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Published in:
Antimicrobial Agents and Chemotherapy

DOI:
10.1128/AAC.49.7.2845-2850.2005

Published: 2005-01-01

Citation for published version (APA):

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Antimicrobial and Chemoattractant Activity, Lipopolysaccharide Neutralization, Cytotoxicity, and Inhibition by Serum of Analogs of Human Cathelicidin LL-37

Cristina D. Ciornei,† Thorgerdur Sigurdardottir, Artur Schmidtchen, and Mikael Bodelsson

Department of Anesthesiology and Intensive Care and Department of Dermatology and Venereology,
Lund University, Lund, Sweden

Received 16 December 2004/Returned for modification 13 January 2005/Accepted 3 April 2005

Antimicrobial peptides have been evaluated in vitro and in vivo as alternatives to conventional antibiotics. Apart from being antimicrobial, the native human cathelicidin-derived peptide LL-37 (amino acids [aa] 104 to 140 of the human cathelicidin antimicrobial peptide) also binds and neutralizes bacterial lipopolysaccharide (LPS) and might therefore have beneficial effects in the treatment of septic shock. However, clinical trials have been hampered by indications of toxic effects of LL-37 on mammalian cells and evidence that its antimicrobial effects are inhibited by serum. For the present study, LL-37 was compared to two less hydrophobic fragments obtained by N-terminal truncation, named 106 (aa 106 to 140) and 110 (aa 110 to 140), and to a previously described more hydrophobic variant, the 18-mer LLKKK, concerning antimicrobial properties, lipopolysaccharide neutralization, toxicity against human erythrocytes and cultured vascular smooth muscle cells, chemotactic activity, and inhibition by serum. LL-37, fragments 106 and 110, and the 18-mer LLKKK inhibited the growth of Escherichia coli, Pseudomonas aeruginosa, Staphylococcus aureus, and Candida albicans in a radial diffusion assay, inhibited lipopolysaccharide-induced vascular nitric oxide production, and attracted neutrophil granulocytes similarly. While fragments 106 and 110 caused less hemolysis and DNA fragmentation in cultured cells than did LL-37, the 18-mer LLKKK induced severe hemolysis. The antibacterial effect of fragments 106 and 110 was not affected by serum, while the effect of LL-37 was reduced. We concluded that the removal of N-terminal hydrophobic amino acids from LL-37 decreases its cytotoxicity as well as its inhibition by serum without negatively affecting its antimicrobial or LPS-neutralizing action. Such LL-37-derived peptides may thus be beneficial for the treatment of patients with sepsis.

Sepsis is an infection with bacteria, viruses, or fungi that causes an overwhelming inflammatory host response which can lead to multiple organ dysfunction and, ultimately, death (3). The treatment of this complex condition has been confined to antibiotics, surgery, and the support of failing vital functions. The inflammatory response during sepsis is triggered by bacterial components such as lipopolysaccharides (LPS) released from gram-negative bacteria (3). Thus, agents that are able to limit the effects of LPS may be of clinical benefit in the treatment of gram-negative sepsis. Furthermore, progressive antibiotic resistance in both gram-negative and gram-positive pathogens requires improved targeted therapies.

Antimicrobial peptides have been evaluated in vitro and in some in vivo trials as alternatives to conventional antibiotics. The human cationic antimicrobial protein of 18 kDa (hCAP-18) belongs to the class of cathelicidins. It is released from activated neutrophil granulocytes (10, 23). After release, the 37-amino-acid α-helical C-terminal end is cleaved off, forming the functional antimicrobial peptide LL-37 (6, 23). Apart from being antimicrobial, LL-37 also binds LPS, and it was previously shown that this binding reduces LPS-induced nitric oxide release from the rat aorta (2) and protects mice from LPS lethality (10). LL-37 has also been found to have immunomodulatory and chemotactic activities mediated via the formyl peptide receptor FPRL1 (1, 21, 29).

However, it has been observed that LL-37 causes hemolysis (18) and is toxic to human leukocytes and the T-lymphocyte MOLT cell line (8), probably due to hydrophobic interactions with the eukaryotic cell membrane (18). LL-37 has also been shown to induce apoptosis in vascular smooth muscle cells (2). The cytotoxic effects of LL-37 liberated into the circulation are inhibited by its binding to plasma proteins, e.g., apolipoprotein A-I, but unfortunately, the antimicrobial effects are also inhibited by this binding (8, 24, 28). Thus, the use of native LL-37 to treat septic patients would either not have beneficial effects due to binding of the peptide to plasma proteins or, if the plasma binding capacity were exceeded, be harmful due to the cytotoxicity of the peptide. In fact, the results of a recent study suggested that LL-37 was toxic at high doses when given in an attempt to treat experimental sepsis in neonatal rats (5). The present study was designed to test the hypothesis that the removal of hydrophobic amino acids from the N-terminal end of LL-37 would decrease its cytotoxicity and plasma protein binding, leaving the antimicrobial and LPS-binding capacities unchanged. We also evaluated a previously described variant of LL-37, the 18-mer LLKKK (16), which has enhanced hydrophobicity and cationicity, in this respect.

MATERIALS AND METHODS

Peptides. Peptides were synthesized by AgriSera AB, Växjö, Sweden, by 9-fluorenylmethoxy carbonyl chemistry. The purity of the peptides (>95%) was...
confirmed by mass spectrometry. The amino acid sequences of all peptides used for this study are presented in Table 1.

**Antimicrobial testing by radial diffusion assay.** Exserichia coli (4), *Pseudomonas aeruginosa* (15159), *Staphylococcus aureus* (F18), and Candida albicans (ATCC 90028) isolates were grown for 18 h at 37°C in 10 ml (3% [wt/vol]) of DMEM, Gibco, N.Y.) saturated with a gas mixture containing 8% CO₂ in 100/19262 (both from Sigma-Aldrich) for 2 h at room temperature (2). After reduction, 100/19262 (ATCC 90028) isolates were grown for 18 h at 37°C in 10 ml (3% [wt/vol]) of DMEM with known concentrations of sodium nitrate (Sigma-Aldrich). To exclude any direct interference of the peptides with the assay, we added the peptides (2 μM) to DMEM with a 1.5 μM nitrate standard in separate experiments. The assay was performed as described above, and no interference was detected.

**Hemolysis assay.** Blood was drawn from the antecubital veins of seven healthy donors into plastic tubes containing EDTA (2 mg ml⁻¹). After centrifugation at 800 × g for 10 min, the plasma and Buffy coat were removed. The erythrocytes were rinsed three times by centrifugation for 10 min at 800 × g and resuspension in 5% (vol/vol) phosphate-buffered saline (pH 7.4). Next, 400 μl of the erythrocyte suspension was incubated for 1 h at 37°C with gentle end-over-end rotation in the presence of LL-37, fragment 106 or 110, the 18-mer LLLKKK, or BMAP-27 at a concentration of either 0 (negative control), 0.6, 2, 6, 20, or 60 μM. Triton X-100 at 2% (Sigma-Aldrich) served as a positive control. After incubation, the samples were centrifuged at 800 × g for 10 min. The release of hemoglobin was monitored by measuring the absorbance of the supernatant at 540 nm and is expressed as a percentage of the value for Triton X-100-induced hemolysis.

**DNA fragmentation assay.** Confluent human aortic vascular smooth muscle cells (CC-2571, BioWhittaker, Walkersville, Md.) from passages 5 to 7 were cultured in 24-well plates and incubated in serum-free DMEM for 16 h in the absence (control) or presence of either LL-37, fragment 106, or fragment 110 at a concentration of either 2, 6, or 20 μM. Internucleosomal DNA fragmentation was measured by use of a Cell Death Detection ELISA kit (Roche Molecular Biochemicals, Mannheim, Germany) according to the manufacturer's instructions. In short, the cells were lysed in the culture wells and the DNA fragments in the lysate were bound to a microtiter plate coated with monoclonal antihistone antibodies. The bound DNA fragments were then detected with peroxidase-conjugated monoclonal anti-DNA antibodies and 2,2'-azino-di-[3-ethylbenzthiazoline-6-sulfonate]. The optical density was measured at 415 nm and is expressed as the increase (fold) in absorbance over that of untreated controls.

**Chemotaxis assay.** Twenty milliliters of blood was drawn from the antecubital veins of four healthy donors into plastic tubes containing EDTA (2 mg ml⁻¹). Polymorphonuclear cells were isolated by centrifugation over Polymorphprep (Axis-Shield PoC, Oslo, Norway) according to the manufacturer’s instructions. The cells were washed and resuspended in RPMI 1640 containing L-glutamine (Gibco) to achieve 2 × 10⁶ cells ml⁻¹. LL-37, fragments 106 and 110, the 18-mer LLLKKK (all diluted in RPMI to 0.01, 0.1, 1, or 10 μM), and N-formyl-Met-Leu-Phe (SMLP 0.1 μM) (Sigma-Aldrich) were added to the lower wells of a 48-well microchemotaxis chamber (AP48, Neuro Probe Inc., Gaithersburg, Md.). Fifty microliters of the cell suspension was added to the upper chamber, which was separated from the lower chamber by a polycarbonate membrane with 5-μm pores. The chamber was incubated for 1 h at 37°C in a humidified gas mixture containing 5% CO₂ in air. After incubation, cells that had not migrated were wiped off the upper face of the membrane. After fixation in methanol and drying, the membrane was stained with MGG quick stain (Bio-Optica, Milan, Italy) according to the manufacturer's instructions, dried, and mounted under coverslips on microscope slides by using Pertex medium (Histolab Products AB, Gothenburg, Sweden). The number of transmigrated cells was counted in at least three 0.03-mm² fields with a light microscope at a magnification of ×1,000 and is expressed as the number of cells per mm².

**Effects of serum on antimicrobial activity.** Blood was drawn from the antecubital veins of five healthy donors into glass tubes without additives and left to coagulate for 1 hour at room temperature. Sera were collected after centrifugation for 10 min at 2,000 × g. LL-37 or fragment 106 or 110 was diluted in sterile distilled water. Serum was added to achieve a peptide concentration of 20 μM in 0.4, or 99% serum. The peptide-serum mixtures were applied to the wells of a plate in a radial diffusion assay using E. coli (4, 37), as described above.

**Statistics.** When a peptide was found to be active against the pathogen in the radial diffusion assay, the diameter of the wells was subtracted from the diameters of the clear zones. For experiments with several peptide concentrations, the resulting values were plotted against the log₁₀ peptide concentration, and a linear relationship was always found. The x-axis intercept of the regression line corresponds to the log₁₀ minimal effective concentration, which was calculated with linear regression software (Sigma Plot 8.0; SPSS Inc., Chicago, Ill.). The minimal effective concentration was used as an estimation of antimicrobial potency. One-way or two-way repeated-measurement analysis of variance (ANOVA), followed by post hoc testing using the Holm-Sidak method when appropriate, and Student’s paired t test were used as indicated in the figure legends. Significance was accepted at P values of <0.05. The data are reported as means ± standard errors of the means (SEM). "n" equals the number of independent experiments for experiments with cultured prokaryotic or eukaryotic cells or the number of rats or humans.

**TABLE 1. Amino acid sequences of the peptides used for this study**

<table>
<thead>
<tr>
<th>Peptide</th>
<th>Amino acid sequence (N terminal to C terminal)</th>
</tr>
</thead>
<tbody>
<tr>
<td>LL-37</td>
<td>LLGDFRRKSSKEGKFEKRIVKLKDRLNLVPRTES</td>
</tr>
<tr>
<td>Fragment 106</td>
<td>GDFRRKSSKEGKFEKRIVKLKDRLNLVPRTES</td>
</tr>
<tr>
<td>Fragment 110</td>
<td>RKSKEGKFEKRIVKLKDRLNLVPRTES</td>
</tr>
<tr>
<td>18-mer LLLKKK</td>
<td>KLPIVRKLRKLFLKL</td>
</tr>
<tr>
<td>BMAP-27</td>
<td>GRFRRKFFKFLKPSVFLHLH-am</td>
</tr>
</tbody>
</table>

*Note that the bovine cathelicidin BMAP-27 is amidated at the C-terminal end. The underlined amino acids of the 18-mer LLLKKK have been changed compared to the native peptide, LL-37.*
TABLE 2. Minimal effective concentrations obtained by a radial diffusion assay for LL-37, fragments 106 and 110, the 18-mer LLKKK, and BMAP-27 for gram-negative and -positive bacteria and C. albicans.

<table>
<thead>
<tr>
<th>Pathogen</th>
<th>NaCl concn (mM)</th>
<th>Minimal effective concn (μM)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>LL-37 Fr 106 Fr 110 18-mer BMAP-27</td>
<td></td>
</tr>
<tr>
<td>E. coli</td>
<td>0 1.2 1.8 0.6 0.36</td>
<td></td>
</tr>
<tr>
<td>P. aeruginosa</td>
<td>0 0.19 0.22 0.15 0.06</td>
<td></td>
</tr>
<tr>
<td>S. aureus</td>
<td>0 1.5 0.86 0.8 1.2</td>
<td></td>
</tr>
<tr>
<td>C. albicans</td>
<td>0 4.6 2.6 2.4 0.39</td>
<td></td>
</tr>
</tbody>
</table>

The values were determined at a low (0 mM) or physiological (150 mM) concentration of NaCl. Each value is based on data from three independent experiments.

RESULTS

Radial diffusion assay. All of the peptides tested were antimicrobial. The minimal effective concentration values are presented in Table 2. The minimal effective concentration values for E. coli, P. aeruginosa, and S. aureus at low salt concentrations were similar between the different peptides, while the shorter fragments 106 and 110 as well as the 18-mer LLKKK and the bovine cathelicidin BMAP-27 were more active against C. albicans than was LL-37. It has been found that the antimicrobial activity of LL-37 against gram-positive bacteria and C. albicans is reduced at physiological salt concentrations (26, 27). We found that the presence of NaCl at 150 mM did not affect the antimicrobial activities of the peptides for E. coli and P. aeruginosa to any major extent, with the only exception being LL-37, which appeared to lose some of its potency against E. coli. NaCl reduced the activity against S. aureus for LL-37 and fragments 106 and 110. In the presence of 150 mM NaCl, all of the peptides lost their activity against C. albicans at the concentrations tested. We concluded that the N-terminal truncation of LL-37 does not affect its antimicrobial activity negatively.

Nitrate/nitrite accumulation. Next, we wanted to see if the peptides could inhibit LPS-induced NO production in isolated rat aortas, leading to a subsequent decrease in the accumulation of nitrate/nitrite in the incubation medium. LPS induced a more than fivefold increase in nitrate/nitrite accumulation (Fig. 1). All peptides tested inhibited nitrate/nitrite accumulation with similar potencies, except fragment 106, which at 2 μM was significantly less efficient than LL-37. The incubation of aortic segments with the peptides in the absence of LPS did not affect the baseline nitrate/nitrite accumulation (not shown). This suggests that the peptides do not have any proinflammatory effects in this model. We concluded that the N-terminal truncation of LL-37 does not affect LPS binding and neutralization to any major extent.

Hemolysis. All peptides induced a concentration-dependent hemolysis (Fig. 2). The hemolysis induced by the 18-mer LLKKK and BMAP-27 was significantly more pronounced than that induced by LL-37, indicating the severe cytotoxicity of these peptides. Fragments 106 and 110 caused significantly less hemolysis than LL-37. Fragment 106 was found to be the least cytotoxic peptide to erythrocytes.

DNA fragmentation. Having ruled out the 18-mer LLKKK and BMAP-27 as potential therapeutic agents due to their severe, rapidly developing cytotoxicities, we compared the toxicities of the remaining fragments, 106 and 110, with that of LL-37 after a longer exposure time. As shown in Fig. 3, LL-37 at concentrations of 6 and 20 μM induced significant DNA fragmentation in human vascular smooth muscle cells compared to the control, confirming the previously found toxicity at these concentrations (2). Fragment 106 also induced significant DNA fragmentation, while fragment 110 did not. Thus, the removal of the N-terminal hydrophobic amino acids reduces the cytotoxicity of LL-37.

Chemotactic activity. LL-37 and its N-terminally truncated analogs, fragments 106 and 110, all displayed similar concentration-dependent chemotactic activities on granulocytes (Fig. 4). The concentration-response curves were biphasic, with a maximum effect at 0.1 μM amounting to nearly half that achieved with the classical chemoattractant formyl pep-
both the x (concentrations followed by post hoc testing by the Holm-Sidak method for the factors of different peptides and peptide concentrations). The data were analyzed by two-way repeated-measurement ANOVA for the factors of different peptides and peptide concentrations followed by post hoc testing by the Holm-Sidak method (P < 0.05). Values are means ± SEM (n = 7). Note the log scales on both the x and y axes.

Effect of serum on antibacterial activity. LL-37 and fragments 106 and 110 inhibited the growth of E. coli to the same extent as indicated by the similar sizes of the clear zones around the wells containing the peptides (Fig. 5). Although serum alone was weakly antibacterial, it markedly decreased the antibacterial activity of LL-37 and, to a significantly smaller extent, the activity of fragment 106, while the activity of fragment 110 was not affected. These results indicate that the N-terminal truncation of LL-37 decreases its binding and neutralization by plasma proteins.

DISCUSSION

We tested the antimicrobial effects of LL-37 and derivative peptides with some pathogens known to cause sepsis. The antimicrobial potency of LL-37 found in the present study was within the range that was previously reported (11, 15, 17, 26, 27). LL-37 was also found to bind and neutralize the effects of LPS as described in the literature, with a potency similar to that of the well-characterized LPS-binder polymyxin B (2, 10, 20, 27). However, we also confirmed earlier observations of short- and long-term cytotoxic effects of the peptide (2, 8, 18). This precludes any therapeutic use of native LL-37. LL-37 has an abundance of hydrophobic amino acids at its N terminus. Oren and colleagues found that the removal of four N-terminal amino acids from LL-37 reduces its hemolytic activity (18). A corresponding removal of the hydrophobic C-terminal tails of the bovine cathelicidins BMAP-27 and BMAP-28 also markedly reduced their hemolytic activities (22). We chose to reduce the hydrophobicity of LL-37 in a stepwise fashion by removing the first two N-terminal leucines (fragment 106) and the first six amino acids, including two leucines, one glycine, and two phenylalanines (fragment 110). This N-terminal truncation did not seem to reduce the antimicrobial potency of LL-37 at a low or physiological salt concentration. Interestingly, it was recently found that a peptide identical to fragment 110 is formed naturally on the skin, where it may protect against microbial colonization (15). The N-terminal truncation of LL-37 did not eliminate its ability to inhibit LPS-induced NO production in the rat aorta, a model which is relevant to gram-negative septic shock. In these experiments, fragment 110 was equipotent with LL-37.

As expected, fragments 106 and 110 were less cytotoxic to human cells than the parent peptide LL-37. Interestingly, this did not seem to be due to a reduction of nonspecific toxicity to eukaryotic cells, since truncation in fact increased the suppressive effect on the growth of C. albicans. This suggests that the mechanisms underlying the antifungal action of LL-37-derived peptides are complex and require further investigation. We found that the activities of all of the peptides against C. albicans decreased profoundly in the presence of a physiological salt concentration. The present results do not provide any explanation for this. It has previously been demonstrated that the antibacterial activity of LL-37 correlates with the formation of the antibacterial activity of LL-37 and fragments 106 and 110 was equipotent with LL-37.

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The underlying infection. Infusion of the chemoattractant in-
infectious foci is decreased, thereby impairing the clearance of
reasonable to assume that the migration of immune cells into
tions of this remain to be elucidated (25). However, it seems
creased in septic patients, but the pathophysiological implica-
tides tested, a variant with an increased hydrophobicity and
-37 are retained as well. However, although it was re-
tment of sepsis. Further studies are needed to
the chemotactic domains of the LL-37 analogs and to
explore the effects of amino acid substitutions in this region on
their chemotactic activity.

It has been demonstrated that LL-37 binds to the plasma
protein apolipoprotein A-I and that this binding inhibits its
antimicrobial and cytotoxic effects (28). We found that serum
did not inhibit the antimicrobial action of LL-37 after the
removal of hydrophobic N-terminal amino acids. This suggests
that these amino acids are important for binding to apolipo-
protein A-I, probably due to the hydrophobic nature of the
binding, as suggested by Sørensen and colleagues (24). The
fact that the actions of fragments 106 and 110 were only mar-
ginally inhibited by serum must be regarded as fundamental if
they are to be used as a systemic treatment for sepsis patients.

In conclusion, the removal of N-terminal hydrophobic ami-
no acids from LL-37 decreases its cytotoxicity for human cells
as well as its inhibition by serum without negatively affecting its
antimicrobial or LPS-neutralizing action. While fragment 110
inhibits bacterial growth and neutralizes LPS at least as effect-
ively as LL-37, it is significantly less hemolytic and cytotoxic in
the long term. We believe that our results will facilitate the
development of novel peptide-based strategies for the treat-
ment of sepsis.

FIG. 5. Inhibition of antibacterial activity by serum, as assessed by
a radial diffusion assay using E. coli. In the absence of serum (open
bars), LL-37 and fragments 106 and 110 (all at 20 μM) inhibited
bacterial growth to the same extent. Although serum alone was weakly
antibacterial (*), it markedly decreased the antibacterial activity of
LL-37 and, to a smaller extent, the activity of fragment 110 (*). The
activity of fragment 106 was not significantly affected. The data were
analyzed by two-way repeated-measurement ANOVA for the factors of different
peptides and serum concentrations followed by post hoc testing by the Holm-Sidak method (P < 0.05). Values are means ± SEM (n = 5).
ACKNOWLEDGMENTS

This work was supported by Swedish Research Council grants 2002-6270, 2004-3874, and 13471, by the Medical Faculty of Lund University, by Lund University Hospital Research funds, by the Region Skåne Research Council, and by the Royal Physiological Society.

We thank Emma Andersson Nordahl and Adrian Ionescu for scientific discussions and advice regarding the radial diffusion assay and the staining of cells, respectively, and Pia Andersson and Tyberius Moska for their excellent technical assistance.

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