In vitro potential of equine DEFA1 and eCATH1 as alternative antimicrobial drugs in rhodococcosis treatment

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Rhodococcus equi, the causal agent of rhodococcosis, is a severe pathogen of foals but also of immunodeficient humans causing bronchopneumonia. The pathogen is often found together with Klebsiella pneumoniae or Streptococcus zooepidemicus in foals. Of great concern is the fact that some R. equi strains are already resistant to commonly used antibiotics. In the present study, we evaluated the in vitro potential of two equine antimicrobial peptides (AMPs), eCATH1 and DEFA1, as new drugs against R. equi and its associated pathogens. The peptides led to growth inhibition and death of R. equi and S. zooepidemicus at low micromolar concentrations. Moreover, eCATH1 was able to inhibit growth of K. pneumoniae. Both peptides caused rapid disruption of the R. equi membrane leading to cell lysis. Interestingly, eCATH1 had a synergic effect together with rifampin. Furthermore, eCATH1 was not cytotoxic against mammalian cells at bacteriolytic concentrations and maintained its high killing activity even at physiological salt concentrations. Our data suggest that equine AMPs, especially eCATH1, may be promising candidates for alternative drugs to control R. equi in mono- and co-infections.

Keywords: Defensin, cathelicidin, DEFA1, eCATH1, synergism, antimicrobial peptide, rhodococcosis, cytotoxicity, peptide antibiotics.
Rhodococcus equi, previously known as Corynebacterium equi, is a facultative intracellular, Gram-positive coccobacillus that causes infection in a wide variety of animal species and humans. Rhodococcosis occurs preferentially in organisms whose immune systems are compromised, either naturally, or due to illness or medical treatment (21).

The infection is typically described in one to six month-old foals (41, 46) and is one of the most common causes of mortality at this age. The high susceptibility of foals to the pathogen is due to their immature immune system combined with the decrease in maternal specific antibodies transmitted through the colostrum (4). Foals are infected by R. equi while grazing or by inhalation of contaminated soil dust. The disease then occurs mainly as bronchopneumonia and less often as intestinal manifestations or septic arthritis and osteomyelitis (21, 50). The survival rate has increased dramatically since the introduction of a combination of rifampin and a macrolide such as erythromycin, or more recently azithromycin or clarithromycin for treatment (20, 26). These combinations are therefore considered to be the first-line treatment of foals for rhodococcosis. In France, a retrospective study performed on the necropsies of 1617 foals between 1986 and 2006 showed that in 60% of rhodococcosis cases, R. equi was solely responsible for lethal lesions. In the other 40%, R. equi was found in co-infection with another pathogen, mainly Klebsiella pneumoniae in lung lesions (24.3%) and Streptococcus zooepidemicus (9.3%) which can sometimes cause the treatment to fail, due to the difference in antibiotic sensitivity (30, 32). Combinations of such pathogens have already been described previously (30).

In humans, the infection is rare in immunocompetent patients (15, 28) but more than 300 cases have been reported in immunocompromised subjects (42, 47). Since the first human case report was described in 1967, reports of the infection have increased substantially, with more than 200 cases in the last three decades (23, 42, 47). The increase in cases appears to be
correlated with the HIV pandemic and with expansions in transplantation medicine and cancer (45, 47). Infections in humans, especially immunocompromised patients, appear to be strongly associated with the farming environment. Contamination is likely to occur through the same route as in foals, via contaminated soil dust. However, no suggestive epidemiological exposure has been identified for half of the immunocompetent patients reported (47). The mortality rate among immunocompromised patients is relatively high, the range of 20-25% among non-HIV-infected patients and 50-55% among HIV-infected patients (13, 25). This high mortality rate can be attributed to an incorrect or late diagnosis of the disease, as the bacteria may be mistaken for a contaminant diphtheroid or Mycobacterium species.

It is a cause for concern that the susceptibility of bacteria to rifampin and erythromycin tends to decrease over time. Buckley et al. highlighted a two-fold increase in minimum inhibitory concentrations (MICs) over a ten-year period (10). Moreover, the emergence of rhodococci resistant to these antibiotics has already been reported in humans and animals (2, 7, 10, 29). This suggests that there may be a problem in the treatment of R. equi infection and new effective broad-spectrum drugs will be needed in the near future. Antimicrobial peptides (AMPs) have been attracting greater interest as new therapeutic molecules besides antibiotics, because of their broad spectrum of action and a lower risk of resistance acquisition (31). In general, AMPs are small cationic peptides participating in the innate immune response in almost all living organisms (including plants and invertebrates). Defensins and cathelicidins are the principal families in vertebrates. Defensins are characterized by intramolecular disulfide bonds and a β-sheet structure while the predominant secondary structure of cathelicidins is α-helical (14). AMPs are active against Gram-negative and Gram-positive bacteria, viruses, fungi and parasites. The principal mechanism of action of these peptides is attributed to membrane destabilization leading to cell lysis. Several AMPs are potential
alternative antimicrobial drugs and some have already undergone clinical trials (http://clinicaltrials.gov). To our knowledge, 30 mature antimicrobial peptides have already been identified in horses but only a few of them have been characterized (8, 9, 36). Among them are the α-defensin DEFA1 and the cathelicidin eCATH1.

The aim of the present study was to evaluate the in vitro potential of these two equine antimicrobial peptides for the treatment of rhodococcosis, and the effect on its associated pathogens.

Materials and methods

Antibiotics and antimicrobial peptides

The antimicrobial peptide eCATH1 was chemically synthesized by GenScript USA Inc. (Piscataway, NJ, USA) and dissolved in 10 mM acetic acid. DEFA1 was chemically synthesized (Biosyntan GmbH, Berlin, Germany), refolded as previously described by Jung et al. for another synthetic peptide (27) and dissolved in 0.01% trifluoroacetic acid. Nisin (ref N5764; Sigma Aldrich, St. Louis, MO, USA) was suspended in 20 mM HCl to obtain a 100 μg/ml stock solution. Erythromycin (ref E5389) and rifampin (ref R7382) were purchased from Sigma Aldrich (St. Louis, MO, USA), and stock solutions were freshly diluted in sterile water prior to each experiment.

Circular dichroism (CD) spectroscopy and liposome preparation

CD measurements were performed on a Jasco J-720 spectropolarimeter (Japan Spectroscopic, Tokyo, Japan) using suitable quartz cuvettes (Helma GmbH, Germany) with different cell lengths. Each CD spectrum represents the mean of three scans at a bandwidth of 2 nm and a data pitch of 1 nm. The scanning speed was adjusted to 5 nm/min with a response time of 8 s.
CD experiments were performed in the absence and presence of liposomes in order to compare the secondary structure of the peptides in aqueous and hydrophobic environments. Liposomes were prepared essentially as described by Pick et al. (35) using defined phospholipids and 50 mM sodium phosphate buffer, pH 5.2. Initially crude liposome samples were refined by passing them over a NAP-5 column (Amersham Biosciences). The eluate served as a stock suspension for the subsequent experiments and was stored at 4 °C. The phospholipids purchased from Avanti Polar Lipids Inc. (Alabaster, AL) were L-α-phosphatidyl-DL-glycerol (PG) and L-α-phosphatidylcholine (PC). Due to the net negative charge at the membrane surface, PG liposomes serve as highly simplified models for bacterial membranes whereas PC liposomes serve as corresponding models for eukaryotic membranes due to their electrostatic neutral surface.

800 µl of the liposome stock, diluted 1:100 in 50 mM sodium phosphate buffer, pH 7.0 was applied to one chamber of a tandem quartz cuvette (2x 4.375 mm). The other chamber was filled with the peptide sample. eCATH1 was applied in a 50 mM sodium phosphate buffer, pH 7.0, at a concentration of 9 µg/ml. DEFA1 was applied in a sodium phosphate buffer, pH 5.2, at a concentration of 17 µg/ml. After initial measurements of separated peptide and liposome samples, the tandem cuvette was inverted 40 times to mix the sample. The spectra of the mixed samples were recorded after 20 min of incubation.

Antimicrobial assays

MICs of eCATH1 on the reference strains *R. equi* ATCC 33701 P+,* S. zooepidemicus* CIP 102.228 T and *K. pneumoniae* CIP 82.91T were determined using the standard broth microdilution method outlined by the CLSI M07-A8 document (12) with modifications proposed by the Hancock Laboratory to avoid AMP adsorption to the microplate (24). 100 µl of bacterial suspension at 5 x 10⁵ CFU/ml in Mueller Hinton broth (MHB) was incubated on
polypropylene NUNC microplates with 11 µl of serially diluted peptides in 10 mM acetic acid supplemented with 0.2% bovine serum albumin (BSA). BSA was used to avoid adsorption of cationic peptides to the test microplate. Plates were sealed and incubated at 37°C for 24 to 48 h until visible growth. Cultures without the peptides were used as positive controls. Non-inoculated MHB was used as a negative control. The MIC was defined as the lowest concentration of the peptide causing an 80% decrease in turbidity compared to the growth of a control well. The experiments were carried out in triplicate.

**Salt tolerance**

Salt tolerance of eCATH1 was determined using the microdilution assay as described previously with minor modifications (27). The *R. equi* ATCC 33701 P+ suspension was adjusted to 10^4 to 10^5 bacteria per ml in 10 mM sodium phosphate, pH 7.2, supplemented with 1% Brain-Heart Infusion (BHI) broth and sodium chloride at final concentrations of 0, 50, 100 or 150 mM. 11 µl of the eCATH1 dilutions (range of final concentrations tested: 0.22–35.5 µg/ml) were added to 100 µl of the bacterial suspension and incubated at 37°C for 2.5 h at 250 rpm before colony forming units were determined. The eCATH1 solvent (10 mM acetic acid) served as negative control. The antibacterial activity of the peptide was given either as a LD90 (90% lethal dose) or as minimum bactericidal concentrations (MBCs) (99.9% killing). Each experiment was performed in triplicate.

**Scanning electron microscopy (SEM)**

1 ml of a mid-exponential phase culture of *R. equi* ATCC 33701 P+ (OD_{600 nm} = 0.5-0.6) was exposed to 100 µg/ml of eCATH1, DEFA1 or peptide diluents, as a control, in BHI broth for 5 minutes at 37 °C. The cell:peptide ratio used for the SEM assay was at least 20 times higher
than in the conditions used to determine the MIC values of these peptides in order to observe
the effect of the peptides on the bacterial membrane before their lysis. Bacteria were
sedimented by centrifugation at 4,000 xg for 5 min and washed twice in PBS, pH 7.2. The
pellets were fixed with 2.5% glutaraldehyde in 0.1 M cacodylate buffer, pH 7.4, at 4°C
overnight. Meanwhile, cells were dispersed and sedimented on Thermanox® coverslips
coated with poly-L-lysine. The cells were then rinsed in 0.2 M cacodylate buffer, pH 7.4, in
the presence of 0.2 M sucrose and post-fixed for 1 h with 1% osmium tetroxide in 0.1 M
cacodylate buffer, pH 7.4, in the presence of 0.1 M sucrose (at 4°C protected from light).
Bacteria were then washed in 0.2 M cacodylate buffer, pH 7.4 in the presence of 0.2 M
sucrose and dehydrated in progressive baths of ethanol (70-100%). Samples were critical-
point dried (CPD 030 LEICA Microsystems) sputtered with platinum (JEOL JFC 1300) and
observed with a JEOL 6400F scanning-electron microscope at the Electron Microscopy
Center of the University of Caen Basse-Normandie (CMABio, France).

Synergy study

*R. equi* P103 P- was used to test the antimicrobial combinations by the checkerboard titration
method using 96-well polypropylene microtiter plates. The experiment was performed in
triplicate. Concentrations tested ranged from 0.031-2 x MIC of each respective antimicrobial
(eCATH1, erythromycin, and rifampin). The final inoculum was verified by counting.
Positive (containing no antimicrobials) and negative growth controls were included.
Microtiter plates were sealed and incubated at 37°C for 48 h. AlamarBlue® (Invitrogen,
Cergy Pontoise, France), a colorimetric redox indicator without known effects on organism
growth (3), was used for the reading of checkerboard plates. Growth was determined visually
by observing the reduction in the colorimetric redox indicator (a color change from blue to
purple or pink). The Lowest FIC (Fractional Inhibitory Concentration) index was calculated according to the following equation: $\text{FIC index} = \frac{\text{MIC}_A + \text{MIC}_B}{\text{MIC}_A + \text{MIC}_B}$, where respectively, $A$ and $B$ are the MICs of drug $A$ and drug $B$ in combination, $\text{MIC}_A$ and $\text{MIC}_B$ are the MICs of drug $A$ and drug $B$ alone, and $\text{FIC}_A$ and $\text{FIC}_B$ are the FICs of drug $A$ and drug $B$.

The FIC indexes were interpreted as follows: $<0.5$, synergy; $0.5$ to $4.0$, indifferent; and $>4.0$, antagonism (1). In some cases, the interpretation may vary (6), therefore, a second method (“two-well”) was used for confirmation. The two-well method defined synergy as the absence of turbidity in the two wells containing $0.25 \times \text{MIC}$ of both drugs and $2 \times \text{MIC}$ of both drugs. Antagonism was defined as the presence of turbidity in both of these wells, whereas indifference was defined as all other possibilities (16).

204 Cytotoxicity

205 The effects of eCATH1 and DEFA1 on plasma membrane integrity of RK13 CCL-87 and VERO CCL-81 cell lines were assessed by lactate dehydrogenase (LDH) release assay. Epithelial cell lines (ATCC, USA) were grown according to the ATCC guidelines. The viability of test cells prior to cytotoxicity assays exceeded 99%, as determined by exclusion of the vital dye Trypan blue. The LDH release assay was carried out according to the manufacturer’s instructions using a commercially available kit (TOX-7, Sigma-Aldrich, Saint Louis, USA). Briefly, cells were incubated with serial dilutions (ranging from 0.31 to 100 $\mu$g/ml) of either eCATH1, DEFA1, nisin or 1% (v/v) Triton X-100 (positive control) for 24 h. Nisin was used here as a “safe control” because of its GRAS status in the food industry. The percentage of cytotoxicity was calculated as described by Vaucher et al. (44). Each experiment was performed in triplicate and values were expressed as mean ± standard error.
Hemolytic activity

The hemolysis of fresh defibrinated sheep (Biomérieux, Marcy l’Etoile, France) and horse (collected from a healthy 8-year-old mare) erythrocytes was evaluated in triplicate using a hemoglobin release assay (37). Briefly, red blood cells were rinsed three times with PBS (pH 7.2) by centrifugation for 15 min at 800 xg and resuspended in PBS, pH 7.2, at a final concentration of 4% (v/v). Samples of 100 µl of suspension were transferred to a microplate and treated with eCATH1, DEFA1, nisin (safe control) or 1% (v/v) Triton X-100 (positive control) at 37°C for 1 h. After centrifugation at 1000 xg for 5 min, supernatants were transferred to a clean microtiter plate where hemoglobin release was monitored by measuring the absorbance at 414 nm. The percentage of hemolysis was calculated as \( \frac{AT-AC}{AX-AC} \times 100 \); where AT is the experimental absorbance of treated supernatants, AC is the control absorbance of untreated cell supernatant, and AX is the absorbance of 1% (v/v) Triton X-100 lysed cells.

Resistance studies

10 µl of \( R. \) equi P103 P- suspension was seeded from the well equal to one-half of the MIC to a fresh microtiter plate containing 75 µl of antimicrobial dilution and 65 µl of fresh MHB (49). Antimicrobial dilutions (of eCATH1, rifampin or erythromycin) were double the desired concentration (0.25 x MIC to 4 x MIC of the agent) as a two-fold dilution was applied in the microplate. Plates were sealed and incubated at 37°C. Due to the slow growth of \( R. \) equi, MICs were determined every 48 h for 50 passages (580 generations) or the selection of resistance for the antibiotics tested. Clones with a lower sensitivity to eCATH1 were frozen at -80°C until further analysis. Because the resistance and susceptibility MIC breakpoints for \( R. \) equi have not been defined, the strain was considered as resistant for rifampicin at MIC > 8.
µg/ml and resistant for erythromycin at MIC > 4 µg/ml. To verify the stability of resistance to eCATH1, frozen clones with a lower sensitivity to the peptide were transferred one to four times on unsupplemented agar medium before MIC measurement as described in the “Antimicrobial assays” section.

Results

Circular dichroism spectroscopy (CD)

In the absence of liposomes, DEFA1 had a CD-spectrum whose maximum was at 230 nm which is typical for proteins with a β-sheet structure (Fig. 1). After mixing DEFA1 with PG liposomes, precipitates were formed leading to strong light scattering. This effect hindered the interpretation of the secondary structure content of DEFA1 by CD-spectroscopy. In contrast, no precipitation was observed after mixing DEFA1 with PC liposomes. The CD spectra of DEFA1 had the same shape before and after mixing with PC liposomes, indicating a constant secondary structure content.

Regarding eCATH1, the CD-spectra exhibited the typical shape of a linear peptide in the absence of liposomes (Fig. 1). After mixing eCATH1 with PC liposomes there was no detectable change of secondary structure composition, comparable to DEFA1, but there was a change after eCATH1 mixing with PG liposomes. Interaction of the peptide with the liposomal membranes changed the secondary structure from linear to an α-helical character with the typical minimum at 222 and 208 nm.

Antimicrobial activity
The antibacterial activity of eCATH1 and DEFA1 on reference strains of *R. equi* (ATCC 33701 P+ and P103 P-), *K. pneumoniae* (CIP 82.91T) and *S. zooepidemicus* (CIP103228T) is presented in Table 1. Equine CATH1 inhibited the growth of the Gram-positive bacteria *R. equi* (3.5 µg/ml, 1.1 µM) and *S. zooepidemicus* (7.1 µg/ml, 2.3 µM), and was also effective against the Gram-negative bacterium *K. pneumoniae* (7.1 µg/ml, 2.3 µM) at low micromolar concentrations. Similar results were obtained for DEFA1 with the Gram-positive strains: *R. equi* ATCC 33701 P+ and *S. zooepidemicus* were inhibited by 10 µg/ml (2.45 µM) and 5 µg/ml (1.22 µM) of peptide, respectively. However, *K. pneumoniae* was not sensitive to DEFA1 as no growth inhibition was observed at the maximal concentration (40 µg/ml; 9.81 µM) tested.

In the absence of sodium chloride, eCATH1 was able to kill 90% of *R. equi* ATCC 33701 P+ at 2.2 µg/ml (LD90) and 99.9 % (MBC) at 4.4 µg/ml (Fig. 2). The MBC and the MIC values were similar, indicating that eCATH1 has a bactericidal rather than bacteriostatic effect on *R. equi*. In the presence of 50 mM of sodium chloride, the LD90 was twice as high but the MBC remained at 4.4 µg/ml. At a physiological salt concentration (150 mM), eCATH1 maintained its relatively high killing activity, since the MBC was only increased by a factor of two (8.8 µg/ml) compared with the no-salt conditions (Fig. 2).

The antibacterial activity of eCATH1 in combination with DEFA1 or an antibiotic (rifampin, erythromycin) against *R. equi* P103 P- is shown in Table 2. Interestingly, there was synergy when eCATH1 was combined with the RNA polymerase inhibitor rifampin (FIC < 0.5). However, this peptide was indifferent in combination with DEFA1 or erythromycin (0.5 < FIC ≥ 4). All these data were confirmed by the “Two-well” method (data not shown).

**Scanning-electron microscopy**

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SEM was used to examine the effect of eCATH1 and DEFA1 on the morphology of *R.* equi ATCC 33701 P+. In the negative control, the bacterial cell membrane was intact, with a mucoid aspect, and small filopodia-like structures were observed. A similar morphology has also been described based on micrographs published for another reference strain of *R.* equi (40). Cellular fragments were absent in the control sample. Treatment of bacteria with 100 µg/ml of DEFA1 or eCATH1 appeared to result in membrane destabilization already after 5 min of incubation. Both peptides clearly led to altered membrane morphology. Moreover, numerous cellular fragments could be observed after treatment indicating cellular lysis (Fig. 3).

**Cytotoxicity of the antimicrobial peptides**

The cytotoxicity of eCATH1 and DEFA1 was assessed by the LDH release assay using RK13 and VERO epithelial cells and a maximum of 100 µg/ml of peptide (Fig. 4). For both cell lines, eCATH1 did not significantly affect plasma membrane integrity of cells. Compared to the negative control, no cytotoxicity was observed up to 50 µg/ml and only minor cytotoxicity (10%) was observed for the VERO cell line at 100 µg/ml (Fig. 4A). The RK13 cells were unaffected by 100 µg/ml of eCATH1 (Fig. 4B). In contrast, DEFA1 was found to be more cytotoxic, with a substantial effect on VERO cells at 50 µg/ml. At 100 µg/ml of DEFA1, the membrane integrity of RK13 and VERO cells was strongly affected (Fig. 4A & B). In addition, eCATH1 and DEFA1 were tested for hemolytic activity against sheep and horse erythrocytes. For both peptides no significant hemolytic activity (< 3%) was observed up to 100 µg/ml (data not shown).

**Resistance study**
When cultures of *R. equi* P103 P- were serially transferred 50 times in the presence of sub-inhibitory concentrations, the final MIC of eCATH1 was slightly higher when compared with the value determined initially. The MIC of the peptide increased two-fold after 34 passages (400 generations), then by four-fold after 43 passages (500 generations) and remained stable until the end of the experiment (50 passages). In comparison, resistance to rifampin or erythromycin appeared more quickly, after 4 passages (45 generations) or 10 passages (115 generations), respectively. The lower sensitivity of the strain to eCATH1 appeared to be only transient since a single passage in a peptide-free medium led to the reversion to the MIC of the parent strain (data not shown).

**Discussion**

Giacometti *et al.* (17-19) analyzed the activity of several AMPs as well as different conventional antibiotics on *R. equi*. MICs of these peptides were comparable to or higher than those of DEFA1 and eCATH1. Moreover, eCATH1 had similar bactericidal activity to vancomycin (median MBCs: 4 µg/ml), used to treat rhodococcosis in humans and a higher activity than rifampin and clarithromycin (median MBCs: 32 µg/ml), commonly used to treat rhodococcosis in foals (17-19). As DEFA1 was more or less ineffective against the rhodococcosis-associated pathogen *K. pneumoniae*, eCATH1 appears to be more suitable in terms of therapeutical usage. Therefore, we investigated its tolerance at physiological salt concentrations. The activities of several AMPs differ greatly in the presence or absence of salt (22, 43); however, eCATH1 was still able to kill *R. equi* at low micromolar concentrations (also at higher salt concentrations) despite a slight decrease in bactericidal activity at physiological sodium chloride concentrations. Moreover, we observed that the MBC of eCATH1 against *R. equi* at salt concentrations of 150 mM was more than 10 times lower than
the cytotoxic concentration for epithelial cells. In addition, eCATH1 did not harm erythrocytes, making this peptide more useful for therapy. These data are consistent with the findings of Skerlavaj et al. (38) who also observed the salt tolerance of eCATH1 and the lack of cytotoxicity against human and horse erythrocytes.

Bell et al. do not advocate the use of antimicrobial peptides to treat human or animal diseases because they may increase host sensitivity to infections (5). Although resistance mechanisms to AMPs have been described in different bacterial species (33), naturally sensitive strains are unlikely to acquire stable resistance because AMPs can interact with membranes without a specific target; Therefore, resistance involves biochemical modifications to the entire membrane, incurring metabolic costs that may be too high to maintain over several generations (48, 49). Only a few studies have been performed in vitro on the experimental evolution of resistance among a continuous exposition of antimicrobial peptide. Perron et al. exposed different strains of Escherichia coli and Pseudomonas fluorescens to increasing concentrations of pexiganan, a synthetic analog of magainin. Most of the strains developed stable resistance after 80 passages (34). In two other studies, the decrease in sensitivity of bacteria to antimicrobial peptides, when detectable, was found to be modest, took much longer to select in comparison to conventional antibiotics, and was transient (31, 39, 49). Our data are consistent with these studies as only a modest decrease in sensitivity (four-fold) was observed after 50 passages (580 generations). In contrast, when we tested conventional antibiotics under the same selection conditions it became evident that resistant mutants to erythromycin and rifampin appeared after only 11 and 4 passages, respectively. Moreover, the lower sensitivity of the strain to eCATH1 was reversed by a single passage in a peptide-free medium. Although our in-vitro study showed that the acquisition of stable resistance to eCATH1 by R. equi is unlikely to occur, in a therapeutic setting any new anti-effective has to be carefully monitored again in the in-vivo situation.
Interestingly, a synergistic effect was observed between eCATH1 and the RNA polymerase inhibitor rifampin. Previous studies have already reported such interactions between AMPs and hydrophobic antibiotics (reviewed in (11)) and it was hypothesized that AMPs allow the antibiotic to access its intracellular target by permeabilization of the bacterial membrane. Therefore, AMPs represent a way of enhancing the activity of classical antibiotics but even more they could potentially tackle the problem of the rise in multidrug-resistant pathogens.

Both, DEFA1 and eCATH1 interacted with liposomal membranes that have a net negative surface charge. In contrast, there was no interaction with liposomes with a neutral surface. Furthermore, the tested liposomes were free of any membrane proteins. Therefore, the electrostatic attraction was apparently sufficient and probably solely responsible for mediating the initial interaction of DEFA1 and eCATH1 with their target membranes. Whereas DEFA1 already had a β-sheet secondary structure character in an aqueous environment, eCATH1 was linear. CD measurement results clearly showed that eCATH1 adopted an α-helical fold upon interaction with the liposomal membranes. Together with the absence of a precipitation effect as observed for DEFA1, both peptides might exert different mechanisms. However, according to SEM, the comparable killing effect of both peptides appeared to be mediated through a rapid membrane disruption of the bacteria. Further studies are necessary to clarify the interplay of structure and activity/cytotoxicity that might also explain the different MIC values, and cytotoxicity of both peptides.

In conclusion, the in vitro therapeutic potential of equine DEFA1 for rhodococcosis treatment was found to be lower than envisaged mainly due to its cytotoxicity but also to its inefficacy in killing K. pneumoniae. In contrast, eCATH1 proved to be a promising candidate for development of a suitable drug in the fight against rhodococcosis in mono- and co-infections and warrants further research in view of its in vivo potential in human or veterinary medicine. Furthermore, among the other equine peptides that have not yet been expansively studied in
vitro, there might be additional promising candidates for the treatment of rhodococcosis and other infectious diseases in humans and animals.
References


Table 1. MICs of DEFA1 and eCATH1 on *R. equi*, *K. pneumoniae* and *S. zooepidemicus* reference strains.

<table>
<thead>
<tr>
<th>Microorganisms</th>
<th>MIC (µg/ml)</th>
<th>DEFA1</th>
<th>eCATH1</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Rhodococcus equi</em> ATCC 33701 P+</td>
<td>10</td>
<td></td>
<td>3.5</td>
</tr>
<tr>
<td><em>Rhodococcus equi</em> P103 P-</td>
<td>ND&lt;sup&gt;a&lt;/sup&gt;</td>
<td></td>
<td>3.5</td>
</tr>
<tr>
<td><em>Klebsiella pneumoniae</em> CIP 82.91T</td>
<td>&gt;40</td>
<td></td>
<td>7.1</td>
</tr>
<tr>
<td><em>Streptococcus zooepidemicus</em> CIP 103228T</td>
<td>5</td>
<td></td>
<td>7.1</td>
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<sup>a</sup> ND, not determined.
Table 2. Antibacterial interaction of eCATH1 with DEFA1, rifampin or erythromycin on *R. equi* P103 P-.

FIC indices indicate synergy when value is < 0.5 or antagonism when value is > 4.

<table>
<thead>
<tr>
<th>Drug combination</th>
<th>FIC</th>
<th>Interaction</th>
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</thead>
<tbody>
<tr>
<td>DEFA1-eCATH1</td>
<td>0.53</td>
<td>Indifferent</td>
</tr>
<tr>
<td>Rifampin-eCATH1</td>
<td>0.49</td>
<td>Synergy</td>
</tr>
<tr>
<td>Erytromycin-eCATH1</td>
<td>1.25</td>
<td>Indifferent</td>
</tr>
</tbody>
</table>
Figure 1. **Impact of phospholipid membranes on the secondary structure of DEFA1 and eCATH1.** The secondary structure of both DEFA1 (left-hand panels) and eCATH1 (right-hand panels) was investigated by CD spectroscopy in the absence (black lines) and presence (grey lines) of liposomes composed of negatively charged (PG, upper panels) or electrostatically neutral (PC, lower panels) phospholipids.

Figure 2. **Salt dependence of the antimicrobial activity of eCATH1.** The salt tolerance was tested against *R. equi* ATCC 33701 P+ by measuring the MBC values in the presence of 0 (▲), 50 (■), 100 (◊) and 150 mM (□) of sodium chloride. A) Mortality curves, values are expressed as the mean of three independent experiments ± standard error, B) LD90 and MBC values in the absence or presence of salt.

Figure 3. **Scanning electron micrographs of *R. equi* ATCC 33701 P+ treated with DEFA1 or eCATH1.** *R. equi* in mid-logarithmic growth was incubated with 100 µg/ml of antimicrobial peptide eCATH1, DEFA1 or with the peptide solvent (as a negative control) for 5 minutes. Observation at low (A) and high magnification (B).

Figure 4. **Cytotoxic activity of DEFA1, eCATH1 and nisin.** A) VERO CCL-81 and B) RK13 cells were incubated with increasing amounts of DEFA1 (◆), eCATH1 (■) and nisin as a safe control (▲). Cytotoxicity was measured spectrophotometrically using the LDH release assay.
<table>
<thead>
<tr>
<th>NaCl concentration (nM)</th>
<th>LD90 (µg/ml)</th>
<th>MBC (ng/ml)</th>
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<td>8.8</td>
</tr>
<tr>
<td>150</td>
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