Liposomal Therapy Attenuates Dermonecrosis Induced by Community-Associated Methicillin-Resistant Staphylococcus aureus by Targeting α-Type Phenol-Soluble Modulins and α-Hemolysin

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1. Introduction

Community-associated methicillin-resistant Staphylococcus aureus (CA-MRSA), typified by the pulse-field type USA300, is an emerging endemic pathogen that is spreading rapidly among healthy people. CA-MRSA causes skin and soft tissue infections, life-threatening necrotizing pneumonia and sepsis, and is remarkably resistant to many antibiotics. Here we show that engineered liposomes composed of naturally occurring sphingomyelin were able to sequester cytolytic toxins secreted by USA300 and prevent necrosis of human erythrocytes, peripheral blood mononuclear cells and bronchial epithelial cells. Mass spectrometric analysis revealed the capture by liposomes of phenol-soluble modulins, α-hemolysin and other toxins. Sphingomyelin liposomes prevented hemolysis induced by pure phenol-soluble modulin-α3, one of the main cytolytic components in the USA300 secretome. In contrast, sphingomyelin liposomes harboring a high cholesterol content (66 mol%) were unable to protect human cells from phenol-soluble modulin-α3-induced lysis, however these liposomes efficiently sequestered the potent staphylococcal toxin α-hemolysin. In a murine cutaneous abscess model, a single dose of either type of liposomes was sufficient to significantly decrease tissue dermonecrosis. Our results provide further insights into the promising potential of tailored liposomal therapy in the battle against infectious diseases.

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2.1. Liposomes

producing dermonecrosis in a murine cutaneous abscess model. Types of liposomes attenuated CA-MRSA virulence by significantly bound by the Sm liposomes revealed α-type PSMs as an interacting target. Sm liposomes, but not Ch:Sm liposomes decreased hemolysis induced by purified recombinant PSM-αc. In contrast to Sm liposomes, Ch:Sm liposomes efficiently bound α-hemolysin. Furthermore, both types of liposomes attenuated CA-MRSA virulence by significantly reducing dermonecrosis in a murine cutaneous abscess model.

2. Materials and Methods

2.1. Liposomes

Unilamellar cholesterol:sphingomyelin (Ch:Sm, 66 mol/% cholesterol, 40 mg/ml, diameter 130 nm) and sphingomyelin (Sm, 40 mg/ml, diameter 60 nm) liposomes in sodium Tyrode’s buffer (140 mM NaCl, 5 mM KCl, 1 mM MgCl₂, 2.5 mM CaCl₂, 10 mM glucose, 10 mM HEPES; pH = 7.4) were provided by Lascco (Geneva, Switzerland, product name CAL02).

2.2. Bacterial strains and supernatants

The MRSA USA300 pulse field type isolate LAC (USA300) was kindly provided by Michael Otto (National Institute of Health, Bethesda, MD) and bioluminescent LAC USA300 was kindly provided by Scott Stibitz (Food and Drug Administration, Silver Spring, MD). Bacteria were cultured in Tryptic Soy Broth (TSB, Becton Dickinson). Overnight cultures were diluted in fresh TSB to an optical density OD₆₀₀ of 0.1 and incubated at 37 °C under shaking conditions for 22 h. Bacteria were pelleted (5000 × g, 10 min) and the resulting supernatants were filter sterilized (pore size 0.2 μm, Nalgene).

If indicated, bacterial supernatants were high-speed centrifuged (100,000 × g) at 4 °C for 1 h. The resulting supernatants were treated with liposomes or sodium Tyrode’s buffer (vehicle) for 5 min. Subsequently, liposomes were pelleted (100,000 × g) at 4 °C for 1 h. The resulting liposome-free supernatants were used for the cytotoxicity assay in Fig. 1e. The liposome/toxin or vehicle/toxin pellets were applied to SDS-PAGE or mass spectrometric analysis.

2.3. Human cells

Peripheral blood mononuclear cells (PBMCs) and red blood cells (RBCs) were isolated from the blood of healthy, consenting human volunteers (following the University of British Columbia ethics guidelines). Blood was collected in sodium heparin anticoagulant collection tubes (BD Biosciences), diluted in phosphate buffered saline (PBS, Thermofisher/Gibco) and layered onto Lymphoprep density gradient medium (STEMCELL Technologies). After centrifugation (500 × g for 20 min) the buffy coat was transferred to a new tube, washed three times with PBS and resuspended in RPMI-1640 Medium (+25 mM HEPES, +l-glutamine, GE Healthcare) supplemented with 10% fetal bovine serum (FBS, Thermofisher/Gibco). PBMCs were seeded at a density of 100,000 cells and rest.

RBCs were collected from the bottom of the density gradient, washed three times with PBS and stored for a maximum of 4 weeks in Alsever’s solution (Sigma Aldrich).

The human bronchial epithelial cell line 16HBE14o- (HBE, RRID: CVCL_0112) was kindly provided by Dr. D. Gruenert (University of California San Francisco). HBE cells were maintained in MEM medium (Thermofisher/Gibco) supplemented with 10% FBS, 2 mM l-glutamine (Thermofisher/Gibco) and 1% penicillin/streptomycin (Thermofisher/Gibco) at 37 °C in 5% CO₂. Cells were dissociated with 0.25% trypsin-EDTA (Thermofisher/Gibco) at 80–90% confluency.

2.4. Hemolysis assay

Prior to use, RBCs were washed three times with TSB (1000 × g, 10 min). Serial dilutions of liposomes were incubated with bacterial supernatants (50 μl) and 2% RBCs in a 200 μl reaction volume with TSB in microtiter plates (Falcon). The hemolytic activity of purified staphylococcal PSM-αc peptide (IBT Bioservices, Cat# 1401–004) was assessed in PBS. Triton X-100 (2% v/v, Sigma–Aldrich)-treated RBCs served as a positive control and TSB-treated RBCs as a negative control. After incubation for 1 h at 37 °C, RBCs were pelleted (1000 × g, 10 min) and the hemoglobin content in the supernatant was measured at OD₅₅₀ (reference 630 nm) using a microplate reader. Relative hemolysis (%) was calculated as (ΔODsample – ΔODnegative control)/(ΔODpositive control – ΔODnegative control) × 100.

2.5. Cytotoxicity assays

Cytotoxicity assays were performed in cell–culture treated microtiter plates (Costar). 100,000 PBMCs were seeded directly after their isolation in RPMI +10% FBS (100 μl) and rested for 1 h. 40,000 HBE cells were seeded two days prior treatment in MEM + 10% FBS and grown to confluence. Shortly before treatment the medium was replaced with MEM + 1% FBS (100 μl). Bacterial supernatants (12.5 μl PBMCs, 50 μl HBE cells) and liposomes (300 μg/ml) or sodium Tyrode’s buffer (vehicle) were added (total reaction volumes: 150 μl PBMCs, 200 μl HBE cells). Triton X-100 (2% v/v, Sigma–Aldrich)-treated PBMCs or HBE cells served as a positive control and TSB-treated PBMCs or HBE cells as a negative control. After incubation for 1 h at 37 °C, PBMCs or HBE cells were centrifuged (500 × g, 5 min) and the lactate dehydrogenase (LDH) content in the supernatant was assessed with the Cytotoxicity Detection Kit Plus (Roche) according to the manufacturer’s instructions. Relative LDH release (%) was calculated by (ΔODsample – ΔODnegative control)/(ΔODpositive control – ΔODnegative control) × 100.

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2.6. Confocal microscopy

Confluent HBE cells in cell-culture treated glass bottom microtiter plates (Greiner bio-one) were stained with the CellTracker Orange CMTMR dye (5 μM, excitation 548/emission 576, ThermoFisher Scientific, Cat# C2927) in serum-free MEM for 30 min. The medium was replaced with 100 μM MEM without phenol red (ThermoFisher/Gibco) and cells were treated with USA300 supernatants and liposomes (300 μg/ml) or sodium Tyrode’s buffer (vehicle) for 1 h. Imaging was performed with a ZEISS LSM 800 confocal microscope equipped with an incubation system at 37 °C and analyzed with the ZEISS ZEN software 2.3 blue edition.

2.7. Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) and silver staining

Samples were resuspended in 2 × SDS-loading buffer (65.8 mM Tris-HCl, pH = 6.8, 26.3% (w/v) glycerol, 2.1% SDS, 0.01% bromophenol blue, 355 mM 2-mercaptopethanol) and were boiled at 95 °C for 5 min. Pellets, bacterial supernatants and a protein standard (Precision Plus Protein 355 mM 2-mercaptoethanol) and were boiled at 95 °C for 5 min. Protein silver staining was performed as described [26]. In brief, the gel was soaked in 50% methanol overnight, washed in deionized water and agitated for 10 min in staining reagent (1.4 ml [26]). In brief, the gel was soaked in 50% methanol overnight, washed in deionized water and agitated for 10 min in staining reagent (1.4 ml ammonium hydroxide, 21.0 ml of 0.36% NaOH, 4.0 ml of 20% in deionized water and agitated for 10 min in staining reagent (1.4 ml ammonium hydroxide, 21.0 ml of 0.36% NaOH, 4.0 ml of 20% SDS-running buffer (25 mM Tris, 192 mM glycine, 0.1% SDS) at 150 V for 30 min. Protein silver staining was performed as described [26]. In brief, the gel was soaked in 50% methanol overnight, washed in deionized water and agitated for 10 min in staining reagent (1.4 ml ammonium hydroxide, 21.0 ml of 0.36% NaOH, 4.0 ml of 20% w/v AgNO₃ increased to 100 ml with deionized water). After washing the gel in deionized water, it was incubated in developer solution (2.5 ml citric acid (1% w/v), 0.25 ml formaldehyde (38% v/v), increased to 250 ml with deionized water). When the gel achieved the desired state of staining, it was soaked in 50% methanol/10% acetic acid. Bands were visualized with an imaging system (Chemidoc Touch Imaging System, Bio-rad).

2.8. Western blotting

All steps were performed at room temperature. SDS-gels were transferred to a PVDF membrane (Immun-Blot PVDF membrane, Bio-rad) in Towbin buffer (25 mM TRIS, 192 mM Glycine, 20% methanol, pH = 8.6) at 30 V overnight. The membrane was blocked in blocking buffer (PBS, 0.3% Tween-20, 3% bovine serum albumin) for 1 h and incubated with 1 μg/ml of a monoclonal mouse anti-alpha-hemolysin antibody (887 N-terminal, ab190467, Abcam) diluted in washing buffer (PBS, 0.3% Tween-20, 1% bovine serum albumin) for 2 h. After washing the membrane three times for 5 min with washing buffer, it was incubated with an ECL mouse IgG, HRP-linked whole antibody from sheep (NXA931, Amersham, RID:AB_772290) at a dilution of 1 to 5000 in washing buffer for 1 h. The membrane was washed three times with washing buffer and the Clarity Western ECL detection Kit (Bio-rad) was used according to the manufacturer’s instructions. Bands were visualized with an imaging system. Black and white values were inverted for data presentation.

2.9. Mass spectrometry

In gel digestion and mass spectrometric analysis of Sm liposome/toxin pellets (35 μl/sample) were performed by the Proteomics Core Facility of the University of British Columbia (Vancouver, BC, Canada). The in gel digestion procedure was performed as described by Shevchenko et al. (1996) [27]. In brief, the protein lanes were excised from SDS-PAGE, chopped into small pieces, washed with 50% digestion buffer (50 mM NH₄HCO₃) and 50% ETOH, dehydrated with absolute ETOH. Gel pieces were incubated with dithiothreitol (10 mM) at 56 °C for 45 min and with iodoacetamide (55 mM) for 30 min at room temperature. After washing with digestion buffer, gel pieces were dehydrated and 150 μl of 0.3% AcOH) and 10 μl of 20% AcOH were added. The samples were vortexed and the liquid was collected. Three gel extractions were performed with the following extraction solutions: [1] 0.5% AcOH, [2] 30% MeCN, 0.5% AcOH, and [3] 100% MeCN. All liquids were combined and the organic portion was removed by vacuum centrifugation. Following digestion, the samples were desalted on C18 STAGE tips [28] eluted with 80% acetonitrile, dried and suspended in 3% acetonitrile +0.1% formic acid. Approximately 5 μg of protein was loaded onto an Agilent 6550 QToF mass spectrometer, through and Agilent 1200 capillary HPLC connected by a 2.1 mm × 250 mm POROShell C18 column. The QToF was in AutoMS/MS mode, at 2 spectra/s for MS and 3 spectra/s for MS/MS scans. LC-MS/MS data was processed using MaxQuant 1.5.3.30 using default values for Agilent QToF data (including 1% FDR), against the Uniprot Staphylococcus aureus USA300 (UP000019393) database.

2.10. Murine cutaneous infection model

The mouse skin infection model was performed as described previously [29]. In brief, the backs of 6-week old female CD-1 mice (Charles River Laboratories, Wilmington, MA) were shaved and depilated. USA300 and bioluminescent USA300 were grown to OD₆ₐ₅ₐ of 1 in TSB, washed twice with PBS and resuspended to a final concentration of 5 × 10⁶ colony forming units (CFU)/5 μl. Bacteria (50 μl) were injected subcutaneously to the right flank of the back. Sm or Ch:Sm liposomes (50 μl of 40 mg/ml –80 mg/kg) were applied intra-abscess injection after 1 h. After 72 h dermonecrosis was measured using a caliper and skin abscesses were excised and homogenized for CFI quantification (non-luminescent USA300). Bioluminescent USA300 LAC bacteria were used to track the disease progress (abscess size and bacterial burden) in real-time. Mice were anesthetized with isoflurane and imaged using the Lumina in vivo Imaging System (IVIS) (Perkin Elmer, Waltham MA) up to 10 days post-infection. Luminescence counts were determined using Living Image® Software, and reported as region of interest (ROI) values. Abscess size measurements were read up to 10 days using a caliper. All animal experiments were performed in accordance with The Canadian Council on Animal Care (CCAC) guidelines and were approved by the University of British Columbia Animal Care Committee.

2.11. Quantification and statistical analysis

Statistical significance was analyzed by Graph Pad Prism 7. All details (statistical test, number of experiments, and definition of significance) are provided in the corresponding figure legends.

3. Results

3.1. Sphingomyelin liposomes protected human cells from necrosis induced by the S. aureus USA300 secretome

Initially we tested the efficacy of Sm and Ch:Sm liposomes in preventing lysis of human red blood cells (RBCs) induced by supernatants of USA300 grown for 22 h. Hemolysis, as measured by the leakage of hemoglobin from ruptured erythrocytes, was reduced by >90% if Sm liposomes were added at concentrations of ≥300 μg/ml (Fig. 1a). Interestingly, the Ch:Sm liposomes did not decrease hemolysis at the highest concentration tested (600 μg/ml) although the same concentration of the sphingomyelin lipid in Sm liposomes (200 μg/ml) led to a reduction of ~80%. Addition of Sm, but not Ch:Sm liposomes (both at 300 μg/ml), significantly diminished necrosis, induced by USA300 supernatants, of human peripheral blood mononuclear cells (PBMCs) (Fig. 1b) and HBE cells (Fig. 1c). Laser scanning micrographs of HBE cells stained with CellTracker Orange, a cell-permeable dye that is intracellularly converted to fluorescent membrane-impermeant products, illustrated the destructive effect of USA300 supernatants leading to disassembly of...
the cells into necrotic blebs, and an overall decline in the fluorescent signal (Fig. 1d). Addition of Ch:Sm liposomes slightly attenuated cell fragmentation, whereas Sm liposomes prevented fatal necrosis, as indicated by the retention of the cell shape and intracellular fluorescent products (Fig. 1d). We further addressed whether cytolytic virulence factors became liposome-bound and thus might be removed with the liposomes. Virulence factors in bacterial supernatants were neutralized by liposomal treatment and the liposomes were subsequently removed by centrifugation. This revealed that the cell cytolytic factors in the supernatants were sequestered by Sm, but not by Ch:Sm liposomes (Fig. 1e).

3.2. Sphingomyelin liposomes neutralized α-type phenol-soluble modulins; cholesterol-containing liposomes bound α-hemolysin

To identify secreted bacterial virulence factors that were bound to the liposome pellets, proteins were separated by SDS-PAGE (Fig. 2a). Protein bands in the liposome-free control (p. vehicle) indicated the presence of a considerable non-specific protein background. However, a prominent band appeared in the Ch:Sm liposome pellet at ~35 kDa (Fig. 2a, lane p; Ch:Sm, band marked with an arrow). Immunoblotting with an anti-α-hemolysin antibody confirmed the identity of this band demonstrating that Ch:Sm liposomes efficiently sequestered α-hemolysin (36 kDa) from USA300 supernatants, while Sm liposomes sequestered lower amounts and the vehicle pellet showed no signal (Fig. 2b; see Supplementary Fig. 1 for the complete Western Blot). Mass spectrometric analysis of the Sm pellet was performed to verify the presence of virulence factors and led to the identification of 159 proteins (Supplementary Table 1) commonly found in 3 independent bacterial supernatant preparations. As expected, proteomic analysis of the Sm/protein pellets reflected most of the proteins secreted by USA300. In addition to α-hemolysin (Hla), the bi-component leukocidin PVL (LukS-PV, LukF-PV), γ-hemolysin components A (HlgA) and B (HlgB), PSM-α1, 3, and 4, and δ-hemolysin (Hld) were also present in the Sm/protein pellets (Table 1). Since PSMs, especially PSM-α3, are the main cytolytic components of USA300 supernatants [6], and can interact with PC liposomes [30, 31], we tested whether engineered liposomes sequestered purified PSM-α3. PSM-α3 (50 μg/ml) led to 60% hemolysis of human RBCs. Sm but not Ch:Sm liposomes (300 μg/ml) significantly diminished PSM-α3-induced hemolysis (Fig. 2c).

3.3. Liposomes reduced dermonecrosis in a murine USA300 abscess model

Since USA300 skin infection studies in rodents have demonstrated the importance of α-type PSM toxins [6, 12] and α-hemolysin [11, 32] in tissue necrosis, we investigated whether Sm and Ch:Sm liposomes could be used therapeutically to target α-type PSMs and α-hemolysin of USA300 in a murine cutaneous abscess model.

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Subcutaneously injected Sm or Ch:Sm liposomes (80 mg/kg) did not induce dermonecrosis, redness or any other sign of inflammation. Intriguingly, a single dose of Sm or Ch:Sm liposomes (80 mg/kg) applied subcutaneously 1 h after infection significantly decreased USA300-induced tissue necrosis measured 72 h post-infection (Fig. 2d). Liposomal treatment did not reduce the bacterial load (Fig. 2e). Abscess sizes and bacterial burden measurements of abscesses induced by bioluminescent USA300 up to 10 days post-infection are shown in Fig. 2f and g, respectively. These results showed that Sm liposomes caused moderate but significant decreases at days 1 and 2, while a single dose of Ch:Sm liposomes caused very substantial to complete abrogation of tissue necrosis at all measured time points up to day 10. In contrast there was no significant change in bioburden on any day, but rather a steady decline in concentrations over the 10-day experiment.

4. Discussion

PSMs and α-hemolysin are critical determinants of CA-MRSA virulence [4, 6, 12, 16, 19, 20, 23]. Studies investigating the effect of PSMs in animal models of SSTIs have shown that dermonecrosis caused by a...
ΔpsmA mutant was highly attenuated compared to the wildtype strain, whereas the deletion of β-toxin showed only a modest reduction of virulence [4, 6, 12]. During SSTIs, PSMs cause the massive recruitment of neutrophils and contribute to tissue damage [6, 18, 20]. Furthermore, PSMs have been shown to influence the expression of virulence-promoting α-hemolysin [11], a toxin that is also involved in abscess formation [11, 32].

Here, we demonstrated that PSM-α3 was bound and neutralized by Sm liposomes in vitro (Fig. 2c) and that dermonecrosis was attenuated by Sm liposome treatment in a cutaneous abscess mouse model (Fig. 2d, f). Therefore we suggest that Sm liposomes sequester α-type PSMs and protect host cells from deleterious PSM effects.

Surewaard et al. (2012) showed that the lytic and pro-inflammatory activities of PSMs were blocked in a serum environment. They identified lipoproteins as PSM scavengers and reasoned that PSMs preferentially bound the lipid rather than protein components. Thus PSM-α1, PSM-α2, PSM-α3, PSM-α4 and β-toxin were efficiently sequestered by high density lipoprotein (HDL) isolated from S. aureus MW2 human blood cultures. They concluded that PSMs mainly contributed to pathogenesis by acting intracellularly after bacterial uptake by neutrophils rather than as secreted toxins [33]. To our knowledge, no data regarding in vivo PSM concentrations during skin infection or other USA300 animal models exist. However in SSTIs it is likely that localized bacterial densities and consequent quorum sensing result in sufficiently high local PSM concentrations to promote receptor-dependent pro-inflammatory responses [8, 18, 19], the potentiation of other virulence factors [11, 20] and liberation of bacterial cytoplasmic protein stores including other factors [22, 34].

In contrast to Sm liposomes, Ch:Sm liposomes efficiently sequestered α-hemolysin [24] (Fig. 2b) but did not target PSM-α3 (Fig. 2c) or other factors responsible for prompt host cell lysis (Fig. 1). Previous studies demonstrated that adding ≥50 mol%/choleratoxin concentrations into dipalmitolyl-phosphatidylcholine (DPPC) liposomes led to increased membrane rigidity and negatively affected but did not completely block the vesicle-lyzing activity of PSMs [31]. This may explain the poor efficacy of the 66 mol%/choleratoxin-containing Ch:Sm liposomes in protecting host cells from PSM-mediated lysis. However, Ch:Sm liposomes were very effective in reducing tissue necrosis in the murine abscess model (Fig. 2d, f).

We point out that the high efficacy of Sm liposomes in neutralizing PSM-α3 and Ch:Sm liposomes in sequestering α-hemolysin in vitro does not exclude the possibility of binding of other staphylococcal or host proteins to the liposomes during the infection. Moreover, the fact that liposomes do not exclusively bind one toxin type (Supplementary Table 1) confer on them even greater therapeutic potency due to broad spectrum protection of host cells.

Blocking PSMs or α-hemolysin in vivo is a desired strategy to attenuate overall virulence. To date several approaches exist affecting staphylococcal PSM expression (8, 29, 35). Recently we demonstrated that the cationic synthetic peptide DJK-5 targeted the bacterial stringent stress response in the USA300 murine cutaneous abscess model, leading to a significant reduction of the lesion size as well as the bacterial burden. In vitro, the expression of stringently regulated PSMs was suppressed at sub-lytic DJK-5 concentrations [29]. This constitutes an indirect approach to target PSM expression. Other studies investigated the potential of blocking bacterial PSM export systems [35] or the human formyl peptide receptor 2 (FPR2/ALX) that senses PSMs and controls PSM-induced inflammatory processes [8]. Although monoclonal antibodies against α-hemolysin have been shown to be protective in a CA-MRSA lung infection model [36], to date no PSM antibodies have been developed, probably because of the high amino acid sequence diversity and overlapping functions of PSMs [37].

In contrast to therapeutic strategies intervening with the expression of staphylococcal virulence-associated genes, we demonstrated here a liposome-based strategy to sequester the most potent S. aureus toxins. The neutralization of α-type PSMs by Sm liposomes and α-hemolysin by Ch:Sm liposomes could beneficially influence the course of disease during localized infections such as necrotizing pneumonia or SSTIs. Liposomal therapy is not strain specific and exerts no known selective pressure on pathogens. To date, incision and drainage followed, in severe cases, by antibiotic therapy are the recommended treatment for cutaneous abscesses [38]. Nevertheless, in killing bacteria, antibiotic treatment can cause massive liberation of host cell-damaging and pro-inflammatory bacterial agents [39]. In contrast, the neutralization of virulence-promoting factors disarms bacteria, prevents tissue damage and supports the immune system [24]. The targeting and neutralization of PSMs and α-hemolysin by liposomes may be a valuable supportive therapy for the treatment of SSTIs. After incision and drainage of abscesses, liposomes added to topical creams or adjunctive to antibiotics may have toxin sequestration and health-promoting effects.

Conflict of Interest

E.B.B. and A.D. are inventors on the patent of tailored liposomes for the treatment of bacterial infections (CA 2875470 A1).

Table 1
Selection of virulence-associated S. aureus USA300 proteins found in the sphingomyelin liposome/toxin pellets identified by mass spectrometry.

<table>
<thead>
<tr>
<th>Protein</th>
<th>Gene Name</th>
<th>Locus Tag</th>
<th>Size (kDa)</th>
<th>Human host cell targets</th>
</tr>
</thead>
<tbody>
<tr>
<td>α-hemolysin</td>
<td>hla</td>
<td>SAUSA300_1058</td>
<td>36</td>
<td>Cholesterol and sphingomyelin enriched microdomains [24]; A Disintegrin And Metalloprotease 10</td>
</tr>
<tr>
<td>γ-hemolysin component A</td>
<td>hlgA</td>
<td>SAUSA300_2365</td>
<td>35</td>
<td>Chemokine receptors [40, 41]</td>
</tr>
<tr>
<td>γ-hemolysin component B</td>
<td>hldg</td>
<td>SAUSA300_2367</td>
<td>37</td>
<td>Chemokine receptors [40, 41]</td>
</tr>
<tr>
<td>Panton-Valentine leukocidin, LukS-PV</td>
<td>lukS-PV</td>
<td>SAUSA300_1382</td>
<td>35</td>
<td>Complement receptors [41, 42]</td>
</tr>
<tr>
<td>Panton-Valentine leukocidin, LukF-PV</td>
<td>lukF-PV</td>
<td>SAUSA300_1381</td>
<td>37</td>
<td>Complement receptors [41, 42]</td>
</tr>
<tr>
<td>δ-hemolysin</td>
<td>hld</td>
<td>SAUSA300_1988</td>
<td>5</td>
<td>Receptor-independent binding to the plasma membrane [6]; formyl peptide receptor 2 (FPR2/ALX) [8]</td>
</tr>
<tr>
<td>Phenol-soluble modulin α1 peptide, PSM-α1</td>
<td>psmA1</td>
<td>SAUSA300_0424.4</td>
<td>2</td>
<td>Receptor-independent binding to the plasma membrane [6]; formyl peptide receptor 2 (FPR2/ALX) [8]</td>
</tr>
<tr>
<td>Phenol-soluble modulin α3 peptide, PSM-α3</td>
<td>psmA3</td>
<td>SAUSA300_0424.2</td>
<td>3</td>
<td>Receptor-independent binding to the plasma membrane [6]; formyl peptide receptor 2 (FPR2/ALX) [8]</td>
</tr>
<tr>
<td>Phenol-soluble modulin α4 peptide, PSM-α4</td>
<td>psmA4</td>
<td>SAUSA300_0424.1</td>
<td>2</td>
<td>Receptor-independent binding to the plasma membrane [6]; formyl peptide receptor 2 (FPR2/ALX) [8]</td>
</tr>
</tbody>
</table>

The full list of proteins commonly found in three bacterial supernatant preparations is given in Supplementary Table 1.
**Funding Sources**

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**Author Contributions**

H.W. and R.E.W.H. designed and interpreted experiments and wrote the manuscript. H.W. and L.T.L. performed all in vitro experiments. S.C.M. performed all mouse experiments. A.D. and E.B.B. contributed to the initial findings. D.P., A.D., and E.B.B. contributed to interpretation of the experiments and editing of the manuscript.

**Appendix A. Supplementary data**

Supplementary data to this article can be found online at https://doi.org/10.1016/j.ebiom.2018.06.016.

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