In Vitro Antibacterial Activity of Acyl-Lysyl Oligomers against Helicobacter pylori

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The gastric pathogen Helicobacter pylori has developed resistance to virtually all current antibiotics; thus, there is a pressing need to develop new anti-H. pylori therapies. The goal of this work was to evaluate the antibacterial effect of oligo-acyl-lysyl (OAK) antimicrobial peptidomimetics to determine if they might represent alternatives to conventional antibiotic treatment of H. pylori infection. A total of five OAK sequences were screened for growth-inhibitory and/or bactericidal effects against H. pylori strain G27; four of these sequences had growth-inhibitory and bactericidal effects. The peptide with the highest efficacy against strain G27, C12K-2β12, was selected for further characterization against five additional H. pylori strains (26695, J99, 7.13, SS1, and HPAG1). C12K-2β12 displayed MIC and minimum bactericidal concentration (MBC) ranges of 6.5 to 26 μM and 14.5 to 90 μM, respectively, across the six strains after 24 h of exposure. G27 was the most sensitive H. pylori strain (MIC = 6.5 to 7 μM; MBC = 15 to 20 μM), whereas 26695 was the least susceptible strain (MIC = 25 to 26 μM; MBC = 70 to 90 μM). H. pylori was completely killed after 6 to 8 h of incubation in liquid cultures containing two times the MBC of C12K-2β12. The OAK demonstrated strong in vitro stability, since efficacy was maintained after incubation at extreme temperatures (4°C, 37°C, 42°C, 50°C, 55°C, 60°C, and 95°C) and at low pH, although reduced killing kinetics were observed at pH 4.5. Additionally, upon transient exposure to the bacteria, C12K-2β12 showed irreversible and significant antibacterial effects and was also nonhemolytic. Our results show a significant in vitro effect of C12K-2β12 against H. pylori and suggest that OAKs may be a valuable resource for the treatment of H. pylori infection.

Helicobacter pylori is a microaerophilic gram-negative bacterium that colonizes the gastric mucosa. It is known to be a principal gastric pathogen of humans and is associated with the development of gastritis, gastric ulcers, duodenal ulcers, and gastric cancer (46, 55, 56, 60). Approximately half of the world’s population is infected with H. pylori (79). Thus, the bacterium poses a significant public health problem, which is further compounded by the fact that H. pylori has developed antimicrobial resistance to virtually all current antibiotics, a phenomenon that is hampering efforts to treat the infection (40, 51).

Since the original isolation of H. pylori in the early 1980s, treatment of the bacterial infection has undergone a significant evolutionary development from initial monotherapy to dual, triple, and in more recent trials quadruple therapy (8, 18). Current treatment strategies employ combination therapy, since single-antibiotic therapy often results in failure to eradicate the infection (21). The highest H. pylori eradication rates have been reported with triple therapy, which involves the utilization of two antibiotics in combination with bismuth or a proton pump inhibitor, PPI (34, 44). Amoxicillin (amoxicilline) with either clarithromycin or metronidazole is often the antibiotic combination of choice as a first- or second-line treatment regimen, respectively. However, in recent years the efficacy of the standard first-line triple therapy has also been decreasing dramatically, mainly due to development of resistance to the drugs (35, 59). Failure to cure H. pylori infection has been noted for more than 20 to 30% of patients (37). In addition, several studies have found an eradication rate lower than 75% (6, 11, 59), and values as low as 25 to 45% have also been recently reported (22, 24). Thus, prolonged standard triple therapy for up to 2 weeks has been recommended (9, 23, 34), and in cases of eradication failure, a quadruple therapy with a proton pump inhibitor, bismuth salt, tetracycline, and metronidazole has been advised as a second-line therapy (8, 13, 44). More recently, sequential therapy (PPI and amoxicillin for 5 days, followed by PPI, clarithromycin, and tinidazole for 5 days) has become very attractive for clinical practice since impressive efficacy was seen (36, 73). However, broad adoption of this strategy as standard first-line therapy for H. pylori infection is still debatable because of impending validation in other geographic locations and studies to demonstrate efficacy superior to that of quadruple therapy, which is still considered a simpler regimen than sequential therapy (74). Of note, all the aforementioned therapies including sequential therapies employ multiple drugs and relatively complex regimens for the treatment of H. pylori infection, hence the search for new/better antibiotics.

The bactericidal activity of amoxicillin results from interference with the interpeptide linkage of peptidoglycan by binding to penicillin binding proteins and blocking their function as transporters during cell wall synthesis. Clarithromycin, like other macrolides, binds to the 50S subunit of bacterial ribosomes, thus inhibiting translocation of tRNA during translation. Binding of clarithromycin to H. pylori ribosomes has been...
shown to be very strong and is irreversible (27). Finally, metronidazole is a 5-nitroimidazole drug whose mode of action is mediated by nitro metabolites, such as the radical anion (NO₂⁻) and perhaps nitroso (RNO) and hydroxylamine (RNOH) derivatives (39). Such metabolites have been demonstrated to cause DNA damage that results in cell death.

*H. pylori* resistance to amoxicillin is very rare, while resistance to clarithromycin varies significantly and may range from 10 to 25% (14). However, in a recent study, it was reported that the first-line anti-*H. pylori* triple therapies containing clarithromycin failed in 7 to 49% of patients (19, 26), indicating the underlying significant increase in antimicrobial resistance and occurrence of refractory *H. pylori* infections (32, 50, 78). Currently, PPI-amoxicillin-metronidazole triple therapy is highly effective as a second-line regimen for the treatment of *H. pylori* infection in patients showing failure of the first-line regimen (PPI-amoxicillin-clarithromycin) (47). However, high rates of resistance have been reported for people with a history of metronidazole treatment (49). Given the immense challenge in rising antimicrobial resistance (38), there is an enormous need for new antibiotics for the treatment of *H. pylori* infection.

One of the pharmacodynamic parameters most studied for antibiotics is the postantibiotic effect (PAE), which describes the suppression of bacterial growth after a short exposure of bacteria to an antimicrobial agent (29). From a clinical standpoint, PAE provides a rationale for the modification of the dosing interval of antimicrobials and could be significant for the optimization of a treatment regimen and the minimization of drug-induced adverse effects. Similarly, the success of intermittent dosing with drugs that exhibit short half-lives has been attributed to the presence of significant PAE. A long and/or positive PAE is considered an attractive characteristic for an effective new antibiotic.

In the last decade, antimicrobial peptides (AMPs) have attracted attention as potential therapeutic agents mainly due to their ability to be promptly synthesized by the host upon induction and their capacity to subsequently lyse cell membranes of pathogens through direct interaction with them. Hence, AMPs are recognized as a cell-free host defense mechanism and are important component of the innate immune systems of living organisms, including plants (76), insects (30), amphibians (75), and mammals (80). These natural membrane-lytic peptides display immense diversity in terms of sequence, secondary structural motifs, charge (cationic and anionic), and/or the abundance of certain specific amino acids (16, 66). Despite the immense diversity, a common feature for cationic AMPs is that they all form amphipathic structures that allow them to bind to the membrane interface of microbes (5, 69). Peptides which are not cationic are known to exhibit less selectivity toward microbes than toward mammalian cells, since electrostatic interactions are critical for initial binding of the peptide to membrane containing anionic lipids (45).

Oligomers of acylated lysines (OAKs) constitute a novel class of synthetic AMP mimics that consists of alternating amino acyl chains and cationic amino acids arranged to create an optimal molecular charge and hydrophobicity for enhanced potency (61, 65). This design has been reported to be advantageous over conventional AMPs by allowing the capacity for fine-tuning of the OAK structure to enhance potency against a broad spectrum of organisms while being devoid of apparent toxicity against mammalian cells (62, 64). This selective activity has been attributed to a design that lacks the secondary structures present in natural peptides (63) and to a mode of action that appears to target multiple sites, such as membranes and DNA (64). Circular dichroism studies of OAKs have demonstrated that they lack secondary structure in the presence of liposomes or hydrophobic media such as trifluoroethanol and sodium dodecyl sulfate (63). Additional characterization of OAKs with microbial pathogens other than *H. pylori* has demonstrated significant stability in the presence of serum and serum components and has shown no hemolysis of host erythrocytes (64). Two recent in vivo studies have also shown that administration of OAKs protected mice from an *Escherichia coli* lethal challenge (63, 64). Therefore, OAKs display characteristic features that are attractive for the development of a potent therapeutic drug.

Given the increasing antibiotic resistance rates of *H. pylori* and the current complicated treatment regime, the need for new potent antibiotics has never been greater. Given the potent effect of OAKs on other pathogens, we investigated the in vitro antibacterial activities of five representative OAKs against *H. pylori*. The selected sequences belong to two distinct groups: one group consisted of C₁₂-K-7ₘₖ₈ and its shorter analog, C₁₂-K-5ₘ₆₅, two well-characterized compounds (15, 63, 64) both of which are known for potent activity against gram-negative bacteria (25); the second group consisted of the less-characterized OAKs C₁₂-K-2B₁₂ and two shorter analogs, C₁₂-2B₁₂ and 2B₁₂, for which a preliminary study (62) predicted broad-spectrum activities at least for the longer analogs. Together, these representative OAKs were anticipated to provide a preliminary structure-activity assessment on the potential activity of OAKs against *H. pylori*. Our results indicate that four of the tested peptides show efficacy against the pathogen. Of these, C₁₂-K-2B₁₂ demonstrated the most potent activity, was active against a spectrum of strains, and was remarkably stable at low pH and after exposure to extreme temperatures.

**MATERIALS AND METHODS**

**Peptide synthesis, reagents, and antibiotics.** Oligo-acyl lysyls used in this study are listed in Table 1 and were synthesized as described previously (61–63). Briefly, a solid-phase method was used to synthesize peptides applying 9-fluorenylmethyloxycarbonyl active ester chemistry. Peptide purity was 98 to 99% on assessment of chromatographic homogeneity by reverse-phase high-performance liquid chromatography (HPLC) (Alliance-Waters). Using a linear gradient of acetonitrile in water (1%/min), with both solvents containing 0.1% trifluoroacetic acid.

**Table 1. Antimicrobial OAK peptide sequences and biophysicalchemical characteristics**

<table>
<thead>
<tr>
<th>OAKα</th>
<th>Sequenceβ</th>
<th>MWγ</th>
<th>Qβ</th>
<th>H'</th>
</tr>
</thead>
<tbody>
<tr>
<td>C₁₂-K-7ₘ₆₅</td>
<td>C₁₂-K-oKoKoKoKoKoKoK</td>
<td>2,212.9</td>
<td>8</td>
<td>47.5</td>
</tr>
<tr>
<td>C₁₂-K-5ₘ₆₅</td>
<td>C₁₂-K-oKoKoKoKoKoK</td>
<td>1,674.1</td>
<td>6</td>
<td>49.7</td>
</tr>
<tr>
<td>C₁₂-K-2B₁₂</td>
<td>C₁₂-K-KIK-KIK-KIK</td>
<td>1,234.8</td>
<td>5</td>
<td>51.0</td>
</tr>
<tr>
<td>C₁₂-2B₁₂</td>
<td>C₁₂-KIK-KIK</td>
<td>1,106.6</td>
<td>4</td>
<td>53.3</td>
</tr>
<tr>
<td>2B₁₂</td>
<td>KIK-KIK</td>
<td>924.3</td>
<td>5</td>
<td>38.1</td>
</tr>
</tbody>
</table>

α OAK designation, where oₘ₆ and βₘ₆ represent aminooctanoyl-lysyl and lysyl-aminoacidocanoyl-lysyl subunits, respectively; C₁₂, dodecanoic acid; K, lysine.

β a, aminoacetic acid; l, aminoacidic acid. For other symbols, see footnote α.

γ Molecular weight.

δ Net charge.

ε Hydrophobicity measured using reverse-phase HPLC.
TABLE 2. Antimicrobial activity of C 12K-2β12

<table>
<thead>
<tr>
<th>H. pylori strain</th>
<th>Reference</th>
<th>OAK concn (µM)</th>
<th>MIC</th>
<th>MBC</th>
</tr>
</thead>
<tbody>
<tr>
<td>G27</td>
<td>3</td>
<td>6.5–7.0</td>
<td>15–20</td>
<td></td>
</tr>
<tr>
<td>7.13</td>
<td>20</td>
<td>&lt;9.0</td>
<td>14.5–15</td>
<td></td>
</tr>
<tr>
<td>J99</td>
<td>1</td>
<td>10.5–11.0</td>
<td>20–25</td>
<td></td>
</tr>
<tr>
<td>HPAG1</td>
<td>57</td>
<td>10.5–11.0</td>
<td>20–45</td>
<td></td>
</tr>
<tr>
<td>SS1</td>
<td>43</td>
<td>25.5–26</td>
<td>45–50</td>
<td></td>
</tr>
<tr>
<td>26695</td>
<td>72</td>
<td>25–26</td>
<td>70–90</td>
<td></td>
</tr>
</tbody>
</table>

a MIC (100% survival) and MBC (99.9% killing) data represent results from at least three independent experiments.
Based on data shown in Fig. 1, tighter OAK doses were designed, with 0.5 \( \mu \)M and 5 \( \mu \)M intervals for the MIC and MBC, respectively. Table 2 summarizes the results for determination of the MICs and MBCs for C\(_{12}\)K-2\( \beta \)\(_{12} \) against the strains tested. All six strains of \( H. \) pylori tested were sensitive to treatment with C\(_{12}\)K-2\( \beta \)\(_{12} \). G27 was the most sensitive (MIC = 6.5 to 7 \( \mu \)M; MBC = 15 to 20 \( \mu \)M), whereas 26695 was the least susceptible (MIC = 25 to 26 \( \mu \)M; MBC = 70 to 90 \( \mu \)M), suggesting that there are strain differences that may affect either the mode of action or the kinetics of interaction of the OAK. Importantly, efficacy of the OAK was dose dependent (Fig. 1 and data not shown), indicating that the peptides interact with a fixed number of targets on the bacteria.

**OAK killing kinetics.** The rate at which an antibiotic is effective is important due to the ability to maintain suitable concentrations for an affective length of exposure. Therefore, we performed time-kill assays to determine the rate of OAK-dependent killing of strains G27, 7.13, and J99. As shown in Fig. 2, C\(_{12}\)K-2\( \beta \)\(_{12} \) exhibited rapid killing of strain G27 at both concentrations tested (20 \( \mu \)M and 40 \( \mu \)M). At 40 \( \mu \)M (twofold the MBC of strain G27), no colonies were recovered after 10 h of treatment in liquid cultures containing the peptide. Similar results were obtained with strains 7.13 and J99 at the same peptide concentration (data not shown). It was also observed by determining the slope of the kill curves that C\(_{12}\)K-2\( \beta \)\(_{12} \) exhibited concentration-dependent killing kinetics (Table 3 and Fig. 2). Following mathematical modeling of the curves, it was demonstrated that at the MBC, the OAK could kill 90% of bacteria in liquid culture two times slower than at concentrations twofold higher than the MBC. Thus, 90% of the bacteria for strains G27, 7.13, and J99 could be killed after incubation with the MBC of peptide in 6, 6, and 4 h, respectively, but the bactericidal rates could be increased to 3, 3.5, and 2 h upon incubation with twofold the MBC of the peptide, respectively (Table 3). A comparison of the killing rates between amoxicillin and C\(_{12}\)K-2\( \beta \)\(_{12} \) demonstrated superior efficacy by the OAK (Fig. 2). Additionally, testing of the killing rate of C\(_{12}\)K-2\( \beta \)\(_{12} \) in liquid medium without vancomycin to rule out any potential interaction of the drugs revealed similar efficacy (data not shown). Taken together, these data indicate dose-dependent killing of \( H. \) pylori by C\(_{12}\)K-2\( \beta \)\(_{12} \).

**Mode of action: reversibility studies and killing kinetics under bacteriostatic conditions.** Whether suppression of bacterial growth persists after limited exposure to an antibiotic has been established as an important pharmacodynamic parameter that is usually considered in choosing antibiotic dosing regimens. This is because in a host, there is often a gradual decrease in the antibiotic concentration to subinhibitory levels. Thus, the question of whether the damage to the bacteria is irreversible or not comes into play once antibiotic levels fall below the effective concentration. Therefore, in an attempt to evaluate whether \( H. \) pylori could recover from the damage imposed by exposure to C\(_{12}\)K-2\( \beta \)\(_{12} \), the killing kinetics were evaluated under conditions in which \( H. \) pylori bacteria were exposed to the peptide for 2 h and the peptide withdrawn by washes. The time-kill curves were then compared to those for conditions in which the peptide was not withdrawn. The data

**TABLE 3. Dose-dependent killing kinetics of C\(_{12}\)K-2\( \beta \)\(_{12} \)**

<table>
<thead>
<tr>
<th>( H. ) pylori strain</th>
<th>Time-kill curve(^a) slope (h for 90% killing)</th>
<th>1 MBC</th>
<th>2 MBC</th>
</tr>
</thead>
<tbody>
<tr>
<td>G27</td>
<td>0.163 (6.1)</td>
<td>0.164 (6.1)</td>
<td>0.260 (3.8)</td>
</tr>
<tr>
<td>7.13</td>
<td>0.164 (6.1)</td>
<td>0.377 (2.7)</td>
<td>0.279 (3.5)</td>
</tr>
<tr>
<td>J99</td>
<td>0.260 (3.8)</td>
<td></td>
<td>0.567 (1.8)</td>
</tr>
</tbody>
</table>

\(^a\) The data represent results from at least three independent experiments.
from these studies are presented in Fig. 3 and demonstrate that although complete killing was abrogated, the killing rate remained similar to that when the bacteria were grown under conditions where the peptide was not withdrawn. These data suggest that the killing effects of C12K-2 are irreversible. In contrast, amoxicillin showed no PAE, an observation that is consistent with previously reported findings (70).

Since some antibiotics are ineffective against slowly growing bacteria and since some bacteria grow slowly at sites of infection (17, 48), we next sought to determine whether the OAK efficacy was maintained when H. pylori growth was inhibited. Therefore, the killing profile of the peptide was examined under chloramphenicol-induced bacteriostatic conditions. Notably, the OAK effects were increased and antibacterial activity was sustained under bacteriostatic conditions (Fig. 4). Sequential addition of C12K-2β12 after 4 h of growth under chloramphenicol-induced bacteriostatic conditions was unable to further increase the activity of C12K-2β12 (data not shown). Taken together, these data indicate that the C12K-2β12 peptide does not require active bacterial growth to be effective.

OAK stability after exposure to different ambient temperatures and at low pH. Inactivation by low pH in the gastric environment as well as poor stability in ambient temperatures during transport, storage, and/or after delivery in vivo may be factors that contribute to the limited clinical efficacies of antimicrobial agents that are active in vitro against H. pylori. Therefore, we tested the effect of exposure to various temperatures and low pH on the stability of the OAK. As shown in Fig. 5, incubation of C12K-2β12 at 4°C, 50°C, 55°C, 60°C, or 95°C for 1 h prior to testing had no effect on the efficacy of the peptide against strain G27 (Fig. 5A). Similar data were obtained with peptide preincubated at 37°C or 42°C (data not shown). Similarly, the OAK showed antimicrobial efficacy against strain G27 at pH 4.5 and pH 6.9 despite a reduced rate of killing at pH 4.5 (Fig. 5B).

Hemolytic assay. Most peptides are cationic, and hence their interaction with anionic membrane phospholipids provides a ready explanation for their specificity for bacterial membranes (7, 10). However, some AMPs exhibit hemolytic activities (42), and delivery of such peptides becomes problematic, especially via an intravascular route. Therefore, we tested the hemolytic activity of C12K-2β12. As shown in Fig. 6, the OAK was nonhemolytic at concentrations from 0.625 to 40 μM. We observed only minor hemolytic activity (4 to 8%) following incubation of 80 μM peptide with erythrocytes for 10 h. These results suggest that C12K-2β12 is nonhemolytic and may be able to be administered via various routes.

DISCUSSION

Considering the increasing resistance observed among H. pylori strains worldwide (38, 81), therapeutic options are becoming significantly limited. Therefore, the aim of the present study was to evaluate the antimicrobial activity of OAKs against H. pylori. OAKs are a class of AMPs with a novel design of linear peptidomimetic sequences consisting of alternating acyl chains and cationic amino acids (63). They have previously been tested against several strains of both gram-positive and gram-negative bacteria, including clinically challenging species (Acinetobacter, Klebsiella, and Pseudomonas spp.), but not against Helicobacter spp. (64). Here we provide in vitro experimental evidence suggesting that the OAK C12K-2β12 displays potent antimicrobial activity against H. pylori.
We evaluated the in vitro susceptibility of *H. pylori* to OAKs by using time-kill assays. This methodology is superior to measuring the 3-log₁₀ decrease in the number of CFU per milliliter in a 24-h period (71), since it has been shown that the 3-log₁₀ difference method may sometimes leave enough bacteria to establish culture. All *H. pylori* strains tested were sensitive to treatment with C₁₂K-2β₁₂, which was the most potent of the five OAKs displaying antimicrobial activity. *H. pylori* was unable to resume growth on untreated agar plates after a 6- to 10-h treatment with concentrations equivalent to the MBC. Moreover, in a molar-to-molar comparison, the antimicrobial activity of C₁₂K-2β₁₂ was superior to that of the commercial antibiotic, amoxicillin. Notably, the six *H. pylori* strains tested exhibited various levels of sensitivity to C₁₂K-2β₁₂. While the reason for this difference is not completely clear, it is possible that the strain-specific sensitivity observed may be related to differential expression of molecules in the anionic phospholipid cell membrane, such as lipopolysaccharides and/or some unknown specific glycoprotein(s) that interacts with C₁₂K-2β₁₂. Like other cationic peptides, C₁₂K-2β₁₂ is believed to form pores by interacting with anionic phospholipids. It is therefore expected that the stability and permeability of the cell membrane would play a fundamental role in the adaptation to different peptides/antibiotics and that these properties would be closely related to the lipid and fatty acid content. In keeping with this idea, lipopolysaccharide has been demonstrated to protect *Bordetella bronchiseptica* from the activity of AMPs (4). To our knowledge this has not been tested for *H. pylori*; however, it should be noted that strain-specific differences in sensitivity and resistance to other antibiotics have been demonstrated. Differential sensitivity to metronidazole has been shown to be due to changes in expression of pyruvate oxidoreductase (33) or gene mutations in the NADP (NADPH)-dependent nitroreductase (encoded by rdxA) (28) and the NADPH flavin oxidoreductase enzyme (encoded by frxA) (41). This suggests that *H. pylori* strain-specific effects can occur with various classes of antibiotics, and future work from our group will seek to understand the nature of these differences for C₁₂K-2β₁₂.

One of the five peptides evaluated, 2β₁₂, failed to show any antimicrobial activity against *H. pylori*. This OAK also was inactive when tested against a panel of gram-positive and gram-negative bacteria (62). It is therefore possible that this short peptide may not display enough charge and/or hydrophobicity to interact well with the anionic *H. pylori* membrane,
which is consistent with the fact that optimal charge and/or hydrophobicity is critical for potency (2, 62, 64). It is also noteworthy to mention that although the alpha-OAKs C_{12-5a} and C_{12-5a} showed only weak efficacy against *H. pylori*, these peptides demonstrated very strong antimicrobial activity against various gram-negative bacteria, including *E. coli* (assessed by both in vitro and in vivo studies), *Salmonella* spp., and *Klebsiella pneumoniae* (63, 64). Although differences in cell membrane composition could explain the disparity in these results, the differential antimicrobial activity among the gram-negative bacteria may signal the underlying differences in specificity of peptide-target interaction in different pathogens.

An advantage of OAK peptide design is the possibility to fine-tune the structure to potentiate activity by manipulation of the acyl length and/or lysine residues (63, 64). This is evidenced in our study by comparing the antibacterial effects of C_{12-2β_12} and C_{12-2β_12}; C_{12-2β_12} showed stronger efficacy. Thus, the differential cationic charge created by the addition of an extra lysine residue results in increased efficacy of C_{12-2β_12}. These results are similar to those obtained by Rotem and colleagues when they compared the effects of C_{12-5a} and C_{12-7a} against *Pseudomonas aeruginosa*: the two extra α subunits in C_{12-7a} were able to enhance potency (64). Taken together, these data confirm the possibility of modifying OAK peptides to optimize potency and enhance activity.

As with most bacteria, doubling times of *H. pylori* at the site of colonization are likely longer than those in vitro. Cozens and colleagues have extensively studied the influence of growth rate on the susceptibilities of members of the family *Enterobacteriaceae* and of *P. aeruginosa* to antimicrobial agents and have shown that the susceptibilities of slowly growing bacteria to antimicrobial agents are greatly reduced (12). This phenomenon may explain the failure of many promising antimicrobial agents when tested in vivo. To address this concern, we asked the following question: is the efficacy of C_{12-2β_12} against *H. pylori* influenced by the growth rate? Our data demonstrate that C_{12-2β_12} exhibits antibacterial activity regardless of whether the bacteria are actively growing, indicating that slow growth in the stomach may not influence efficacy of the peptide.

We determined the OAK stability by looking at the effect of extreme temperatures (range, 0 to 95°C) and pHs (4.5 and 6.9) on activity. Our data demonstrated that C_{12-2β_12} is stable at the afore-mentioned temperatures and low pH, albeit reduced activity was observed at low pH. pH influences the ionization of charged groups and consequently affects downstream interactions. This fact may explain the slightly reduced kinetics of the C_{12-2β_12} peptide at low pH. The robust stability suggests slow OAK peptide degradation, sustained antimicrobial activity in the acidic environment of the stomach, and the possibility of overcoming cold-chain storage problems in a clinical setup. Indeed, these results are in accordance with those in studies with the cationic peptide nisin, which have shown low-pH-induced reduction of peptide net charge and reduced potency (76). In the host, however, *H. pylori* survives strong acidity of the stomach using the enzyme urease to convert gastric urea into ammonia, which then neutralizes the bacterial cytoplasm and microenvironment (52, 58, 67, 68, 77). Thus, the reduced kinetics observed in vitro might not apply in the host, since the local microenvironment inhabited by the bacteria would have a near-neutral pH.

Persistent suppression of bacterial growth after a short exposure to an antibacterial agent, PAE, was first noted and described more than 65 years ago. Since then, several studies have been undertaken to determine the PAE of numerous antimicrobial agents that have further established the significance of PAE in drug development. Today, it is one of the minimum recommendations in a preclinical evaluation of all new antimicrobial agents that determination of the PAE be performed. This is essentially because PAE is a factor that influences optimal antimicrobial dosing intervals. It is generally accepted that antibiotics without a PAE would usually require more-frequent administration than agents exhibiting PAE. PAE is thus an important pharmacodynamic predictor of clinical application of antibiotic dosage in the drug development process. We performed a PAE assay for C_{12-2β_12} against *H. pylori* and made a direct comparison of time-kill curves of treated and untreated bacterial cultures using the classical viable-count procedure. Our data demonstrate a significant and irreversible PAE of the OAK against *H. pylori*, a characteristic feature that makes the peptide promising for future drug development. The cellular and molecular events involved in the significant PAE observed here are largely unknown. However, it is reasonable to suggest that the irreversible significant PAE observed might be related to the level of damage done by the peptide to the bacterial cell. Thus, this might indicate that the damage to the bacterial cell is very profound or at least irreparable, a speculation that is consistent with the fact that if the damage is not fixable, then the bacterial cell dies. It is also noteworthy that the amoxicillin data are consistent with the results of a previous study (31) in which other β-lactams were shown to lack PAE against slowly growing *H. pylori*.

In conclusion, our data demonstrate strong in vitro antimicrobial activity of C_{12-2β_12} against *H. pylori*. Our results suggest that the activity of the OAK is irreversible and sustainable regardless of bacterial growth. Additionally, the peptide is stable at a wide range of temperature and pH conditions. This is the first characterization of synthetic OAK peptides against *H. pylori*, and our results indicate that C_{12-2β_12} may, in principle by itself, have strong therapeutic potential against *H. pylori*. Future work will investigate the in vivo efficacy of C_{12-2β_12} using *H. pylori* animal models.

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REFERENCES


