

A CONCISE REVIEW ON THE ANTIMICROBIAL PEPTIDES AND THEIR CRITICAL ACTIVITY AGAINST INTRACELLULAR TARGETS OF BACTERIA

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<https://doi.org/10.55251/jmbfs.6006>

ARTICLE INFO

Received 26. 3. 2022
Revised 4. 11. 2022
Accepted 28. 11. 2022
Published 1. 2. 2023

Review



ABSTRACT

Multi-drug resistance, which is the consequence of overusing antibiotics, has been shown to become a common problem in the medical environments. Accordingly, finding a substitute for daily used antibiotics is a topic of interest in medical microbiology and biotechnology. Antimicrobial peptides (AMPs) are among the main candidates for controlling this problem. These peptides are regarded as the critical defensive line in many organisms. These AMPs act as an innate immunity against pathogenic microorganisms; such as bacteria or fungi. AMPs could destroy their target via different methods; including membrane pore-formation or by targeting their intracellular targets and disrupting the normal cellular activity. Some AMPs have the property of targeting constructs like DNA, RNA, protein synthesis and folding and inhibiting cell life activities; such as normal metabolism or cell division. At this study, we reviewed more than 130 papers that were concerning the importance of intracellular targeting AMPs, by searching the valuable data sources such as PubMed, Scopus, and Web of Science. These AMPs can be considered as one of the possible options to improve the treatment of infected patients. In this review, it was aimed to discuss the activity of intracellular AMPs and provide an outlook for future studies.

Keywords: Antimicrobial peptides, Intracellular targets, Multi-drug resistance, bacterial infection

INTRODUCTION

The increased use of antibiotics for humans and animal husbandry has caused a cycle of resistance to be constantly rotating between other species and humans. Also, the indiscriminate use of antibiotics has made these therapeutic agents even less effective (Dorado et al., 2021, Besharati et al., 2020, McCollum et al., 2021). Bacterial pathogens have shown to become more resistant toward antibiotics; therefore, finding new antimicrobial compounds is necessary to provide an efficient therapy. Antimicrobial peptides (AMP) are one of the main candidates to be considered for therapeutics development against various pathogens (Moghaddam et al., 2015). It has been indicated that the activity and selectivity of AMPs could be influenced by the different factors; such as cell density and peptide entrapment in the target cells (Scheffer et al., 2021, Talledo et al., 2018).

Previous studies have shown that cationic and non-cationic peptides found in a variety of organisms, including bacteria, and could act synergistically to improve the immune responses toward infections (Lei et al., 2019, Seyfi et al., 2020). AMPs are one of the most important defensive lines of the organisms' immunity and often protect them from microbial pathogens. These peptides have multifunctional influences on the innate immunity and provide antimicrobial effect on a wide range of pathogens; such as bacteria, fungi, and viruses. Their important role as a defensive mechanism has attracted the attention of many scientists who wish to find a more effective therapeutic and better outcome for the infection treatment.

Generally, AMPs are low molecular weight peptides with cationic (in most cases) and amphipathic properties (Kardani and Bolhassani, 2021, Moravej et al., 2018). So far, many of AMPs have been isolated from bacteria, animals, plants, various vertebrate and invertebrate species. Regarding the AMPs mode of actions, the membrane disruption and intracellular targeting have been investigated and discussed by previous studies (Nayab et al., 2022).

The activity of AMPs is very critical in a situation where the number and variety of antibiotic-resistant microorganisms has been increased (Amani et al., 2015). Initially, AMPs affect the cell membrane and afterward, they could also influence the components inside of the cell. Due to the amphipathic identity of AMPs, they first interact electrostatically with the LPS in Gram-negative and the teichoic acid

in Gram-positive bacteria via their hydrophilic region, then they penetrate the membrane using the hydrophobic region and form pores that can lead to membrane permeability, which ultimately induces cell destruction. Also, AMPs can affect the intracellular components; such as RNA, DNA, ribosomes, proteins, and chaperones. It is known that some antimicrobial peptides could destroy their targets via different roles, meaning that some of them could affect internal targets and meanwhile cause membrane disruption. In the current review, we aimed to stay focused on AMPs with intracellular activity.

Moreover, it needs to be mentioned that some of these intracellular AMPs could act as multifunctional agents (Le et al., 2017b, Madani et al., 2011, Nicolas, 2009). So far many studies have been performed to clarify the targets for AMPs, for example differential gene expression analysis of RNA-Seq data for detecting the internal targets of AMPs (Mohammadi et al., 2020), yet more in depth investigations are required.

Regarding the AMPs that have been suggested to target DNA, there are some controversy, since the binding of a cationic peptide to anionic nucleic acids is not surprising. Therefore, showing that some peptides associate with DNA is not sufficient to demonstrate that this interaction is responsible for bacterial killing, and it could be just a consequence of the accessibility of DNA (Snoussi et al., 2018). Accordingly, still far more information is required to exactly and completely make clear their exact activity that provides anti-microbial effect. In addition to affecting various components of the intracellular target, AMPs could inhibit a wide range of disorder causing pathogenic constructs, including the biofilms formation of bacteria, which can increase the drug resistance (Davarzani et al., 2021, Duan et al., 2022, Yasir et al., 2018).

Considering the importance of AMPs against infections, this field is an open area for research and practice. One of the important perspectives for future of AMPs is the application of bioinformatics and biotechnology methods to design and develop new AMPs. In this regard, the study by Madanchi et al., could be named as an example of designing and synthesis of an AMP for medical application. In that study, they introduced novel AMPs, based on truncated rabbit and human CAP18 peptides, and evaluated their action mechanism against Lipopolysaccharide (Madanchi et al., 2020a). Another study by the same author was focused on designing the novel truncated derivatives based on direct and reverse mirror repeats of first six residues of Caerin 4 antimicrobial peptide and investigated their activity

and toxicity. Their study showed that the site and arrangement of amino acids are crucial for a peptide function. Moreover, GLWQKI sequence is necessary for the antimicrobial role of Caerin 4 antimicrobial peptide family (Madanchi et al., 2020b).

In the current review, we tried to provide a brief outlook and discuss the importance of antimicrobial peptides and their crucial role to suppress the bacterial infection by disrupting the internal targets. Figure 1 represents some antimicrobial peptides with their intracellular targets.

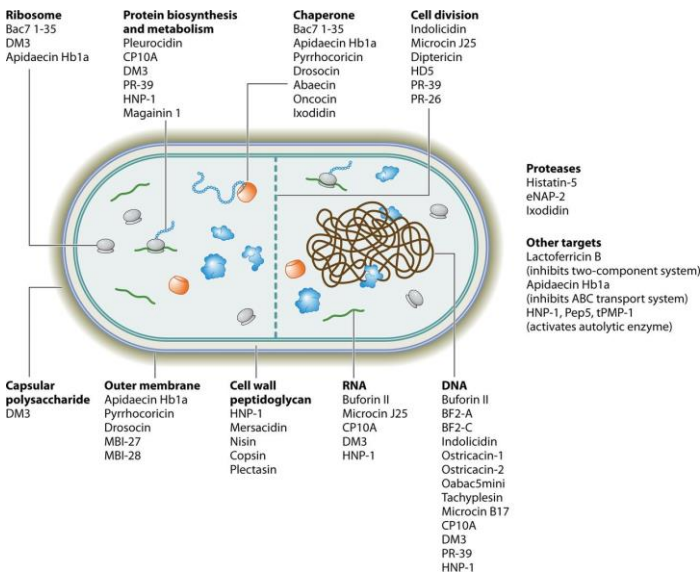


Figure 1. Schematic depiction of some intracellular targets in the bacterial cells which could be affected by AMPs. Taken with permission from Le et al., Intracellular Targeting Mechanisms by Antimicrobial Peptides, Antimicrobial Agents and Chemotherapy, American Society for Microbiology, doi.org/10.1128/AAC.02340-16 (Le et al., 2017a).

EVIDENCE ACQUISITION

To provide conclusive data for the current review, more than 130 papers were fetched from valuable scientific data resources including Web of Science, Scopus, and Pubmed by searching keywords such as multi-drug resistance, anti-microbial peptides, bacterial infection, and intracellular targets.

RESULTS

AMPs can inhibit basic processes in the cells; such as nucleic acid synthesis, protein biosynthesis, and cell wall biosynthesis. For example, AMPs like DM3, CP 10A, and Microcin j25 are effective on RNA and DNA. Apidaecin Hb1a peptides are effective on ribosome; Pleurocidin, PR-39 and HNP-1 peptides are effective on protein biosynthesis and metabolism, and Indolicidin and Diptererin peptides are effective on cell division. In this paper, we tried to provide a brief overview of the AMPs that are capable of suppressing bacterial infection by targeting their intracellular components. Table1 provides some examples regarding the AMPs that target intracellular components and activities.

AMPs with inhibitive effect on DNA, RNA and metabolism

AMPs could attach to the negative charge of the nucleic acids due to their positive charge. This way, they can target these component which eventually causes disrupting their activity. Some of these peptides are discussed in this section.

Burofins are a class of DNA inhibitor peptides. Burofin II (Seq: TRSSRAGLQFPVGRVHRLLRK) is a 21 amino acid peptide with a strong antimicrobial effect on a wide variety of bacteria and fungi, without posing any considerable hemolytic activity. This peptide was initially isolated from the stomach of Asian toad (*Bufo gargarizans*) (Park et al., 1996). These peptides could suppress the cellular activities of bacteria by attaching to their DNA and RNA content and inhibiting the cellular processes by disrupting DNA and RNA activity after penetrating the cell membrane, eventually causing an immediate cell death (Cardoso et al., 2019, Park et al., 1998). Burofin II is more active than Burofin I. Burofin I has been shown to induce membrane penetration in *Escherichia coli*. Proline hinge plays an important role in the cellular penetration of Burofin II and determines the penetration efficiency of the peptides into their target bacterial cells. Its removal destroys the ability of a peptide to enter the cells. Degradation of four amino acids from the C-terminus of Burofin II can lead to complete degradation of the antimicrobial effect of these peptides (Park, Yi, 2000). Burofin II can kill *E. coli* without losing the cell membrane and shows to decrease the number of viable cells (Park, Kim, 1998).

Ostricacins are AMP, which could be isolated from ostrich leukocytes. These AMPs have bacteriostatic effect against Gram-negative bacteria via the interactions between the peptide and cytoplasmic processes; such as DNA and protein synthesis and enzymatic activities. These peptides are made of 36-42 amino acids. This class of AMPs cause minor abnormalities in the integrity of the cytoplasmic membranes, allowing them to cross the cytoplasmic membrane, enter the cytoplasm, and interact with the bacterial DNA (Sugiarto and Yu, 2007). By binding to DNA, they could inhibit the activity of DNA in bacterial cells (Ganz et al., 1985). From this family, Ostricacin-1 (Seq: LFCRKGTCHFGGCPAHLVKVVGSCFGRACCKWPWDV) and Ostricacin-2 (Seq: APGNKAECEREKGYCGFLKCSFPFVVSCKSRFFFCCKNIW) are two of the known members for their antibacterial effects.

Indolicidin (Seq: ILPWKWPWPWRR) is a 13 amino acid peptide, derived from the cytoplasmic granules of bovine neutrophils (Marchand et al., 2006). This peptide belongs to the cathelicidin family, as a tryptophan/proline-rich AMP. This peptide has antibacterial properties against Gram-positive and -negative bacteria. In high concentrations, Indolicidin could increase the permeability of the bacterial cell and exclusively inhibits the DNA biosynthesis by reaching the cytosol (Hsu et al., 2005, Subbalakshmi and Sitaram, 1998). Earlier studies have shown that this peptide has a high affinity toward ds [AT], ds [CG], and ds [AG] and a low affinity to ds [GT]. Also, the binding affinity of peptides to DNA duplex is higher than to the single-strand DNA (Fimland, Eijsink, 2002, Ghosh et al., 2014, Subbalakshmi and Sitaram, 1998). Indolicidin is effective on *E. coli* (MIC 12.5 μM), but has a stronger effect on bacteria such as *Staphylococcus aureus* (MIC 0.2–0.4 μM) and *Bacillus cereus* (MIC 0.8 μM) (Brahma et al., 2015, Falla et al., 1996).

CP10A (Seq: ILAWKWAWWAWRR) is a member of the cathelicidin family, a 13 amino acid peptide derived from indolicidin, which has alanine residues substituted for proline residues with the improvement of antibacterial activity against Gram-positive bacteria. CP10A Inhibits DNA and RNA biosynthesis (Fimland, Eijsink, 2002, LUO, 2008). Studies have shown that in CP10A-treated bacteria, peptides affect thymidine, histidine, and uridine incorporation into DNA and RNA.

Tachypleisin (Seq: KWCFRVCYRGICYRRRCR) is a cationic peptide, derived from the hemocytes of horseshoe crab (*Tachypleustridentatus*). Tachypleisin has a unique antiparallel β-sheet construct for binding to the DNA duplex. This peptide is made of 17 residues and provides broad-spectrum and potent antimicrobial activity against many bacterial pathogens, especially multidrug-resistant (MDR) isolates in low concentrations. However, the clinical application of this peptide is limited due to its highly hemolytic effects (Nakamura et al., 1988, Yonezawa et al., 1992). Tachypleisin I is effective on Gram-positive and -negative bacteria, viruses, and yeasts (Erdem Büyükkiraz and Kesmen, 2022).

As the first step, tachypleisin can interact with lipid membranes and enhance the permeability of bacterial membranes, contributing to bacteria death. In the second step and upon entering the cell and binding to DNA, it could even lead to cell death. **Microcins** are very small bacteriocins, composed of relatively few amino acids, produced by bacteria such as *Enterobacteriaceae*. These peptides are secreted under the conditions of inadequate nutrients and have a strong antibacterial effect on closely related organisms. Seven types of microcins including A, B, C, D, E, H, and J are classified according to their cross-safety, genetic and biochemical criteria. Microcin B17 (MccB17, Seq: VGIGGGGGGGGGSCGGQGGGCGGCSNGCSGGNGGSGGSGSHI) is a peptide produced by *E. coli* (Novikova et al., 2007b). Microcin B17 inhibits DNA topoisomerase II or gyrase (like quinolone antibiotics) (Blond et al., 2000) and leads to the fragmentation of bacterial chromosomes (Herrero and Moreno, 1986, Vizán et al., 1991).

Microcin J25 (MccJ25, Seq: VGIGTPIFSYGGGAGHVPEYF) can inhibit transcription by affecting bacterial RNA polymerase. Previous studies have indicated that suppression of transcription is induced through NTP uptake or NTP attachment via RNA polymerase inhibition. Transcription suppression occurs by attachment of MccJ25 within the RNAP secondary channel (Bayro et al., 2003, Wang et al., 2020). This peptide could act against a variety of gram-negative bacteria from the Enterobacteriaceae family; including *E. coli*, *Salmonella* sp. and *Shigella* sp. (Salomon and Farías, 1992).

PR-39 (Seq: RRRPRPPYLPRPRPPFFPPRLPPRIPPFPFRPPFRFP) is a linear proline-rich cathelicidin, isolated from the porcine small intestine, which has an inhibitory effect on Gram-negative and -positive bacteria. This AMP not only promotes cell death via membrane disruption, but also could translocate across the cell membrane and disrupts some of the cellular activities; including synthesis of DNA and protein (Agerberth et al., 1991). PR-39 could affect various cellular processes like regulation of apoptosis, promoting the repair of the wound, inhibition of NADPH oxidase activity, induction of angiogenesis, and neutrophil chemotaxis (Zanetti, 2004). All of these multiple actions indicate the active involvement of catalytidine peptides, such as PR-39, in regulation of the antimicrobial host defense (Gallo et al., 1994). Examination of PR-39 peptide proteomic microarrays has shown that this peptide can inhibit some metabolic pathways; such as coenzyme transport and metabolism, nucleotide transport, and metabolism (Sang and Blecha, 2009, Zanetti, 2004). This peptide is structurally similar to the calcitonin (CGRP) and amylin gene peptides. Also, it has similarities with β-defensins and participates in the mechanisms of bacterial membrane

penetration. This peptide is present in various tissues; such as the adrenal medulla, brain, kidneys, and lungs. This peptide is involved in behavioral and biological

reactions, like inhibition of drinking, nutrition, and appetite for salt (Samson, 1999, Samson et al. , 1998).

Table 1 Cellular targets of AMPs and some of the peptides that affect these targets

Intracellular targets	Examples of AMPs	Reference
RNA	DM3 Bofurin II HNP-1 CP 10A Microcin j25 BF2-C	(Friedrich et al. , 2001, Le, Fang, 2017a, Le et al. , 2016, Pardi et al. , 1992, Park et al. , 2000, Yuzenkova et al. , 2002)
	DM3 CP 10A Microcin j25 Ostricacin-1 Ostricacin-2 PR-39 HNP-1 Bofurin II BF2-A Indolicidin Oabac5mini Tachyplesin	
Ribosome	DM3 Bac7 1-35 Apidaecin Hb1a	(Benincasa et al. , 2010, Le, Fang, 2017a, Le, Gudimella, 2016)
Protein biosynthesis and metabolism	CP10A Pleurocidin PR-39 HNP-1 DM3 Magainin 1	(Fimland et al. , 2002, Le, Gudimella, 2016, Matsuzaki et al. , 1996, Pardi, Zhang, 1992)
	Indolicidin HD5 PR-26 PR-39 Diptericin Microcin J25	
Cell division	Mersacidin Nisin Plectasin	(Mor et al. , 1991, Water et al. , 2015, Wiedemann et al. , 2001)
Chaperone	Pyrrhocoricin Bac7 1-35 Drosocin Abaecin Oncocin Ixodidid ApidaecinHb 1a	(Benincasa, Pelillo, 2010, Knappe et al. , 2011, Le, Fang, 2017a, Lele et al. , 2017)

Seminalplasmin

(SPLN, Seq: SDEKASPDKTRFSLSR YAKLANRLANPKLLETFLSKWIGDRGNSV) is an AMP that inhibits RNA in *E. coli* and RNA polymerase I and II in yeast. This peptide is a 47 residues AMP isolated from bovine seminal fluid. Also, it is active against pathogens; such as bacteria, and fungi (Shivaji, 1988).

AMPs with inhibitory effect on protein synthesis

Some AMPs can suppress protein synthesis in bacteria. For protein synthesis, DNA is first transcribed into mRNA, then mRNA is translated. AMPs can interfere with protein biosynthesis by inhibiting any of these stages. Several AMPs including Drosocin, Oncocin, Ixodidid could target protein synthesis. Some of these types of peptides are discussed below.

Oncocin is a class of proline-rich AMPs analogs from the *oncopeltus* antibacterial peptides that were initially isolated from *Oncopeltus sfasciatus*. This peptide (Seq: VDKPPYLPRPRPRRIYNR) has a high antibacterial effect on Gram-negative bacteria at a minimal inhibitory concentration (around 1 µg/mL). Oncocin inhibits protein synthesis by binding to the bacterial ribosome (Mattiuzzo et al. , 2007). Also, previous studies have shown that Oncocin can form a complex with DnaK, as a chaperone, and inhibit protein folding (Agerberth, Lee, 1991).

Bactenecin 7 (Bac 7, Seq: RRIRPRPRLPRPRPLPFPRPGPRPIPRPLPFPRPGPRPIPRPLPFPRPGPRPI PRPL) is an AMP with 60 residues that has been isolated from large granules of bovine neutrophils. This peptide is rich in proline and arginine. This peptide has been shown effective on Gram-negative bacteria by inhibiting DnaK and ribosomal proteins (Schnapp et al. , 1996).

Microcin C7 (MccC7) is an anti-microbial peptide that suppresses protein expression without influencing DNA replication or RNA transcription (Garcia-

Bustos et al. , 1985, Guijarro et al. , 1995). Microscine C7 can enter bacterial cells with the help of membrane transducers; including YejABEF (Novikova et al. , 2007a), then it would be processed by intracellular proteases. These actions eventually cause protein synthesis inhibition by releasing Asp-NH-adenosine monophosphate (Meditskaya et al. , 2006, Roush et al. , 2008).

AMPs with inhibitory effect on protein-folding and bacterial proteases

Chaperones are a group of proteins that promote the folding of newly expressed polypeptide chains and proteins in the cell, and support the refolding of misfolded proteins and protein trafficking. Chaperones play an important role in preventing the accumulation of proteins. Also, they are involved in the assembly and transport of newly synthesized polypeptides (Georgopoulos and Welch, 1993). Previous studies have declared that some AMPs can interfere with chaperones, which leads to their inactivation and cell lysis. It has been indicated that a group of proline-rich AMPs; including pyrrhocoricin and apidaecin, could have inhibitory activity on bacterial chaperones. Also, some peptides can disrupt the pathogenesis of bacteria by inactivating some secreted proteases (Le, Fang, 2017a).

Pyrrhocoricin is a proline-rich AMP with 20 residues that could be isolated from *Pyrrhocoris apterus* with an inhibitory effect on both Gram-negative and -positive bacteria by interacting with heat shock protein DnaK (Cociancich et al. , 1994). Only the N-terminal region of pyrrhocoricin is required to suppress the ATPase activity of DnaK, while the C-terminal region of this peptide supports its cell entry and suppresses the ATPase activity of the chaperone, thus preventing the chaperone-assisted protein folding.

By inactivation of DnaK, this peptide causes the folding of newly synthesized proteins and refolding of the misfolded proteins (Cociancich, Dupont, 1994). Pyrrhocoricin can also interact with the GroEL chaperone in a non-specific manner, while the interactions with DnaK is specific. The activity of this peptide against Gram-negative *P. aeruginosa*, *E. cloacae*, *E. coli* and some Gram-positive

ones like *B. megaterium* and *M. luteus* has been reported by earlier studies (Bernini et al., 1995, Kolda et al., 2020, Rosetto et al., 1996).

Apidaecins are a group of proline-rich AMPs with 18 to 20 residues expressed by insects (Casteels and Tempst, 1994). They are effective against many Gram-negative bacteria without any significant toxicity on human cells (Li et al., 2006, Singh et al., 2002). Apidaecin (Seq: GNNRPVYIPQRPHPRI) that could be harvested from lymph fluid of *Apis mellifera*, has an inhibitory effect on Gram-negative and -positive bacteria by suppressing DnaK and GroEL (Otvos et al., 2000, Troxler et al., 1990). From this family of AMPs, Apidaecins Ia, Ib and II are heat-stable and non-helical ones expressed by *A. mellifera* upon bacterial infection (Casteels et al., 1989).

Drosocin (Seq: GKPRPYSRPTSHRPIRV) is a glycosylated AMP with 19 residues, which is synthesized in the hemolymph of *Drosophila melanogaster* upon the bacterial challenge. Drosocin is an arginine and proline-rich AMP that contains an O-glycosylated threonine residue, with antibacterial effect on Gram-negative bacteria like *S. enterica* subsp. *Enterica* serovar Typhimurium and serovar Typhi, and *E. coli*, by entering the cells and inhibiting the DnaK chaperone, which could affect the protein folding (Bulet et al., 1993, Lele et al., 2015).

Lipid II binding peptides

Despite many antibiotics that show their effect by binding and inhibiting enzymes involved in PGN synthesis, some AMPs attach to the peptidoglycan precursors and interfere with their enzymatic activities; leading to the suppression of peptide expression by sterically suppressing the activity of enzymes (Mahapatra et al., 2015). Among these targets, Lipid II, which is a membrane-anchored cell-wall precursor, is regarded as a critical target that has been mentioned to have a good potential for suppressing bacterial infection (Breukink and de Kruijff, 2006). In this section, we provide a brief list of some peptides, such as members from lantibiotic, that have proven to be efficient against lipid II.

Mersacidin (Seq: CTFTLPGGGGVCALTSEIC) is a lantibiotic AMP with 20 amino acids. This peptide is ribosomally expressed by *Bacillus* sp. strain HIL Y-85, 54728. Mersacidin is an uncharged molecule forming four intramolecular thioether bridges, which confer a globular shape. This peptide acts by complexing the sugar phosphate head group of lipid II as a peptidoglycan precursor. Accordingly, this peptide could inhibit the transglycosylation reaction of peptidoglycan biosynthesis (Brötz et al., 1998, Sass et al., 2008).

Nisin (Seq: IOAIULAAPGAKAGALMGANMKAAAANASHIVUK) is a lantibiotic AMP, expressed by a group of bacteria. This compound belongs to *Lactococcus lactis* and suppresses a wide variety of Gram-positive bacteria (Wiedemann, Breukink, 2001). This peptide contains several unusual amino acids, because of the post-translational modifications. Nisin could suppress bacterial growth by making pores on the cell membrane and interrupting cell-wall biosynthesis through specific interaction with lipid II. The N-region of Nisin is very important for attaching to the lipid II, as a cell wall precursor, by electrostatic interactions between negative and positive charges on the cell wall (Alkhatib et al., 2014, Najmi et al., 2020, Yamauchi et al., 2003).

This peptide could act against a wide range of Gram-positive bacteria; such as *S. aureus*, *S. pyogenes*, *L. monocytogenes*, and *C. botulinum*, as well as, Gram-negative bacteria including *E. coli*, *Salmonella enterica* subsp. *Enterica* serovar Typhimurium, *Klebsiella* spp., *Aeromonas* spp., *Neisseria* spp., and *Yersinia enterocolitica* (Rodríguez, 1996).

Plectasin (Seq: GFGCNGPWDEDDMQCHNHCKSIKGYKGGYCAKGGFVCKCY) is composed of 40 residues and is a member of the defensins. This peptide is the first defensin isolated from a fungus, the saprophytic ascomycete *Pseudoplectanigrella*. This peptide exhibits strong bactericidal effects on several Gram-positive pathogens; such as *Staphylococcus*, *Streptococcus*, *Corynebacterium*, and *Enterococcus*. For example, MIC of this peptide against Gram-positive bacteria like *S. pyogenes* (MIC 0.015 IM), *Corynebacterium jeikeium* (MIC 0.2 IM), *Corynebacterium diphtheriae* (MIC 0.5 IM), and MRSA (MIC 0.9 IM) shows a good efficiency and high potential for therapeutic applications (Mygind et al., 2005).

This peptide acts by coalescing with the pyrophosphate moiety of the cell wall precursor, lipid II; therefore, it interferes with bacterial cell wall biosynthesis. However, plectasin derivatives can be effective on both cell membrane and cytoplasmic targets (Li et al., 2017).

hBD3 (Seq: GIINTLQKYYCRVRGGRCVLSCLPKKEEQIGKCSRGRKCCRRKK) or Human β -defensin 3 is a highly charged (+11) cationic AMP, expressed by neutrophils and epithelial cells. This peptide has an antimicrobial effect on a broad range of pathogens; such as multidrug-resistant *S. aureus*. Based on the earlier studies, suppression of cell wall biosynthesis is a major activity of hBD3 by directly interfering with the membrane-bound cell wall precursor lipid II. Increased acylation reduces the bacterial membrane fluidity and inhibits resistance to CAMPs by preventing peptide insertion (Escobar-Salom et al., 2022).

Lipopolysaccharide-binding AMPs

Inflammation, which could be caused by LPS, is a critical issue along with the infection process (Johari et al., 2021, Maghsood et al., 2020). In addition to the broad-spectrum antibacterial effect of AMPs, these peptides are also anti-inflammatory agents. Neutralization of LPS, an endotoxin from Gram-negative bacteria, is an important activity. Some AMPs can penetrate the cell wall barrier by neutralizing LPS to kill the Gram-negative bacteria that can cause infection. Conversely, AMPs could also reduce the inflammatory response by inhibiting the production of inflammatory cytokines by neutralization of LPS (Sun and Shang, 2015). Increased acylation reduces bacterial membrane fluidity and increases the resistance toward cationic antimicrobial peptides (CAMPs) by preventing the peptide insertion. Changes in Lipid A could increase CAMP resistance in bacteria, which has been observed in some gram-negative bacteria, including *P. aeruginosa*. This has been shown to increase the CAMP resistance in a PhoP-dependent manner, in response to low levels of Mg^{2+} (Ernst et al., 1999, Guo et al., 1998). PhoP-PhoQ virulence regulators in *Salmonella* bacteria could cause resistance to host cationic CAMP upon infection and Mg^{2+} or Ca^{2+} restriction (Guo, Lim, 1998). CAMP resistance happens because of multifactorial factors. In *Legionella*, PgtE is an outer membrane CAMP protease and waaP is effective in altering the lipopolysaccharide core. In *Salmonella*, CAMP resistance is regulated by the pagP gene with PhoPQ. The PmrAB gene is a two-component system that regulates PmB resistance which increases amino arabinosis (Guina et al., 2000, Gunn and Miller, 1996).

Cecropins (A, B, and D) are linearly positive peptides. Cecropins A and B are isolated from Boman's group from the hemolymph of the giant silk moth. They can lead to cell lysis by forming membrane channels. These AMPs are more effective on Gram-negative bacteria. Cecropin B is 40 times more effective against *E. coli* (MIC 1.7–3.3 μ M) than *S. aureus* (Hancock, 2001, Moore et al., 1996).

MBI-27 (formerly CEME, Seq: KWKLFKKIGIGAVLKVLTTLGLPALIS) and **MBI-28** (Seq: KWKLFKKIGIGAVLKVLTTLGLPALKLTK) are peptides harvested from parts of silk moth cecropin and bee melittin. They have both anti-endotoxic and anti-bacterial effects against Gram-negative bacteria. However, peptide MBI-28 is more powerful than MBI-27 (Piers et al., 1994). The binding of AMP to endotoxin and its neutralization prevents the uncontrollable activation of inflammatory responses by reducing the related cytokines; such as IL-1 and TNF (Crittenden et al., 2005, Sun and Shang, 2015).

CAP18 is 18-kDa cationic antimicrobial protein that was originally identified from rabbit leukocytes due to its capacity to bind and inhibit various activities of lipopolysaccharide (LPS). CAP18 (Sun and Shang, 2015) has been reported to have therapeutic potential for conditions related to increased levels of LPS. hCAP18 is found in humans, and its carboxyl-terminal antibacterial peptide, which is known as LL-37, (Seq: LILGDFFRKSKEKIGKEFKRIVQRIKDFLRNLLVPRTES37) has been identified to bind LPS and neutralize its biological activities (Nagaoka et al., 2002).

Inhibition of cell-division

FtsZ is one of the main factors of the cell division process in bacteria. This factor is necessary for Z-ring formation in the bacterial cell division. Accordingly, it is regarded as an attractive target for the development of new antibacterial drugs. Suppression of Z-ring and septum formation could lead to bacterial filaments disruption and eventual cell death (Lutkenhaus, 1990). Earlier studies have demonstrated that a series of peptides could cause bacterial cell death via binding to FtsZ. Some of these types of peptides are discussed below:

MciZ is a 40 residues AMP, which acts during spore formation in *B. subtilis*, as an endogenous inhibitor for Z-ring formation in the mother cells, by perturbing the assembly of FtsZ. This peptide binds to the C-terminal polymerization interface of FtsZ and inhibits its polymerization (Han et al., 2021, Ray et al., 2013).

CRAMP or cathelin-related antimicrobial peptide is a biological construct with 37 amino acid residues, necessary for the host defense response in mammals. CRAMP (16-33) with the sequence GEKLLKIGQKIKNFFQKL could inhibit the bacterial growth of *B. subtilis* and *E. coli* by targeting FtsZ and blocking the formation of Z-ring and FtsZ polymerization (Ray et al., 2014).

Edeine are polypeptide AMPs that have been harvested from *B. brevis*. Edeine could suppress the growth of *B. subtilis* bacteria by blocking Z-ring formation. Edeine has two subtypes; including edeine A and edeine B as biologically active (A1 and B1), and inactive ones (A2 and B2) (Shimotohno et al., 2010).

Kil is an AMP composed of 47 amino acid residues. This peptide could be isolated from phage λ , which can prevent cell division in *E. coli* by filamentation of bacterial cells. This peptide interacts with FtsZ-GDP and inhibits the overall GTPase activity, and could block the Z-ring formation (Chen et al., 2012, Hernández-Rocamora et al., 2015).

Resistance toward AMPs

Despite the effect of AMPs on microorganisms, some cases indicate resistance to peptides in bacteria, which could happen via various routes such as sensing systems, resistance by proteases, production of external AMP-binding molecules (trapping), modification of membrane and cell wall (surface remodeling), capsule

production (exopolymers), modulation of host AMP gene expression and the other possible ways (Moravej, Moravej, 2018).

In this regard, integration of molecules with positive charge on the surface of bacterial cells to reduce the interaction and binding of cationic AMPs is one of the common routes of resistance toward AMPs. Resistance to AMP in Gram-positive bacteria can occur due to the concatenation of positively charged molecules on the cell wall teichoic acids (TA). One example of such a defense is the activity of pagP gene in *Salmonella* that increases resistance toward the antibacterial activity of CAMPs. As an example of such a resistance, the *rep* gene in *L. pneumophila* has been determined by Robey et al. (Robey et al., 2001).

Regarding to quorum sensing methods against AMPs, PhoP-PhoQ virulence regulators in *Salmonella* bacteria causes resistance toward host cationic CAMP (Guo, Lim, 1998). Outer membrane (OM) changes and lipopolysaccharide (LPS) are mechanisms of resistance of gram-negative bacteria to CAMPs (Madanchi, Ebrahimi Kiasari, 2020a). A RosA and RosB proteins efflux pump/potassium antiporter system is a recently discovered mechanism of resistance toward CAMPs in *Yersinia* bacteria (Bengoechea and Skurnik, 2000).

In spite of all the probable microbial defensive mechanisms against AMPs, they seem to be more effective than the regular antibiotics due to their broad-spectrum activity. Another advantage of these AMPs compared to the conventional antibiotics is their immediate onset of killing the targets, along with respectively lower levels of resistance than regular antimicrobial agents (Moravej, Moravej, 2018). In recent years, so many studies have been performed regarding the mechanisms by which the pathogens act against AMPs, and increased knowledge about these activities have been of a great help to the scientists to find a solution for this issue. To overcome such a problem, scientists have come up with solutions; such as insertion or deletion or change of amino acids in the structure of AMPs, modifying biochemical characteristics; such as cationicity, hydrophobicity, and amphipathicity. Also, co-therapy using AMPs and regular antibiotics has showed promising results to reduce the resistance via their synergic effect (Amani, A Barjini, 2015, Mohammadi Azad et al., 2017, Mojsoska and Jenssen, 2015, Moravej et al., 2019).

Challenges of AMPs application

Prior to clinical application of AMPs, issues such as toxicity, hemolytic activity, immunogenicity, resistance, and the other potential downsides need to be considered (Moravej, Moravej, 2018). Some peptides could have toxic side effects on mammalian cells in the long-term application, or causing hemolytic activity (Lei, Sun, 2019, Starr et al., 2018). For example, Indolicidin indicates a broad spectrum of antimicrobial, but has shown some hemolytic activity which restricts its clinical use (Mirski et al., 2018). Considering these limitations, scientists have been working on modifying the structure of AMPs through bioinformatics and biotechnology methods, which has indicated to be helpful for both increasing their efficacy and reducing the undesired side effects.

CONCLUSION

The growing resistance toward several antibiotics, including extensively Drug-Resistant (XDR) and MDR, among various bacteria has become a concern in medical society, and this has made the treatment process very difficult. Increased drug resistance is faster than the discovery and approval of new antimicrobial agents. All of these issues has increased the need for the international community to find a new group of antimicrobials. AMPs are a group of the main candidates in the design of the new generation of antimicrobial agents. This has led to an increased proposal to study peptides and discovery of natural AMPs and designing effective treatments for patients. In this review, AMPs with intracellular targets were briefly discussed. These targets include DNA, RNA, protein biosynthesis, cell wall, and some other intracellular components. AMPs usually have several targets, rather than a single target. Despite the efforts to investigate AMPs with intracellularly targets, still more studies are required to be carried out.

Acknowledgments: The authors wish to thank Baqiyatallah University of medical sciences.

Conflict of interest: None to declare

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