Defining Daptomycin Resistance Prevention Exposures in Vancomycin-Resistant Enterococcus faecium and E. faecalis

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Daptomycin is used off-label for enterococcal infections; however, dosing targets for resistance prevention remain undefined. Doses of 4 to 6 mg/kg of body weight/day approved for staphylococci are likely inadequate against enterococci due to reduced susceptibility. We modeled daptomycin regimens in vitro to determine the minimum exposure to prevent daptomycin resistance (Dapr) in enterococci. Daptomycin simulations of 4 to 12 mg/kg/day (maximum concentration of drug in serum \( C_{\text{max}} \) of 57.8, 93.9, 123.3, 141.1, and 183.7 mg/liter; half-life \( t_{1/2} \) of 8 h) were tested against one Enterococcus faecalis strain (S447) and one Enterococcus faecium strain (S613) in a simulated endocardial vegetation pharmacokinetic/pharmacodynamic model over 14 days. Samples were plated on media containing 3 × the MIC of daptomycin to detect Dapr. Mutations in genes encoding proteins associated with cell envelope homeostasis (yycFG and liaFSR) and phospholipid metabolism (cardiolipin synthase \([\text{cls}]\) and cyclopropane fatty acid synthetase \([\text{fca}]\) ) were investigated in Dapr derivatives. Dapr derivatives were assessed for changes in susceptibility, surface charge, membrane depolarization, cell wall thickness (CWT), and growth rate. Strains S447 and S613 developed Dapr after simulations of 4 to 8 mg/kg/day but not 10 to 12 mg/kg/day. MICs for Dapr strains ranged from 8 to 256 mg/liter. Some S613 derivatives developed mutations in liaF or cls. S447 derivatives lacked mutations in these genes. Dapr derivatives from both strains exhibited lowered growth rates, up to a 72% reduction in daptomycin-induced depolarization and up to 6-nm increases in CWT \((P < 0.01)\). Peak/MIC and AUC_{0–24}/MIC ratios \((AUC_{0–24} \) is the area under the concentration-time curve from 0 to 24 h) associated with Dapr prevention were 72.1 and 780 for S447 and 144 and 1561 for S613, respectively. Daptomycin doses of 10 mg/kg may be required to prevent Dapr in serious enterococcal infections.

Enterococcus spp. are among the leading causes of nosocomial infections (1). Vancomycin-resistant Enterococcus faecium has been recognized as an important multidrug-resistant pathogen for which new or improved therapies are urgently needed (2, 3). Daptomycin is a lipopeptide antibiotic with potent in vitro bactericidal activity against Gram-positive bacteria, including vancomycin-resistant enterococci (VRE). Although daptomycin lacks an approved indication from the FDA, it is frequently utilized as an alternative agent for the management of VRE infections. However, the optimal pharmacokinetic/pharmacodynamic (PK/PD) targets for resistance prevention and therapeutic success with daptomycin have not been defined (4). In fact, the susceptibility breakpoint designating resistance in enterococci also remains questionable; however, for ease of presentation, we will use the term resistance to refer to nonsusceptible enterococci with daptomycin MICs of >4 mg/liter. Most experts agree that the daptomycin doses of 4 to 6 mg/kg of body weight/day used for staphylococcal infections are likely inadequate for VRE infections due to reduced susceptibility observed in enterococci (3–5). Daptomycin MIC_{50} and MIC_{90} are 2 and 4 mg/liter for E. faecium, and 0.5 and 1 mg/liter for Enterococcus faecalis versus 0.25 and 0.5 mg/liter for staphylococci (6). Reports of daptomycin resistance are now becoming more common, emphasizing the need for improved daptomycin dosing paradigms to help preserve the utility of this drug against these difficult to treat pathogens (7–10). Due to the substantial morbidity and mortality associated with enterococcal infections, it is critical to identify characteristics that correlate with treatment failure and therefore improve antimicrobial optimization and patient outcomes.

In order to derive daptomycin exposure targets for resistance prevention, we evaluated simulated daptomycin regimens from 4 to 12 mg/kg/day in a 14-day PK/PD model of simulated endocardial vegetations (SEVs) against two daptomycin-susceptible clinical VRE strains (E. faecium S447 and E. faecalis S613). Resistant strains derived from these models were then subjected to a variety of phenotypic and genotypic analyses to evaluate characteristics associated with development of daptomycin resistance.

MATERIALS AND METHODS

Bacterial strains. Two daptomycin-susceptible and vancomycin-resistant enterococcal strains, E. faecalis S613 and E. faecium S447 recovered from the bloodstream and urine, respectively, of patients before daptomycin therapy, were evaluated (11, 12). Both isolates developed daptomycin-resistant derivatives in vivo during daptomycin therapy (11, 12) and...
have been previously characterized. Additionally, the draft sequences of both genomes are available (11, 12).

**Antimicrobial agents and media.** Daptomycin was commercially purchased (Cubist Pharmaceuticals, Inc., Lexington, MA). Mueller-Hinton broth II (MHB) (Difco, Detroit, MI) with 50 mg/liter of calcium and 12.5 mg/liter magnesium was used for susceptibility testing. Due to the dependency of daptomycin on calcium for antimicrobial activity and protein binding of calcium, MHB supplemented to 75 mg/liter of calcium was used for in vitro SEV model experiments (13). Colony counts were determined using brain heart infusion agar (BHIA) (Difco, Detroit, MI). Emergence of resistance was assessed with BHIA supplemented with 50 mg/liter of calcium and 3 × MIC of daptomycin of each original strain, *E. faecalis* S613 and *E. faecium* S447.

**Susceptibility testing.** Daptomycin MICs were determined in duplicate by broth microdilution according to the Clinical and Laboratory Standards Institute (CLSI) guidelines (14). Any colonies growing on resistance screening plates were evaluated for changes in susceptibility by broth microdilution.

**In vitro PK/PD model.** A well-characterized in vitro PK/PD model of simulated endocardial vegetations (SEVs) previously validated against an in vivo endocarditis model with *Staphylococcus* and *Enterococcus* spp. and developed by our laboratory was utilized (15). The SEVs were prepared as previously described using human cryoprecipitate as the source of fibrin, a platelet suspension, bovine thornin in siliconized microcentrifuge tubes, and an organism suspension to reach a final bacterial density of 10⁹ CFU/g. The resultant SEVs were removed from the tubes and suspended in the model via a sterile monofilament line. The model apparatus was prefilled with growth media containing human albumin at a concentration of 3.5 g/dl. Fresh medium was continuously added and removed from the compartment along with the drug via a peristaltic pump set to simulate of 3.5 g/dl. Fresh medium was continuously added and removed from the compartment along with the drug via a peristaltic pump set to simulate a dependency of daptomycin on calcium for antimicrobial activity and protein binding with elemental calcium, the daptomycin-calcium complex is positively charged, and its degree of binding with the cell membrane has been postulated to be dependent on the attractive forces between the drug and cell surface (19). Cytochrome c is a cationic peptide that has been used as a surrogate marker for changes in surface charge. A cytochrome c binding study was performed by the method of Kraus et al. (20) Resistant derivatives from each model were evaluated for changes in cytochrome c binding and compared to the unexposed parent strain.

**Characterization of daptomycin-resistant derivatives. (i) Cationic peptide and daptomycin binding determination.** When daptomycin is bound with elemental calcium, the daptomycin-calcium complex is positively charged, and its degree of binding with the cell membrane has been postulated to be dependent on the attractive forces between the drug and cell surface (19). Cytochrome c is a cationic peptide that has been used as a surrogate marker for changes in surface charge. A cytochrome c binding study was performed by the method of Kraus et al. (20) Resistant derivatives from each model were evaluated for changes in cytochrome c binding and compared to the unexposed parent strain.

(ii) **Binding of fluorescent daptomycin.** Bacteria were grown to an optical density at 600 nm (OD₆₀₀) of 0.6 and then incubated with 16 µg/ml daptomycin–boron-dipyrromethene (bodipy) for 10 min, washed three times in medium to remove unincorporated label, stained with 2 µg/ml DAPI (4,6-diamidino-2-phenylindole), and placed on a 1.2% agarose pad for imaging in an Applied Precision deconvolution fluorescence microscope as described previously (21). For quantitation of daptomycin-bodipy fluorescence, images from each sample were collected using identical camera exposures. Cell Profiler was used to measure the average fluorescence intensity of individual pixels for >200 cells for the parent and resistant strains. The average fluorescence intensity of individual pixels for the background was also measured and subtracted from the cells to generate an accurate measurement of daptomycin-bodipy binding. Daptomycin binding to the resistant strains was compared to the binding observed with the parent strains.

(iii) **Binding of fluorescent cathelicidin LL37.** Bacteria were grown in LB broth to an OD₆₀₀ of 0.5 to 0.6, diluted 1:1 in phenol red-free RPMI medium (Invitrogen) in a final volume of 200 µl with 6-carboxytetramethylrhodamine (TAMRA)-labeled LL37 (American Peptide, Sunnyvale, CA) (TAMRA-LL37) to a final concentration of 1 µM for *E. faecium* and 32 µM for *E. faecalis*, and incubated for 45 min at 37°C with shaking. These concentrations were chosen based on previous LL37 susceptibility data in order to maintain bacterial integrity for microscopy. Bacteria were pelleted, washed three times with RPMI medium, counterstained with DAPI (2 µg/ml) in the final wash, and visualized using a Delta Vision Deconvolution microscope (Applied Precision, Inc., Issaquah, WA).

(iv) **Determination of cytoplasmic membrane depolarization.** The ability of daptomycin to depolarize the cytoplasmic membrane of parent and resistant strains was carried out as previously described using a kinetic spectrophoelurometric assay (22). Upon membrane potential dissipation from daptomycin or another cationic antimicrobial peptide, 3,3-dipropylthiatricarboxylic acid (DIPC₃) is released from the cell membrane into the surrounding medium, causing an increase in the fluorescence intensity at a wavelength of 670 nm. Daptomycin concentrations of 11.3 mg/liter (correlating with an average free peak of a 10-µg/kg/day dose) were utilized for each experiment. The membrane depolarization profiles over 1 h of the resistant strains and the parent strains were determined and compared. Nisin was used as a positive control to demonstrate that the assay was functioning properly.

(v) **Cell wall thickness.** Cell wall thickness was determined by transmission electron microscopy (TEM) as described previously (23). Ultra-thin sections were evaluated at a magnification of ×48,000 with a JEOL 100CX electron microscope, and images were captured with a MegaView III side-mounted digital camera. The resulting images were analyzed us-
ponent regulatory system that is part of the cell envelope response to phospholipid metabolism and have been previously associated with dap-synthase, respectively) that are likely to be involved in cell membrane coding two enzymes (cardiolipin synthase and cyclopropane fatty acid two-component regulatory system involved in cell wall homeostasis (yycG and yycG, respectively) (12); (ii) encoding a predicted yycFG, cliaFSR, and cfa, en-
coding two enzymes (cardiolipin synthase and cyclopropane fatty acid synthase, respectively) that are likely to be involved in cell membrane phospholipid metabolism and have been previously associated with daptomycin resistance in E. faecalis (11) and E. faecium (11, 12, 25). A non-

sociated with daptomycin resistance were evaluated using Sanger se-
mibrated (PCR products obtained from the entire open reading frame.

(vi) Growth kinetics. Bacterial growth kinetics of daptomycin-resis-
tant strains derived from the final time points of each model were evalu-
ated and compared to the parent strains. Briefly, using a 96-well, flat-
bottom plate, 200 µl of MHB was inoculated with 10^6 CFU/ml of each test

organism in triplicate. The plate was incubated in a spectrophotometer at
37°C for 8 h, and the optical density at 600 nm was automatically mixed
and measured every 15 min. Turbidity measurements were plotted over
time to construct growth curves. Daptomycin-resistant strains were com-
pared to unexposed parent strains.

(vii) Mutation screening by PCR. Mutations in genes previously associ-
ated with daptomycin resistance were evaluated using Sanger se-

quencing of PCR products obtained from the entire open reading frame.

The following genes were investigated: (i) mutation was defined as a nucleotide change that resulted in an amino acid substitution not present in daptomycin-susceptible parent

teral enterococci (S447 and S613), whose sequences are published and pub-

licly available. E. faecalis V583 (26) and E. faecium DO (27) (closed ge-

genomes were used as the template for sequence assembly. Primers utilized to

amplify the genes above are listed in Table 1.

(viii) Statistical analysis. Changes in CFU/g, cytochrome c binding,
daptomycin-bodipy binding, TAMRA-LL37 binding, total daptomycin-

induced depolarization, and growth curve AUCs were compared by one-

way analysis of variance with Tukey’s post hoc test or by t test as appro-

riate. A P value of ≥0.05 was considered significant. All statistical analyses

were performed using SPSS statistical software (release 21.0; SPSS, Inc.,

Chicago, IL).

RESULTS

Susceptibility testing. Daptomycin MICs for E. faecium S447 and
E. faecalis S613 were 2 and 1 mg/liter, respectively. MICs of daptomycin-resistant derivatives recovered from the in vitro models

ranged from 8 to 256 mg/liter.

In vitro PK/PD model. Observed PK parameters and achieved PK/PD ratios are summarized in Table 2. Quantitative changes in log_{10} CFU/g for each regimen are illustrated in Fig. 1 and 2 for each


ting ImageJ 1.39t software. Cell wall thickness was determined for at least

15 cells per sample using four separate quadrants of each cell for a total of

±100 measurements per sample.

Achieved PK parameter$^c$

<table>
<thead>
<tr>
<th>Dose in mg/kg/day</th>
<th>C_{max}</th>
<th>t_{1/2}</th>
<th>AUC_{0-24}</th>
<th>AUC_{0-24}/MIC</th>
<th>Peak/MIC</th>
<th>E. faecium S447 with a DAP MIC of 2 mg/liter</th>
<th>E. faecium S613 with a DAP MIC of 1 mg/liter</th>
</tr>
</thead>
<tbody>
<tr>
<td>12</td>
<td>184.1 ± 2.5</td>
<td>7.75 ± 0.35</td>
<td>2,036.3 ± 145.1</td>
<td>1,018.15</td>
<td>92.05</td>
<td>2,036.3</td>
<td>184.1</td>
</tr>
<tr>
<td>10</td>
<td>144.3 ± 1.8</td>
<td>8.0 ± 0.14</td>
<td>1,567.1 ± 37.2</td>
<td>780.85</td>
<td>72.15</td>
<td>1,561.7</td>
<td>144.3</td>
</tr>
<tr>
<td>8</td>
<td>122.4 ± 0.1</td>
<td>8.15 ± 0.07</td>
<td>1,342.9 ± 7.6</td>
<td>671.45</td>
<td>61.2</td>
<td>1,342.9</td>
<td>122.4</td>
</tr>
<tr>
<td>6</td>
<td>94.3 ± 1.9</td>
<td>7.25 ± 0.21</td>
<td>959.1 ± 35.7</td>
<td>479.55</td>
<td>47.15</td>
<td>959.1</td>
<td>94.3</td>
</tr>
<tr>
<td>4</td>
<td>57.6 ± 1.7</td>
<td>8.05 ± 0.07</td>
<td>627.3 ± 22.9</td>
<td>313.65</td>
<td>28.8</td>
<td>627.3</td>
<td>57.6</td>
</tr>
</tbody>
</table>

$^c$ C_{max} = maximum concentration of drug in serum; $t_{1/2}$ = half-life; AUC_{0-24} = area under the concentration-time curve from 0 to 24 h.

$^b$ DAP, daptomycin.

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organism. Against Enterococcus faecium S447, all regimens were bactericidal within the first 24 h, but only 10- and 12-mg/kg/day exposures remained bactericidal for the duration of the models. These exposures produced similar reductions in bacterial densities ($P = 0.55$) by 336 h but offered significantly greater CFU/g reductions compared to 4- to 8-mg/kg/day regimens ($P = 0.0005$). Against Enterococcus faecalis S613, 6- to 12-mg/kg/day regimens were bactericidal within the first 24 h, but only 12-mg/kg/day exposures remained bactericidal for the duration of the model. This regimen maintained statistically superior CFU/g reductions compared to 4- to 10-mg/kg/day regimens by 336 h ($P = 0.0005$). Daptomycin resistance, defined as recovery of isolates with an MIC of $>4$ mg/liter, emerged in both strains from models simulating 4-, 6-, and 8-mg/kg/day regimens but not during simulated exposures of 10 and 12 mg/kg/day. Resistant isolates were observed as early as 120 h and 144 h from the Enterococcus faecalis S613 strain and the Enterococcus faecium S447 strain, respectively. The peak/MIC and AUC$_{0-24}$/MIC ratios observed with the 10-mg/kg/day simulations were 72 and 781 for strain S447 and 144 and 1,562 for strain S613, respectively.

Characterization of daptomycin-resistant derivatives. (i) Cationic peptide and daptomycin binding determination. Cytochrome c binding studies revealed a significant reduction in the bound fraction of cytochrome c in daptomycin-resistant isolates derived from our models. On average, Enterococcus faecalis S613-derived resistant strains bound 42% (median) less cytochrome c than the parent strain, with a range from 2% to 94% ($P = 0.01$). Enterococcus faecium S447-derived resistant strains bound 28% (median) less cytochrome c than the parent strain with a range of 13% to 40%. This difference was significant for some of the S447-derived resistant strains tested, but not all.

(ii) Binding of fluorescent daptomycin. Two representative daptomycin-resistant derivatives were chosen from the SEV model for microscopy experiments: (i) a derivative of Enterococcus faecalis S613 that was obtained on day 10 at a simulated dose of 4 mg/kg (Enterococcus faecalis S613$_{D4}$, harboring an insertion of isoleucine in position 177 of the putative LiaF protein with an MIC of 16 $\mu$g/ml), and (ii) a derivative of Enterococcus faecium S447, obtained on day 14 at a simulated dose of 4 mg/kg (Enterococcus faecium S447$_{D4}$, with no mutations in target genes with an MIC of 128 $\mu$g/ml). Results of daptomycin-bodipy binding for selected parent and derivative strains are depicted in Fig. 3. The mean fluorescent intensity of bound daptomycin-bodipy at 16 $\mu$g/ml was 2.3× higher for Enterococcus faecalis S613 than for Enterococcus faecium S613$_{D4}$ (671.29 ± 11.80 versus 282.16 ± 19.40, respectively [mean ± standard error shown]; $P < 0.0001$). Similarly, the mean fluorescent intensity of bound daptomycin-bodipy for Enterococcus faecium S447 cells was 334.83 ± 5.65 but was below the level of detection for Enterococcus faecium S447$_{D4}$.

(iii) Binding of fluorescent LL37. Changes in fluorescent labeled LL37 binding between Enterococcus faecalis S613 and Enterococcus faecium S447 versus their daptomycin-resistant derivatives (Enterococcus faecalis S613$_{D4}$ and Enterococcus faecium S447$_{D4}$, respectively) are illustrated in Fig. 4. Similar to daptomycin binding, TAMRA-labeled LL37 (TAMRA-LL37) was found to bind less to their daptomycin-resistant derivatives obtained from the SEV model. The mean fluorescence intensity of bound TAMRA-LL37 at 1 $\mu$M was 3.4× higher in Enterococcus faecium S447 than in Enterococcus faecium S447$_{D4}$ (601.99 ± 37.99 versus 177.30 ± 17.08, respectively [mean ± standard error shown]; $P < 0.0001$). Similarly, the mean fluorescence intensity of bound TAMRA-LL37 at 32 $\mu$M in Enterococcus faecalis S613 cells was 2.4× higher than those in Enterococcus faecalis S613$_{D4}$ (154.35 ± 20.83 versus 65.09 ± 17.08, respectively; $P < 0.05$).

(iv) Determination of cytoplasmic membrane depolarization. Daptomycin-induced membrane depolarization of parent strains and selected resistant derivatives is depicted in Fig. 5A and...
B. Both the total amount of membrane depolarization and the rate of depolarization were substantially reduced among daptomycin-resistant strains. The total percentage depolarization was 19.7% to 37.2% for \textit{E. faecalis} S613 derivatives and 12.8% to 53.3% in \textit{E. faecium} S447-derived strains compared to 100% for both parent strains \((P < 0.0001)\).

\textbf{(v) Cell wall thickness.} Transmission electron microscopy (Fig. 6 and 7) revealed multiple morphological abnormalities in \textit{E. faecium} S447 compared to its daptomycin-susceptible parental strain. \textit{E. faecium} S447 was found to have a 4.5-nm increase in cell wall thickness compared to \textit{E. faecium} S447 (31.7 \pm 4.9 nm versus 27.2 \pm 4.9 nm, respectively; \(P < 0.001\)), while the cell wall thickness of \textit{E. faecalis} S613 increased by an average of 6.2 nm compared to S613 (26.2 \pm 4.4 nm versus 20.0 \pm 4.1 nm, respectively; \(P < 0.001\)). Qualitatively, the daptomycin-resistant derivatives of both species were found in clusters, demonstrating poor cell separation and abnormal septum formation. Another prominent finding observed in this study was the development of abnormal protrusions from the cell wall. These abnormalities have previously been reported in daptomycin-resistant VRE, but it is unclear whether they are a cause or effect of daptomycin resistance \((11, 24)\).

\textbf{(vi) Growth kinetics.} Growth kinetic analysis revealed that the majority of the resistant derivatives from either strain developed daptomycin resistance at the cost of fitness. Interestingly, the degree of growth rate inhibition appeared to be proportional to the daptomycin exposures in the model from which they were derived. Daptomycin-resistant strains derived from the 4-mg/kg/day simulations had less growth rate inhibition, while resistant derivatives from 6- and 8-mg/kg/day simulations tended to have lower growth rates. The growth rates of \textit{E. faecalis} S613 (harboring an insertion in \textit{liaF}) and an S613-derived mutant with a three-codon deletion in \textit{cls} were unchanged compared to that of the parent strain \((P = 0.28\) and \(P = 0.055\), respectively). The time to mid-exponential growth was 286 \pm 3.15 min versus 323 \pm 34.5 min for \textit{E. faecalis} S613 and its resistant derivatives, respectively, and 338 \pm 0.9 min versus 405 \pm 50.2 min for \textit{E. faecium} S447 and its resistant derivatives, respectively. Exponential-phase doubling times for strains S613 and S447 were both 50 min. \textit{E. faecalis} S613-derived strains demonstrated a median doubling time of 75 min with a range of 52 to 91 min. \textit{E. faecium} S447-derived strains demonstrated a median doubling time of 60 min with a range of 57 to 74 min. The overall growth rate, assessed by comparison of the area under the growth-versus-time curves, was significantly lower in \(50\%\) of \textit{E. faecalis} S613-derived strains compared to S613 \((P \leq 0.001)\) and \(83\%\) of \textit{E. faecium} S447-derived strains relative to S447 \((P \leq 0.001)\).

\textbf{(vii) Mutation screening by PCR.} Mutations in \textit{liaFSR} and \textit{cls} were assessed in all derivative strains. Additionally, \textit{yycFG} and \textit{cfa} were also evaluated in \textit{E. faecium} derivatives. The mutations identified are summarized in Table 3. Nonsynonymous point mutations in \textit{liaF} and \textit{cls} were identified in six \textit{E. faecalis} S613 derived from the 4-mg/kg/day simulations but were not found in strains derived from other exposures. No mutations in the target genes were identified in \textit{E. faecium} S447-derived strains.

\section*{DISCUSSION}

Infections with VRE are a major therapeutic challenge due to intrinsic resistance to multiple antibiotic classes, a paucity of bactericidal agents, and the rapid emergence of acquired antibiotic resistance. Antimicrobial dose optimization is necessary for the preservation of the clinical utility of currently available antimicrobials, but there are insufficient data to recommend resistance prevention dosing targets for most drugs. In this study, we have demonstrated that for daptomycin-susceptible strains of vancomycin-resistant \textit{E. faecium} and \textit{E. faecalis}, daptomycin exposures associated with doses of at least 10 mg/kg/day are likely to be

\begin{figure}[h]
\centering
\includegraphics[width=\textwidth]{figure3.png}
\caption{Membrane-bound fluorescently labeled daptomycin (green) in the parent strains (\textit{E. faecium} S447 and \textit{E. faecalis} S613) (left images) and representative daptomycin-resistant (Dap-R) strains (right images). Cells are stained with DAPI (blue).}
\end{figure}

\begin{figure}[h]
\centering
\includegraphics[width=\textwidth]{figure4.png}
\caption{Membrane-bound fluorescently labeled human cathelicidin LL37 (red) in the parent strains (\textit{E. faecium} S447 and \textit{E. faecalis} S613) (left images) and representative daptomycin-resistant (Dap-R) strains (right images). Cells are stained with DAPI (blue).}
\end{figure}
required to prevent resistance emergence. These doses were associated with an AUC0–24/MIC ratio of 781 for *E. faecium* S447 and 1,562 for *E. faecalis* S613. These exposures are clinically achievable and have been shown to be safe in multiple studies (17, 28–30). While we did not detect resistant derivatives from the models at the 4-mg/kg/day exposures. However, these mutations, although present in the same genes, were different from those previously described under daptomycin exposure (11). Moreover, resistant derivatives of *E. faecium* S613, mutations in LiaF and cfs were observed in resistant strains derived from the 4-mg/kg/day exposures. However, these mutations, although present in the same genes, were different from those previously described under daptomycin exposure (11). Moreover, resistant derivatives of *E. faecium* S447 selected in the SEV model harbored none of the mutations in yycG, cfs, or cfa previously described in an S447-resistant derivative (designated R446) obtained from the bloodstream of a patient after daptomycin therapy. Our findings suggest that there are multiple alternative genetic pathways leading to daptomycin resistance. Our results also highlight the remarkable ability of enterococci to adapt to the attack of antimicrobial peptides.

Recent insights into the complex mechanism of daptomycin resistance suggest that in certain enterococcal strains, the mechanism of resistance may not involve “repulsion” of cation-decorated daptomycin from the cell surface, as previously shown. Tran et al. recently postulated that diversion of daptomycin from the bacterial septum with subsequent “trapping” of the antibiotic away from septal areas may be an alternative mediator of daptomycin resistance in *E. faecalis* (24). This antibiotic diversion was associated with redistribution of cardiolipin arrays away from the septum, which appeared to be mediated by an Ile177 deletion in the predicted LiaF protein. Interestingly, instead of an Ile177 deletion, our *E. faecalis* S613-derived mutant (S613D4) harbored an Ile insertion at the same position. However, our microscopy data with bodipy-labeled daptomycin and TAMRA-labeled LL37 indicate that the mechanism of daptomycin resistance for this mutant involves the classical “repulsion” of the antibiotic from the cell surface, highlighting different strategies under various conditions. Resistant derivatives also developed thicker cell walls with more septum formation and poor cell separation. It is believed that some organisms may use this strategy of forming “false” division septa in order to draw daptomycin molecules away from critical binding sites at the “true” division septum. It is possible that di-

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**FIG 5** Daptomycin-induced membrane depolarization over 1 h in *E. faecalis* S447 and resistant derivatives (A) and *E. faecalis* S613 and resistant derivatives (B). Nisin (25 mg/liter) was used as a positive control for membrane depolarization (thin solid line). The parent strain exposed to daptomycin (11.3 mg/liter) (line of long dashes), average resistant derivative exposed to daptomycin (11.3 mg/liter) (thick solid line) with upper and lower standard deviation (lines of short dashes), and negative control (dotted line) are shown. The emission wavelength is shown on the y axes.

increased intrinsic resistance to antimicrobial peptides in *E. faecalis* may be related to the fact that it causes 90% of enterococcal endocarditis, compared to 5 to 10% for *E. faecalis* (32). Reflective of this difference in LL37 MIC, which approximates 1 to 4 μM in *E. faecium* and 16 to 64 μM in *E. faecalis*, was the concentrations of LL37 used in the LL37 binding assay experiments. These findings highlight the cross-resistance between endogenous antimicrobial peptides produced by innate immune defenses and pharmaceutical antibiotics like daptomycin. It also points to the important role that in *vivo* peptide exposure might play in driving antibiotic resistance in the absence of administered drugs. Peptide-mediated predisposition for daptomycin resistance *in vivo* makes achieving the critical AUC0–24/MIC threshold of utmost importance in the treatment of infective endocarditis, where suboptimal exposure to cationic antimicrobial peptides is likely.

The mechanisms of daptomycin resistance in enterococci have not been fully elucidated. It appears that resistance to daptomycin can emerge through a variety of genetic pathways (33), but a common theme involves mutations in two group of genes: (i) genes involved in cell envelope homeostasis (*yycFG* and *liaFSR* systems) and (ii) genes encoding enzymes involved in phospholipid metabolism (i.e., *cls*, *gdpD*, and *cfa* encoding cardiolipin synthase, glycerophosphodiester phosphodiesterase, and cyclopropane fatty acid synthase, respectively) (11, 12, 24, 34). However, the absence of mutations in some of these target genes in some of our resistant derivatives suggests that alternative genetic pathways remain to be discovered. In *E. faecalis* S613, mutations in LiaF and cfs were observed in resistant strains derived from the 4-mg/kg/day exposures. However, these mutations, although present in the same genes, were different from those previously described under daptomycin exposure *in vivo* (11). Moreover, resistant derivatives of *E. faecium* S447 selected in the SEV model harbored none of the mutations in *yycG*, *cfs*, or *cfa* previously described in an S447-resistant derivative (designated R446) obtained from the bloodstream of a patient after daptomycin therapy. Our findings suggest that there are multiple alternative genetic pathways leading to daptomycin resistance. Our results also highlight the remarkable ability of enterococci to adapt to the attack of antimicrobial peptides.
version of daptomycin from critical sites is an initial strategy at early stages of the development of daptomycin resistance. While daptomycin is not shown to be diverted in the daptomycin-resistant mutant *E. faecalis* S613D4 (as previously shown in other strains), the genotypic characterization of such resistant derivatives suggest that different mutations than those previously described *in vivo* occurred, making comparisons difficult to establish. Additionally, other unknown mutations may have occurred, and their role in manifestation of this phenotype is unclear at this time. Given that it was not feasible to perform fluorescent drug

**FIG 6** TEM of the parent strain *E. faecium* S447 illustrating baseline cell wall thickness and the absence of abnormal surface projections and division septa. Bars, 500 nm.

**FIG 7** TEM of the parent strain *E. faecium* S447D4 illustrating increased cell wall thickness and the presence of abnormal surface projections and division septa. Bars, 500 nm.
binding studies or TEM on more than two of the daptomycin-resistant derivatives, it may also be possible that some of the other strains would have behaved differently in these experiments. Further studies are warranted to clarify the genetic changes associated with these phenotypes in *E. faecalis* (24).

To our knowledge, this is the first study that explores the daptomycin resistance prevention breakpoint in enterococci using clinically relevant drug exposures over the substantial time period of 14 days. Based on our observations, it is clear that the dose of daptomycin for the management of VRE infections and prevention of resistance is much higher than the labeled dose of 6 mg/kg/day indicated for staphylococcal bacteremia and is likely around 10 mg/kg/day for average patients with MICs in the susceptible range. However, this study is limited to some extent by the number of strains tested and the potential variability between enterococcal species (*E. faecium* versus *E. faecalis*). Furthermore, this resistance prevention breakpoint was derived in a model with very high bacterial densities (9 log10 CFU/g), so these data may be more representative of serious high-inoculum infections such as infective endocarditis and less relevant to more-benign infections. Emerging data suggest that certain strains of VRE with genetic predisposition toward daptomycin resistance, specifically those with lasF mutations, may require clinically unachievable daptomycin exposures to prevent resistance. Further research in this area should focus on characterizing this resistance prevention exposure in other strains and exploring strategies, such as combination therapy, to lower this breakpoint.

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**REFERENCES**


**TABLE 3 E. faecalis S613 mutants derived from 4-mg/kg/day exposures**

<table>
<thead>
<tr>
<th>Time derived (h)</th>
<th>DAP MIC (mg/liter)</th>
<th>Gene</th>
<th>Mutation in gene</th>
</tr>
</thead>
<tbody>
<tr>
<td>120</td>
<td>32</td>
<td>iaf</td>
<td>Insertion of Ile at position 177</td>
</tr>
<tr>
<td>144</td>
<td>32</td>
<td>clsf</td>
<td>G653→A (R218Q)</td>
</tr>
<tr>
<td>16</td>
<td>16</td>
<td>clsf</td>
<td>G800→A (R267H)</td>
</tr>
<tr>
<td>168</td>
<td>8</td>
<td>clsf</td>
<td>Deletion of NFQ77–79</td>
</tr>
<tr>
<td>240</td>
<td>16</td>
<td>iaf</td>
<td>Insertion of Ile at position 177</td>
</tr>
<tr>
<td>336</td>
<td>16</td>
<td>clsf</td>
<td>Deletion of NFQ77–79</td>
</tr>
</tbody>
</table>

**TABLE 4 Distribution of mutations in G653, G800, and NFQ77–79**

<table>
<thead>
<tr>
<th>Mutation</th>
<th>G653</th>
<th>G800</th>
<th>NFQ77–79</th>
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</table>


