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Cationic amphipathic peptide analogs of cathelicidin LL-37 as a probe in the development of antimicrobial/anticancer agents

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Eugenia Panou-Pomonis, Department of Chemistry, University of Ioannina, 45110 Ioannina, Greece. Email: epanou@uoi.gr Cathelicidin LL-37 belongs to the class of human defense peptides and is overexpressed in many cancers. Segments of LL-37 derived through biochemical processes have a wide range of activities. In this study, novel analogs of the 13-amino acid cathelicidin 17-29 amide segment F¹⁷KRIV²¹QR²³IK²⁵DF²⁷LR-NH₂ were prepared and examined for their antimicrobial and hemolytic activities, as well as for their cytotoxicity on cancer bronchial epithelial cells. Selected substitutions were performed on residues R^{23} and K^{25} in the hydrophilic side, V^{21} and F^{27} in the hydrophobic side of the interphase, and F¹⁷ that interacts with cell membranes. Specific motifs IIKK and LLKKL with anticancer and antimicrobial activities isolated from animals were also inserted into the 17-29 fragment to investigate how they affect activity. Substitution of the amino-terminal positive charge by acetylation and replacement of lysine by the aliphatic leucine in the peptide analog Ac-FKRIVQRIL²⁵DFLR-NH₂ resulted in significant cytotoxicity against A549 cancer cells with an IC₅₀ value 3.90 µg/mL, with no cytotoxicity to human erythrocytes. The peptide Ac-FKRIVQI²³IKK²⁶FLR-NH₂, which incorporates the IIKK motif and the peptides FKRIVQL²³L²⁴KK²⁶L²⁷LR-NH₂ and Ac-FKRIVQL²³L²⁴KK²⁶L²⁷LR-NH₂, which incorporate the LLKKL motif, displayed potent antimicrobial activity against gram-negative bacteria (MIC 3-7.5 µg/mL) and substantial cytotoxicity against bronchial epithelial cancer cells, (IC₅₀ 12.9-9.8 µg/mL), with no cytotoxic activity for human erythrocytes. The helical conformation of the synthetic peptides was confirmed by circular dichroism. Our study shows that appropriate substitutions, mainly in positions of the interphase, as well as the insertion of the motifs IIKK and LLKKL in the cathelicidin 17-29 segment, may lead to the preparation of effective biological compounds.

KEYWORDS

amphipathic α -helical peptides, antimicrobial activity, cathelicidin LL-37 analogs, cytotoxicity, hemolytic assay

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1 | INTRODUCTION

According to the Schiffer-Edmunson projection, amphipathic helical cationic peptides isolated over the last few decades from a variety of plant and animal organisms are characterized as natural antimicrobials.^{1,2} They represent the first line of defense for organisms and target a wide variety of microbes that include bacteria, viruses, parasites, and fungi. Antimicrobial peptides that also inactivate a wide range of cancer cell types and act as anticancer agents have been isolated. The inappropriate and irrational use of antibiotics has induced the worldwide emergence and spreading of resistant microorganisms. As well, radiation and chemotherapy are conventional treatments for cancer, which is one of the main causes of disease-related death worldwide. These treatments suffer from low performance and serious side effects.³⁻⁶ The development of new antimicrobial/anticancer therapeutics is of urgent priority. Amphipathic peptides or their analogs may be a potential alternative.

Many relatively small-size peptides have a number of advantages. These include favorable pharmacokinetic profiles and bioavailability, good solubility, lessened potential for development of tolerance because of the short interaction time with cells, low toxicity, and selective recognition by microbial and cancer cells.⁷ Cationic antimicrobial amphipathic peptides rupture the cell membrane through membrane-disrupting mechanisms (carpet, barrel-stave, and toroidal models), do not act via receptors, and decrease tolerance. Antimicrobial peptides can be divided into those that cause cell death by direct cell lysis and those that penetrate the cell membranes and kill the cell without lysis by interacting with critical intracellular targets. Interestingly, peptides that are active in microbial and cancer cells but inactive in normal cells have also been reported.⁸ Peptides that contribute to the defense of an organism are expected to show strong toxicity and selectivity to cancer cells compared with normal cells.

The detailed mechanisms of action of anticancer peptides are not fully understood, but it is accepted that in most cases, they cause necrosis and/or apoptosis as they affect the cell or the mitochondria.^{3,9–14} The net negative charge of cancer and microbial cells, due to the presence of anionic compounds in the cell membrane, such as phospholipids, phosphatidylserine, glycosyl, and sialyl compounds, is an important difference from the zwitterion-neutral form of normal mammalian cells. Other important aspect is cholesterol, which modulates membrane fluidity and facilitates the destabilization of cancer cells by anticancer peptides.^{15–22}

Cathelicidin is the 18 kDa precursor human protein of the active 37 amino acid form, LL-37, that results following proteolysis. LL-37 belongs to the class of human defense peptides and is secreted from bone marrow, leukocytes, epithelial tissues, and the gastrointestinal system. LL-37 is overexpressed in many cancers, including ovarian, breast, and lung cancer.^{23–28} Segments of LL-37 derived from bio-chemical processes have diverse actions that include antiseptic, antibacterial, antimicrobial, apoptotic, metastatic, and immunological activities.^{29–34}

Two- and three-dimensional nuclear magnetic resonance spectroscopy conducted in a membrane-like environment comprised of dodecylphosphocholine and sodium dodecyl sulfate (SDS) has revealed that aromatic residues F^5 , F^6 , F^{17} , and F^{27} on the hydrophobic nonpolar side of the helical 2-31segment of LL-37 are important sites for the interaction of the protein with cell membranes. The same is also true for residues R^7 , R^{19} , R^{23} , R^{29} , and R^{34} on the polar hydrophilic side of the helix.²³

With the aim of further contributing to the development of new effective antimicrobial/anticancer compounds, we report the design, synthesis, and study of cationic amphipathic peptide analogs of the cathelicidin 17-29 segment. Selected substitutions were made on residues R²³, K²⁵, V²¹, and F²⁷ of both sides of the interface, as well as on residue F¹⁷, which is related to cell membrane interactions.^{8,23} Sequences containing two consecutive lysines and the hydrophobic residues of leucine and isoleucine (e.g., IIKK, IIKKI, IKK, and LLKKL) with anticancer and antimicrobial activities have been isolated from animals.^{4,5} The IIKK and LLKKL motifs were inserted into the 17-29 segment and studied.^{8,35-37} Peptide-based factors as polarity/hydrophobicity, aromaticity, total charge, and side chain stereochemical volume are discussed in relation to their biological properties.

The anticancer activity of the synthesized peptide analogs was investigated by measuring the cytotoxicity of the peptides on the cancer obronchial epithelial cell line A549, using the (3-4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium (MTT) photometric assay, and concentration that causes 50% inhibition (IC₅₀) was determined.⁸ The antimicrobial properties of the synthesized peptides were studied in gram-negative and gram-positive bacteria, the minimum inhibitory concentration (MIC) was estimated, and the concentration of the peptide that causes lysis of 50% of erythrocytes (EC₅₀) was established.^{38–40}

The data concerning the correlation of the anticancer and antimicrobial properties of the peptide analogs will help to understand the prerequisites for the development of effective pharmaceuticals.

2 | MATERIALS AND METHODS

2.1 | Peptide synthesis

The synthesis of the peptides was performed by the stepwise solid-phase synthesis procedure on a Rink-Amide (AM) resin (0.37 mmol/g resin) using the 9-fluorenylmethyloxycarbonyl (Fmoc) methodology. Arginine was used as Fmoc-Arg (Pbf)-OH (Pbf: 2,2,4,6,7-pentamethyl-dihydrobenzofurane-5-sulfonyl), lysine as Fmoc-Lys (Boc)-OH (Boc: tert-butyloxycarbonyl), aspartic acid as Fmoc-Asp (OtBu)-OH (OtBu: Otert-butyloxy), and glutamine as Fmoc-Gln (Trt)-OH. Fmoc-groups were removed using 20% piperidine in dimethylformamide. The coupling reactions were performed using an Fmoc-amino acid/HBTU/HOBt/DIEA/resin with a molar ratio of 3/3/3/6/1 (HBTU: O-benzotriazol-1-yl-N,N,N',N' tetramethyluronium hexafluorophosphate, HOBt: hydroxybenzo-1.2,3-triazole, and DIEA: N, N-diisopropylethylamine). Completion of coupling reactions was ensured by the use of the ninhydrin-

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based Kaiser test. The peptides were cleaved from the resin by treatment with trifluoroacetic acid/triisopropylsilane/water (TFA/TIS/H₂O, 95/2.5/2.5). The resin was removed by filtration, the filtrate was evaporated under reduced pressure, and the product was precipitated with cold diethyl ether. The crude products were purified by semipreparative reverse phase-high performance liquid chromatography (RP-HPLC) using a C18 column. Appropriate programs were applied using eluent A ($H_2O/0.1\%$ TFA) and B (acetonitrile [CH₃CN]/0.1% TFA). Yields ranged from 40% to 55%. The purity of the peptides was checked by analytical HPLC, and the correct molecular masses were confirmed by electrospray ionization-mass spectrometry (ESI-MS) (Table 1).

TABLE 1 Parameters and characterization of the synthesized peptides

Peptides	RP-HPLC gradient elution ^a	t _R (min) ^b	ESI-MS	Net charge
$1 F^{17} KRIV^{21} QR^{23} I^{24} K^{25} D^{26} F^{27} LR-NH_2$	A:B 90:10	12.5	Calculated [M + 3H] ³⁺ : 573.7	+5
	A:B 30:70		Found [M + 3H] ³⁺ : 573.96	
2 L ¹⁷ KRIVQRIKDFLR-NH ₂	A:B 90:10	12.5	Calculated [M + 3H] ³⁺ : 562.36	+5
	A:B 30:70		Found [M + 3H] ³⁺ : 562.68	
3 A ¹⁷ KRIVQRIKDFLR-NH ₂	A:B 90:10	13.0	Calculated [M + 3H] ³⁺ : 548.33	+5
	A:B 30:70		Found [M + 3H] ³⁺ : 548.97	
4 Ac-FκRIVQRIL ²⁵ DFLR-NH ₂	A:B 80:20	17.0	Calculated [M + 3H] ³⁺ : 582.7	+3
	A:B 20:80		Found [M + 3H] ³⁺ : 581.61	
5 Ac-FK (SA)RIVQRIL ²⁵ DFLR-NH ₂	A:B 90:10	17.0	Calculated [M + 3H] ³⁺ : 704.14	+2
	A:B 0:100		Found [M + 3H] ³⁺ : 703.36	
6 FKRIVQRIR ²⁵ DFLR-NH ₂	A:B 90:10	13.5	Calculated [M + 3H] ³⁺ : 583.00	+5
	A:B 30:70		Found [M + 3H] ³⁺ : 582.04	
7 Ac-FKRIVQRIR ²⁵ DFLR-NH ₂	A:B 90:10	17.5	Calculated [M + 3H] ³⁺ : 59 5.05	+4
	A:B 30:70		Found [M + 3H] ³⁺ : 595.94	
8 FKRIVQκ ²³ IKDFLR-NH ₂	A:B 90:10	12.5	Calculated [M + 3H] ³⁺ : 564.37	+5
	A:B 30:70		Found [M + 3H] ³⁺ : 563.26	
9 FKRIVQL ²³ IKDFLR-NH ₂	A:B 90:10	10.5	Calculated [M + 3H] ³⁺ : 559.03	+4
	A:B 30:70		Found [M + 3H] ³⁺ : 558.12	
10 Ac-FKRIVQL ²³ IKDFLR-NH ₂	A:B 90:10	14.5	Calculated [M + 3H] ³⁺ : 573.25	+3
	A:B 30:70		Found [M + 3H] ³⁺ : 572,21	
11 FKRIVQRIKDL ²⁷ LR-NH ₂	A:B 90:10	10.2	Calculated [M + 3H] ³⁺ : 562.37	+5
	A:B 30:70		Found [M + 3H] ³⁺ : 561.09	
12 Ac-FKRIVQRIKDL ²⁷ LR-NH ₂	A:B 90:10	13.8	Calculated [M + 3H] ³⁺ : 576.38	+4
	A:B 30:70		Found [M + 3H] ³⁺ : 575.10	
13 FKRIVQI ²³ IKK ²⁶ FLR-NH ₂	A:B 90:10	17.5	Calculated [M + 2H] ²⁺ : 845.60	+5
	A:B 30:70		Found [M + 2H] ²⁺ : 843.69	
14 Ac-FKRIVQI ²³ IKK ²⁶ FLR-NH ₂	A:B 90:10	22.5	Calculated [M + 2H] ²⁺ : 866.62	+4
	A:B 30:70		Found [M + 2H] ²⁺ : 864.72	
$15 \ FKRIVQL^{23}L^{24}KK^{26}L^{27}LR-NH_2$	A:B 90:10	14.5	Calculated [M + 3H] ³⁺ : 552.34	+5
	A:B 30:70		Found [M + 3H] ³⁺ : 551.10	
16 Ac-FKRIVQL $^{23}L^{24}$ KK $^{26}L^{27}$ LR-NH $_2$	A:B 90:10	18.0	Calculated [M + 3H] ³⁺ : 566.40	+4
	A:B 30:70		Found [M + 3H] ³⁺ : 565.12	
17 FKRIL ²¹ QRIKDFLR-NH ₂	A:B 90:10	15.5	Calculated [M + 3H] ³⁺ : 578.05	+5
	A:B 30:70		Found [M + 3H] ³⁺ : 577.09	
18 Ac-FKRIL ²¹ QRIKDFLR-NH ₂	A:B 90:10	20.5	Calculated [M + 2H] ²⁺ : 887.59	+4
	A:B 30:70		Found [M + 2H] ²⁺ : 886.79	

Abbreviations: ESI-MS, electrospray ionization-mass spectrometry; RP-HPLC, reverse phase-high performance liquid chromatography. ^aA: H₂O/0.1%TFA, B: CH₃CN/0.1%TFA.

2.2 | Circular dichroism

Circular dichroism (CD) spectra were recorded from 260 to 180 nm at a scan speed of 50 nm/min. The average of three scans was determined. The procedure was performed using a Jasco J-710 spectropolarimeter equipped with a 0.1-cm path-length quartz cell and peptide concentration 10^{-4} M at 25°C. Phosphate-buffered saline (PBS, p 7.4), trifluoroethanol (TFE) in PBS, and sodium dodecylsulfate (SDS) were used in all experiments. The spectra were smoothed after subtraction of the solvent contribution. The α -helical content was estimated on the basis of [θ]₂₂₂ nm values ([θ] in deg.cm².dmol⁻¹) according to the Chen equation⁴¹ as follows:

 $\%\alpha$ – helical content = $[\theta]_{222}/[\theta]^{\infty}(1-k/n)$,

where n is the number of residues of the peptide and $[\theta]_{222}$ the molar ellipticity at 222 nm. The estimated value $[\theta]^{\infty}$, which corresponds to a 100% helical content at 222 nm, is 39,500 and the constant k = 2.57.

2.3 | Antimicrobial activity

The peptides were tested for their antimicrobial activity against gramnegative bacteria (Escherichia coli DH5a, Pseudomonas aeruginosa PAO, and Zymomonas mobilis ATCC 10988), gram-positive bacteria (Bacillus subtilis DELTA and Mycobacterium smegmatis mc² 155), and the fungus Candida parapsilosis. E. coli is a representative of potent pathogens, and P. aeruginosa PAO and Z. mobilis ATCC 10988 possess natural multidrug resistance. The selection of the gram-positive bacteria was based on differences of their membrane lipid components. Aliquots (100 μ L) containing 2 \times 10⁶ logarithmic phase bacteria per milliliter obtained from microorganisms grown in the appropriate culture medium were dispensed into wells of 96-well microplates. Peptide stock solution was obtained by solubilizing the peptides in water followed by filter sterilization using a 0.22-µm pore size filter. After serial dilutions of the stock solution, 100 µL was added to each well to obtain a final concentration of 5 to 500 µg/mL. Control wells contained filter-sterilized water instead of peptide solution. The experiments were performed in triplicate. Inhibition of the growth was determined by measuring the absorbance at 620 nm after incubation for 24 h at the appropriate temperature for each microorganism. The antimicrobial activities were expressed as the minimum concentration at which 100% inhibition of growth was observed (the MIC).

2.4 | Hemolytic activity assay

The hemolytic activity of the peptides was monitored by determining hemoglobin release from a suspension of erythrocytes suspension as previously described.⁴² In brief, fresh human red blood cells were washed three times in 10 mM Tris buffer containing 150 mM NaCl, pH 7.4. Cell suspensions containing 1.9×10^8 cells/mL were incubated with varying amounts of peptides solubilized in Tris buffer. Zero

hemolysis and 100% hemolysis were determined by using Tris buffer and 0.5% NH₄OH, respectively. The experiments were performed in triplicate. Concentrations causing 50% hemolysis (EC_{50}) were derived from the dose-response curves.

2.5 | Cytotoxicity test

The possible anticancer activity of the peptide analogs of cathelicidin LL 17-29 was assessed using A549 cancer bronchial epithelial cells, with comparison against DLF lung fibroblasts as normal control cells. We investigated the cytotoxicity of the peptides for cancer and control cells using the MTT photometric viability assay as previously described.^{43,44} The results were used to determine the IC₅₀. A549 or DLF cells (18,000 cells/well) were precultured in a sterile 96-well plate. After 24 h of incubation, cells were treated with 100 µL of peptide solutions (10-200 µg/mL) and incubated for a further 24 h. Then, 10 µL of MTT solution (5 mg/mL) was added to each well and incubated for 4 h. The supernatant was removed from each well and the formazan crystals that had formed in each well were dissolved in 100 µL dimethyl sulfoxide (DMSO). After 2 h, the absorbance intensity was measured at 570 nm using a microplate reader and compared with a standard curve to determine the number of viable cells in each sample. Wells without peptides were used as a positive control and wells without cells as a negative control (blank) of the assay. The experiments were carried out three times independently

3 | RESULTS AND DISCUSSION

3.1 | Design of the peptides

The design of the peptides was based on the Schiffer-Edmunson helical wheel projection of the cathelicidin 17-29 amide segment. The aim of the design was to preserve and improve the amphipathic character of the peptides Figure 1. Generally, the amides are more proteolytic



FIGURE 1 Schiffer-Edmundson α -helical wheel projection of the sequence 17-29 of LL-37, FKRIVQRIKDFLR-NH₂

stable and enhance the α -helical conformation inducing better activity. Selected substitutions were performed on residues R²³, K²⁵, V²¹, and F²⁷ of both sides of the interface, as well as on residue F¹⁷. The specific motifs IIKK and LLKKL, which are found in animal peptides, were inserted into the 17-29 segment and their influence on antimicrobial and anticancer activities was evaluated.

Table 1 shows the sequence 17-29 amide of LL-37(1) and the synthesized analogs (2-18). The aromatic phenylalanine residue in position 17 of the hydrophobic side of the amphipathic helix was substituted by the aliphatic leucine and alanine residues in compounds 2 and 3, respectively. The positively charged lysine in position 25 of the interface was replaced by the aliphatic leucine residue, in analogs 4 and 5 and by arginine, another positively charged residue, in analogs 6 and 7. Arginine in position 23, which is also located in the interface, was substituted by lysine in analog

8 and by leucine in analogs 9 and 10. Leucine replaced phenylalanine in position 27 of the hydrophobic side in analogs 11 and 12. Leucine also replaced valine in position 21 of the hydrophobic side in analogs 17 and 18. The IIKK segment (23-26) substituted for aspartic acid 26 and arginine 23 of the hydrophilic face in analogs 13 and 14,while the LLKKL segment (23-27) substituted for arginine 23 and aspartic acid 26 of the hydrophilic face as well as F²⁷ and I²⁴ of the hydrophobic face in analogs 15 and 16. Finally, sialic acid, which is successfully incorporated in microbial pathogens where it assists in evasion of host immunity,⁴⁵ was inserted into the ε - amino group of lysine in position 18.

The location of the replaced residues within the amphipathic helix, their charges, and hydrophilic/hydrophobic properties, as well as their stereochemical volume, were investigated in relation to their biological activities.



FIGURE 2 Circular dichroism (CD) spectra of the peptides 1(--), 4(--), 14(--), 15(---), and 16(--), 100μ M). A, Phosphate-buffered saline (PBS); B, sodium dodecyl sulfate (SDS) 8 mM; C, trifluoroethanol (TFE)/PBS (50/50, v/v)

3.2 | CD analysis

All the CD experiments of the peptides in this study were carried out in PBS (pH 7.4), TFE in PBS (50/50, v/v), and in the SDS membrane mimic at the critical micelle concentration of 8 mM³⁸⁻⁴⁰ Figure 2. The percent helicity of the peptides was calculated on the basis of $[\theta]_{222}$ nm values (Table 2). The hydrophobic moment of the peptides was also calculated Table 2.^{46,47} The native sequence 17-29 of LL-37 (peptide 1) indicated a percent helicity of 51% in SDS and 83% in TFE/PBS. All the synthesized analogs preserved or increased, in some cases, their alpha helical content indicating that the selected substitutions did not affect the overall helical conformation, which might be critical for their activity. The calculated hydrophobic moments of all free peptides were almost the same.

3.3 | Antimicrobial activity

The antimicrobial activity of the peptides was studied using gramnegative bacteria (*E. coli* DH5a, *P. aeruginosa* PAO, and *Z. mobilis* 10,988), gram-positive bacteria (*B. subtilis* DELTA and *M. smegmatis* mc² 155), and the fungus *C. parapsilosis*. The MIC values of the peptides are shown in Table 3. Differences in the MIC values could be attributed to the different composition of the outer envelope of each microorganism. The native sequence 17-29 of LL-37 (peptide 1) showed weak antimicrobial activity, with an MIC of 200 µg/mL, for *E. coli* DH5a and *C. parapsilosis*, and an MIC of 50 µg/mL for *M. smegmatis* mc² 155. Substitution of the aromatic phenylalanine in position 17 (which interacts with cell membranes) of the hydrophobic side of the amphipathic helix, by aliphatic residues leucine and alanine in peptides 2 and 3, respectively, did not substantially affect the activity of the natural sequence (peptide 1), indicating that phenylalanine may not interact with the cell membranes in this analog. Substitution of the positively charged lysine in position 25 of the interface by leucine and acetylation of the amino-terminal group increased the activity in peptide 4. Analog 5, which incorporates sialic acid into the ε -amino group of lysine in position 18, displayed reactivity only against *B. subtilis* DELTA, although the native sequence (peptide 1) was inactive to this microorganism. Substitution of lysine 25 by arginine, another positively charged residue, did not substantially change the reactivity in analog 6. The same finding was also found for the acetylated N-terminus peptide 7.

Replacement of arginine in position 23, which is also located in the interface, by lysine in peptide 8 did not enhance the activity of the peptide compared with the peptide 1. Arginine in position 23 was also substituted by leucine in peptides 9 and 10. This substitution increased the activity against *E. coli* DH5a (MIC 30 µg/mL and 100 µg/mL for peptide 9 and 10, respectively), whereas these peptides showed low reactivity (MIC 20 and 100 µg/mL, same respective order) against *P. aeruginosa* PAO. On the contrary, peptides 9 and 10 were not effective against the tested gram-positive bacteria and the fungus. These findings highlighted the role of position 23 in the interphase. Replacement of the aromatic phenylalanine in position 27 of the hydrophobic side by leucine produced comparable reactivities against all tested bacteria and fungus, for peptides 11 and 12.

Insertion of the IIKK motif (23-26) in peptides 13 and 14 and the LLKKL motif (23-27) in peptides 15 and 16 found in many defense proteins improved the antimicrobial activity. The substitutions of R^{23}

TABLE 2 Percent helicity on the basis of $[\theta]_{222}$ nm values and hydrophobic moment μ H of the peptides

	Peptides	μH	PBS	SDS (8mM)	TFE/PBS (50/50 v/v)
1	FKRIVQRIKDFLR-NH ₂	8.846	5.8	50.7	83.1
2	L ¹⁷ KRIVQRIKDFLR-NH ₂	0.840	7.6	51.5	90.1
3	A ¹⁷ KRIVQRIKDFLR-NH ₂	0.743	8.0	58.3	46.6
4	Ac-FKRIVQRIL ²⁵ DFLR-NH ₂	-	25.8	70.6	88.6
5	Ac-FK (SA)RIVQRIL ²⁵ DFLR-NH ₂	-	46.1	68.4	58.4
6	FKRIVQRIR ²⁵ DFLR-NH ₂	0.847	8.4	87.0	55.8
7	Ac-FKRIVQRIR ²⁵ DFLR-NH ₂	-	9.2	70.9	57.4
8	FKRIVQK ²³ IKDFLR-NH ₂	0.846	6.0	53.0	62.0
9	FKRIVQL ²³ IKDFLR-NH ₂	0.847	15.0	81.6	60.5
10	Ac-FKRIVQL ²³ IKDFLR-NH ₂	-	9.8	79.3	52.0
11	FKRIVQRIKDL ²⁷ LR-NH ₂	0.843	12.1	55.6	44.6
12	Ac-FKRIVQRIKDL ²⁷ LR-NH ₂	-	7.2	77.4	76.0
13	FKRIVQI ²³ IKK ²⁶ FLR-NH ₂	0.863	7.7	51.9	66.4
14	Ac-FKRIVQI ²³ IKK ²⁶ FLR-NH ₂	-	9.9	70.6	56.5
15	$FKRIVQL^{23}L^{24}KK^{26}L^{27}LR-NH_2$	0.848	5.2	39.7	53.4
16	Ac-FKRIVQL ²³ L ²⁴ KK ²⁶ L27LR-NH ₂	-	14.6	67.8	76.5
17	FKRIL ²¹ QRIKDFLR-NH ₂	0.864	2.8	44.7	71.6
18	Ac-FKRIL ²¹ QRIKDFLR-NH ₂	-	6.3	89.8	99.5

Abbreviations: PBS, phosphate-buffered saline; SDS, sodium dodecyl sulfate; TFE, trifluoroethanol.

values of the peptides
ц ш
, µg/
(MIC
concentration
inhibitory
Minimum
TABLE 3

	Gram (–) bacteria			Gram (+) bacteria		Fungus
Peptides	Escherichia coli DH5a	Pseudomonas aeruginosa PAO	Zymomonas mobilis 10,988	Bacillus subtilis DELTA	Mycobacterium smegmatis mc ² 155	Candida parapsilosis
1 F ¹⁷ KRIV ²¹ QR ²³ I ²⁴ K ²⁵ D ²⁶ F ²⁷ LR-NH ₂	200				50	200
2 L ¹⁷ KRIVQRIKDFLR-NH ₂	200	,	200	ı	200	
3 A ¹⁷ KRIVQRIKDFLR-NH ₂					200	
4 Ac-FkRIVQRIL ²⁵ DFLR-NH ₂	100	1		100		
5 Ac-FK (SA)RIVQRIL ²⁵ DFLR-NH ₂	1		ı	200		
6 FKRIVQRIR ²⁵ DFLR-NH ₂	100	,		50	20	200
7 Ac-FKRIVQRIR ²⁵ DFLR-NH ₂	100		200	40	30	
8 FKRIVQK ²³ IKDFLR-NH ₂		,	200	ı	50	
9 FKRIVQL ²³ IKDFLR-NH ₂	30	20	ı	50	200	100
10 Ac-FKRIVQL ²³ IKDFLR-NH ₂	100	100	100	20	200	100
11 FKRIVQRIKDL ²⁷ LR-NH ₂	200	200	200	200	200	200
12 Ac-FKRIVQRIKDL ²⁷ LR-NH ₂	200	40	40	200	200	200
13 FKRIVQI ²³ IKK ²⁶ FLR-NH ₂	100	S	5	20	20	20
14 Ac-FKRIVQI ²³ IKK ²⁶ FLR-NH ₂	50	с	5	20	100	30
15 FKRIVQL ²³ L ²⁴ KK ²⁶ L ²⁷ LR-NH ₂	200	S	7.5	30	30	30
16 Ac-FKRIVQL ²³ L ²⁴ KK ²⁶ L ²⁷ LR-NH ₂	100	с	5	10	50	40
17 FKRIL ²¹ QRIKDFLR-NH ₂	100	30	100	100	40	100
18 Ac-FKRIL ²¹ QRIKDFLR-NH ₂	100	20	50	100	20	40

Note. (–) not active.

by I and D²⁶ by K (peptides 13 and 14) significantly increased the activity of peptide 13 against *P. aeruginosa* PAO (MIC 3 μ g/mL) and *Z. mobilis* 10,988 (MIC 5 μ g/mL). Peptide 14 also was effective against *P. aeruginosa* PAO (MIC 3 μ g/mL) and *Z. mobilis* 10,988 (MIC 7.5 μ g/mL).

The substitutions of R²³ and I²⁴ by L, D²⁶ by K ,and F²⁷ by L in the peptides 15 and 16 also significantly increased the activity against *P. aeruginosa* PAO (MIC 3 μ g/mL in both peptides) and *Z. mobilis* 10,988 (MIC 7.5 and 5 μ g/mL for peptides 15 and 16, respectively), and against *B. subtilis* DELTA (MIC 10 μ g/mL for peptide 16).

Replacement of valine by leucine in position 21 of the hydrophobic side in peptide analogs 17 and 18 increased the activity of peptide 18 against P. *aeruginosa* PAO (MIC 20 μ g/mL) and M. *smegmatis* mc² 155 (MIC 20 μ g/mL).

The overall data of Table 3 demonstrated that the incorporation of the IIKK and LLKKL motifs into the native sequence 17-29 of the cathelicidin LL-37 significantly improved the antimicrobial activity against most of the tested microorganisms. Substitution of the positively charged arginine in position 23 and lysine in position 25, which are located in the interface, by aliphatic residues (leucine or isoleucine) increased the activity against almost all the tested bacteria. Replacement of phenylalanine, an aromatic residue, in positions 17 and 27 of the hydrophobic side of the amphipathic helix by aliphatic residues leucine and alanine did not enhance the activity of peptide 1.



FIGURE 4 Hemolytic activity of peptides versus concentration (µg/mL), A: 12(_____), 13(_____), 14(_____), 15(____), and 16(____); B: 17(____) and 18(____). The experiments were performed in triplicate



FIGURE 3 Hemolytic activity of peptides versus concentration (μ g/mL), A: 1(\rightarrow), 2(\rightarrow), 3(\rightarrow), and 4(\rightarrow); B: 6(\rightarrow), 7(\rightarrow), 7(\rightarrow), and 10(\rightarrow). The experiments were performed in triplicate

TABLE 4 Hemolytic activity of the peptides

Peptides	EC ₅₀ , μg/mL
$1 \ F^{17} KRIV^{21} QR^{23} I^{24} K^{25} D^{26} F^{27} LR \cdot NH_2$	-
2 L ¹⁷ KRIVQRIKDFLR-NH ₂	-
3 A ¹⁷ KRIVQRIKDFLR-NH ₂	-
4 Ac-FKRIVQRIL ²⁵ DFLR-NH ₂	450
5 Ac-FK (SA)RIVQRIL ²⁵ DFLR-NH ₂	-
6 FKRIVQRIR ²⁵ DFLR-NH ₂	-
7 Ac-FKRIVQRIR ²⁵ DFLR-NH ₂	-
8 FKRIVQx ²³ IKDFLR-NH ₂	-
9 FKRIVQL ²³ IKDFLR-NH ₂	114
10 Ac-FKRIVQL ²³ IKDFLR-NH ₂	227
11 FKRIVQRIKDL ²⁷ LR-NH ₂	-
12 Ac-FKRIVQRIKDL ²⁷ LR-NH ₂	-
13 FKRIVQI ²³ IKK ²⁶ FLR-NH ₂	361
14.Ac-FKRIVQI ²³ IKK ²⁶ FLR-NH ₂	292
15 FKRIVQL ²³ L ²⁴ KK ²⁶ L ²⁷ LR-NH ₂	411
$16 \text{ Ac-FKRIVQL}^{23} \text{L}^{24} \text{KK}^{26} \text{L}^{27} \text{LR-NH}_2$	185
17 FKRIL ²¹ QRIKDFLR-NH ₂	-
18 Ac-FKRIL ²¹ QRIKDFLR-NH ₂	-

Note. (-) not active.

3.4 | Hemolytic assay

The cathelicidin 17-29 segment and all its analogs were also tested for their toxicity against human erythrocytes. Peptides 1-3, 5-8, 11, 12, 17, and 18 did not exhibit any toxicity against erythrocytes, while peptides 4, 9, 10, and 13-16 displayed low toxicity at concentrations much higher than their MIC values Figures 3 and 4 and Table 4. The lack of hemolytic activity can be attributed to the different lipid composition of the bacteria and erythrocyte membranes. The cationic AMPs interact with the anionic surface of bacterial membranes, which lead to the lysis of the bacteria, whereas they cannot interact with the neutral surface of the erythrocytes.

3.5 | Cytotoxicity test

The cytotoxicity of the peptides against A549 bronchial epithelial cancer cells and the control DLF normal lung fibroblasts was investigated using the MTT photometric assay. The IC_{50} values of the peptides are shown in Table 5.

The native sequence 17-29 of LL-37 (peptide 1) was cytotoxic to A549 cells, with an IC₅₀ of 20.13 μ g/mL Figure 5. Substitution of phenylalanine in position 17 by the aliphatic residues leucine and alanine in compounds 2 and 3, respectively, and replacement of phenylalanine in position 27 of the interphase by leucine in peptides 11 and 12 did not enhance their cytotoxicity compared to peptide 1. Substitution of the positively charged lysine in position 25 of the interface by leucine in analogs 4 and 5 increased the cytotoxicity, as evidence by the IC₅₀

TABLE 5	IC_{50} (µg/mL) of the peptides for A549 cancer cells and
DLF normal c	ells

Peptides	A549	DLF
$1 \ F^{17} KRIV^{21} QR^{23} I^{24} K^{25} D^{26} F^{27} LR \cdot NH_2$	20.1	29.3
2 L ¹⁷ KRIVQRIKDFLR-NH ₂	33.7	56.9
3 A ¹⁷ KRIVQRIKDFLR-NH ₂	29.8	-
. 4 Ac-FKRIVQRIL ²⁵ DFLR-NH ₂	3.9	20.1
5 Ac-FK (SA)RIVQRIL ²⁵ DFLR-NH ₂	10.7	24.3
6 FKRIVQRIR ²⁵ DFLR-NH ₂	56.0	-
7 Ac-FKRIVQRIR ²⁵ DFLR-NH ₂	12.5	54.1
8 FKRIVQK ²³ IKDFLR-NH ₂	145.1	-
9 FKRIVQL ²³ IKDFLR-NH ₂	18.9	23.5
10 Ac-FKRIVQL ²³ IKDFLR-NH ₂	13.9	22.5
11 FKRIVQRIKDL ²⁷ LR-NH ₂	75.0	-
12 Ac-FKRIVQRIKDL ²⁷ LR-NH ₂	45.5	-
13 FKRIVQI ²³ IKK ²⁶ FLR-NH ₂	20.0	27.0
14 Ac-FKRIVQI ²³ IKK ²⁶ FLR-NH ₂	12.9	15.7
15 FKRIVQL ²³ L ²⁴ KK ²⁶ L ²⁷ LR-NH ₂	12.8	23.7
16 Ac-FKRIVQL ²³ L ²⁴ KK ²⁶ L ²⁷ LR-NH ₂	9.8	17.3
17 FKRIL ²¹ QRIKDFLR-NH ₂	19.2	76.8
18 Ac-FKRIL ²¹ QRIKDFLR-NH ₂	29.2	160.9



FIGURE 5 Cytotoxicity of peptide 1, $F^{17}KRIV^{21}QR^{23}I^{24}K^{25}D^{26}F^{27}LR-NH_2$; IC₅₀ (µg/mL), 20.13. The experiments were carried out three times independently

values of 3.90 and 10.70 µg/mL, respectively. The incorporation of SA into the ε -amino group of lysine in position 18 (analog 5) improved the cytotoxicity compared with peptide 1. Substitution of lysine in position 25 by arginine in analog 6 did not enhance the cytotoxicity, while acetylation of analog 6 increased the cytotoxicity of analog 7 (IC₅₀ 12.46 µg/mL). Replacement of arginine in position 23 by lysine in analog 8 did not enhance the cytotoxicity. Arginine in position 23 was also substituted by leucine in analogs 9 and 10. This substitution did not enhance the cytotoxicity of analog 9, but enhanced the cytotoxicity of the acetylated analog 10 (IC₅₀ 13.92 µg/mL).

Insertion of the IIKK motif (23-26) in peptides 13 and 14, and the LLKKL motif (23-27) in peptides 15 and 16 improved the cytotoxicity, with IC₅₀ values of 12.92 μ g/mL (peptide 14), 12.83 μ g/mL (peptide 15), and 9.8 μ g/mL (peptide 16). Substitution of valine in position 21 by leucine in analogs 17 and 18 did not enhance cytotoxicity.

All the peptides were also tested against normal DLF cells. Lower cytotoxicity was evident compared with A549 cells, as indicated the significantly higher IC_{50} values (Table 4).

The collective data of Table 5 demonstrated that the incorporation of the IIKK and LLKKL motifs, which are present in many defense peptides, into the native sequence 17-29 of the cathelicidin LL-37 significantly improved cytotoxicity against cancer cell line A549 cells as compared with the native sequence 17-29 of LL-37 (peptide 1). Substitution of the positively charged arginine in position 23 and lysine in position 25, which are located in the interface, by aliphatic residues significantly increased the cytotoxicity of the acetylated analogs compared with the native sequence 17-29 of LL-37 (peptide 1). Substitution of phenylalanine, an aromatic residue, in positions 17 and 27 of the hydrophobic side of the amphipathic helix by aliphatic residues did not enhance the cytotoxicity of peptide 1. Peptide 4, Ac-FKRIVQRIL²⁵DFLR-NH₂, displayed the best



FIGURE 6 Schematic representation (SAR) of the % helical content of the peptides 1(_), 4(_), 14(_), 15(_), and 16(_) in sodium dodecyl sulfate (SDS) against antimicrobial and anticancer activity. The experiments were performed in triplicate

cytotoxicity (IC₅₀ 3.90 μ g/mL), highlighting the significance of position 25 in the interphase, as well as the importance of the N-terminus neutralization.

4 | CONCLUSIONS

In this study, we present the design, synthesis, and analysis of cationic amphipathic peptide analogs of the cathelicidin 17-29 segment. The aim of this study is to further contribute to the development of new effective antimicrobial/anticancer compounds. The native sequence 17-29 of LL-37 (peptide 1) showed weak antimicrobial activity with an MIC of 200 μ g/mL against the gram-negative bacterium *E. coli* DH5a and fungus *C. parapsilosis* and an MIC of 50 μ g/mL against the gram-positive bacterium *M. smegmatis* mc² 155. Peptide

1 was not toxic for human erythrocytes but was cytotoxic to A549 cells (IC_{50} 20.13 $\mu g/mL).$

Selected substitutions were performed on residues R²³, K²⁵, V²¹, and F²⁷ of the interphase and the aromatic residue F¹⁷. The IIKK and LLKKL motifs were inserted into the 17-29 fragment, and their antimicrobial/anticancer reactivity was studied. The substituted peptide Ac-FKRIVQRIL²⁵DFLR-NH₂ (4) exhibited the best cytotoxicity against A549 cancer cells, with an IC₅₀ value of 3.90 µg/mL, probably due to its increased helical content. The peptide was not toxic for human erythrocytes and displayed relatively low antibacterial activity, with an MIC of 100 µg/mL for both gram-negative (*E. coli* DH5a) and gram-positive (*B. subtilis* DELTA) bacteria.

The peptides Ac-FKRIVQI²³IKK²⁶FLR-NH₂ (14), FKRIVQL²³L²⁴ KK²⁶L²⁷LR-NH₂ (15), and Ac-FKRIVQL²³L²⁴KK²⁶L²⁷LR-NH₂

FIGURE 7 Schematic representation (SAR) of the % helical content of the peptides 1(_), 4(_), 14(_), 15(_), and 16(_) in trifluoroethanol (TFE)/ phosphate-buffered saline (PBS) 50/50 v/v against antimicrobial and anticancer activity. The experiments were performed in triplicate



(16) displayed potent antimicrobial activity against the gramnegative species *P. aeruginosa* PAO and *Z. mobilis* 10,988, with MIC values ranging from 3 to 7.5 μ g/mL, were not toxic for human erythrocytes and were cytotoxic for A549 cancer cells (IC₅₀ values of 12.9, 12.8, and 9.8 μ g/mL, respectively). All the peptides were also tested against normal DLF cells. Toxicity was lower as compared with A549 cancer cells, as indicated by their significantly higher IC₅₀ values. Schemes were added in understanding the SAR studies and the conclusion achieved (Figures 6 and 7).

We conclude that the selected substitutions in positions located in the interphase of the amphipathic helix of the cathelicidin 17-29 segment is crucial role in the antimicrobial/anticancer activities of the peptide. Even residues within the IIKK and LLKKL motifs belong to the interphase. The net positive charges of the most active peptides, ranging from 3 to 5 (Table 1), may also contribute to their reactivity against the negatively charged cancer and microbial cells, whereas changes of the side chain stereochemical volume (Ala, Ile, Val) did not affect the overall reactivity of the peptides. N-terminal acetylation, which increased the peptide stability, increased the antibacterial and anticancer activity of most of the peptide analogs.

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