Human Antimicrobial Peptide LL-37 Induces MefE/Mel-Mediated Macrolide Resistance in Streptococcus pneumoniae

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Macrolides are in widespread use and are recommended as the first line of treatment for community-acquired pneumonia (CAP), except in areas compromised by high rates of macrolide resistance (25). Macrolide resistance is therefore a major concern in the treatment of *Streptococcus pneumoniae*, a major causative agent of CAP, sinusitis, otitis media, and meningitis. In *S. pneumoniae*, macrolide resistance is conferred primarily by the methylase *ermB* (MIC ≥ 64 μg/ml) or the macrolide efflux pump *mef* (1, 20, 30). *Mef* mediated efflux has been shown to be specific for 14- and 15-membered macrolides (2, 32). *Mef* is encoded by two variants, either *mefE* or *mefA*, with *mefE* being more prevalent in the United States (2). *MefE/Mel* is encoded on the mobile genetic element mega (8) and has been shown to be inducible by 14- and 15-membered macrolides (1, 2, 32). *MefE/Mel*-mediated MICs for erythromycin range from 1 to 32 μg/ml and increase by 4-fold upon macrolide induction, on average (37). The clinical implications of low-level macrolide resistance (1 to 8 μg/ml) are controversial (3, 14, 17, 26). Recent studies provide evidence that infection with low-level macrolide-resistant pneumococci constitutes a risk factor for treatment failure (5, 4, 13, 22, 23). About 35% of all pneumococcal isolates from community-acquired respiratory tract infections in the United States are macrolide resistant (15).

Cationic antimicrobial peptides (CAMPs) are small cationic, amphiphilic peptides. The major mammalian CAMPs are cathelicidins and defensins, which are constitutively expressed in macrophages and neutrophils and inductibly produced by epithelial cells and at mucosal surfaces. They play an important role in host defense against bacterial infections and are a major component of the innate immune response (11, 19). Sublethal concentrations of CAMPs are known to alter the levels of bacterial gene expression (9). In this respect, we determined that the sole human cathelicidin, LL-37, could alter *mef* and *mel* expression and that this alters pneumococcal susceptibility to macrolides and LL-37.

**LL-37 induces the mefE promoter.** In a screen for inducers of the *MefE/Mel* efflux pump, several cationic antimicrobial peptides were tested in a plate diffusion assay with a *mef* promoter-*lacZ* reporter strain. The reporter strain was constructed by introducing a 1.1-kb fragment containing the *mefE* promoter (*PmefE*) region of *S. pneumoniae* strain GA17457 (bp 1 to 1,178 based on the published, identical mega nucleotide sequence of strain GA3488; GenBank accession number AF274302 [8]) as an XbaI/EcoRI fragment upstream of the *lacZ* gene in vector pPP2 (10). The resulting plasmid was used to transform *S. pneumoniae* strain GA17457, leading to the integration of *PmefE-lacZ* in the *bga* locus in reporter strain XZ87042. GA17457 is a clinical isolate (serotype 19A), which has a major element as its sole erythromycin resistance determinant. For plate diffusion assays, XZ7042 was streaked onto indicator plates (Todd-Hewitt [TH] medium supplemented with 1.5% agarose, 0.5% yeast extract, 300 U/ml catalase, and 0.004% 5-bromo-4-chloro-3-indolyl-β-D-galactopyranoside [X-Gal]), and a test compound was applied to the center of the plates. After 36 h at 37°C with 5% CO2, the plates were evaluated for a zone of growth inhibition and an adjacent zone of induction. Under inducing conditions, as shown for erythromycin (Fig. 1A), the zone of induction appears as a blue halo around the inhibition zone.

We tested several CAMPs of different origins, including polymyxin B (bacterial, 750 μg), cathespin G-derived peptide (CG117-136; human, 75 μg), protegrin 1 (porcine, 75 μg), and tachyplesin 1 (horseshoe crab, 75 μg), and a mixture of α-defensins, containing the human neutrophil peptides HNP1-3 (25 μg) and the cathelicidins LL-37 (human, 75 μg) and CRAMP38 and CRAMP39 (both murine, 75 μg each). CRAMP38 and CRAMP39 are two alternatively processed forms of the LL-37 mouse homolog CRAMP (7). All peptides were prepared synthetically, except for HNP1-3 (Hycult Bio-

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in 5-fold-diluted TH medium supplemented with 0.5% yeast extract was added to serial dilutions of LL-37 or erythromycin. After 1 h at 37°C, samples were plated on TSA II blood agar plates (BD), and after 16 h at 37°C with 5% CO2, the MICs and the minimal bactericidal concentrations (MBCs) were determined.

Wild-type strain GA17457 and the PmeF-lacZ reporter derivative XZ7042 showed high levels of resistance to LL-37 (Table 1), which were further increased upon growth in subinhibitory concentrations of LL-37 (Table 1). Concomitantly, the MIC for erythromycin increased by 2- to 16-fold. Growth in the presence of erythromycin caused an increase in LL-37 resistance, as well as a 4-fold increase in erythromycin resistance. Taken together, independent of the nature of the inducer, induction increased resistance toward both compounds. In regard to the MBCs, LL-37 induction of resistance was less pronounced than that with erythromycin, consistent with the weaker induction observed with LL-37 in the plate diffusion assay (Fig. 1A and C).

To determine whether the increased resistance to LL-37 and erythromycin relied on the mega element, two mega deletion mutants were constructed. By allelic replacement, the 5.5-kb mega region (bp 1 to 5,532; GenBank accession number AF274302) was replaced in GA17457 and XZ7042 with the spectinomycin resistance cassette (containing the aad9 gene) from pUC-spc (12). The resulting mutants XZ8006 and XZ8004, respectively, were less resistant to LL-37 than their parental strains and were susceptible to erythromycin, confirming that mega was required for resistance (Table 1). In addition, growth in the presence of subinhibitory concentrations of LL-37 did not induce increased resistance to LL-37 or erythromycin (Table 1); hence, inducible resistance in the wild-type strains required the mega element.

We analyzed whether pneumococcal resistance to LL-37 required the MefE/Mel efflux pump encoded on mega. A mefE-mel deletion mutant, XZ8009, was constructed by replacing the region containing the mefE and mel genes (from bp 83 in mefE to bp 3,858 in mel) with the kanamycin resistance cassette (containing the aph3 gene) of pSF191 (33) in GA17457. XZ8009 showed the same levels of resistance to LL-37 as the mega-deletion mutants under all tested conditions (Table 1), demonstrating that the

TABLE 1. MICs and MBCs of wild-type, mega, and mefE-mel mutant strains for LL-37 and erythromycin

<table>
<thead>
<tr>
<th>Strain</th>
<th>Genotype</th>
<th>MIC (MBC)c</th>
<th>Etest valued</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Uninduced</td>
<td>Induced with LL-37b</td>
<td>Induced with Emc</td>
</tr>
<tr>
<td>GA17457</td>
<td>Wild type, parent</td>
<td>500 (1,000)</td>
<td>2,000 (2,000)</td>
</tr>
<tr>
<td>XZ8006</td>
<td>mega::aad9</td>
<td>125 (250)</td>
<td>125 (250)</td>
</tr>
<tr>
<td>XZ8009</td>
<td>mefE-mel::aph3</td>
<td>125 (250)</td>
<td>64 (250)</td>
</tr>
<tr>
<td>XZ7042</td>
<td>bga::PmefE-lacZ</td>
<td>500 (1,000)</td>
<td>2,000 (2,000)</td>
</tr>
<tr>
<td>XZ8004</td>
<td>mega::aad9</td>
<td>250 (500)</td>
<td>125 (250)</td>
</tr>
<tr>
<td></td>
<td>bga::PmefE-lacZ</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

a MICs and MBCs (μg/ml) determined by microdilution assays adapted to CAMPs (28). E, erythromycin; N/A, not applicable because the strain was erythromycin sensitive.

b Subinhibitory concentrations used for induction: GA17457 and XZ7042, 200 μg/ml; XZ8006 and XZ8009, 50 μg; and XZ8004, 100 μg.

c Subinhibitory concentration used for induction: 1 μg/ml.

d Etest was performed according to the manufacturer’s instructions (AB Biodisk, Solna, Sweden).

Shown are the results obtained from one representative experiment, and at least three independent experiments were performed.
Serum concentrations of LL-37 are reported to be in the range of 14- and 15-membered macrolides had been described as inducers/substrates of this efflux pump (32, 37). The potential clinical implications of this finding are 2-fold, as follows: (i) failure of macrolide-based treatment of mega-containing isolates, that increase upon incubation with LL-37 altered expression of msr

S. pneumoniae is naturally resistant to high levels of CAMPs, which has been attributed to mechanisms altering the surface charge, thereby decreasing CAMP affinity, and to several other factors that await further characterization (18, 21, 24, 31, 35, 36). Recently, Majchrzykiewicz et al. (24) have shown that incubation with LL-37 altered expression of ~10% of the genome in S. pneumoniae, including genes of known and putative regulatory proteins, suggesting the possibility of an indirect induction of MeF/Mel by LL-37. Our data suggest that the MeF/Mel efflux pump can further contribute to cathelicidin resistance and may thereby contribute to increased survival in the human host. Due to the limitations of our in vitro assay system, which required high concentrations of LL-37 at or beyond the soluble concentration of LL-37 (~2,000 µg/ml), this important observation needs to be further evaluated for biological significance with in vivo experiments. Actual efflux-mediated cathelicidin resistance has been demonstrated for the MtrCDE efflux pump of Neisseria spp. (28, 34). This additional function of MeF/Mel could account for an increasing number of pneumococcal isolates that contain both macrolide resistance determinants ErmA and MeF/Mel (15). Due to the high-resistance levels associated with ErmA, MeF/Mel does not contribute to macrolide resistance, but it may help protect MeF/Mel-containing strains from antimicrobial host defenses.

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