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Antimicrobial Peptides in Microorganisms and Lower Eukaryotes: Diversity, Mechanisms, and Applications

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Abstract

The rapid emergence of multidrug-resistant (MDR) microorganisms has intensified the search for novel antimicrobial agents that can overcome the limitations of conventional antibiotics. Antimicrobial peptides (AMPs), evolutionarily conserved components of innate immunity, have emerged as promising alternatives owing to their broad-spectrum antimicrobial activity, low propensity for resistance development, and immunomodulatory functions. This review comprehensively examines the diversity, structural characteristics, mechanisms of action, and applications of AMPs, with particular emphasis on their therapeutic potential. AMPs are widely distributed across diverse organisms, including bacteria, fungi, mushrooms, plants, and invertebrates. Their key physicochemical properties, such as cationic charge, amphipathic nature, and structural diversity, are discussed in relation to antimicrobial efficacy. Their mechanisms of action primarily involve membrane-targeting processes, including barrel-stave, toroidal pore, carpet, and lipopolysaccharide-binding models. AMPs can also act through intracellular mechanisms by inhibiting nucleic acid and protein synthesis, disrupting enzymatic pathways, inducing oxidative stress, and interfering with cellular homeostasis. Structurally, AMPs are categorised into α-helical, β-sheet, extended, and cyclic classes, highlighting the relationship between molecular architecture and biological function. The review further summarises AMP diversity across taxa, including bacterial bacteriocins, fungal and mushroom peptides, plant cysteine-rich peptides, and major invertebrate AMP families. Their applications in medicine, agriculture, food preservation, and industrial biotechnology are also discussed. Despite their considerable therapeutic potential, challenges related to peptide stability, bioavailability, extraction, purification, large-scale production, and manufacturing costs continue to hinder clinical translation. Mushrooms are highlighted as particularly attractive and economically viable sources of natural AMPs due to their high protein content, relatively simple extraction procedures, low toxicity, and significant antimicrobial activity. Overall, this review highlights AMP sources, extraction strategies, mechanisms, applications, and translational prospects, emphasising sustainable and cost-effective natural sources for developing peptide-based therapeutics against MDR pathogens.

Major Findings: Mushrooms emerge as promising, safe, and economically viable sources for direct AMP extraction due to their high protein content, relatively simple extraction procedures, low toxicity, and significant antimicrobial activity.

Keywords: Antimicrobial Peptides, β-sheet, Bacteriocins, Cellular Homeostasis, Mushroom Peptides, Natural Antibiotics, Toxicity

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1. Introduction

The alarming global intensification of multidrug-resistant (MDR) bacterial strains, primarily driven by the overuse and misuse of conventional antibiotics, has become a critical public health challenge[1]. Pathogens such as *Staphylococcus aureus* and *Pseudomonas aeruginosa* are major contributors to hospital-acquired infections, posing serious risks, especially to immunocompromised patients[2]. For example, individuals with Cystic Fibrosis (CF) who suffer from chronic *P. aeruginosa* infections often develop resistance to key antibiotics such as aminoglycosides and ciprofloxacin. This persistent cycle of lung inflammation and disease is a leading cause of respiratory failure in late-stage CF. Similarly, the use of drug-resistant *Salmonella* strains has reduced the effectiveness of conventional antibiotic regimens for treating pediatric meningitis. In contrast, these regimens remain more effective for treating *E. coli* infections[3].

In response to this escalating crisis, alternative therapeutic agents with novel mechanisms of action are urgently needed. One promising avenue lies in the innate immune system, an ancient and widely conserved defence mechanism present across many biological systems[4]. This system enables organisms to respond swiftly to invading pathogens such as bacteria, viruses, fungi, and parasites[5].

Among the key effectors of innate immunity are Antimicrobial peptides (AMPs), short, naturally occurring peptides first identified in 1942[6]. These are evolutionarily conserved molecules of innate immunity and have appeared as promising alternatives because of their broad-spectrum antimicrobial activity and low propensity for resistance development. AMPs have since been recognised for their ability to eliminate a broad spectrum of pathogens[7]. The Antimicrobial Peptide Database (APD3), as reported in its 2016 release, catalogues over 2,600 AMPs, including 1,972

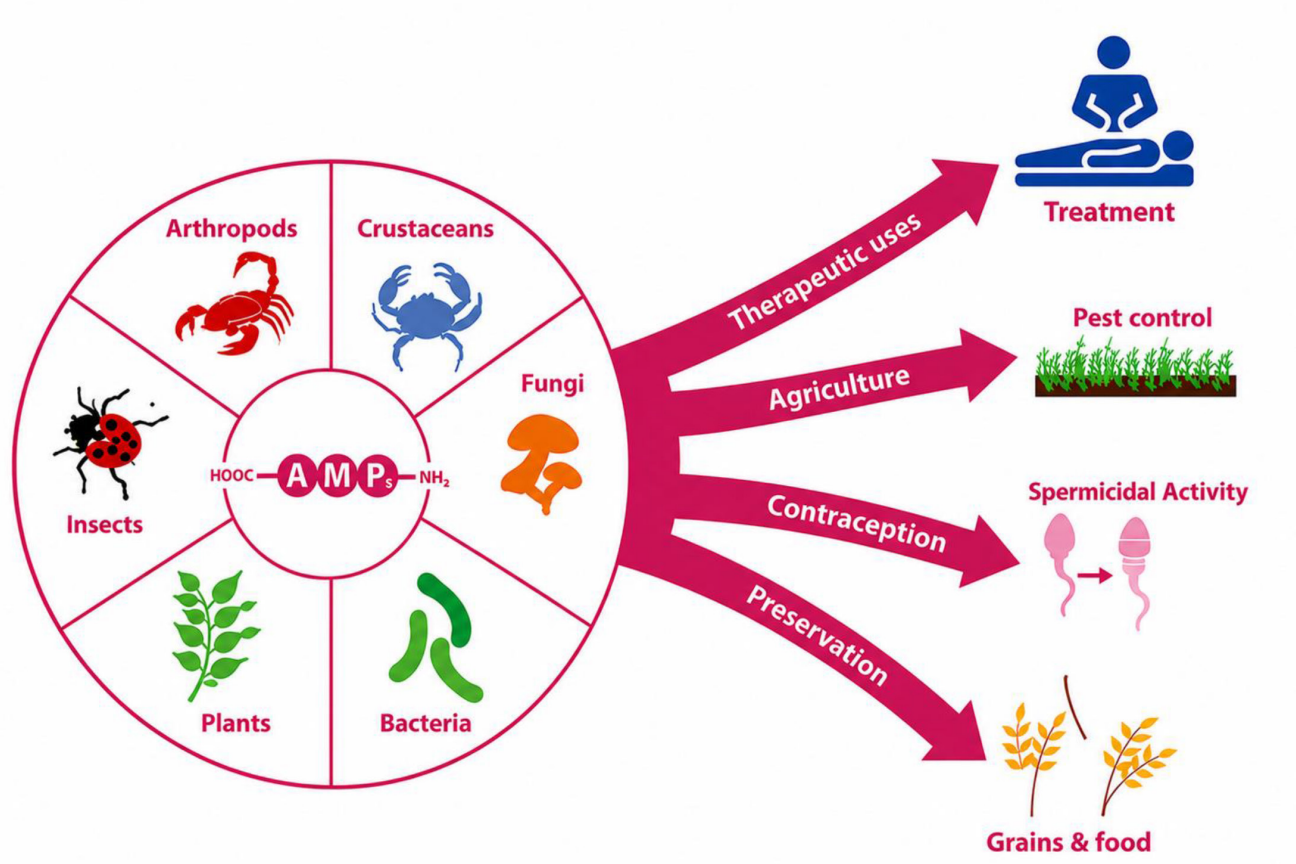


Figure 1. Schematic representation of AMPs, highlighting their diverse biological sources, including bacteria, fungi, plants, invertebrates and their wide-ranging applications in treatment, agriculture, contraception, preservation, and pest control.

from animals, 321 from plants, and 261 from bacterial bacteriocins[8]. As the contents of AMP databases are updated on an ongoing basis, subsequent releases have expanded these figures further, and readers are advised to consult the database directly for current counts. Unlike traditional antibiotics, AMPs can directly kill microbes without readily inducing resistance and are generally nontoxic to host cells at their effective concentrations (minimum inhibitory concentrations)[9].

In a significant study, researchers identified substantial levels of antibacterial peptides in heart tissue from slaughtered animals, including poultry and goats, highlighting the potential for large-scale, cost-effective extraction of AMPs from underutilised by-products[10]. Further investigations assessed the antibacterial efficacy of crude protein extracts derived from bovine cardiac tissue[11] and of serum samples subjected to additional SDS treatment[12], providing insights into their antimicrobial properties. Within this context, the present review explores diverse biological sources of AMPs, from prokaryotes to mammals, with an emphasis on their structural diversity, underlying mechanisms, and prospective applications in human health, agriculture, and biotechnology. Special attention is given to identifying viable, economically scalable sources of natural AMPs for therapeutic development.

2. Characteristic Features of AMPs

AMPs are evolutionarily conserved molecules present across most living organisms, ranging from unicellular organisms to higher plants and animals, as shown in Figure 1. These peptides play essential roles in innate immune defence against microbial invaders[13,14].

2.1 Size, Charge, and Structure

AMPs are typically short peptides composed of 10–100 amino acids with a low molecular weight (generally <30 kDa). They carry a net positive charge at physiological pH because of the prevalence of lysine and arginine residues[15]. This cationic nature allows them to bind to negatively charged microbial membranes via electrostatic interactions. Most AMPs are amphipathic with both hydrophobic and hydrophilic domains, enabling their insertion into lipid bilayers. Their secondary structures vary but are most commonly α-helices, β-sheets (often stabilised by disulfide bridges), or mixed/hairpin motifs[4,8].

2.2 Amphipathicity and hydrophobicity

An amphipathic nature is vital for their selective interaction with microbial versus host membranes. Hydrophobic residues interact with membrane lipids, whereas polar residues engage aqueous environments. An optimal hydrophobicity index (typically 40–60%) enhances antimicrobial activity while reducing cytotoxicity to host cells[16].

2.3 Tissue Localisation and Expression

In multicellular organisms, AMPs are predominantly localised on epithelial surfaces exposed to environmental microbes, such as the skin, lungs, oral mucosa, and urinary and reproductive tracts[17]. These peptides are either constitutively expressed or induced by microbial stimuli. For example, human β-defensins and cathelicidin (LL-37) are upregulated during infection via Toll-like receptor signalling[18,19].

2.4 Mechanisms of Action and Broad-spectrum Activity

AMPs exert antimicrobial activity through various mechanisms, primarily by disrupting microbial membranes via models such as toroidal pore formation, barrel-stave, or carpet-like membrane disruption[20]. Some AMPs additionally compromise intracellular machinery by interfering with genetic material (DNA and RNA) or inhibiting protein synthesis pathways[8]. The engagement of multiple cellular targets complicates the emergence of resistant pathogen strains. AMPs show activity against a broad spectrum of organisms, including Gram-positive and Gram-negative bacteria, fungi, protozoa, and enveloped viruses. They are typically active at concentrations ranging from 0.1 to 100 μg/mL[15].

2.5 Synergistic and Immunomodulatory Roles

AMPs often act synergistically with other innate molecules such as lysozyme and lactoferrin[21]. In addition to their direct killing capacity, many AMPs modulate immune responses by recruiting immune cells, promoting wound healing, or dampening excessive inflammation[22]. The dual antimicrobial and

immunomodulatory functions of AMPs make them promising therapeutic candidates.

2.6 Cross-taxa Comparison

- Bacterial AMPs (e.g., bacteriocins): Usually, narrow-spectrum AMPs are involved in interbacterial competition. It is often post-translationally modified[23].
- Fungal and plant AMPs: Rich in cysteine residues with stable disulfide bonds. Defensin-type peptides are standard[24].
- Invertebrates: Exhibit highly diverse AMPs such as tachyplesins, penaeidins, and cecropins.

3. Mechanisms of Action and Structural Classes of AMPS

3.1 Mechanism of Action

Many AMPs exert their effects by disrupting microbial membranes through distinct biophysical models, such as in Figure 2. The key mechanisms of action are classified into membrane targeting and intracellular mechanisms as follows;

3.1.1 Membrane Targeting Mechanisms of AMPs

3.1.1.1 Barrel-Stave Model

Amphipathic peptides orient themselves perpendicularly into the lipid bilayer and oligomerise to form a transmembrane pore resembling a barrel. The peptide "staves" line the pore and create a channel through which ions and cell contents leak. This model, first proposed in early AMP studies, explains how peptides such as alamethicin form well-defined ion channels in membranes[15,25]. The resulting loss of ion homeostasis leads to cell death[26].

3.1.1.2 Toroidal Pore Model

Here, peptides also insert into the membrane but induce the lipid monolayers to bend continuously through the pore, so that both peptides and lipid head groups line the pore. In contrast to the barrel-stave model, the pore includes lipid molecules and is often described as a "wormhole" through the membrane. AMPs such as melittin form toroidal pores; the peptide-lipid arrangement causes curvature stress and transient channels in the membrane[25,27]. These pores are dynamic and can expand, leading to membrane disintegration if enough peptides aggregate[26].

3.1.1.3 Carpet Model (Detergent-like Mechanism)

Cationic AMPs accumulate parallel to the membrane surface, coating it like a "carpet" without initially being inserted deeply. Once a threshold concentration is reached, this peptide mixture disrupts membrane integrity in a detergent-like manner, leading to wholesale membrane destabilisation and micelle formation. The membrane is essentially disintegrated rather than pierced by stable pores. For example, cecropins can permeabilise membranes via this mechanism[28]. The carpet model explains the rapid lysis in which the cell membrane "boils apart" into vesicles, leading to cell death[15].

3.1.1.4 Lipopolysaccharide (LPS) Binding and Outer Membrane Disruption

Many AMPs selectively target Gram-negative bacteria by binding to LPS in the outer membrane. Sequestering LPS neutralises its endotoxin activity and destabilises the outer membrane structure. Certain AMPs like thanatin inhibit the LPS transport machinery, preventing proper outer membrane assembly[29,30]. By breaching the outer membrane or blocking its maintenance, these peptides render Gram-negative bacteria more susceptible to killing.

3.1.1.5 Membrane Thinning and Destabilisation

In addition to forming discrete pores, AMPs can disrupt membranes by altering lipid packing and membrane curvature. Even in the absence of stable pore formation, peptide binding can cause local membrane thinning, pessimistic curvature induction, or domain formation, thereby compromising barrier function[31]. This generalised membrane destabilisation results in leaky membranes and is often an outcome of the carpet mechanism or peptide-induced phase separation[32]. The net effect is the loss of membrane potential and entry of peptides into the cell. Notably, some peptides (e.g., melittin from bee venom) cause extensive membrane perturbation, leading to cell lysis without well-defined pore structures[33].

3.1.1.6 Cellular Uptake via Macropinocytosis

Certain AMPs (especially those with cell-penetrating peptide properties) can trigger their own uptake into eukaryotic or bacterial cells through energy-dependent endocytic pathways. For example, arginine-rich AMPs have been shown to induce macropinocytosis, a process

in which the cell membrane engulfs extracellular fluid and peptides into large vesicles[34,35]. While bacteria do not perform endocytosis, this mechanism is relevant for AMPs to target intracellular pathogens or cancer cells.

By exploiting macropinocytic uptake, AMPs or their analogues can cross cell membranes without immediately lysing them, and then escape endosomes to reach intracellular targets. This mode is akin to that of cell-penetrating peptides and has been used to deliver AMPs into host cells infected with pathogen[36]. In summary, macropinocytosis offers an alternative route for AMPs to breach cell membranes and function inside cells, complementing direct lytic pathways.

All these membrane-centric mechanisms result in the loss of membrane integrity and homeostasis. Whether through defined pores (barrel-stave, toroidal), detergent-like dissolution (carpet), or other destabilisation mechanisms, the common outcome is the leakage of ions and essential metabolites, leading to membrane depolarisation and cell death. Membrane-targeting AMPs act rapidly and are less dependent on specific metabolic processes, which is why bacteria struggle to develop resistance to membrane disruption[26,32]. These mechanisms underpin the potent, broad-spectrum activity of many AMPs against bacteria, fungi, and even enveloped viruses[37].

3.1.2 Non-membrane (Intracellular) Mechanisms of AMPs

In addition to membrane disruption, many AMPs can enter cells (or be actively transported into them) and interfere with vital intracellular processes, as illustrated in Figure 3. These non-membrane mechanisms include the following:

3.1.2.1 Inhibition of DNA/RNA Synthesis

Several antimicrobial peptides (AMPs) from prokaryotes and invertebrates inhibit nucleic acid synthesis by targeting DNA, RNA, or enzymes involved in transcription and replication. Among bacterial AMPs, microcin J25, a lasso peptide produced by *E. coli*, enters susceptible Gram-negative bacteria through specific membrane transporters and binds within the secondary channel of RNA polymerase, thereby blocking transcription elongation and preventing

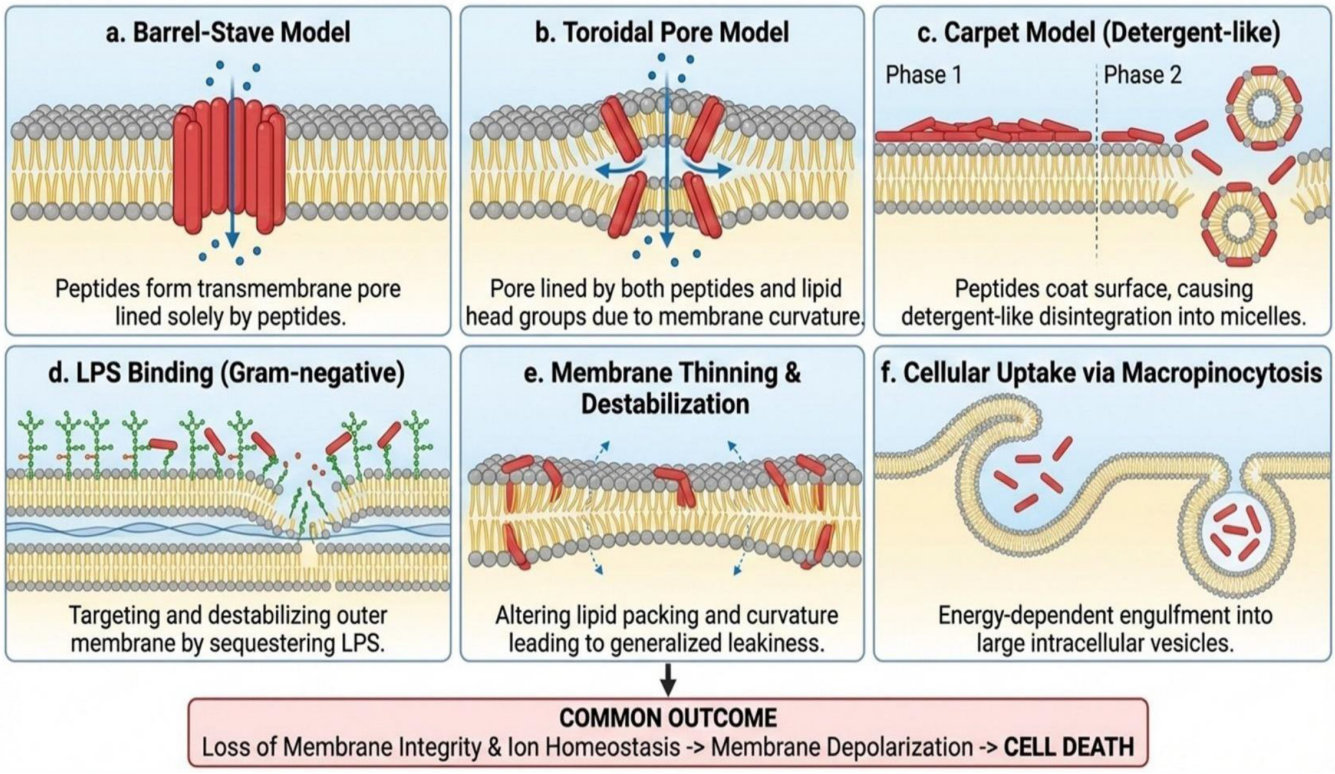


Figure 2. Various membrane-targeting mechanisms of AMPs.

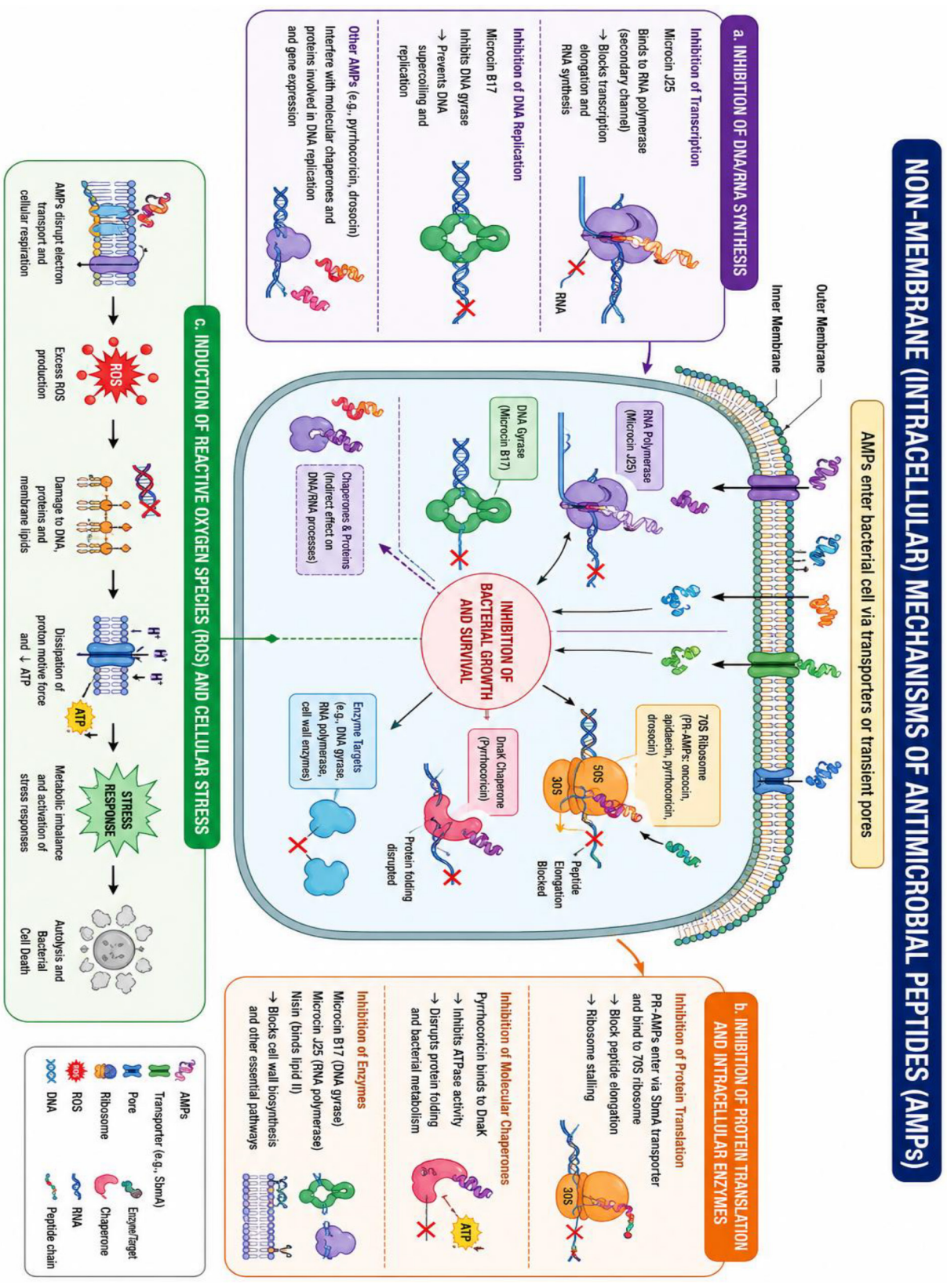


Figure 3. Intracellular (non-membrane) mechanisms of AMPs.

RNA synthesis[38]. Similarly, microcin B17 inhibits DNA gyrase, preventing DNA supercoiling and replication, ultimately leading to bacterial cell death. Certain insect-derived peptides, such as pyrrhocoricin and drosocin, also interfere with intracellular nucleic acid-related processes indirectly through inhibition of molecular chaperones essential for DNA replication and gene expression. By disrupting DNA replication, transcription, or associated regulatory proteins, these AMPs effectively suppress the expression of essential genes, resulting in inhibition of bacterial growth and eventual cell death[39].

3.1.2.2 Inhibition of Protein Translation and Intracellular Enzymes

Several AMPs exert their antibacterial activity by targeting intracellular proteins and enzymes essential for bacterial survival. The lantibiotic nisin, produced by *L. lactis*, binds to lipid II, thereby inhibiting peptidoglycan biosynthesis while simultaneously promoting membrane pore formation[40]. Proline-rich antimicrobial peptides (PR-AMPs) from insects, including oncocin, apidaecin, pyrrhocoricin, and drosocin, are transported into bacterial cells via the SbmA transporter, where they bind to the bacterial 70S ribosome and inhibit protein synthesis by blocking peptide elongation. Pyrrhocoricin additionally targets the molecular chaperone DnaK, disrupting protein folding and impairing bacterial metabolism[41]. Similarly, bacterial bacteriocins such as microcin B17 and microcin J25 inhibit DNA gyrase and RNA polymerase, respectively, thereby blocking DNA replication and transcription. Collectively, these AMPs interfere with multiple intracellular targets—including ribosomes, DNA replication enzymes, RNA polymerase, molecular chaperones, and cell wall biosynthetic proteins—resulting in effective inhibition of bacterial growth and survival[42,43]. Some peptides bind and inhibit enzymes involved in cell wall synthesis or metabolism. Nisin, for example, binds to lipid II (the peptidoglycan precursor), blocking cell wall biosynthesis in bacteria[44]. Cationic peptides can also destabilise bacterial protein complexes and induce the release of autolytic enzymes: θ-defensins (cyclic peptides in primates) attach to the cell envelope and trigger bacteria to activate their own cell-wall lytic enzymes, causing self-destruction[45].

3.1.2.3 Induction of Reactive Oxygen Species (ROS) and Cellular Stress

Several AMPs from prokaryotes and invertebrates induce bacterial death through oxidative and metabolic stress. Following intracellular entry, certain bacteriocins and insect-derived peptides disrupt electron transport processes and cellular respiration, resulting in excessive production of reactive oxygen species (ROS)[46]. The accumulated ROS damage DNA, proteins, and membrane lipids, leading to irreversible cellular injury. Some insect defensins have also been reported to interfere with bacterial redox homeostasis, thereby enhancing oxidative stress-mediated killing. In addition, intracellular AMPs can dissipate the proton motive force, disturb ATP production, and trigger metabolic imbalance, ultimately activating bacterial stress-response pathways and autolytic mechanisms[47]. The combined effects of oxidative damage, metabolic dysfunction, and impaired cellular homeostasis culminate in bacterial cell death[48].

These multi-targeted mechanisms enhance antimicrobial efficacy and substantially reduce the probability of resistance development. Consequently, AMPs derived from prokaryotes and invertebrates exhibit broad-spectrum antimicrobial activity through coordinated inhibition of nucleic acid synthesis, protein translation, enzymatic function, and cellular homeostasis, making them promising alternatives to conventional antibiotics[20,37].

3.2 Structural Classification of AMPs

AMPs are remarkably diverse in size and structure, yet their secondary structural motifs commonly categorise them as in Figure 4. The primary structural classes of AMPs include the following;

3.2.1 α-Helical Peptides

These AMPs are typically linear and unstructured in free solution, but fold into amphipathic α-helices upon contact with membranes. They often have a clear separation of hydrophobic and cationic faces in the helix, which facilitates membrane insertion. Many α-helical AMPs such as cecropins are found in invertebrates chiefly in insects[49]. The helical conformation favours the disruption of microbial membranes[50]. Such helical peptides tend to have a broad spectrum of bioactivity

and form the largest class of AMPs[15]. The efficacy of these peptides is often attributed to the helix's ability to span lipid bilayers, damaging bacterial membranes so as to leak the protoplasmic materials[51].

3.2.2 β-Sheet Peptides

These peptides are stabilised by one or more disulfide bonds that form β-strands and sheet-like structures. They often have rigid, globular folds. Defensins are the prime example found in plants and invertebrates. Defensins contain 3 or 4 disulfide bonds that lock them into a β-sheet-rich structure[52]. β-sheet architectures exert antimicrobial activity by permeabilising membranes and neutralising LPS[53,54]. β-sheet AMPs are typically short (under 50 amino acids) and often highly positively charged. Their disulfide-bonded structures confer stability under harsh conditions (e.g., protease resistance and heat stability), an advantage for therapeutic development[55].

3.2.3 Extended (Unstructured) Peptides

This category comprises antimicrobial peptides (AMPs) that do not adopt well-defined α-helical or β-sheet secondary structures because of their high content of specific amino acids such as proline, glycine, tryptophan, and arginine, which confer considerable conformational flexibility[56]. These peptides generally exist in an extended or random-coil conformation in aqueous environments and frequently undergo structural rearrangements upon interaction with microbial membranes or intracellular targets[57]. Despite lacking a stable folded structure, they exhibit potent antimicrobial activity through membrane translocation and interference with essential cellular processes.

Several prokaryotic and invertebrate AMPs belong to this structural class. Pyrrhocoricin, a proline-rich AMP isolated from the European firebug (*Pyrrhocoris apterus*), penetrates bacterial cells and binds to the molecular chaperone DnaK, thereby disrupting protein folding and inhibiting bacterial growth[57]. Likewise, apidaecin, a proline-rich peptide from the honeybee (*Apis mellifera*), traverses the bacterial membrane without causing extensive membrane disruption and inhibits intracellular protein synthesis by interacting with translation-associated factors. Drosocin, isolated from the fruit fly (*Drosophila melanogaster*), exhibits a similar intracellular mode of action by targeting bacterial protein-folding machinery and translation processes[56]. The structural flexibility of extended AMPs enables them to adapt to diverse molecular targets and, in many cases, adopt more ordered conformations only after binding to their intracellular receptors[35].

3.2.4 Cyclic Peptides

Cyclic AMPs have their peptide backbone cyclized (often via a peptide bond between the N- and C-termini, or through head-to-tail cyclisation, or via the formation of a loop by a disulfide or lactam bridge). Cyclisation often enhances stability against exopeptidases and can constrain the peptide in an active conformation. Examples span many life forms. In plants, cyclotides, such as kalata B1 (from *Oldenlandia affinis*), are circular peptides with multiple disulfide bonds; they are highly stable and can disrupt microbial membranes via a detergent-like mechanism. Bacterial cyclic AMPs include nisin, a linear peptide containing five intramolecular cyclic thioether rings (rings A, B, C, D, and E) formed by lanthionine bridges, that targets Gram-positive bacteria by binding lipid II and forming pores. Another bacterial example is microcin J25, a bicyclic lasso peptide (a loop with a tail threaded through) that, as noted, can inhibit RNA polymerase in target cells. Cyclic AMPs often have unique mechanisms due to their rigid structures; for example, the lasso structure enables them to withstand proteases and to thread into enzyme pockets[39]. The cyclic class also includes many bacteriocins produced by bacteria to kill other bacteria. Overall, cyclic AMPs demonstrate natural engineering for stability and specificity, and they inspire drug development due to their potent activity and resilience[55].

3.2.5 Distribution Across Taxa

Notably, these structural classes are found across virtually all living entities. Organisms have evolved convergently distinct peptide scaffolds as antimicrobial agents. For example, insects predominantly yield linear α-helical AMPs (e.g., dermaseptins and cecropins). Plants synthesise a variety of cysteine-rich peptides (many β-sheets and cyclic peptides such as plant defensins and cyclotides) to fight pathogens[58]. Even bacteria produce AMPs (bacteriocins), which can be α-helical, extended, or cyclic/lantibiotic in nature, to eliminate competitors[59]. This broad distribution

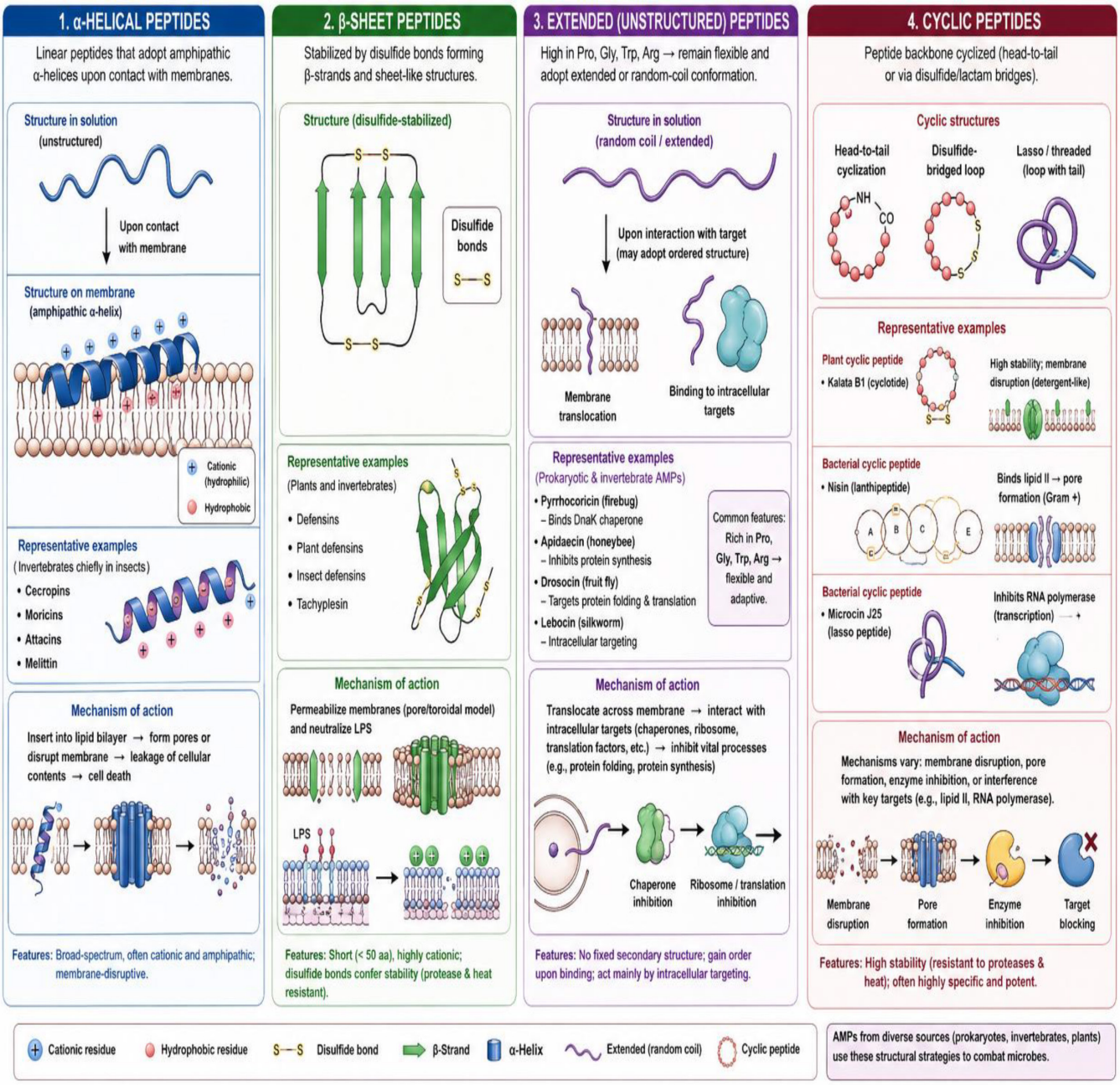


Figure 4. Structural classification of antimicrobial peptides. Representative 3D structures of the four major AMP classes.

highlights the fundamental importance of AMPs: they are ancient, conserved weapons in the evolutionary arms race against microbes. As of now, over 4380 AMPs have been catalogued from organisms ranging from single-celled microbes to humans (Figure 5). The structural classifications above provide a valuable framework for understanding how these diverse peptides achieve their effects. Each structure type confers particular properties, for example, helices for membrane insertion, sheets for stable folds, extended coils for multitarget flexibility, and cyclic loops for stability- yet all converge on the ability to kill microbes selectively. This combination of structural diversity and functional convergence is a hallmark of AMPs and underpins their potential as templates for the development of new anti-infective drugs[60].

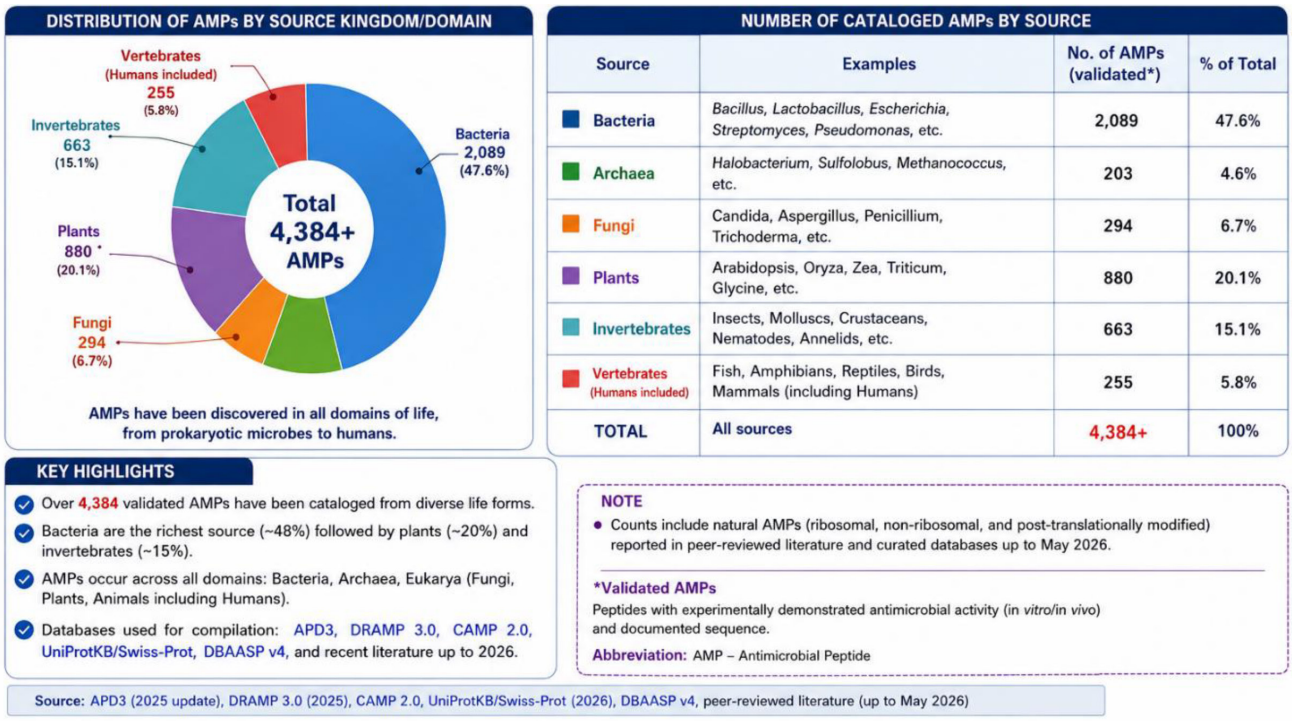


Figure 5. Global catalogue of AMPs (up to May 2026).

4. Diversity of AMPS

Figure 6 indicates the independent shapes of AMPs in bacteria, fungi, plants, and invertebrates. In bacteria, AMPs are represented by bacteriocins—further categorised into lantibiotics and non-lantibiotics in Gram-positive bacteria, and colicins and microcins in Gram-negative types. Fungal AMPs include defensins and peptaibols, while plants produce structurally diverse peptides such as thionins, defensins, lipid transfer proteins (LTPs), snakins, and hevein-like peptides. In invertebrates, specialised peptides have evolved in arachnids, crustaceans, and insects, reflecting the complexity of immune defence in these phyla.

4.1 Bacterial AMPs

Substantial advances have been achieved in discovering diverse antibacterial peptides, leading to the profiling of an extensive spectrum of bioactive compounds. Many *Bacillus* strains produce AMPs that significantly suppress the growth of pathogens such as *Salmonella, Shigella, E. coli*, and *S. aureus*[61]. In an earlier study, a *Bacillus*-derived AMP was shown to have activity against *S. aureus,* the *Alteromonas* sp. strain CCSH174, and *K. pneumoniae*. Further discoveries include an extracellular AMP sourced from *Propionibacterium jensenii,* and *Pseudomonas*-derived peptides were found to be effective against *Shigella, Salmonella, E. coli*, and *S. aureus*. In 2015, a notable peptide with remarkable biofilm-inhibitory properties was identified[62].

Scientists have also discovered glycocin, a tiny but powerful AMP produced by a thermophilic bacterium known for its ability to withstand high temperatures, and successfully produced the glycocin gene in *E. coli*[63]. This ever-changing environment of bacterial AMPs, enhanced by novel findings and combined potential, highlights the potential of these peptides in the continuous fight against bacterial infections. Bacteriocins, a distinct and well-studied subset of bacterial AMPs, have attracted increased attention, particularly those from *Bacillus, Pseudomonas*, and *Propionibacterium*.

Bacteriocins are well-known proteins or peptides produced by bacteria via ribosomal synthesis that either inhibit or kill closely related or rival bacterial species. Owing to their heat stability, nontoxicity, and protease sensitivity, they are becoming recognised as alternatives to conventional antibiotics and as natural food preservatives[64]. Nisin represents one of the

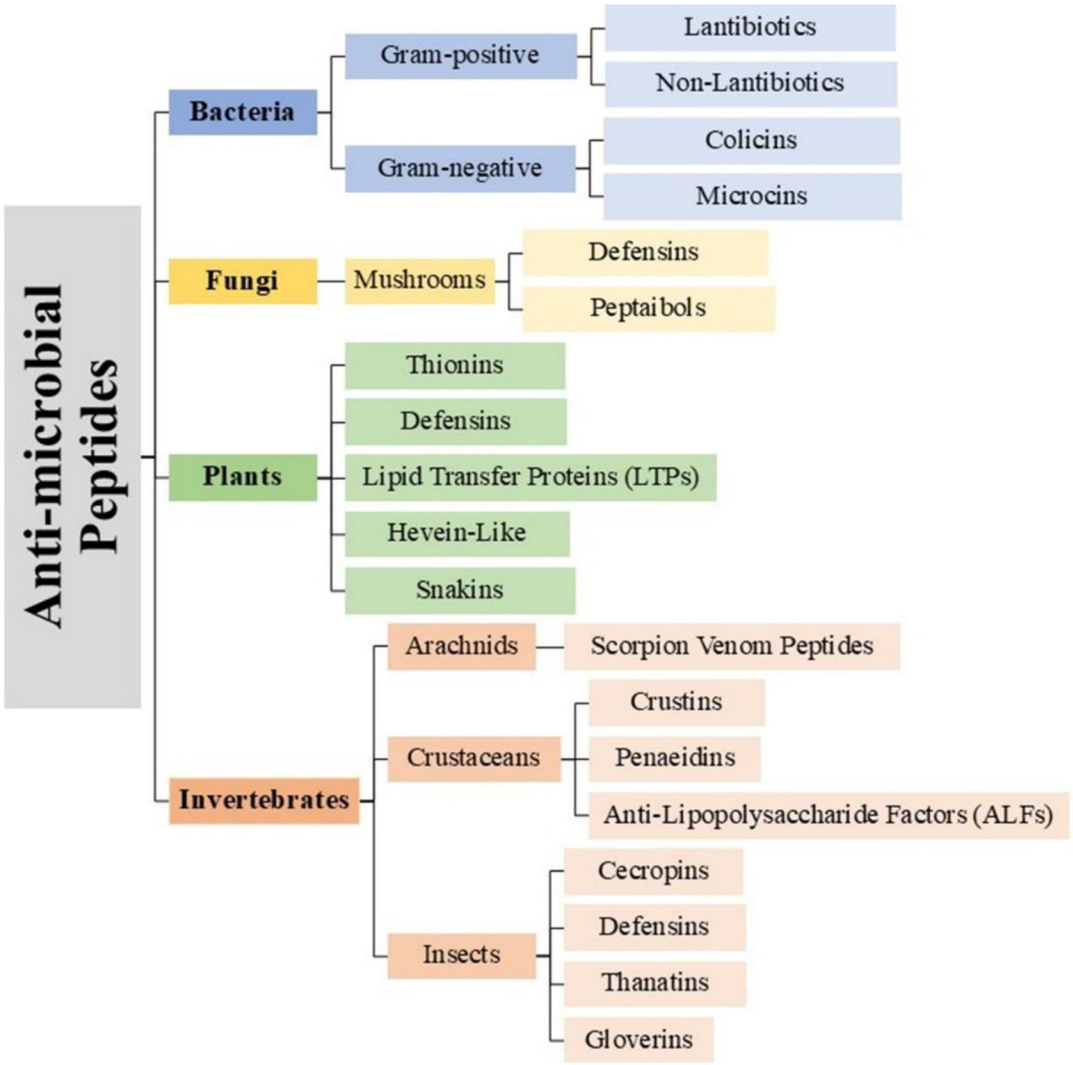


Figure 6. Biological sources and classification of AMPs. A schematic overview of AMP diversity across kingdoms. It highlights key peptide families derived from Bacteria (Bacteriocins), Fungi (Defensins/Peptaibols), Plants (Thionins/Snakins), and Invertebrates (Crustins/Cecropins), illustrating the evolutionary conservation of innate immunity.

most extensively studied bacteriocins, produced by specific strains of *L. lactis* and approved for preserving various foods, including poultry products[64]. Notably, not all peptides produced by ribosomal synthesis are considered bacteriocins, as they can serve a variety of purposes. Bacteriocins operate through diverse antimicrobial mechanisms, enabling them to target broad bacterial taxa, thereby reinforcing their applicability as antimicrobial therapeutics[65]. To date, a substantial number of bacteriocins from various bacterial origins, totalling over 1000, have been identified.

Based on the type of bacterium producing them, bacteriocins are broadly classified into Gram-positive and Gram-negative bacteriocins. Gram-negative bacteriocins are divided into two major groups: the small peptide-structured microcins and the larger protein-structured colicins, which are produced by Gram-negative bacteria such as *E. coli*. Similarly, Gram-positive bacteriocins are classified into two major groups: lantibiotics (Class I), which contain thioether-based ring structures such as lanthionine or β-methyllanthionine, and non-lantibiotics (Class II), which comprise unmodified antimicrobial peptides (AMPs)[66].

Another important group, Lactic Acid Bacteria (LAB), also produces three classes of bacteriocins[67], as described below;

(a) Class I comprises Subclass I-A and Subclass I-B bacteriocins, each with molecular masses of <5 kDa. (b) Class II consists of larger peptide bacteriocins with molecular masses of <10 kDa. (c) Class III bacteriocins are high-molecular-weight proteins (>30 kDa). Unlike the other classes, they exhibit antimicrobial mechanisms that do not conform to the conventional AMP classification.

Numerous LAB produce certain typical AMPs similar to pediocin, so-called pediocin-like AMPs, which are distinguished by their cationic, membrane-permeabilising qualities, including Leucocin A, Sakacin P, Curvacin A, and Mesentericin Y105. These peptides exhibit activity against a range of bacterial strains, including *Lactobacillus, Pediococcus*, *Enterococcus, Carnobacterium, Leuconostoc*, *Lactococcus, Clostridium*, and *Listeria*. As a result of their disruption of target cell membranes, cells rapidly deplete adenosine triphosphate (ATP)[68].

4.2 Fungal and Mushroom AMPs

The history of fungal use for health and healing is particularly deep-rooted in Asian regions, such as Japan, China, and Korea[69]. In 1928, Alexander Fleming's discovery of penicillin from *Penicillium notatum* established an era for research into fungal-derived antibiotics, including antimicrobial peptides. A wide range of AMPs is produced by both types of fungi (traditional moulds and mushrooms), thereby generating a distinct variety of natural defence molecules as mentioned in Table 1.

Diverse AMPs have been discovered in several fungal species, including *A. giganteus*, *A. niger*, *Z. bailii*, *P. eryngii*, and *T. giganteum*. Extracts containing crude proteins from specific fungi in phosphate buffer have exhibited notable antibacterial activity[76]. Wild mushrooms collected locally have been found to possess antimicrobial activity against hospital pathogens, including a 44 kDa antibacterial protein identified in *Clitocybe sinopica*[77]. Wang *et al.*, have identified thirteen AMPs from various fungal species[8]. Fungal defensins, such as plectasin from *P. nigrella,* have shown efficacy against *S. pneumoniae* infections. Additionally, AMPs, such as those from *F. tricinctum*, target plant pathogens, including *F. oxysporum*. *Eurotium amstelodami* produces a newly identified defensin named Eurocin. These fungal defensins often work by binding to lipid II precursor molecules, thereby blocking cell wall synthesis[78].

Fungal and mushroom-derived AMPs may induce osmotic stress in microbial cells while also stimulating host immune responses against fungal pathogens. However, some fungi produce mycotoxins that pose significant health risks, including hepatic carcinogenesis and neurological disorders, highlighting the need for effective prevention and control strategies. Nevertheless, Sundaramoorthy and Sabarimanikandan reported that 10% TCA-precipitated proteins from the acid extract of the wild mushroom *Ganoderma lucidum* exhibited significant antibacterial activity against clinical isolates with minimal haemolytic activity[79]. Further investigation may provide valuable insights into the development of mushroom-derived AMPs.

Mushrooms contain a wide array of bioactive compounds with high therapeutic value. They yield a unique variety of peptides, known as mushroom bioactive peptides (MBAPs), which exhibit antihypertensive, antioxidant, and antimicrobial effects[80]. MBAPs are either extracted directly from mushrooms or generated by the enzymatic breakdown of mushroom proteins with specific enzymes into smaller fragments. Notably, the MBAPs included Cordymin from *Cordyceps militaris* and a 17 kDa antifungal peptide isolated from *Lentinus squarrosulus*. While their antimicrobial activity might lack strong specificity, their amphipathic and cationic characteristics enable them to bind effectively to microbial cell membranes that carry a negative charge[81]. Although the exploration of fungal and mushroom-derived AMPs is still in its early stages, their distinctive structures and low toxicity profile highlight their promise for use in medical treatments, farming, and food industry preservation.

4.3 Plant AMPs

Plants utilise a wide range of defence mechanisms to protect themselves from invading pathogens, including the use of secondary metabolites such as hydrogen peroxide, phenolics, terpenoids, alkaloids, polyacetylenes, phytoalexins, and tannins[24]. Furthermore, AMPs are immune proteins that are often cysteine-rich peptides (CRPs) stabilised by multiple disulfide bonds, thereby increasing their chemical and structural resilience. Wang *et al.*,[8] documented the discovery and characterisation of 321 plant-derived AMPs from various plant tissues.

Table 1. AMPs derived from fungi and mushrooms

Source	Protein	Sensitive Pathogen	Molecular Weight (Daltons)	References
C. sinopica	Antibacterial	*S. aureus*	44,000	[70]
Marine bacterium	Antibacterial	*S. aureus*, *P. aeruginosa*	90,000	[71]
Cordyceps sinensis	CS-AMP/Cordymin-like	*B. subtilis*, *S. aureus*	35,000	[72]
Bullfrog	Ranalexin/Gaegurin	Broad-spectrum bacteria	1,865	[73]
Bullfrog	Ranalexin/Gaegurin	Broad-spectrum bacteria	3,691	[73]
Scylla serrata	Scyllin/ Antilipopolysaccharide factor	*Vibrio* spp., Gram-negative bacteria	10,800	[74]
Bombyx mori–I	Cecropin/ Moricin	Gram-positive/Gram-negative bacteria	5,500	[75]
Bombyx mori–II	Cecropin/Moricin	Gram-positive/Gram-negative bacteria	4,500	[75]
Tricholoma giganteum	Trichogin	*Fusarium* spp.	27,000	[69]
Polyporus alveolaris	Alveolarin	Antifungal/Ribosome-inactivating	28,000	[69]
Pleurotus eryngii	Eryngin	*Fusarium* spp., *Mycosphaerella*	10,000	[69]
Lyophyllum shimiji	Ls-AMP (Antifungal protein)	*Physalospora*, *Arachis*	20,000	[69]
Ganoderma resinaceum	Ganodermin-like Protein	*B. cereus, C. krusei, A. fumigatus*	~15,000	[69]
Mycena pura	MP-AMP/Lectin	*E. coli, B. cereus, C. krusei, A. fumigatus*	17,000	[69]
Russula fragilis	Lectin/AMP	*B. cereus, C. krusei*	-	[69]
Inocybe grammata	Lectin/AMP	*B. cereus, C. krusei*	-	[69]
M. pura	MP-AMP	*E. coli, Staphylococcus, Salmonella poona, E. coli, S. aureus, S. epidermalis, C. glabrata, C. parapsilosis, A. flavus, C. albicans, C. krusei, A. niger*	17,000	[69]
G. resinaceum	Ganodermin-like Protein	*Staphylococcus, S. poona, C. glabrata, C. parapsilosis, A. flavus, C. albicans, C. krusei, A. niger*	~15,000	[69]
Russula delica	Rd-Lectin	*S. aureus, M. luteus, M. flavus, B. cereus, C. albicans*	30,000	[69]
Calatia craniiformis	Calvatan/AMP	*S. aureus*	18,000	[69]
Cordyceps sobolifera	Cordysobin	*S. aureus*	31,000	[69]
Dictyophora indusiata	Ribonuclease /AMP	*S. aureus*	28,000	[69]
Oudemansiella mucida	Mucidermin	*S. aureus*	~12,000	[69]
Pholiota adipose	PA-Lectin/AMP	*S. aureus*	-	[69]
Pycnoporus cinnabarinus	Pycnoporin	*S. aureus*	-	[69]
Pycnoporus coccineus	Pycnoporin-like	*S. aureus*	-	[69]
Stereum ostrea	Stereum-AMP	*S. aureus*	-	[69]

These peptides are categorised into families such as thionins, plant defensins, lipid transfer proteins, hevein-type, knottin-type, systemin, and snakin[24].

4.3.1 Thionin Peptides

Thionins are cationic peptides with a molecular mass of approximately five kDa and contain either 6 or 8 conserved cysteine residues[82]. Studies have demonstrated their potent toxicity toward plant-pathogenic bacteria and fungi, and they are present in both monocots and dicots[24]. In both barley and wheat, a 47-amino-acid-long thionin peptide is present and exhibits antimicrobial activity against yeasts and both Gram-positive and Gram-negative bacteria[83].

Wheat thionin has antagonistic activity even at low concentrations against the human parasite *Leishmania donovani*. Research by Kragh *et al.*,[84] revealed that the sugar beet thionins AX1 and AX2 possess antifungal activity but are largely ineffective against bacteria. In contrast, Fabatin, a 47-residue peptide from fava beans, has antibacterial properties but does not inhibit the growth of *Candida* or *Saccharomyces* species[85]. Additionally, Ligatoxin B, a 46-amino-acid basic thionin with DNA-binding activity, was purified from the mistletoe *Phoradendron ligustrum*, whose antagonistic activity against invading pathogens has yet to be explored[86].

4.3.2 Plant Defensins

Like thionins, plant defensins are cationic, cysteine-rich peptides that comprise 45 to 54 amino acids, are stabilised with 4 to 5 disulfide bonds, and are prevalent in diverse plant tissues[24,87]. First identified in the seeds of wheat and barley[88,89], plant defensins have structures highly similar to those of thionins, which are distinguished by their unique disulfide bridge patterns[85]. Since then, researchers have reported the isolation of more than 100 plant defensins from a range of plant tissues, including leaves, tubers, flowers, pods, and seeds[24]. In addition to being present in various plant parts, these peptides are localised in tissues such as xylem, stomata, and parenchyma cells. Owing to their proven antibacterial and antifungal properties, they are now used in crop biotechnology to increase fungal disease resistance[87].

4.3.3 Lipid Transfer Proteins

Lipid transfer proteins (LTPs) are small, roughly nine-kDa peptides composed of approximately 90–93 amino acids, held together by eight disulfide-bridged cysteine residues. LTPs account for approximately 4% of total soluble protein in plants and exhibit antimicrobial activity against a broad spectrum of pathogenic organisms[90]. Depending on the source, LTPs vary in their ability to target different pathogens. Onion seed LTP, for example, is especially effective against fungi. In contrast, LTPs from radish seeds offer only moderate protection, whereas those from maize and wheat are mostly inactive in this regard. Some varieties also act against bacteria, all without damaging plant cells[90].

4.3.4 Hevein- and Knottin-type Antimicrobial Peptides

Chitin-binding proteins are prevalent in plants, with Hevein and Knottin being the most notable types. Chitin-binding proteins are widespread in plants, and Hevein and Knottin exhibit significant antifungal activity[87]. Studies have identified homologous peptides with relatively strong antimicrobial activity against amaranth and sweet pepper seeds. Knottins, on the other hand, are short peptides of 36-37 amino acids with six disulfide-linked cysteines that also exhibit robust antimicrobial activity against both bacteria and fungi[91].

4.3.5 Systemin

Produced by the proteolytic cleavage of the 200-amino-acid prosystemin, systemin is an 18-amino-acid peptide involved in a prominent role in defence signalling pathways as well as growth in *Solanaceae* plants[92]. In addition, studies have shown that mung bean peptides 0.5 to 5 kDa in size are linked to enhanced plant defence mechanisms[93].

4.3.6 Snakins

Extracted from potato tubers, Snakin-1 (63 residues) and Snakin-2 (66 residues) each contain 12 cysteine residues and show high antagonism against fungal and bacterial pathogens. Even at very low concentrations (1–20 μM), these peptides effectively aggregate both bacteria and fungi and show notable resemblance to thionins and α-hairpinins, underscoring the evolutionary links among cysteine-rich plant peptides[94].

Although plant AMPs play a crucial role in innate immunity of plants and hold significant potential for developing disease-resistant crops, their extraction and purification remain highly challenging. The presence of abundant phytochemicals, including chlorophyll, interferes significantly with downstream processing. Nevertheless, because plant AMP families exhibit diverse structural features and broad-spectrum antimicrobial activity, they are primary targets for sustainable agriculture. Ectopic expression or enhancement of AMPs in crops effectively confers resistance to major phytopathogens, thereby offering a viable alternative to chemical pesticides.

4.4 Invertebrate AMPs

In invertebrates, hemolymph and hemocyte granules contain AMPs[72]. Secretion of AMPs from the fat body into hemolymph is the dominant mechanism for curing injured or infected insects. In contrast, hemocytes are the primary source of immunity in horseshoe crabs[95]. The characteristics of AMPs vary with the invertebrate animals from which they are isolated and are grouped into different families, such as carcinine and crustin, defensin, attacin, cecropin, diptericin, tachylectin, coagulogen, tachyplesin, tachycitin, and tachystatin. Persulcatusin, an AMP derived from ticks (*Ixodes persulcatus*), has strong antibacterial properties against two clinically challenging pathogens, methicillin-resistant *S. aureus* (MRSA) and vancomycin-resistant *S. aureus* (VRSA)[96].

4.4.1 Crustacean AMPs

Crustacean-derived AMPs, identified across numerous species including crabs, shrimp, and crayfish, are designated "crustins" and are cationic peptides rich in cysteine residues[97]. Initial crustacean AMPs were a 6.5 kDa proline-enriched cationic protein and an 11.5 kDa antibacterial protein isolated from hemocytes of *Carcinus maenas*, the shore crab[98]. These proteins bear the alternative name 'carcinins' due to their origin in Carcinus species. Barreto C. *et al.*, described a novel type I crustin participating in antibacterial and antifungal defence mechanisms in the red claw crayfish *Cherax quadricarinatus*[99]. Hemocytes and hemolymph of *Tachypleus tridentatus*, the Japanese horseshoe crab, yield over 47 AMPs, which include coagulogen, tachylectin-1, tachystatin, and tachyplesin-I. Within this repertoire, the tachystatin family, localised in hemocyte small granules, stands out as exceptionally potent, with efficacy against fungi, Gram-negative bacteria, and Gram-positive bacteria[100].

Penaeidins constitute a peptide family derived from shrimp (*Penaeus* species) exhibiting antimicrobial efficacy primarily against Gram-positive bacteria and fungal organisms. *Litopenaeus vannamei*, the Pacific white shrimp, led to the discovery of the initial shrimp penaeidin[101]. Investigations documented comparable peptides from multiple penaeid shrimp species, including *Litopenaeus setiferus*[102], *Penaeus monodon*[103], and *Fenneropenaeus chinensis*[104]. Crustin Pm1, which predominates among penaeidins in *P. monodon* hemocytes, possesses an amino-terminal Gly-Pro-rich region and a carboxyl-terminal single whey acidic protein (WAP) domain[105]. Recombinant production of crustin Pm1 (14.7 kDa, predicted pI 8.3) yielded a peptide with antimicrobial capability against Gram-positive bacteria, notably exhibiting robust inhibitory effects on *S. aureus* and *S. iniae*[99]. Additionally, the anti-lipopolysaccharide factor (ALF) from shrimp functions as a highly cationic polypeptide exhibiting extensive antimicrobial activity across Gram-positive and Gram-negative bacteria (including vaginal pathogens), and fungal species[106].

4.4.2 Arachnid AMPs

Arachnid species, particularly scorpions, have evolved an extensive repertoire of venom peptides displaying multiple biological activities and pharmacological roles in response to environmental microbial threats[107]. These scorpion venom peptides fall into two primary categories: disulfide-bridged peptides (DBPs), which predominantly interact with ion channels integrated in cell membranes, and non-disulfide-bridged peptides (NDBPs), a more limited category characterised by diverse functional capabilities[108]. Typically, scorpion-derived DBPs are stabilised by three to four disulfide bridges and bind to multiple channel types within membranes, such as those permeable to Na^+, K^+, Ca^{2+}, and Cl^- ions, compromising normal cellular homeostasis and leading to cell death[107]. NDBPs constitute distinct scorpion venom peptide families that have been discovered and functionally profiled only in the last decade. Research interest in NDBPs has intensified because these molecules demonstrate a wide range of biological functions with multifunctional characteristics, including antimicrobial, anticancer, hemolytic, anti-inflammatory, immunomodulatory, and bradykinin-potentiating activities.

4.4.3 Insect AMPs

Insects represent the dominant and most species-rich arthropod group on Earth, encompassing in excess of one million described species and comprising over half of documented living organisms worldwide. These insect-derived AMPs offer potential utility in agricultural settings, control strategies for disease vectors, and medical applications[109]. Among the thoroughly investigated AMPs originating from insects are cecropins, defensins, thanatins, and gloverins.

4.4.3.1 Cecropins

The cecropin family stands as the most numerous group of linear insect AMPs, including hyphancin, enbocin, spodopsin, and cecropin-related peptides totalling over 60 characterised sequences. Characterised by an α-helical conformation, these peptides contain 29-42 residues, possess molecular weights of 3-4 kDa, and are found in insect hemolymph. These peptides lack cysteine residues and feature two discrete helical domains: a basic N-terminal region and an elongated hydrophobic C-terminal helix, joined by a compact hinge structure. The initial discovery of cecropins as inducible AMPs occurred through isolation from hemolymph of experimentally challenged diapausing pupae of the moth *Hyalophora cecropia* (*Lepidoptera*)[56]. Subsequently, over 150 insect AMPs have been described[109]. Most insect cecropins characteristically display a tryptophan residue at positions 1 or 2 and feature an amidated C-terminus; C-terminal amidation is crucial for cecropin binding to liposomes and may underlie their extensive antimicrobial spectrum[110].

However, the cecropins of mosquitoes (*Aedes albopictus* and *Aedes aegypti*) and cecropin D of the *Lepidoptera* silk worm moth (*Bombyx mori*) lack this tryptophan residue. However, mosquito-derived cecropins (*Aedes albopictus* and *Aedes aegypti*) and cecropin D from the Lepidopteran silk moth (*B. mori*) represent exceptions lacking this tryptophan. Findings indicated that cryptonin, a 24-amino-acid, 2,704 Da α-helical AMP from the adult Korean blackish cicada (*Cryptotympana dubia)*, manifested strong antibacterial and antifungal activities (MIC of 1.56-50 μg/ml), including potency against two antibiotic-resistant strains: methicillin-resistant *S. aureus* and vancomycin-resistant *Enterococci* (MIC of 25 μg/ml). Cecropins and cecropin-derived peptides also possess anti-parasitic capabilities (SB-37 and Shiva targeting Plasmodium and trypanosome), anti-HIV properties, anticancer activities, and anti-inflammatory effects (papiliocin)[109].

4.4.3.2 Defensins

Insect defensins comprise a widely distributed family of small (~4 kDa), cationic/basic AMPs consisting of 36 to 46 amino acids stabilised by six cysteines forming three disulfide bridges[111]. The predominant insect defensins, such as phormicins, sapecins, royalisi, tenecin, holotricin, heliomicin, spodoptericin, gallerimycin, coprisin, and lucifensin, exhibit uniform cysteine pairing patterns: Cys1-Cys4, Cys2-Cys5, and Cys3-Cys6. These peptides also exhibit effectiveness against extensive Gram-positive bacterial populations and limited Gram-negative bacteria, fungi, and yeasts in environments with reduced salt concentrations[110]. Numerous reports demonstrate that phormia and aeschna insect defensins can eliminate specific mosquito life stages of the *Plasmodium gallinaceum* parasite[112]. Over 60 defensins have been characterised from insects representing both phylogenetically recent orders (*Diptera, Lepidoptera, Coleoptera, Hymenoptera*) and the ancient order *Odonata* (dragonfly)[110].

4.4.3.3 Drosomycin

Drosomycin was identified as the initial inducible antifungal peptide characterised from insects, consisting of 44 residues including eight cysteines involved in generating four internal disulfide connections: Cys1-Cys8, Cys2-Cys5, Cys3-Cys6, and Cys4-Cys7[113], reported in the fruit fly *D. melanogaster*. Unlike insect defensins stabilised by three disulfide bonds, drosomycin possesses an extra disulfide linkage between the first and C-terminal cysteine residues, resulting in a highly compact molecular structure[114]. This structural characteristic indeed accounts for drosomycin's remarkable resistance to protease degradation observed under both *in vitro* and *in vivo* experimental conditions[113].

4.4.3.4 Thanatins

Among AMPs, thanatins are the most compact, comprising only 21 amino acids (GSKPVPIIYCNRRTGKCQRM), including two cysteine residues. This cationic AMP was initially discovered in the hemipteran insect *Podisus maculiventris*, the spined soldier bug. Thanatin displays comprehensive antimicrobial activity, eliminating both Gram-positive and Gram-negative bacteria, filamentous fungi, and yeasts at micromolar concentrations without observable hemolytic effects on red blood cells[30].

4.4.3.5 Gloverins

Glycine-rich polypeptides known as gloverins, ranging from 8-30 kDa, have been isolated from multiple insect species[115]: *Diptera* (diptericins, attacins and sarcotoxins II), *Lepidoptera* (attacins), *Hymenoptera*

(hymenoptaecins), *Coleoptera* (coleoptericin, holotricin II and III, tenecin III), and *Hemiptera* (hemiptericin). The constitutive glycine-rich peptides holotricin II and III, and tenecin III, exhibit activity against *Candida* spp. These peptides are effective against Gram-negative bacteria but show no activity against Gram-positive bacteria, yeasts, mammalian cell lines, or pestiviruses[109,116,117].

5. Conclusion and Future Perspective

As one of the most primary and adaptable immune defence strategies in nature, AMPs are evolutionarily conserved and are present in all living entities from bacteria to higher animals and plants. Their notable structural diversity and ability to combat a wide range of pathogens make them potent alternatives to conventional antibiotics in an era of increasing multidrug resistance.

AMPs have received enormous attention, particularly for their efficacy against MDR pathogens. AMPs operate via receptor-independent mechanisms, which limit bacteria's ability to acquire resistance[118,119]. Given their widespread availability, broad-spectrum activity and natural origin, AMPs have been proposed as a next-generation class of antibiotics[92]. Moreover, their functions extend beyond microbial clearance. AMPs have been shown to act as immunomodulators, anti-inflammatory agents, and anti-endotoxin (LPS) compounds[120]. They modulate inflammation, counteract endotoxins such as LPS[121], and play roles in wound healing, angiogenesis, adaptive immune regulation, and both septic and nonseptic immune responses[22].

This review highlights the essential features, modes of action, and source diversity of AMPs, underscoring their broad functional applicability. In addition to their well-established role in combating pathogens, AMPs also contribute substantially to immune homeostasis and tissue repair. Owing to their natural origin and selective toxicity, AMPs are emerging as viable candidates for applications in clinical medicine, agriculture, and industrial biotechnology.

This study primarily investigates the diversity of AMPs across living organisms, from microbes to invertebrates and plants, to identify abundant and accessible sources for the cost-effective extraction of natural peptide-based antibiotics. Despite their therapeutic potential, the high production cost and limited bioavailability of AMPs remain major challenges. Based on the available evidence, mushrooms emerge as promising, safe, and economically viable sources for the direct extraction of AMPs[122,123].

In this review, the direct extraction of AMPs from readily available mushroom fruiting bodies could serve as a cost-effective strategy for large-scale peptide production. A study reported that the wild mushroom *Ganoderma lucidum* yielded a significant amount of AMPs following 10% TCA precipitation of acid-extracted crude proteins[79]. The favourable properties of AMPs include their short length, structural stability, hydrophobicity, and strong cationic charge. These peptides are all key contributors to their broad antimicrobial efficacy. Among them, cyclic peptides, such as θ-defensins, fulfil these criteria and are of particular interest due to their enhanced stability and potent antimicrobial activity. Owing to their cyclic backbone, their extraordinary antimicrobial potency, and improved resistance to proteolytic degradation, they are promising leads for pharmaceutical applications[124]. Screening these peptides across multiple species may yield new candidates for pharmaceutical use.

As the global threat of AMR intensifies, current research continues to expand opportunities for AMP-based therapeutics. With these innovations, AMPs are well-positioned to become powerful alternatives to traditional antibiotics in combating infectious diseases, offering hope for a new generation of safe, effective, and sustainable antimicrobial agents.

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Authorship Contribution

Sundaramoorthy Marimuthu: Conceptualisation, Writing – original draft; S. Lenita: Conceptualisation, Writing – original draft; Parvathi Velan: Conceptualisation, Writing – original draft; Mohiraa Shafreen: Conceptualisation, Writing – original draft. Mahfeera Mubeen: Conceptualisation, Writing – review and editing; Kumaran Shanmugam: Writing – review and editing; Nitin Kumar: Conceptualisation, Writing – review and editing, supervision. All authors have read and agreed to the published version of the manuscript.