Inhibition of expression of a staphyloccocal superantigen-like protein by a soluble factor from Lactobacillus reuteri

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INTRODUCTION

Bacteria utilize chemical communication systems to control gene expression within populations (Waters & Bassler, 2005). Although most research has focused on communication within a single species, there has been increasing interest towards understanding interspecies bacterial communication in order to understand cell–cell communication in natural environments, and to identify novel ways to attenuate undesirable bacteria (Visick & Fuqua, 2005). The term ‘quorum sensing’ (Fuqua et al., 1994) is used to describe a communication system employed by many bacteria to co-ordinately change gene expression in response to microbial density and the environment. Gram-negative bacteria characteristically use acylhomoserine lactones (AHLs) for their communication systems, and these are generally able to diffuse through the cell membrane, and interact directly with their intracellular target proteins when present in sufficient concentrations (Bassler, 1999). Gram-positive bacteria typically employ small post-translationally modified peptides for inter- and intraspecies communication (Dunny & Leonard, 1997). These communication peptides are usually processed from larger propeptides, and most interact with two-component histidine kinase receptors to initiate an intracellular phosphorylation cascade. In addition, many bacteria produce the autoinducer-2 (AI-2) furanosyl borate ester signal, which is encoded by the luxS gene (Surette et al., 1999). The luxS gene is found in approximately 50% of sequenced bacterial genomes, and it may represent a conserved interspecies communication signal (Waters & Bassler, 2005).

Lactobacillus reuteri RC-14 has previously been shown to inhibit Staphylococcus aureus infection in a rat surgical-implant model. To investigate the basis for this, communication events between the two bacterial species were examined. L. reuteri RC-14 and Staph. aureus Newman were grown in a co-culture apparatus that physically separates the two species, while allowing the passage of soluble compounds. Using two-dimensional gel electrophoresis (2D-E), protein expression changes in Staph. aureus were analysed in response to co-culture with medium alone, L. reuteri RC-14, and a Lactobacillus strain that did not inhibit Staph. aureus infection in the rat model. It was observed that one protein in particular, identified as staphyloccocal superantigen-like protein 11 (SSL11), showed a dramatic decrease in expression in response to growth with L. reuteri RC-14. Genetic reporters that placed both gfp and lux under the transcriptional control of the SSL11 promoter confirmed the 2D-E results. Interestingly, using similar reporter gene experiments, it was observed that the Staph. aureus P3 promoter from the staphylococcal accessory gene regulator (agr) locus also showed a decrease in expression in response to growth in the presence of L. reuteri RC-14. It was further demonstrated that L. reuteri RC-14 supernatant contained small unidentified molecules that were able to repress the SSL11 and P3 promoters, but the repression of SSL11 occurred independently of the agr system. These results suggest that L. reuteri RC-14 has the potential to alter the virulence of Staph. aureus via secretion of cell–cell signalling molecules.
It is evident that there are additional mechanisms for interspecies communication in bacteria. For example, McKenney et al. (1995) demonstrated that the addition of concentrated cell-free culture supernatant from *Pseudomonas aeruginosa* increased the production of quorum-sensing-regulated virulence factors in *Burkholderia cepacia*, and this was attributed to AHLs in the added supernatant. The host microbiota have also been shown to have the ability to upregulate genes involved in the virulence of *P. aeruginosa*, via interspecies communication of AI-2 (Duan et al., 2003). In addition to this, a recently characterized communication system between *Streptococcus gordonii* and *Veillonella atypica*, which are both colonizing members of early dental plaque, was shown to result in increased expression of α-amylase from *Strep. gordonii*, and when grown in an open system, the signal worked only when the bacterial species were in close proximity (Egland et al., 2004). *Staphylococcus aureus* has been shown to produce a peptide in a cell-density-independent manner, termed *staph*-CAM373, and this may act as a sex pheromone for certain *Enterococcus faecalis* strains (Muscholl-Silberhorn et al., 1997). The pAM373 plasmid-specific peptide may function to enhance gene transfer from *Ent. faecalis* to *Staph. aureus*, and this is a major concern for the transfer of antibiotic-resistance genes. Alternatively, interference with bacterial cell–cell communication has been termed ‘quorum quenching’ (Waters & Bassler, 2005); an example of this has been demonstrated in which *Bacillus subtilis* produces an AHL-lactonase called AiiA, which hydrolyses the lactone ring of AHTLs, and destroys their function (Dong et al., 2000, 2001). Expression of the *Bacillus anthracis* aiiA gene in *Burkholderia thailandensis* has been shown to inhibit the accumulation of the quorum-sensing molecules *N*-decanoylhomoserine lactone and *N*-octanoylhomoserine lactone, and alter motility in *B. thailandensis* (Ulrich, 2004).

*Staph. aureus* is a common hospital and community-acquired pathogen that causes infections ranging from relatively uncomplicated skin infections, such as boils and impetigo, to more severe and life-threatening deep tissue infections, including endocarditis and osteomyelitis. One well-characterized quorum-sensing system in *Staph. aureus* is the accessory gene regulator (*agr*) (Recsei et al., 1986; Yarwood & Schlievert, 2003). The *agr* locus includes an operon (*agrBDCA*) encoding an autoinducing prepeptide (*AgrD*), which is exported and processed by *AgrB* to become the active autoinducing peptide (*AIP*), and this is sensed by a two-component system (*AgrC/A*). At high cell density, AIP accumulates, and results in activation of the *agr* locus. The effector molecule of the *agr* system is an RNA molecule termed RNAIII, which is under control of the P3 promoter, and is transcribed divergently from the *agrBDCA* operon (Novick et al., 1993). Expression of RNAIII results in the up-regulation of many secreted proteins, and the simultaneous down-regulation of many cell-surface-expressed factors (Dunman et al., 2001; Recsei et al., 1986), by a mechanism that has yet to be characterized. The ability of *Staph. aureus* to cause human disease of such a range of severity is consistent with its ability to express a large number of surface and secreted virulence factors (Kuroda et al., 2001). The emergence of highly resistant strains of *Staph. aureus*, including those resistant to last-resort antibiotics (Anonymous, 2002a, b), has led to an increased interest in identifying novel antimicrobial therapies to combat this pathogen (Ji et al., 1997; Wright et al., 2005).

The Gram-positive bacterium *Lactobacillus reuteri* RC-14 (formerly *Lactobacillus fermentum*) (Reid et al., 2005) has previously been shown to inhibit *Staph. aureus* infection in a rat surgical-implant model (Gan et al., 2002). To investigate this phenomenon, we hypothesized that the inhibition may result from specific communication events between the two bacterial species. To address this, we analysed staphylococcal protein expression changes when *Staph. aureus* was grown in the presence and absence of *L. reuteri* RC-14. We show that the expression of staphylococcal superantigen-like protein 11 (SSL11) is dramatically decreased in response to growth with *L. reuteri* RC-14. Furthermore, using gene-reporter systems, we show that *L. reuteri* RC-14 supernatant contains small molecules that are able to repress both the SSL11 and P3 promoters, with repression of SSL11 occurring independently of the staphylococcal *agr* system.

**METHODS**

**Bacterial strains and plasmids.** Bacterial strains and plasmids used in this study are listed in Table 1. *Escherichia coli* was grown in Luria–Bertani broth (Difco), *Staph. aureus* was grown in brain heart infusion (BHI) broth (Difco), and lactobacilli were grown in BHI medium or Man–Rogosa–Sharpe (MRS) medium (Merck Froost Canada), as required. Solid media were obtained by the addition of 1.5 % (w/v) Bacto agar (Difco). All strains were grown at 37 °C. For plasmid selection, chloramphenicol was used at 10 μg ml−1 for *Staph. aureus* and *E. coli*, and ampicillin and kanamycin were used at 100 μg ml−1 and 50 μg ml−1, respectively, for *E. coli*. Mannitol salt agar (Difco) and Rogosa agar (Difco) were used as selective media for *Staph. aureus* and lactobacilli strains, respectively. To assay for α- and β-haemolysis, *Staph. aureus* was plated on sheep blood agar (Becton Dickinson). All reagents were made with water purified using a Milli-Q water-purification system (Millipore).

**Preparation, manipulation and analysis of DNA.** Standard DNA manipulations were performed as described (Sambrook & Russell, 2001), using enzymes supplied from New England Biolabs, in accordance with the manufacturer’s instructions. Oligonucleotides were obtained from Invitrogen, and are described in Table 1. PCRs were performed in a Peltier Thermocycler (MJ Research), in 50 μl reaction volumes, with PFX DNA polymerase (Invitrogen). PCR products were purified using the QIAquick PCR purification kit (Qiagen). DNA sequencing was performed at the Sequencing Facility, Robarts Research Institute, London, Canada. Plasmids were introduced into *Staph. aureus* RN4220 using bacteriophage 80a, as described (Sebulsky et al., 2000), before they were transduced into other *Staph. aureus* strains.

**Co-culture experiments.** Co-culture experiments were performed using a two-chamber device containing two 30 ml glass compartments separated by a 0.45 μm mixed cellulose ester membrane (Millipore). Co-cultures were grown in BHI at 37 °C, with slow shaking (~30 r.p.m.) to improve diffusion of small molecules between the compartments. *L. reuteri* RC-14 or *Lactobacillus rhamnosus* GR-1 (5 %, v/v, ...
inoculum) were inoculated first, and grown to an OD₆₀₀ of 0.15 (~5 h), before inoculation of Staph. aureus Newman (1%, v/v, inoculum) in the second compartment. After overnight growth, co-cultures were examined using selective agar media to ensure that cross-contamination had not occurred.

### Extraction of Staph. aureus cell-wall-associated proteins, and two-dimensional gel electrophoresis.

Cell-surface-associated proteins were extracted from Staph. aureus Newman, essentially as described (Hermann et al., 2000). Specifically, 30 ml cultures were harvested (5000 g, 10 min, 4 °C) at late-exponential phase, and subsequently washed in 50 mM Tris/HCl, pH 7.5. The final pellet was resuspended in 2 ml Sarcosyl buffer (50 mM Tris/HCl, pH 7.5, 150 mM NaCl, 1 mM MgCl₂, and 2%, w/v, N-lauroyl-sarcosine), and incubated on ice for 20 min. The cell wall suspensions were then centrifuged (10 000 g, 10 min, 4 °C), and the supernatant was recovered, aliquoted and stored at −80 °C prior to analysis. For two-dimensional gel electrophoresis (2D-E), the Sarcosyl-extracted proteins were precipitated with the Perfect Focus Kit (Geno Technology), following the manufacturer’s specifications. Precipitated proteins were resuspended in 200 μl rehydration buffer (9 M urea, 4% (w/v) CHAPS, 0.5% (v/v) Bioyltes (3-10; Bio-Rad Laboratories) and 20 mM dithiothreitol), and left at room temperature for 1 h, with occasional mixing. Insoluble material was removed by centrifugation (16 000 g, 1 h, 15 °C). The concentration of each protein sample was then determined by a modified Bradford procedure (Bio-Rad Laboratories). Aliquots of the solubilized proteins (6 μg for analytical gels, and up to 200 μg for preparative gels) were applied to immobilized pH gradient (IPG) strips (7 cm, pH range 4–7; Bio-Rad Laboratories), which were rehydrated overnight at 50 V in an IEF cell (Bio-Rad Laboratories). The following day, first-dimension IEF was carried out with increasing voltage [200 V for 100 Volt-hours (Vh), 500 V for 250 Vh, 1000 V for 500 Vh, and 8000 V for 8000 Vh], and then the strips were immersed in an equilibrium buffer containing 6 M urea, 2% (w/v) SDS, 50 mM Tris/HCl (pH 8–8), 30% (v/v) glycerol, and 65 mM dithiothreitol. After 15 min, the strips were placed in the equilibrium buffer, which contained 135 mM iodoacetamide instead of dithiothreitol, for a further 15 min. The second-dimension SDS-PAGE was performed using the Mini-Protean III electrophoresis unit (Bio-Rad Laboratories). Stacking gels and separating gels were used at 4 and 10%, respectively. Following electrophoresis, the analytical gels were stained with SYPRO Ruby (Bio-Rad Laboratories), and preparative gels were stained with Coomassie blue R-250. Gel images were captured using an AlphaInnotech camera, and the 2D-E protein profiles were analysed using Phoretix-2D (version 5.1) software (Non-linear Dynamics). Relative volumes were estimated by calculating the ratio of the volume of a spot to the volume of the spots from the entire gel. Results are the means of at least three independent experiments. In experiments that compared two conditions, proteins were considered to be induced or repressed if the mean relative volume for an individual protein was at least twofold higher or lower than that for the control.

### Identification of proteins of interest.

Peptide mass fingerprints were obtained using facilities provided by The Biological Mass Spectrometry Laboratory at the Dr Don Rix Protein Identification Facility at The University of Western Ontario (London, Canada).

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**Table 1. Bacterial strains, plasmids and oligonucleotides used in this study**

<table>
<thead>
<tr>
<th>Strain, plasmid or primer</th>
<th>Description</th>
<th>Source or reference</th>
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<tbody>
<tr>
<td><strong>Strains</strong></td>
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<tr>
<td>Staph. aureus Newman</td>
<td>Wild-type</td>
<td>Dajcs et al. (2002)</td>
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<tr>
<td>RN4220</td>
<td>Restriction-deficient derivative of 8325-4; accepts foreign DNA, (rKm m&lt;sup&gt;+&lt;/sup&gt;)</td>
<td>Kreiswirth et al. (1983)</td>
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<tr>
<td>RN6390</td>
<td>Prophage-cured wild-type strain</td>
<td>Novick et al. (1993)</td>
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<tr>
<td>RN6011</td>
<td>agr-null mutant of RN6390 containing a 3 kb fragment with 'G' marker in place of the 3-4 kb agr Cid–HinCII fragment</td>
<td>Peng et al. (1988)</td>
</tr>
<tr>
<td>MSSA476</td>
<td>Invasive community-acquired methicillin-sensitive strain</td>
<td>Holden et al. (2004)</td>
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<tr>
<td><strong>E. coli</strong></td>
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<tr>
<td>DH5α</td>
<td>F&lt;sup&gt;−&lt;/sup&gt; δ80dialcZAM15 Δ(lacZYA–argF) U169 endA1 recA1 hsdR17 (rKm m&lt;sup&gt;+&lt;/sup&gt;) deoR</td>
<td>Gibco-BRL</td>
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<tr>
<td><strong>Lactobacillus species</strong></td>
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<tr>
<td>L. reuteri RC-14</td>
<td>Isolated from the urogenital tract of a healthy woman</td>
<td>G. Reid</td>
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<tr>
<td>L. rhamnosus GR-1</td>
<td>Isolated from the urogenital tract of a healthy woman</td>
<td>G. Reid</td>
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<td><strong>Plasmids</strong></td>
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<tr>
<td>pSB2034</td>
<td>P3 promoter controlling expression of both luxABCDE (from Photobacterium phosphoreum) and translationally enhanced gfp3 (red-shifted gfp variant); Cm&lt;sup&gt;′&lt;/sup&gt;, Ap&lt;sup&gt;′&lt;/sup&gt;</td>
<td>Qazi et al. (2001)</td>
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<tr>
<td>pJLED1</td>
<td>SSL11 promoter amplified by PCR from Staph. aureus Newman inserted into EcoRI- and Xmal-digested pSB2034; Cm&lt;sup&gt;′&lt;/sup&gt;, Ap&lt;sup&gt;′&lt;/sup&gt;</td>
<td>This study</td>
</tr>
<tr>
<td><strong>Primers</strong></td>
<td></td>
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<tr>
<td>P&lt;sub&gt;ssl11&lt;/sub&gt; :: gfp/lux (forward)</td>
<td>CACCGATTCTAAGTGGATAAATAGATAG</td>
<td>This study</td>
</tr>
<tr>
<td>P&lt;sub&gt;ssl11&lt;/sub&gt; :: gfp/lux (reverse)</td>
<td>CATCAACCGGATTCTATGTCCTCCAAATT</td>
<td>This study</td>
</tr>
<tr>
<td>ssl11 (forward)</td>
<td>CACTCAACATATGAGTAGTTAGGTTAGT</td>
<td>This study</td>
</tr>
<tr>
<td>ssl11 (reverse)</td>
<td>CACCCCTGAGGGTCCTGCAATATTTTA</td>
<td>This study</td>
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</table>

*Restriction sites for subsequent cloning of the PCR products are underlined.*
The proteins were prepared according to the protocol provided by the facility. Briefly, the excised gel pieces were washed and dried in acetonitrile, and the proteins were subjected to reduction/alkylation by using dithiothreitol (10 mM) and iodoacetamide (55 mM). After several washing steps in 100 mM ammonium bicarbonate, and dehydration in acetonitrile, a solution of trypsin (15 ng μl⁻¹) was added to each gel piece, and the digestions were performed overnight at 37°C. The digested fragments were then recovered with a solution of acetonitrile/formic acid (50:5, v/v), and dried under vacuum. The dried peptides were stored at -80°C until needed, and, as required, the peptide mixture was diluted 1:1 with α-cyano-4-hydroxy-cinnamic acid. Matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF MS) analysis of the samples was performed using a Reflex III (Bruker), operating in a linear positive-ion mode with the N₂ laser, to obtain MS fingerprints and sequence tags. A Mascot Database search was then performed to identify proteins based on their pl, molecular mass and mass fingerprint (only protein databases were searched). The peptide sequence data (Table 2) were also used as query sequences in BLAST searches of all complete Staph. aureus genomes. The ORFs within the contigs retrieved by the BLAST search were identified, and their theoretical tryptic peptide fingerprints were determined via the ExPASy web site (http://www.expasy.ch), and compared with the peptide mass fingerprints obtained by MALDI-TOF MS analysis of the proteins. For confirmation, the peptide sequence data were also used as query sequences in BLASTP searches of all complete Staph. aureus genomes.

**Generation of anti-SSL11 antisera.** The ssl1 gene, lacking the DNA encoding the N-terminal signal peptide, was PCR amplified using primers ssl1F (forward) and ssl1R (reverse), and cloned into the multiple cloning site of pET28a. SSL11 was expressed and purified from E. coli BL21 (DE3), transformed with pET28::ssl1, using Ni²⁺ affinity chromatography, as specified by the manufacturer (Qiagen). The N-terminal His₆ tag was removed by cleavage with 1 unit thrombin (Sigma) per milligram of recombinant protein (16 h at 21°C). The recombinant protein was purified from the His₆ tag and thrombin by anion-exchange chromatography using a DEAE column pre-equilibrated in 20 mM Tris/HCl buffer, pH 7 (24/22-3, 34/33, 25/22-2, 24/22-3, 24/22-3, 24/22-3, 24/22-3) and adjusted to neutral pH with 5 M NaOH. To examine the heat stability of the compound, the supernatant was boiled for 30 min, and the volume was adjusted to the theoretical theoretical). The proteins were prepared according to the protocol provided by the facility. Briefly, the excised gel pieces were washed and dried in acetonitrile, and the proteins were subjected to reduction/alkylation by using dithiothreitol (10 mM) and iodoacetamide (55 mM). After several washing steps in 100 mM ammonium bicarbonate, and dehydration in acetonitrile, a solution of trypsin (15 ng μl⁻¹) was added to each gel piece, and the digestions were performed overnight at 37°C. The digested fragments were then recovered with a solution of acetonitrile/formic acid (50:5, v/v), and dried under vacuum. The dried peptides were stored at -80°C until needed, and, as required, the peptide mixture was diluted 1:1 with α-cyano-4-hydroxy-cinnamic acid. Matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF MS) analysis of the samples was performed using a Reflex III (Bruker), operating in a linear positive-ion mode with the N₂ laser, to obtain MS fingerprints and sequence tags. A Mascot Database search was then performed to identify proteins based on their pl, molecular mass and mass fingerprint (only protein databases were searched). The peptide sequence data (Table 2) were also used as query sequences in BLAST searches of all complete Staph. aureus genomes. The ORFs within the contigs retrieved by the BLAST search were identified, and their theoretical tryptic peptide fingerprints were determined via the ExPASy web site (http://www.expasy.ch), and compared with the peptide mass fingerprints obtained by MALDI-TOF MS analysis of the proteins. For confirmation, the peptide sequence data were also used as query sequences in BLASTP searches of all complete Staph. aureus genomes.

**Preparation of L. reuteri RC-14 supernatant.** Cell-free supernatants were prepared by growing L. reuteri RC-14 in BHI to an OD₆₀₀ of 0.4–0.6, and then removing the cells by centrifugation (5000 g, 10 min, 4°C). The remaining cell-free supernatant was filtered using 0.45 μm pore-size filters, checked for sterility by plating an aliquot on MRS agar, and assayed as described below. To rule out effects from hydrogen peroxide or pH, the supernatant was treated with catalase (1000 U ml⁻¹, Sigma), or adjusted to neutral pH with 5 M NaOH. To examine the heat stability of the compound, the supernatant was boiled for 30 min, and the volume was adjusted to the original volume by the addition of sterile water. To examine the role of lactic acid, BHI medium was treated with lactic acid to a pH of 2 or 7 (at concentrations of 20 mM, 50 mM or 100 mM), and, to rule out nutrient limitation in the BHI medium, a 1:175 dilution of 200-fold concentrated L. reuteri RC-14 supernatant was added to fresh BHI medium. The supernatant was also treated with proteases (0.5 mg ml⁻¹ Pronase, proteinase K or trypsin, or a combination of all three enzymes; Sigma) for 12 h at 55°C.

**Creation of the gfp/lux gene reporter construct.** Plasmid pSB2034 is an E. coli/Gram-positive bacterial shuttle vector that contains both gfp and lux under the transcriptional control of the staphylococcal P3 promoter (Qazi et al., 2001). The Plux::gfp/lux fusion was constructed by PCR amplification of a 385 bp DNA fragment from Staph. aureus Newman, corresponding to the untranslated 5’ end of
the ssl1 gene (bases −1 to −385), using primers PSSL1::gfp/lux (forward), and PSSL1::gfp/lux (reverse). The PCR product was cloned as an EcoRI–XmaI fragment into the unique EcoRI/XmaI sites of pSB2034. The resulting plasmid created a transcriptional fusion (pJLED1), and was confirmed to contain the SSL11 promoter region directly upstream of the vector-borne lux/gfp by sequencing the promoter region and the insertion sites. Both pJLED1 and pSB2034 were recovered from E. coli, and introduced into Staph. aureus Newman as described above.

Green fluorescent protein (GFP) and Lux expression analysis. For quantification of bioluminescence in the absence of exogenous aldehyde, overnight cultures of Staph. aureus Newman, harbouring either pSB2034 or pJLED1, were diluted 1:50 in medium containing the necessary antibiotics. Samples of each condition were prepared in triplicate, and loaded into a 96-well microtitre plate (320 μl), and incubated at 37 °C, without shaking, in a Luminoskan luminometer (Thermo). OD600 and luminescence were measured every hour over a 48 h period, and results were calculated as relative light units (RLUs). The data were normalized by taking the maximum RLU detected, and dividing by the corresponding maximum c.f.u. value for each condition. GFP was detected using fluorescence spectroscopy (Olympus BX-61 light microscope with a FITC filter), and fluorescent images were analysed using the Pro-Image Plus program version 5.0.1 (Media Cybernetics). All media used to grow Staph. aureus Newman in the promoter expression analysis were diluted 1:1 in Milli-Q water. For repression of an active SSL11 promoter, a 1:150 dilution of concentrated RC-14 supernatant (in Milli-Q water) was added to a culture of Staph. aureus Newman that had been growing in BHI medium for 24 h, and, at the same time point, an equivalent volume of Milli-Q water was added to Staph. aureus Newman growing in BHI medium and Staph. aureus Newman growing in L. reuteri RC-14 supernatant.

Screening for cell–cell signalling compounds. L. reuteri RC-14 cell-free supernatant was lyophilized and resuspended in 100% methanol (1:20 of the original supernatant volume). Centrifugation (5000 g, 10 min, 4 °C), followed by passage through Whatman No. 1 filter paper and a 0.45 μm pore-size filter, removed insoluble material. Rotary evaporation was used to concentrate the methanol-soluble material to 1/100 of the original volume of the culture supernatant. An aliquot (400 μl) of the concentrated supernatant was passed across a P-10 gel-filtration column (Bio-Rad Laboratories), and 2 ml fractions were collected. The fractions testing positive for biological activity in the luminescence 96-well plate assay were dried, resuspended in water, and further purified by HPLC on an Agilent 1100 HPLC, using a Zorbax 300SB-C8 (4.6 × 250 mm, 5 μm diameter) column (Agilent Technologies). Solvent A consisted of trifluoroacetic acid (0.1%) in water, and solvent B consisted of trifluoroacetic acid (0.085%) in acetonitrile. All solvents used were HPLC grade (Fischer Scientific). The chromatographic method used was as follows (flow rate 1.5 ml min−1): 2% solvent B for 2 min, followed by a gradient of 2–80% solvent B over 30 min, and a final step of 80% solvent B for 2 min. Fractions were collected off the HPLC C8 column, and tested in the luminescence 96-well plate assay. In order to determine whether the repression of both the SSL11 promoter and the staphylococcal P3 promoter was dependent on the same compound from the L. reuteri RC-14 supernatant, we performed the 96-well luminescence assay with Staph. aureus Newman containing either pJLED1 or pSB2034, grown in BHI medium, L. reuteri RC-14 supernatant, and an HPLC fraction that had previously tested positive for the ability to repress the SSL11 promoter. Isolated HPLC fractions were further evaluated by electrospray ionization mass spectrometry (ESI-MS) and MS/MS analysis in the QTOF instrument (Micromas), in positive-ion mode at a cone voltage of 20 V. For controls, MS analysis was performed on the two antecedent fractions, and the fraction collected directly after the active fraction (these fractions were shown to be biologically inactive).

Statistical analysis. Statistical comparisons between independent means were made by Student’s t test, assuming unequal variances.

RESULTS

2D-E of the Staph. aureus Newman cell-wall-associated proteins produced in response to growth with L. reuteri RC-14

The goal of this study was to evaluate cell–cell communication events between Staph. aureus and L. reuteri RC-14, in order to elucidate the mechanism by which L. reuteri RC-14 inhibits Staph. aureus infection (Gan et al., 2002). We initially analysed protein expression patterns from Staph. aureus in response to growth with L. reuteri RC-14. Since we initially reasoned that the inhibition may be due to an alteration in the adhesive properties of Staph. aureus, we focused on a subproteome enriched for surface proteins of Staph. aureus. Controls for the experiment included growth of Staph. aureus in medium alone, and growth with L. rhamnosus GR-1, a strain previously shown to lack the ability to inhibit Staph. aureus infection in the rat surgical-implant model (Gan et al., 2002). The protein expression profiles of the cell-wall-associated preparations analysed by 2D-E were very similar for all the gels. The total number of spots detected varied between 118 and 130, and the number of spots per gel for a given condition remained constant. Specifically, when Staph. aureus Newman was co-cultured with BHI, L. reuteri RC-14 and L. rhamnosus GR-1, the gels had 122, 130 and 118 detectable spots, respectively (Fig. 1). In each of these co-culture conditions, there were no significant differences detected between the OD600 values of Staph. aureus Newman when samples were taken during the late-exponential phase (results not shown). Each condition was repeated a minimum of three times, and the gels shown in Fig. 1 are from a representative experiment.

We were interested in staphylococcal proteins that either decreased or increased in expression in response to co-culture with L. reuteri RC-14, and, based on this, we selected seven of the spots in the preparative gels for further analysis (labelled in Fig. 1A, B). The identifications of the proteins are listed in Table 2, and the genes encoding each of the seven proteins were found in all complete Staph. aureus genomes published to date (Baba et al., 2002; Gill et al., 2005; Holden et al., 2004; Kuroda et al., 2001). We noted that expression of protein 1, annotated as SSL11, decreased considerably when co-cultured with L. reuteri RC-14. SSL11 belongs to a larger group of genetically clustered proteins known as the staphylococcal superantigen-like proteins (SSL proteins) (Lina et al., 2004), which are proposed to be important virulence factors in Staph. aureus (Al-Shangiti et al., 2004; Arcus et al., 2002; Fitzgerald et al., 2003; Langley et al., 2005).
SSL11 is present in Staph. aureus supernatant, and is repressed by growth in L. reuteri RC-14 supernatant

To further confirm our findings, we cloned and over-expressed recombinant SSL11 from E. coli, and used the pure protein to raise polyclonal rabbit antisera against this protein. We then analysed the supernatant from Staph. aureus spa-515, a strain that is deficient in protein A, to prevent non-specific immunoglobulin binding. Supernatants were analysed from Staph. aureus spa-515 grown to stationary phase in BHI medium, and in L. reuteri RC-14 supernatant. We observed a clear decrease in the expression of an immunoreactive band consistent with the predicted size of SSL11 when Staph. aureus was grown in the L. reuteri RC-14 supernatant (Fig. 2A). We also performed a Western blot experiment with extracted surface proteins from Staph. aureus using goat IgG conjugated to horseradish peroxidase (HRP) to detect protein A. Results from this experiment indicated no noticeable change in protein A expression when grown in the L. reuteri RC-14 supernatant (Fig. 2B). These experiments indicate that production of the SSL11 protein from Staph. aureus is markedly reduced when grown with supernatant from L. reuteri RC-14.

Staphylococcal SSL11 and P3 promoters are both repressed in the presence of L. reuteri RC-14 supernatant

Observing that a potential exotoxin decreased in expression in response to co-culture with L. reuteri RC-14 motivated us.

Fig. 1. 2D-E analysis of cell-surface-associated proteins expressed by Staph. aureus Newman when co-cultured with BHI medium (A), L. reuteri RC-14 (B), and L. rhamnosus GR-1 (C), as described in Methods. Spots were analysed using Phoretix 2D software, and only those spots with at least a two-fold change were analysed. Relative to growth with RC-14, proteins labelled in (A) showed decreased expression, and proteins labelled in (B) showed increased expression. Note that protein 1 showed a dramatic decrease in expression in response to growth with RC-14, but not in response to growth with GR-1. This protein had a pI of ~5-9, and a molecular mass of ~25 kDa, and MS analysis showed that it was homologous to a known staphylococcal superantigen-like protein. Molecular mass markers (kDa) are indicated on the right, and the pI gradient is shown on the bottom.

SSL11 is present in Staph. aureus supernatant, and is repressed by growth in L. reuteri RC-14 supernatant

To further confirm our findings, we cloned and over-expressed recombinant SSL11 from E. coli, and used the pure protein to raise polyclonal rabbit antisera against this protein. We then analysed the supernatant from Staph. aureus spa-515, a strain that is deficient in protein A, to prevent non-specific immunoglobulin binding. Supernatants were analysed from Staph. aureus spa-515 grown to stationary phase in BHI medium, and in L. reuteri RC-14 supernatant. We observed a clear decrease in the expression of an immunoreactive band consistent with the predicted size of SSL11 when Staph. aureus was grown in the L. reuteri RC-14 supernatant (Fig. 2A). We also performed a Western blot experiment with extracted surface proteins from Staph. aureus using goat IgG conjugated to horseradish peroxidase (HRP) to detect protein A. Results from this experiment indicated no noticeable change in protein A expression when grown in the L. reuteri RC-14 supernatant (Fig. 2B). These experiments indicate that production of the SSL11 protein from Staph. aureus is markedly reduced when grown with supernatant from L. reuteri RC-14.

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Fig. 2. Western blot analysis of SSL11 and protein A expression from Staph. aureus. (A) Secreted proteins were separated by 12% SDS-PAGE, and SSL11 was detected using anti-SSL11 antisera. Molecular mass markers (kDa) are shown on the left. SSL11 had a predicted molecular mass of ~24 kDa (indicated by the arrowhead). Staph. aureus spa-515 (a protein-A-deficient mutant) was grown to stationary phase in BHI medium (lane 1) and L. reuteri RC-14 supernatant (lane 2), and surface proteins were extracted as described in Methods. (B) Staphylococcal cell-wall-associated proteins were separated by 12% SDS-PAGE, and protein A was detected using goat IgG–HRP (protein A is an IgG-binding protein). Staph. aureus Newman was grown to stationary phase in BHI medium (lane 1) and L. reuteri RC-14 supernatant (lane 2). Molecular mass markers (kDa) are shown on the left. The expected molecular mass of protein A was ~54 kDa (indicated by the arrowhead).
to construct a dual-gene reporter construct to study ssl11 gene expression, and to confirm our findings. Based on the Staph. aureus COL sequence (Gill et al., 2005), PCR primers PSSL11::gfp/lux forward, and PSSL11::gfp/lux reverse, were used to amplify the SSL11 promoter region from Staph. aureus Newman. This region corresponds to a 385 bp region upstream of the ssl11 gene, and it is immediately downstream of a putative type-IC restriction–modification system (Fig. 3). The nucleotide sequence of this region from Staph. aureus Newman was 100% homologous to the same region in Staph. aureus strains COL (Gill et al., 2005), Mu50 (Kuroda et al., 2001), N315 (Kuroda et al., 2001) and MRSA252 (Holden et al., 2004), although, interestingly, in Staph. aureus strains MSSA476 (Holden et al., 2004) and MW2 (Baba et al., 2002), the first 79 bp of this sequence showed little or no homology to the Newman/COL sequence (Fig. 3). Despite this, we did not detect a difference in SSL11 protein expression between Staph. aureus Newman and Staph. aureus MSSA476, as detected by anti-SSL11 antibody in Western blot experiments (results not shown). The SSL11 promoter region replaced the staphylococcal P3 promoter in the Gram-positive expression vector pSB2034, thereby creating the gene reporter construct pJLED1. Since the expression of many exoproteins in Staph. aureus is regulated by the two-component agr signalling pathway (Dunman et al., 2001; Recsei et al., 1986), the expression of the P3 promoter (pSB2034 construct) was also monitored. P3 is one promoter of the agr system, whose untranslated gene product, RNAIII, is the effector molecule of the agr system (Novick et al., 1993). Reporter constructs pLED1 and pSB2034 were both introduced separately into Staph. aureus Newman. Staph. aureus harbouring these gene reporter constructs was grown in two separate microtitre plates to monitor hourly luminescence and culture density. For optimum activation of both the SSL11 and P3 promoters, Staph. aureus was grown in BHI medium diluted 1:1 with Milli-Q water. As a result of this, all further media used in promoter expression experiments were diluted 1:1 with Milli-Q water. The strains were grown in a 96-well plate in the presence or absence of L. reuteri RC-14 supernatant (Fig. 4A). The results of these experiments indicate that both PSSL11 and P3 are activated in the stationary phase when Staph. aureus Newman is grown in BHI, with a peak of luminescence detected at approximately 30 h of growth (Fig. 4A), while both PSSL11 and P3 are repressed when Staph. aureus is grown in the presence of L. reuteri RC-14 supernatant. The data obtained from the luciferase experiments were also confirmed by monitoring Staph. aureus grown in BHI, and in L. reuteri RC-14 supernatant, for the expression of GFP (results not shown). Importantly, growth of Staph. aureus was slightly inhibited when grown in L. reuteri RC-14 supernatant, compared with growth in BHI; this effect was probably due to a decrease in nutrients available in the spent supernatant, since Staph. aureus grows equally well in BHI and BHI supplemented with concentrated L. reuteri RC-14 supernatant (results not shown). To compensate for the decrease in growth observed for Staph. aureus grown in L. reuteri RC-14 supernatant, we measured the maximum RLU detected for each condition, and divided the result by the corresponding maximum c.f.u. under a variety of different conditions (Fig. 4B). Based upon normalized data, we determined that the SSL11 promoter remained repressed in the presence of the L. reuteri RC-14 supernatant, and that the observed effect was not due to a change in pH, or to the presence of lactic acid or hydrogen peroxide in the L. reuteri RC-14 supernatant (Fig. 4B, and results not shown). Also, we demonstrated that we could alleviate repression of the SSL11 promoter by adding decreasing amounts of L. reuteri RC-14 supernatant to Staph. aureus Newman (pJLED1) growing in BHI medium. We determined that the ability of the L. reuteri RC-14 supernatant to repress SSL11 promoter activation was insensitive to both protease activity (Pronase, proteinase K and trypsin, and a cocktail of all three enzymes) and heat.

![Fig. 3. Schematic representation of the ssl11 locus in Staph. aureus.](image-url)

**Fig. 3.** Schematic representation of the ssl11 locus in Staph. aureus. The arrows are representative of individual coding regions from Staph. aureus COL (Gill et al., 2005). The ssl11 gene is preceded by a 382 bp region lacking predicted ORFs that is directly downstream of SA0447, which is a gene whose product is predicted to belong to a restriction endonuclease complex. SA0479 is predicted to encode a lipoprotein of unknown function. The nucleotide sequence of the intragenic region between SA0477 and ssl11 (nt 479807–480191 in COL) is shown, with the region cloned into pJLED1 shown in upper-case letters. The start of SSL11 is indicated with the corresponding amino acid sequence.
The addition of concentrated L. reuteri RC-14 supernatant to the BHI medium also resulted in SSL11 promoter repression, ruling out the lack of nutrients or other compounds from the BHI medium as a cause of the repression. Of particular note, supernatant from L. rhamnosus GR-1 was not capable of repressing SSL11 or P3 promoter activity, consistent with the proteomic analysis (Fig. 4B).

(Fig. 4B and results not shown).
Since *L. reuteri* RC-14 supernatant repressed transcription of the SSL11 promoter, we were interested in determining if spent culture supernatant could repress an active SSL11 promoter. To accomplish this, an aliquot of concentrated *L. reuteri* RC-14 supernatant was added to *Staph. aureus* Newman (pJLED1) that had been growing in BHI medium for 26 h. The assay was performed in triplicate, and an equivalent volume of water was added to the same strain of *Staph. aureus* growing in either BHI medium or *L. reuteri* RC-14 supernatant. We observed a repression of the SSL11 promoter within 1 h following the addition of concentrated *L. reuteri* RC-14 supernatant (Fig. 4C), indicating that it was able to repress an activated SSL11 promoter. No repression of the SSL11 promoter was observed upon addition of an equivalent volume of water to *Staph. aureus* growing in BHI.

**Expression and repression of the SSL11 promoter is independent of the agr system in *Staph. aureus***

The expression of many virulence factors in *Staph. aureus* is controlled by *agr*, a quorum-sensing system that upregulates the expression of many secreted proteins upon entering the late-exponential phase, while simultaneously repressing the expression of many cell-wall-associated proteins. We were interested in determining if the observed decrease in ssl11 expression was a direct consequence of the decrease in activation of the P3 promoter. In order to analyse this, pJLED1 was introduced into *Staph. aureus* RN6390, and its isogenic *agr* mutant, RN6911. SSL11 promoter activation was observed when RN6390 and RN6911 were grown in control BHI medium, and repression was observed when each strain was grown in *L. reuteri* RC-14 supernatant (Fig. 5), indicating that both expression and repression of the SSL11 promoter are independent of P3 and the *agr* regulatory circuit in *Staph. aureus*.

**Isolation of the signalling molecule**

In order to begin characterization of the molecule(s) mediating the repression of the SSL11 and *agr* promoters, *L. reuteri* RC-14 supernatant was methanol extracted, and subjected to size-exclusion chromatography, followed by reverse-phase HPLC. Fractions were screened for activity using *Staph. aureus* Newman harbouring pJLED1, and luminescence was used as a measure of SSL11 and *agr* promoter activity. As shown in Fig. 6, an active HPLC fraction was able to completely inhibit activation of PSSL11, but it had only moderate inhibitory activity against P3. We performed ESI-MS analysis to determine which ions were present in the biologically active fractions, but were absent, or significantly decreased, in the biologically inactive fractions from adjacent HPLC fractions. Using this process, we were able to restrict our analysis to two candidate ions with *m/z* values of 851 and 437. Because the larger of the two ions appeared to be a dimer of the smaller molecular mass ion, we conducted MS/MS analysis on the larger ion with *m/z* 851, and this fragmented into the smaller 437 Da ion. Experiments are under way to elucidate the identity of the *L. reuteri* RC-14 signalling molecule.

**DISCUSSION**

Data obtained from the proteomic analysis of co-culture experiments, Western blot analysis of supernatant fractions, gene reporter analysis, and purification experiments, indicate that *L. reuteri* RC-14 is able to produce one or more molecules that inhibit the expression of both SSL11, a putative staphylococcal exotoxin, and RNAIII, the effector molecule of the *agr* locus. This decrease in toxin synthesis...
may explain, at least in part, the attenuated ability of Staph. aureus to cause infection in the rat surgical-implant model (Gan et al., 2002). Since L. rhamnosus GR-1 was unable to repress these promoters, this provides additional indirect evidence that these putative communication events may have contributed to the decreased pathogenesis of Staph. aureus in the rat model. While several researchers have shown that inhibiting RNAIII expression through the use of peptides that inhibit RNAIII transcription in vitro inhibits Staph. aureus infection in vivo (Balaban et al., 1998, 2000; Mayville et al., 1999; Wright et al., 2005), others have shown that, depending on the model, expression of RNAIII in vivo may not be required for virulence (Yarwood et al., 2002). We were somewhat surprised to observe the repression of the staphylococcal P3 promoter, since we did not detect a corresponding increase in multiple cell-surface-expressed factors in the 2D-E experiments. Because the surface extracts were analysed at the late-exponential phase, it is possible that RNAII was not yet fully active. Also, it is not clear whether other global regulators have also been affected, and these could override some of the agr-dependent factors. For example, the repressor of toxins (ROT) has been shown to at least partially restore regulation in an agr mutant, although mutation of ROT has not been reported to significantly affect the expression of ssl11 (Said-Salim et al., 2003). Although regulation of protein A expression is complex, the unaltered expression of protein A in the presence of L. reuteri RC-14 supernatant supports our findings (Fig. 2).

Our data indicate that the addition of concentrated L. reuteri RC-14 supernatant to a Staph. aureus culture in stationary phase can repress an activated SSL11 promoter within 1 h (Fig. 3C), implying that this is a specific regulation event. In the reporter experiments, we further showed that the inhibition was independent of the luciferase system, since GFP from pJLED1/pSB2034 was also inhibited. By subjecting Staph. aureus Newman harbouring pSB2034 to the potential communication signal from RC-14 supernatant, we demonstrated that an active HPLC fraction capable of completely inhibiting PSSL11 had only moderate inhibitory activity on P3 (Fig. 6). This result implies that the inhibition of P3 may be mediated by an independent signalling factor, or, alternatively, that the P3 promoter may be much less sensitive to repression by this compound. Although it is well known that many staphylococcal virulence factors are regulated by agr, our results indicate that SSL11 is expressed and repressed independently of the agr locus (Fig. 5). This is not uncommon, since other exotoxins, including staphylococcal enterotoxin A and staphylococcal enterotoxin J (SEA and SEJ), have also been shown to be expressed independently of agr (Tremaine et al., 1993; Zhang et al., 1998). As a consequence, therapeutic agents that decrease toxin production in Staph. aureus via interference with agr are likely to have no effect on the expression of SSL11. It will be of interest to determine if other SSL proteins are also regulated independently of the agr locus.

Despite the clear repression of SSL11 by L. reuteri RC-14, the role of SSL11 in staphylococcal virulence is unclear. The cluster of staphylococcal SSL proteins was first identified by Williams et al. (2000), and these proteins (formerly known as the staphylococcal enterotoxin-like proteins, or SET proteins) (Arcus et al., 2002; Fitzgerald et al., 2003; Williams et al., 2000) share the C-terminal β-grasp domain, and the N-terminal β-barrel domain, which are characteristic of known superantigens, yet they appear to have lost the low-affinity MHC class II binding (Al-Shangiti et al., 2004; Arcus et al., 2002)
et al., 2002). Although SSL1 (formerly Set1) has been shown to induce proinflammatory cytokines from peripheral blood mononuclear cells (Williams et al., 2000), none of the recombinant SSLs examined to date has exhibited key properties expected of superantigens, including MHC class II binding or T-cell activation (Arcus et al., 2002; Langley et al., 2005; Williams et al., 2000). We determined that recombinant SSL1 from Staph. aureus Newman lacks the ability to proliferate T cells (unpublished data), and this provides further evidence that the lack of superantigen activity is not a result of inactive allelic variants present in a select group of strains. However, SSL7 was recently shown to bind to IgA and complement C5 from human serum, inhibit the ability of IgA to bind to its receptor, and block complement-mediated killing of bacterial cells (Langley et al., 2005); none of the other SSLs tested shared this activity, and those authors suggested that the SSL proteins have distinct and possibly non-redundant functions. We were able to detect SSL1 in Staph. aureus supernatant by Western blot (Fig. 2), and, because SSL1 contains a typical 30 aa signal sequence, it is clear that it is a secreted protein. SSL1 was originally detected as a Staph. aureus cell-wall-associated protein, possibly due to its high level of expression, which may have resulted in some protein remaining associated with the cell surface. Contradictory to previous reports examining Staph. aureus COL (Fitzgerald et al., 2003), we found that SSL1 was expressed by Staph. aureus Newman. This difference could be attributed to differences in the regulatory circuits of Staph. aureus Newman and COL strains, since Staph. aureus Newman is a clinical methicillin-sensitive isolate (Dajcs et al., 2002), while Staph. aureus COL is an early methicillin-resistant Staph. aureus (MRSA) isolate (Shafer & Landolfo, 1979). Furthermore, recombinant SSL1 reacted with all five convalescent human sera samples from patients with previous Staph. aureus infections (unpublished data), consistent with previous reports (Arcus et al., 2002; Fitzgerald et al., 2003), although some SSL proteins have been shown to be non-immunoreactive with such sera (Fitzgerald et al., 2003).

The potential communication system that we have uncovered may have evolved as a result of the bacteria sharing similar niches within the host microbiota, since L. reuteri RC-14 is a vaginal isolate from a healthy woman (Gardiner et al., 2002), and Staph. aureus is commonly found on the mucosa of the vagina. A bacterial species able to detect and respond to competitors in a microenvironment would have the advantage of being able to alter its gene expression appropriately (Federle & Bassler, 2003). This potential communication system may actually represent a quorum-quenching mechanism, and whether or not it is broadly conserved, or highly species-specific, remains to be determined. It is interesting to speculate that the compound responsible for the repression of P3 could be similar to an agr AIP, since at least four Staph. aureus agr groups exist, such that an AIP produced from one group inhibits agr expression in other groups (Novick, 2003). Indeed, Lactobacillus plantarum produces a compound that is similar to Staph. aureus AIPs; this compound is produced by the lam operon, which shows similarities to the agr system in Staph. aureus (Sturme et al., 2005). Unfortunately, the L. reuteri genome sequence is currently not available, and we were unable to detect homologues of either the agr or lam operons in other sequenced lactobacilli. We were, moreover, unable to inactivate the L. reuteri RC-14 compound using various protease treatments, leading to the conclusion that this compound may not be a simple peptide. We do not believe that AI-2 is the key mediator in the response we have described, given that Staph. aureus is a producer of AI-2 (Schauder & Basler, 2001; Sun et al., 2004), and it is unlikely that Staph. aureus would respond differently to a similar compound also produced by L. reuteri RC-14. Alternatively, different bacteria may produce different forms of the AI-2 signalling molecule (Miller et al., 2004), and this is thought to be dependent upon the environment in which 4,5-dihydroxy-2,3-pentanedione, the precursor to AI-2, is produced (Chen et al., 2002). It is possible that an altered form of AI-2 acts as an inhibitor.

Confirmation of a bona fide signalling cascade controlling the expression of SSL11 that is inhibited by a compound produced in L. reuteri RC-14 supernatant will require the identification of the putative signalling molecule(s), and this will also be necessary to evaluate the role of this compound in interfering with the virulence of Staph. aureus. The research reported in this study is an important step in the quest to identify novel antimicrobial agents that inhibit Staph. aureus infection, and it also provides insight into natural inhibitors of Staph. aureus infection. The research will also serve to further characterize communication signals produced from non-pathogenic commensal bacteria that may alter the expression of virulence factors in pathogenic bacteria, and it will also aid in further understanding interspecies cell–cell communication.

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