strain used: *B. subtilis* 168 (wild type).

70 SUPPLEMENTARY INFORMATION REFERENCES

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