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Proteinases of common pathogenic bacteria degrade and inactivate the antibacterial peptide LL-37

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Summary
Effectors of the innate immune system, the antibacterial peptides, have pivotal roles in preventing infection at epithelial surfaces. Here we show that proteinases of the significant human pathogens Pseudomonas aeruginosa, Enterococcus faecalis, Proteus mirabilis and Streptococcus pyogenes, degrade the antibacterial peptide LL-37. Analysis by mass spectrometry of fragments generated by P. aeruginosa elastase in vitro revealed that the initial cleavages occurred at Asn-Leu and Asp-Phe, followed by two breaks at Arg-Ile, thus inactivating the peptide. Proteinases of the other pathogens also degraded LL-37 as determined by SDS-PAGE. Ex vivo, P. aeruginosa elastase induced LL-37 degradation in human wound fluid, leading to enhanced bacterial survival. The degradation was blocked by the metalloproteinase inhibitors GM6001 and 1, 10-phenantroline (both of which inhibited P. aeruginosa elastase, P. mirabilis proteinase, and E. faecalis gelatinase), or the inhibitor E64 (which inhibited S. pyogenes cysteine proteinase). Additional experiments demonstrated that dextran sulphate and disaccharides of the structure [ΔUA(2S)-GalNAc(4,6S)], or sucroseoctasulphate, inhibited the degradation of LL-37. The results indicate that proteolytic degradation of LL-37 is a common virulence mechanism and that molecules which block this degradation could have therapeutic potential.

Introduction
Epithelial surfaces of various organisms are continuously exposed to bacteria. During recent years the innate immune system, based on antibacterial peptides originally described in silk worms (Steiner et al., 1981), has been attributed important roles in the initial clearance of bacteria at biological boundaries susceptible to infection (for references see reviews by Selsted and Ouellette, 1995; Lehrer and Ganz, 1999; Schröder and Harder, 1999; Boman, 2000). Cathelicidins, consisting of a conserved N-terminal domain and a C-terminal antibacterial region, constitute one family of such peptides. In humans, the cathelicidin hCAP-18 is processed by proteinase 3 (a serine proteinase) to generate the active peptide LL-37, which exerts antibacterial activity against both Gram-negative and Gram-positive bacteria (Sörensen et al., 2001). LL-37 has been isolated from neutrophils (Zanetti et al., 1995) and subpopulations of lymphocytes and monocytes (Agerberth et al., 2000). This peptide is also found in seminal plasma (Malm et al., 2000), in the lung (Bals et al., 1998; Agerberth et al., 1999), and in keratinocytes during inflammation (Frohm et al., 1997). Furthermore, it has been reported that LL-37 has synergistic effects with α-defensin, another major antibacterial peptide found in the azurophilic granules of neutrophils (Nagaoka et al., 2000). The significance of cathelicidins for bacterial clearance is exemplified by recent findings indicating that the mouse antibacterial peptide CRAMP protects the skin from invasive bacterial infection (Nizet et al., 2001).

Pathogens, however, appear to overcome the innate immune defence systems giving rise to various infections. In some conditions, such as chronic ulcers of the skin, bacteria such as P. aeruginosa, E. faecalis, and P. mirabilis, manage to infect and persist for long periods of time. During infection, these pathogens, which are frequently found in chronic ulcers (P. aeruginosa; 20–30%, E. faecalis 80%, P. mirabilis 15%) (Hansson et al., 1995), use a combination of virulence strategies. For instance, release of various proteinases, such as elastase and alkaline proteinase of P. aeruginosa (Morihara et al., 1965; Fukushima et al., 1989; Okuda et al., 1990), may modulate host responses involving kallikreins, coagulation factors, complement, cytokines, and antiproteinases (for a review, see Travis et al., 1995). Interestingly, degradation of complement, antiproteinases, and matrix components in vitro by the proteinases, closely resembles the
degradation pattern of these molecules seen in wound fluid in vivo (Schmidtchen, 2000, and unpublished data).

The well known bacterial persistence in chronic skin ulcers and the fact that antiproteinase deprivation and uncontrolled proteolysis characterize these ulcers raise the possibility that bacterial proteinases may affect antibacterial peptides. In this study, data are presented showing that bacterial proteinases, such as P. aeruginosa elastase, rapidly degrade and inactivate LL-37, leading to enhanced bacterial survival. Furthermore, we show that this proteolytic degradation may be modulated by proteinase inhibitors and by sulphated poly- and di-saccharides.

Results
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To examine the bactericidal effects of intact LL-37, the activity of the peptide against S. pyogenes, E. faecalis, P. mirabilis and P. aeruginosa was determined. The bacterial strains were separately incubated with 0–20 μg ml⁻¹ of LL-37. Pseudomonas aeruginosa, E. faecalis, P. mirabilis, and S. pyogenes were effectively killed by the peptide at or above concentrations of 2–10 μg ml⁻¹ (Fig. 1). We then investigated the effects of P. aeruginosa elastase on LL-37. Initial experiments indicated that the peptide was rapidly degraded, with no detectable intermediate peptides on SDS-PAGE (not shown). Thus, a titration was performed and proteinase amounts yielding detectable amounts of LL-37 degradation products were used in further experiments. The addition of 30 mM of proteinase (~25 ng protein) to 10 μg peptide (molar ratio enzyme to peptide ~1:2500) yielded intermediate fragments of approximately 3–4 kDa after an incubation period of 1–30 min (Fig. 2A, upper panel). Longer incubations yielded no visible peptides in the SDS-PAGE system used (16.5%). The proteinase amounts used correspond to enzyme levels found in ~5–10 μl of conditioned media from a P. aeruginosa culture grown overnight in TH-medium (as determined by an azocasein assay). Next, the effect of these LL-37 intermediates was investigated. In bactericidal assays, E. faecalis bacteria were incubated with the peptide fractions (corresponding to 10 μg ml⁻¹), and those containing the 3–4 kDa forms (Fig. 2A, 5–30 min incubations) exerted residual bactericidal activity (40–60% bacteria killed), whereas subsequent incubations (1–20 h) contained no such activity (not shown). The finding that the 30 min incubation, which was devoid of intact peptide, exerted residual activity (~40% of control), suggests that the larger ~4 kDa degradation product is bactericidal. Finally, structural analysis of LL-37 fragments generated by P. aeruginosa elastase was performed. Liquid chromatography–mass spectrometry time of flight (LC-MS TOF) and MS-MS TOF analysis of the material corresponding to the 1 min to 1 h degradations (Fig. 2A) yielded major peptides of masses 3708.859, 3178.637, 2822.450, 2326.169 and 1401.748 Da. A correspondence between the peptide intensities of the major 3–4 kDa bands on electrophoresis (Fig. 2A) and the peak heights on mass spectrometry was noted (not shown). The P. aeruginosa cleavage points were determined and are indicated (Fig. 2B). Interestingly, the proteinase acted on a region of LL-37 that has been attributed with antibacterial activity (Oren et al., 1999).

Having proven that fragmentation of LL-37 leads to loss of antibacterial activity (using E. faecalis as the test organism), we examined whether proteinase production was protective for P. aeruginosa. In this context, various experimental approaches were tested. Analyses of P. aeruginosa growth in TH or LB medium before and after addition of proteinase inhibitors (GM6001 or 1, 10-phenanthroline), showed that these, at levels necessary for inhibition of elastase (50–100 μM), inhibited bacterial growth, which prevented us from performing MIC analyses under conditions necessary for P. aeruginosa growth. The effect of supplementing P. aeruginosa with proteinase was therefore investigated. Addition of elastase, corresponding to the concentrations found in overnight cultures of P. aeruginosa, resulted in significant reduction of LL-37-mediated bacterial killing (Fig. 2C and D). Next, to show that degradation abolished bacterial binding, the uptake of fluorescent labelled LL-37 by bacteria was studied using fluorescence microscopy and flow cytometry. As shown in Fig. 3B, Texas red-conjugated LL-37 rapidly bound to and stained P. aeruginosa bacteria. After an incubation of the labelled LL-37 with P. aeruginosa elastase, no binding of LL-37 to the bacteria could be detected (Fig. 3D). Both

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incubations were analysed directly and, hence, identical amounts of Texas red label were added in both cases to the bacteria (this was easily verified by UV-illumination).

The images in Fig. 3B and D were recorded using identical settings for the microscope and CCD camera software. To quantify the fluorescence more stringently, we analysed the fluorescence distribution of bacteria incubated with intact labelled LL-37 (Fig. 3E, rightmost histogram) and bacteria incubated with LL-37 that had been subjected to prior treatment with \textit{P. aeruginosa} elastase (Fig. 3E, lefmost histogram). Non-degraded LL-37 gave rise to a distinct fluorescence, whereas the fluorescence histogram of bacteria incubated with degraded LL-37 did not differ from that of unlabelled bacteria (not shown).

Finally, the effects of other bacterial proteinases on LL-37 were investigated. Incubation of LL-37 with \textit{E. faecalis} growth medium (containing gelatinase), as well as purified \textit{S. pyogenes} cysteine proteinase yielded similar fragments as those generated by \textit{P. aeruginosa} elastase, as determined by SDS-PAGE. \textit{Proteus mirabilis} proteinase did not generate these intermediates. However, for all bacteria, longer incubation periods yielded almost complete digestion of LL-37 (Fig. 4A). Incubation of LL-37 with wound fluid from a patient with a \textit{P. aeruginosa} infected chronic ulcer, also yielded almost complete degradation. Fluid from a surgical (sterile) wound did not exhibit this effect (Fig. 4B). Analysis of additional acute (three samples) and chronic, infected, wound fluids (two samples) from other patients yielded similar results (not shown).

**Ex vivo experiments using human wound fluid and neutrophil extracts**

The finding that wound fluid from infected ulcers degrades LL-37, prompted us to further investigate LL-37 degradation in wound fluids, and the effects on bacterial survival of \textit{P. aeruginosa} proteinase production in these wound fluids. Various ulcer-derived \textit{P. aeruginosa}, producing either undetectable levels of elastase or expressing high levels of elastase (three isolates each, of which one from each group is presented in Fig. 5, see also Schmidtchen \textit{et al.}, 2001a) were grown in TH medium or in wound fluid...
obtained from sterile surgical wounds. *Pseudomonas aeruginosa* elastase was only detected (by zymographic analysis and immunoblotting) in supernatants from cultures of previously characterized elastase-expressing bacteria, and the levels of elastase were similar in TH and in wound fluid (Fig. 5A). The minor 50 kDa enzyme is alkaline proteinase (Schmidtchen et al., 2001a).

Having confirmed elastase production, the various wound fluids were then incubated with Texas red-labelled LL-37. As shown in Fig. 5B, significant degradation of LL-37 was only noted in the wound fluid containing elastase-producing *P. aeruginosa* (ELA +). Thus, the data show that wound fluid infected ex vivo with elastase-producing *P. aeruginosa*, has the capacity to rapidly degrade LL-37. On the basis of these observations, we examined whether the different *P. aeruginosa* isolates, when grown in wound fluid, exhibited variable sensitivity to exogenously added LL-37. In growth assays, overnight cultures of *P. aeruginosa* were inoculated (5%) in 200 μl of 10% human wound fluid (in phosphate-buffered saline). After an incubation period of 5 h, 0–30 μg of LL-37 was added and bacterial growth assessed (by measuring absorbance at 490 nm). Five and 10 μg LL-37 had no effect relative the controls (not shown). Whereas the elastase-producing *P. aeruginosa* was unaffected by LL-37 at all concentrations (in contrast to the results with the same isolate in the bactericidal assays shown in Fig. 1), the non-producing isolate was inhibited by LL-37 doses at or above 20 μg (100 μg ml⁻¹) (Fig. 5C). This concentration of LL-37 exceeded the bactericidal concentration of the peptide (obtained in 10 mM Tris-buffer; 10–20 μg ml⁻¹, see Fig. 1), indicating the presence of inhibitory substances in wound fluid, as previously described for plasma (Wang et al., 1998). These results were similar for all other isolates studied, showing that soluble elastase promotes bacterial survival in wound fluid ex vivo. The fact that neutrophils secrete hCAP18 which is processed into active LL-37, raised the question whether the intact proprotein is affected by *P. aeruginosa* proteinase. To address this, human neutrophil extracts were treated with conditioned medium from elastase-producing or elastase-deficient *P. aeruginosa* (Fig. 6). As shown by immunoblotting using polyclonal antibodies against LL-37, degradation of hCAP18 was only noted after treatment with elastase-producing *P. aeruginosa*. Likewise, addition of purified *P. aeruginosa* elastase to neutrophil extracts resulted in a complete degradation of hCAP18 and LL-37 (not shown).

Identification of substances that inhibit the degradation of LL-37

To find out whether the degradation of LL-37 could be
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inhibited, the effects of proteinase inhibitors were studied. Results showed that degradation was abolished by the metalloproteinase inhibitors GM6001 and 1,10-phenantroline (which both inhibited *P. aeruginosa* elastase, *E. faecalis* gelatinase and *P. mirabilis* proteinase) (Fig. 4C, PAELA, EFGEL and PMMP), or by the inhibitor E64 which inhibits the *S. pyogenes* cysteine proteinase (Björck et al., 1989) (Fig. 4C, SPCP). Previous studies showed that the antibacterial peptide α-defensin specifically bound to glycosaminoglycans, preferably chondroitin sulphate B (CS-B), and that this binding destroyed the antibacterial effect of the peptide (Schmidtchen et al., 2001). Therefore, we investigated whether LL-37 could bind to various glycosaminoglycans. As assessed by slot-binding experiments, LL-37 preferentially bound to CS-B and CS-E (Fig. 7A), and subsequently, in a functional assay, we found that the various glycosaminoglycans blocked the bactericidal effects of the peptide (Fig. 7B). An octasulphated disaccharide, sucroseoctasulphate (SOS), also blocked the bactericidal activity of LL-37. Having shown that LL-37 binds to sulphated polysaccharides, we wanted to investigate whether these polysaccharides, their constituent disaccharides or related carbohydrates, exerted protective effects on LL-37 vis-à-vis added bacterial proteinase. Indeed, intact polysaccharides, preferably CS-B and CS-E, were able to protect LL-37 from degradation by *P. aeruginosa* elastase (Fig. 7C). Interestingly, a protective effect was noted after addition of trisulphated CS-disaccharides of the structure ΔUA(2S)-GalNAc(4,6S) (Fig. 7D), which are found (as co-polymers) in the CS-B fraction used here (Rodén et al., 1973). Notably, a related disaccharide (ΔUA(3S)-GalNAc(4,6S)) was recently identified in CS-E (Kinoshita et al., 2001). Sucroseoctasulphate also exhibited similar protective effects at almost equimolar concentrations of disaccharide relative the peptide (Fig. 7E). Sucrose did not exhibit these effects (not shown). These results show that anionic molecules of various sulphation patterns inhibit the degradation of LL-37. No effect on elastase activity (as determined by an azocasein assay) by either the CS variants or sucroseoctasulphate was detected (not shown).

**Discussion**

Bacterial evasion of peptide-based innate defences may prove to be important for the initial colonization of epithelial surfaces. Recently, pathways aimed at inactivating the innate immune system have been uncovered. For example, proteinases of common pathogenic bacteria, such as *P. aeruginosa*, *E. faecalis* and *S. pyogenes* were shown to release dermatan sulphate chains, leading to inactivation of the antibacterial peptide α-defensin (Schmidtchen et al., 2001b). Independent findings showed that the metalloproteinase lasA from *P. aeruginosa* induced release of another sulphated polysaccharide, heparan sulphate, leading to inactivation of innate defence and increased mortality during *P. aeruginosa* infection (Park et al., 2001). Staphylococcal resistance to defensins has recently been related to modification of bacterial membrane lipids with...
L-lysine (Peschel et al., 2001). During *Shigella* infections, it was shown that this pathogen downregulates the expression of LL-37 and human β-defensins, with bacterial DNA as a potential regulator (Islam et al., 2001). Additional acterial defence mechanisms directed against antibacterial peptides may involve modifications of outer cell wall components, such as lipopolysaccharide (Ernst et al., 1999) or phosphorylcholine (Lysenko et al., 2000) and the modulation of efflux pumps (Shafer et al., 1998).
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Here, we show for the first time that proteinases of the clinically significant bacterial species *P. aeruginosa*, *E. faecalis*, *P. mirabilis* and *S. pyogenes* degrade the major human antibacterial peptide LL-37 and that this degradation leads to loss of LL-37 binding to bacteria and, ultimately, abolished bacterial killing.

*Pseudomonas aeruginosa* elastase was shown to specifically hydrolyse LL-37. The P1¢ position was preferentially occupied by hydrophobic amino acids (L, I, F), whereas the P1 position was less specific (N, D, R, E, K). The P1¢ specificities corresponded well with those reported for the M4 peptidase family (thermolysin family) to which *P. aeruginosa* elastase belongs. *Enterococcus faecalis* gelatinase, as well as the 50 kDa metalloproteinase of *P. mirabilis* are also members of this group, having similar specificities (Rozalski et al., 1997; de Kreij et al., 2000). In this context, it should be noted that, in addition to cationic amino acids, most antibacterial peptides contain a significant (≈50%) portion of hydrophobic amino acids (Hancock and Scott, 2000). Therefore, considering the data discussed above, and taking the specificities of the M4 peptidase family into account, it is conceivable that bacterial proteinases may have profound effects on the actions of antibacterial peptides. This notion is further supported by the fact that human α-defensin was also degraded by *P. aeruginosa* elastase (unpublished results).

From the perspective of chronic ulcers and considering recent observations identifying defensins in wound fluids (Frohm et al., 1996), as well as findings showing that cutaneous injury induces the release of LL-37 in response to infection (Dorschner et al., 2001), it is still an enigma how certain pathogens, such as *P. aeruginosa*, *E. faecalis* or *P. mirabilis* may persist and colonize for long periods of time in these ulcers. In this study, we present several lines of evidence that support the hypothesis that bacterial proteinases degrade and inactivate LL-37.
of evidence indicating a pivotal role for *P. aeruginosa* elastase in the evasion of LL-37 mediated bacterial killing. First, the finding that elastase production made *P. aeruginosa* completely resistant to the action of LL-37 during growth in human wound fluid ex vivo suggests that during *P. aeruginosa* infection of human wounds, release of elastase inactivates LL-37 and protects bacteria from the action of the antibacterial peptide. Second, *P. aeruginosa* elastase also induced degradation of the proprotein hCAP18 in neutrophil extracts. Third, we found that chronic wound fluid collected from *P. aeruginosa* infected leg ulcers, but not acute sterile wound fluid, had the capacity to degrade LL-37. Taken together, these findings correspond well with recent data showing that chronic venous ulcers are devoid of LL-37 and contain low levels of hCAP18, in contrast to normally healing wounds (Frohm-Nilsson, 2001). Because all chronic ulcers contain bacteria able to secrete proteinases, it is plausible that the observed lack of LL-37/hCAP18 is due to degradation by bacterial proteinases.

From a therapeutic point of view, inhibition of bacterially induced proteolysis could lead to increased levels of LL-37 in vivo. As hCAP-18 is processed to LL-37 by extracellular cleavage with proteinase 3, a serine proteinase (Sörensen et al., 2001), the use of specific metalloproteinase inhibitors, such as GM6001, could represent a possible treatment option in future in vivo studies. Considering the action of glycosaminoglycans and sulphated disaccharides, their effects also merits some consideration. The fact that these molecules block the bactericidal effects of LL-37, as well as protect the peptide from proteolysis, highlights the complexity and sometimes dual roles of bacterial virulence mechanisms. For example, it has been shown that bacterial proteinases are able to release *E. faecalis* as the test bacterium. 1, 10-Phenantroline, GM6001, E64, the chondroitin sulphate (CS) preparations CS-A, -C, and -E, and the CS and dermatan sulphate (DS) disaccharides ΔUA-GalNAc, ΔUA(2S)-GalNAc(4S), ΔUA(2S)-GalNAc(6S), ΔUA-GalNAc(4,6S), ΔUA(2S)-GalNAc(4,6S) were purchased from Sigma. CS-B (DS6) was obtained from Dr L.-Å. Fransson. The preparation and characteristics of this fraction have been described previously (Rodén et al., 1973; Fransson et al., 1979). Sucroseoctasulphate (potassium salt, MW 1287.55) was purchased from Toronto Research Chemicals. *Pseudomonas aeruginosa* elastase was purchased from Calbiochem. In some experiments, we used an equivalent elastase enzyme, generously supplied by Dr H. Maeda, Kumamoto University, Japan.

### Bacterial culture and proteinases

*Pseudomonas aeruginosa, E. faecalis,* and *P. mirabilis* isolates were initially obtained from chronic venous ulcer cases and were grown for 18 h at 37°C (stationary phase) in Todd–Hewitt (TH) medium. The *S. pyogenes* strain AP1 (40/58) was from the World Health Organization Collaborating Centre for References and Research on Streptococci (Prague, Czech Republic), and was grown to stationary phase in C-medium (Gerlach et al., 1983). Bacteria were pelleted by centrifugation and supernatants sterile-filtered (0.3 μm) and stored at −20°C. The cysteine proteinase of *S. pyogenes* was purified according to previous protocols (Herwald et al., 1996). Growth culture supernatants from the *E. faecalis* (expressing gelatinase) and *P. mirabilis* strains (expressing a 50 kDa metalloproteinase) (not shown) were sterile-filtered and used directly. The activity of the proteinase preparations was determined using an azocasein assay (Okamoto et al., 1997). For preparation of infected wound fluids, wound fluid from surgical wounds (1 ml diluted 1:1 with TH, denoted 50% WF in the text) was inoculated with 20 μl of overnight cultures of carbohydrates, including glycosaminoglycans and sucrosoctasulphate (Folkman et al., 1991; Klagsbrun, 1992), and that non-infected human wound fluid contains significant levels of CS-B (Penc et al., 1998).

In summary, we have presented data showing that the major human antibacterial peptide LL-37 is degraded and inactivated by proteinases of several significant human pathogens. This observation and the finding that proteinase inhibitors, glycosaminoglycans and sulphated disaccharides protect LL-37 from proteolytic degradation could be utilized in the search for novel antibacterial strategies.

### Experimental procedures

#### Materials

LL-37, LLGDFRKSKEKGKEFKRIVQRKDFLRNLPRTES (MW 4492.08) and Texas-red labelled LL-37 were synthesized by Innovagen AB, Lund. The Texas-red label including an additional cysteine was coupled to the aminoterminus of LL-37. The purity and molecular weight of these peptides was confirmed by mass spectral analysis (MALDI-TOF Voyager).

Both peptides exhibited identical bactericidal activities using *P. aeruginosa* as the test bacterium. 1, 10-Phenantroline, GM6001, E64, the chondroitin sulphate (CS) preparations CS-A, -C, and -E, and the CS and dermatan sulphate (DS) disaccharides ΔUA-GalNAc, ΔUA(2S)-GalNAc(4S), ΔUA(2S)-GalNAc(6S), ΔUA-GalNAc(4,6S), ΔUA(2S)-GalNAc(4,6S) were purchased from Sigma. CS-B (DS6) was obtained from Dr L.-Å. Fransson. The preparation and characteristics of this fraction have been described previously (Rodén et al., 1973; Fransson et al., 1979). Sucroseoctasulphate (potassium salt, MW 1287.55) was purchased from Toronto Research Chemicals. *Pseudomonas aeruginosa* elastase was purchased from Calbiochem. In some experiments, we used an equivalent elastase enzyme, generously supplied by Dr H. Maeda, Kumamoto University, Japan.

P. aeruginosa. Bacteria were pelleted by centrifugation and supernatants were stored at -20°C.

Wound fluids

Wound fluids (100–600 µl) from patients with chronic, infected, venous ulcers were collected under a Tegaderm dressing for 2 h as previously described (Schmidtchen, 2000). Sterile wound fluid was obtained from surgical drainages after mastectomy. Collection was for 24 h after operation. Wound fluids were centrifuged, aliquoted and stored at -20°C. The use of this material was approved by the Ethics Committee at Lund University (LU 509–01, LU 708–01). Informed consent was obtained from the patients.

Sodium dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE)

Electrophoresis was performed using the Ready Gel system (Bio-Rad) on 16.5% precast polyacrylamide gels with 4% stacking gel (Tris-tricine Ready Gel, Bio-Rad). For analysis of LL-37 degradation, peptides solubilized in 10 mM Tris, pH 7.4, were incubated with sterile or infected wound fluids, purified proteinases and, when indicated, additional substances were added (see figure legends for details). The incubations were stopped by boiling (5 min) and samples were supplemented with Tricine sample buffer (Bio-Rad). After fixing, the gels were stained with 0.25% Coomassie brilliant blue, destained and dried between two cellophane sheets in a Gel air dryer (Bio-Rad), and scanned (Duoscan T1222; Agfa). Texas red-labelled LL-37 was visualized directly after electrophoresis by the use of UV-illumination and digital photography. Pictures were processed using the Adobe photoshop software (Adobe).

Zymography

Wound fluids and bacterial supernatants were mixed with sample buffer (0.4 M Tris HCl, 20% glycerol, 5% sodium dodecyl sulphate (SDS), 0.03% bromophenol blue, pH 6.8) and electrophoresed on 10% polyacrylamide gels (1 mg of bovine gelatine per ml of gel). To remove SDS, gels were blocked (PBS, pH 7.4, 0.25% Tween 20, 3% bovine serum albumin) for 1 h and incubated with radiolabelled DS (~10 µg ml⁻¹) for 1 h in the same buffer. Unlabelled polysaccharides (2 mg ml⁻¹) were added for competition of binding. The membranes were washed (3 × 10 min) (PBS, pH 7.4, 0.25% Tween 20). Bas 2000 radioimaging system (Fuji) was used for visualization of radioactivity.

Mass spectrometry

Analysis of LL-37 fragments was performed by electrospray ionisation mass spectrometry on a Q-tof (Micromass, UK) using Masslynx software (performed by Innovagen AB, Lund).

Bactericidal assays

For antimicrobial assays S. pyogenes, E. faecalis, or P. aeruginosa were grown to mid-log phase in TH-medium. Bacteria were washed and diluted in 10 mM Tris-HCl, pH 7.5, containing 5 mM glucose. 50 µl of bacteria (2 × 10⁶ colony-forming units ml⁻¹) were incubated with intact or degraded LL-37, at the indicated concentrations (see figure legends). Incubations were carried out at 37°C for 2 h (S. pyogenes, E. faecalis) or 4 h (P. aeruginosa). To quantify the bactericidal activity, serial dilutions of the incubation mixture were plated on TH agar, incubated at 37°C overnight, and the number of colony-forming units were determined. In one experiment, the agar plates were placed on a light-board, photographed, and pictures further processed using Photoshop software (Adobe).

Bacterial growth assay

Pseudomonas aeruginosa were grown to stationary phase (OD = 1) in TH-medium. Then 200 µl of 10% sterile wound fluid (in PBS) was inoculated with 10 µl of the bacterial suspension in 96-well plates (Falcon). After an incubation period of 5 h at 37°C, LL-37 was added and absorbance measured at 490 nm (using a Bio-Rad 550 microplate reader) after various periods of time. The absorbance value at T = 5 h
(addition of LL-37) was subtracted from the thereafter attained values (see figure legends for further details).

Fluorescence microscopy

Bacteria \((5 \times 10^{10} \text{ ml}^{-1})\) were incubated for 5 min on ice together with either intact Texas red-labelled LL-37 \((10 \mu \text{g ml}^{-1})\) or with Texas red-labelled LL-37 that had been subjected to prior treatment with \(P. \text{ aeruginosa}\) elastase \((5 \text{ ng of elastase} \mu \text{g}^{-1} \text{LL-37 for} 4 \text{ h at} 37°C)\). Complete degradation of the peptide was verified by electrophoresis of the material on 16.5% Tris-tricine gels followed by UV-transillumination. After washing twice with ice-cold PBS, the bacteria were mounted on slides for immediate visual inspection and recording of images. This was performed using a Nicon Eclipse TE300 inverted fluorescence microscope equipped with a Hamamatsu C4742-95 cooled CCD camera, a Plan Apochromat 60X objective, and a high N.A. oil-condenser.

FACS analysis

Flow cytometry measurements were performed using a FAC-SCalibur flow cytometer (Becton-Dickinson) equipped with a 15 mW argon laser tuned at 488 nm. The bacterial population was selected by gating with appropriate settings of forward scatter (FSC) and sideward scatter (SSC). The FL3 fluorescence channel \((\lambda_{\text{em}} = 585 \text{ nm})\) was used to record the emitted fluorescence of Texas red. All experiments were performed at least three times using different preparations of bacteria and the results were analysed using the software CellQuest (Becton Dickinson).

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References


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