

Antimicrobial peptides as promising alternatives to antibiotics in weaning pigs - a review

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Abstract

Antimicrobial peptides are relatively small peptides (< 10kDa), cationic and amphipathic peptides of variable length sequence and structure which are an important component and widely existing in nature as the first line defence in wide range of organisms. Antimicrobial peptides have the widespread distribution of potent, broad spectrum antimicrobial peptides in multicellular organisms that have been suggested to use to resist a wide range of microbes, including bacteria, fungi, viruses, and protozoa. Due to the emergence of spreading antibiotic resistance in the environment, and the presence of chemical residues in animal products which results in the development of antimicrobial peptides, which have a good application prospect in animal husbandry and aquaculture, especially in young animal. The available documents to date has shown that antimicrobial peptides have the potential to prevent the growth of pathogens, improve the intestinal mucosal function, the immune system, digestion, and absorption capacity, as well as useful intestinal flora, and decrease diarrhea rate, keep the weaning pig health, and eventually improve the growth performance in weaning pigs, which is a potential alternatives to replace antibiotics in the diets of weaning pigs. This review will give an overview of (i) the source of antimicrobial peptides, (ii) mode of antimicrobial actions, and (iii) application of antimicrobial peptides on weaning pigs and systematically.

Keywords: antimicrobial peptides; antibiotic, weaning pigs

Introduction

Weaning is a stressful experience for the piglets involving psychological, nutritional, microbiological, and immunological, and environmental stresses because during this weaning transition period piglets have to face with abrupt separation from their dam, mixing with other litters, moving to new environment and switch from highly digestible feed (milk) to a less digestible commercial feed (Lalles, 2008), which could result in economic losses due to decreased growth rate, feed efficiency, diarrhoea, intestinal disturbances, and piglets' health.

Antibiotics have been used very successfully to weaning pigs for the diarrhoea prevention or treatment and growth performance improvement in the worldwide. However, the use of antibiotics as growth promoters in animal feed has been banned in many countries including European Union since 2006 as well as South Korea since 2011 (Nguyen et al., 2018) due to the concern of antibiotic resistance in pathogens and antibiotic residues in animal products. Therefore, massive efforts have been made to find different ways to maintain animal health and performance, many researchers have suggested that the use of organic acids, organic minerals, bacteriophages, probiotics, and prebiotics as potential alternatives (Nguyen et al., 2020). Among a variety of candidates for the replacement of antibiotic growth promoters, antimicrobial peptides (AMPs) are promising alternatives. Antimicrobial peptides are an important component of the first line defence in various animal species, the natural defences of most living organisms against invading pathogens with the widespread distribution of potent, broad spectrum AMPs in multicellular organisms that have been suggested to use to resist a wide range of microbes, including bacteria, fungi, viruses, and protozoa (Reddy et al., 2004; Leeson, 2001).

Unlike conventional antibiotics, which usually function through a defined high-affinity antimicrobial target and which can induce resistance in microorganisms, AMPs exert multiple antimicrobial activities that might provide a strategy to prevent bacteria from developing resistance (Peschel and Sahl, 2006). Apart from directly attacking microbes, AMPs can confer protection by alternative mechanisms, such as maintenance of normal gut homeostasis, and modulation of host inflammatory responses (Lai and Gallo,

2009; Wang et al., 2015). Administrating of various AMPs has been illustrated to improve growth performance, nutrient digestibility, intestinal microflora, intestinal morphology and immune system in pigs (Tang et al., 2008; Yoo et al., 2013). It is therefore this article provides an overview of their common sources, mechanism of action. The response of weanling pigs to antibacterial peptides of the previous reports pigs is also reviewed.

Antimicrobial peptides

Since the identification of the first antibacterial protein family, thionins, during the early 1970s, more than 750 different AMPs have been identified in various organism ranging from insects to plants to animals as well as in humans (Schnapp et al., 1998; Leeson, 2001). Antimicrobial peptides are relatively small (<10kDa), cationic and amphipathic peptides of variable length sequence and structure. These peptides have been grouped based on their primary structure, amino acid composition and their size (Ravichandran et al., 2010).

The diversity of natural AMPs causes difficulty in their classification. According to Huan et al. (2020), AMPs are classified based on (1) sources, (2) activity, (3) structural characteristics, and (4) amino acid-rich species. However, in this work we will summary the classification of AMPs based on the sources.

Source of antimicrobial peptides

Mammalian sources

Mammalian antimicrobial peptides are found in human, sheep, cattle, and other vertebrates. They have common features such size, cationic charge, and an amphipathic nature. Defensins and cathelicidins are the main antimicrobial based on such features in mammals. Defensins can be divided into α -, β -, and θ -defensins depending on the position of disulfide bonds (Reddy et al., 2004). Table 1 further summarizes discovery of various AMPs from variety of mammal.

Table 1. Antimicrobial peptides derived from mammal (Boparai and Sharma, 2020)

| Peptide name | Source | Amino acid number | Antimicrobial activity | References |
|------------------|-------------------------------------|-------------------|------------------------|---------------------------|
| Cathelicidins | Human neutrophils | 30 | F, G, G ⁺ | Sheehan et al., 2018 |
| A Defensins | Human neutrophils | 12 - 80 | F, G, G ⁺ | Schaal et al., 2018 |
| Human Histatin 8 | <i>Homo sapiens</i> | 12 | F, G, G ⁺ | Khurshid et al., 2017 |
| LL37 | Neutrophils (<i>Homo sapiens</i>) | 37 | F, G, G ⁺ | Baxter et al., 2017 |
| Androctonin | <i>Androctonus australis</i> | 25 | F, G, G ⁺ | V Panteleev et al., 2017 |
| Bactenecin | Bovine Neutrophils | 12 | G, G ⁺ | Young-Speirs et al., 2018 |
| Brevinin | <i>Rana brevipora porsa</i> | 24 | G, G ⁺ | Savelyeva et al., 2014 |
| Buforin II | <i>Bufo bufo gargarizans</i> | 21 | F, G, G ⁺ | Sun et al., 2015 |
| Cupiennin | <i>Cupiennius salei</i> | 35 | G, G ⁺ | Upadhyay, 2018 |
| Dermaseptin S1 | <i>Phyllomedusa sauvagii</i> | 34 | G, G ⁺ | Belmadani et al., 2018 |
| Lycotoxin | <i>Lycosa carolinensis</i> | 27 | G, G ⁺ | Tahir et al., 2018 |
| Tachyplesins | <i>Tachyplesus tridentatus</i> | 17 | G | Kuzmin et al., 2017 |

Note: F, Fungus; G-, Gram negative; G+, Gram positive

Plant sources

Plant AMPs have evolved differently from AMPs from other life forms. Most plant AMPs involves host plant resistance to pathogens such as fungi, viruses, and bacteria, whereas a few plant AMPs from the cyclotide family carry insecticidal functions (Noonan, 2017). Ranging size from 2 to 9 kDa, all plant AMPs are globular, compact, and cysteine-rich peptides (Leeson, 2001). Thionins were the first plant AMPs to be described. Subsequently, the antimicrobial activities of various defensins, lipid transfer proteins, hevein-and knottin-like peptides, including MBP-1 from maize, IbAMP from the seeds of impatiens, snakins from potatoes, and shepherdins from roots of shepherd's purse have been identified (Garcia-Olmedo, 2015; Tam, 2015). Table 2 further summarizes discovery of various AMPs from variety of plant.

Table 2. Antimicrobial peptides derived from plant (Shwaik et al., 2021)

| Peptide name | Source | Antimicrobial activity | References |
|-------------------------------------|-----------------------------|------------------------|----------------------------|
| Defensin | | | |
| Rs-AFP1; Rs-AFP2 | <i>Raphanus sativus</i> | F, Y | Shwaiki et al., 2020a |
| IbAMP1 | <i>Impatiens balsamina</i> | F, B | Wu et al., 2013 |
| Cp-thionin II | <i>Vigna unguiculata</i> | F, B | Schmidt et al., 2019 |
| MsDef1; MtDef4 | <i>Medicago sativa</i> | F | Sagaram et al., 2011 |
| Thionins | | | |
| Tu-AMP 1; Tu-AMP 2 | <i>Tulipa gesneriana</i> | F, B | Fujimura et al., 2004 |
| Wheat β -Purothionins | <i>Triticum aestivum</i> | B | Mak and Jones, 1976 |
| Thionin 2.4 | <i>Arabidopsis thaliana</i> | F | Asano et al., 2013 |
| Snakin/ GASA | | | |
| St-SN1 | <i>Solanum tuberosum</i> | F, Y, B | Shwaiki et al., 2020b |
| MsSN1 | <i>Medicago sativa</i> | F, B | García et al., 2014 |
| Snakin-Z | <i>Ziziphus jujuba</i> | F, B | Daneshmand et al., 2013 |
| Cyclotides | | | |
| Cycloviolacin O2 | <i>Viola odorata</i> | F, B | Zarrabi et al., 2013 |
| Cycloviolacin O8 | <i>Viola odorata</i> | F | Parsley et al., 2018 |
| Knottin type | | | |
| PAFP-S | <i>Phytolacca americana</i> | F | Shao et al., 1999 |
| Mj-AMP1; Mj-AMP2 | <i>Mirabilis jalapa</i> | F | Cammue et al., 1992 |
| Hevein-type | | | |
| Ee-CBP | <i>Euonymus europaeus</i> | F | Van Den Bergh et al., 2002 |
| SmAMP3 | <i>Stellaria media</i> | F | Rogozhin et al., 2015 |
| EAFP1 | <i>Eucommia ulmoides</i> | F | Huang et al., 2002 |
| EAFP2 | | | |
| Lipid Transfer Protein (LTP) | | | |
| Ca-LTP1 | <i>Capsicum annum</i> | F | Diz et al., 2011 |
| Mung bean nsLTP | <i>Phaseolus mungo</i> | F, B | Lin et al., 2005 |
| 2S albumin proteins | | | |
| Pe-AFP1 | <i>Passiflora edulis</i> | F, Y | Pelegrini et al., 2006 |
| CW-1 | <i>Malva parviflora</i> | F | Wang and Bunkers, 2000 |

Note: B, Bacteria; F, Fungus; Y, Yeast

Insect sources

It is well known that insects are extremely resistant to bacterial infections. Antimicrobial peptides are mainly synthesized in fat bodies and blood cells of insects, which is one of the main reasons for insects' strong adaptability to survival (Vilcinskis, 2013). The cecropin is the first and most famous family of antimicrobial peptides from insect that was identified in the 1980 from the pupae of *Hyalophora cecropia* (Hultmark et al., 1980). Most insect AMPs are cationic molecules due to the presence of basic residues with activities against bacteria. According to their amino acid sequences and structures, antimicrobial peptides can be classified in four different groups: cysteine-rich peptides (e.g. defensins), the α -helical peptides (e.g. cecropins), glycine (Gly) -rich proteins (e.g. attacins), and proline-rich peptides (e.g. drosocins) (Bulet and Stocklin, 2005; Makarova et al., 2018). Table 3 further summarizes discovery of various AMPs from variety of insects.

Table 3. Antimicrobial peptides derived from insect (Boparai et al., 2020)

| Peptide name | Source | Amino acid number | Antimicrobial activity | References |
|--------------------|--------------------------------|-------------------|------------------------|------------------------|
| Acaloleptin | <i>Acalolepta luxuriosa</i> | 71 | G, G ⁺ | Vogel et al., 2014 |
| Andropin | <i>Drosophila melanogaster</i> | 34 | G ⁺ | Abry et al., 2017 |
| Apidaecin IA | <i>Apis mellifera</i> | 18 | G ⁻ | Farouk et al., 2017 |
| Cecropin | <i>Hyalophora cecropia</i> | 37 | G ⁻ | Lee and Lee, 2015 |
| Defensin- α | <i>Aedes aegypti</i> | 40 | G, G ⁺ | Price et al., 2015 |
| Drosomycin | <i>Drosophila melanogaster</i> | 44 | F | Allocca et al., 2018 |
| Holotricin | <i>Holotrichia diomphalia</i> | 43 | G, G ⁺ | Thiyonila et al., 2018 |
| Sapecin- α | <i>Sarcophaga peregrine</i> | 40 | G, G ⁺ | Manabe et al., 2017 |
| Tenacin 1 | <i>Tenebrio molitor</i> | 43 | G, G ⁺ | Yang et al., 2018 |
| Thanatin | <i>Podisus maculiventris</i> | 21 | G, G ⁺ | Duwadi et al., 2018 |

Note: F, Fungus; G⁻, Gram negative; G⁺, Gram positive

Amphibian sources

Antimicrobial peptides from amphibians play an important role in the protection of amphibians from the pathogens that have

induced the global amphibian population decline (Rollins-Smith, 2009). Frogs are the main source of amphibian AMPs and the most famous AMP from frogs is magainin; the skin secretions of frogs from genera *Xenopus*, *Silurana*, *Hymenochirus*, and *Pseudhymenochirus* under the Pipidae family are rich in AMPs (Conlon and Mechkarska, 2014). Cancrin which had 19 amino acids has been reported as the first AMP from the sea amphibian *Rana cancrivora* (Lu et al., 2008). This marks a broader source of AMPs of amphibians. Table 4 further summarizes discovery of various AMPs from variety of frogs.

Table 4. Antimicrobial peptides derived from frogs (Patocka et al., 2019)

| Peptide name | Source | Antimicrobial activity | References |
|--------------------|--------------------------|------------------------|----------------------|
| Esculentin-1 | <i>Rana esculenta</i> | 46 | Simmaco et al., 1993 |
| Esculentin-1a | <i>Rana esculenta</i> | 46 | Simmaco et al., 1994 |
| Esculentin-1b | <i>Rana saharica</i> | 46 | Marenah et al., 2006 |
| Esculentin-1c | <i>Rana esculenta</i> | 45 | Kang et al., 2010 |
| Esculentin-2a | <i>Rana esculenta</i> | 37 | Simmaco et al., 1993 |
| Esculentin-1SEa | Dusky gopher | 46 | Graham et al., 2006 |
| Esculentin-2SE | Dusky gopher | 37 | Graham et al., 2006 |
| Esculentin-2- OG15 | <i>Amolops soloensis</i> | 78 | Wang et al., 2010 |
| Esculentin-2- OG11 | <i>Amolops soloensis</i> | 78 | Wang et al., 2010 |

Microorganism sources

Antimicrobial peptides can be also obtained from microorganisms like bacteria and fungi, and some famous peptides are nisin, gramicidin from *Lactococcus lactis*, *Bacillus subtilis*, and *Bacillus brevis* (Cao et al., 2018). Microorganism-derived AMPs have long been used as food preservatives. Recently, peptides produced by members of the genus *Bacillus* were shown to have a broad spectrum of antimicrobial activity against pathogenic microbes. *Bacillus*-derived AMPs can be synthesized both ribosomally and nonribosomally and can be classified according to peptide biosynthesis, structure, and molecular weight. Table 5 further summarizes discovery of various AMPs from variety of microorganism.

Table 5. Antimicrobial peptides derived from microorganism (Boparai et al., 2020)

| Peptide name | Source | Amino acid number | Antimicrobial activity | References |
|-------------------|--|-------------------|---------------------------------|---------------------------------|
| Nisin | <i>Lactococcus lactis</i> | 34 | G ⁺ | Mills et al., 2017 |
| Enterocin | <i>Enterococcus</i> | 70 | G ⁺ , G ⁻ | Braiek et al., 2018 |
| Ericin S | <i>Bacillus subtilis</i> | 32 | G ⁺ | Sharma et al., 2018 |
| Plantaricin A | <i>Lactobacillus plantarum</i> | 26 | G ⁺ , G ⁻ | Jiang et al., 2018 |
| Leucocin A | <i>Leuconostoc pseudomesenteroides</i> | 37 | G ⁺ , G ⁻ | Chen et al., 2018 |
| Subtilin | <i>Bacillus subtilis</i> | 32 | G ⁺ | Singh et al., 2017 |
| Microcin J25 | <i>Escherichia coli</i> AY25 | 21 | G ⁺ | Zhao et al., 2016 |
| Gramicidin A | <i>Bacillus brevis</i> | 15 | G ⁺ , G ⁻ | Muhammad et al., 2016 |
| Streptin 1 | <i>Bacillus subtilis</i> A1/3 | 23 | G ⁺ | Bosma and LanthioPep, 2017 |
| Gasserin A | <i>Lactobacillus gasseri</i> LA39 | 58 | G ⁺ , G ⁻ | Maldonado-Barragán et al., 2016 |
| Circularin A | <i>Clostridium beijerinckii</i> ATCC 25752 | 69 | G ⁺ , G ⁻ | Perez et al., 2016 |
| Plantaricin C19 | <i>Lactobacillus plantarum</i> C19 | 37 | G ⁺ | Wang et al., 2018 |
| Enterocin P | <i>Enterococcus faecium</i> P13 | 44 | G ⁺ | Le et al., 2014 |
| Subtilosin A | <i>Bacillus subtilis</i> | 35 | G ⁺ , G ⁻ | Venturina et al., 2016 |
| Plantaricin; ASM1 | <i>Lactobacillus plantarum</i> A-1 | 43 | G ⁺ | Wang et al., 2018 |
| Lichenin | <i>Bacillus licheniformis</i> | 12 | G ⁺ , G ⁻ | Bhat, 2018 |

Note: G⁻, Gram⁻, G⁺, Gram⁺

Aqua sources

Fishes are one of the organisms that have managed to survive in a milieu of pathogenic organisms. The primary interference of fish with their environment happens through a mucous layer that covers its entire body. Marine fishes possess antimicrobial peptides as a part of their defense system, which are mainly present in the mucous layer indicating that they eliminate the pathogenic bacteria before they enter the skin barrier (Ravichandran et al., 2010). Based on both structural features and origins, fish AMPs have classified into four classes: (i) AMPs exhibiting an α -helical structure (pleurocidins, moronecidins and piscidins); (ii) β -sheet structured AMPs containing 4 disulfide bonds (hepcidins); (iii) proteolytic fragments of structural or functional proteins; (iv) AMPs produced by fish-associated bacteria (Desriac et al., 2013). Table 6 further summarizes discovery of various AMPs from variety of fishes.

Table 6. Antimicrobial peptides derived from fishes (Desriac et al., 2013)

| Peptide name | Source | Antimicrobial activity | Antimicrobial activity | References |
|---------------------|-------------------------------|------------------------|------------------------|----------------------------|
| Pleurocidins | | | | |
| WF1 | <i>P. americanus</i> | 25 | G-, G+ | Cole et al., 1997 |
| WF2 | <i>P. americanus</i> | 26 | F, G-, G+ | Douglas et al., 2003 |
| WF1L | <i>Pp. americanus</i> | 24 | F, G-, G+ | Douglas et al., 2003 |
| WFX | <i>Pp. americanus</i> | 21 | F, G-, G+ | Douglas et al., 2003 |
| WFY | <i>Pp. americanus</i> | 21 | F, G-, G+ | Douglas et al., 2003 |
| WF3 | <i>P. americanus</i> | 23 | F, G-, G+ | Douglas et al., 2001 |
| WF4 | <i>P. americanus</i> | 25 | F, G-, G+ | Douglas et al., 2001 |
| Moronecidins | | | | |
| Moronecidin | <i>Morone chrysops</i> | 22 | F, G-, G+ | Lauth et al., 2002 |
| Moronecidin | <i>Morone saxatilis</i> | 22 | F, G-, G+ | Lauth et al., 2002 |
| Dicentracin | <i>Dicentrarchus labrax</i> | 22 | | Salerno et al., 2007 |
| Piscidins | | | | |
| Piscidin-1 | <i>Morone saxatilis</i> | 22 | F, G-, G+ | Lauth et al., 2002 |
| Piscidin-2 | <i>Morone saxatilis</i> | 22 | V, F, G-, G+ | Campagna et al., 2007 |
| Piscidin-3 | <i>Morone chrysops x</i> | 22 | G-, G+ | Silphaduang and Noga, 2001 |
| | <i>Morone saxatilis</i> | | | |
| Epinecidin | | | | |
| Epinecidin-1 | <i>Epinephelus coioides</i> | 25 | G-, G+ | Pan et al., 2007 |
| Grammistins | | | | |
| Grammistin Pp2b | <i>Pogonoperca punctata</i> | 13 | H, G-, G+ | Sugiyama et al., 2005 |
| Grammistin Pp2a | <i>Pogonoperca punctata</i> | 13 | G-, G+ | Kaji et al., 2006 |
| Grammistin Pp4b | <i>Pogonoperca punctata</i> | 24 | H, G-, G+ | Kaji et al., 2006 |
| Grammistin Pp4a | <i>Pogonoperca punctata</i> | 24 | H, G-, G+ | Kaji et al., 2006 |
| Grammistin Pp3 | <i>Pogonoperca punctata</i> | 25 | H, G-, G+ | Sugiyama et al., 2005 |
| Grammistin GsG | <i>Grammistes sexlineatus</i> | 24 | H, G-, G+ | Sugiyama et al., 2005 |
| Grammistin GsF | <i>Grammistes sexlineatus</i> | 25 | H, G-, G+ | Sugiyama et al., 2005 |
| GrammistinGsC | <i>Grammistes sexlineatus</i> | 26 | G-, G+ | Sugiyama et al., 2005 |
| Grammistin GsA | <i>Grammistes sexlineatus</i> | 28 | G-, G+ | Sugiyama et al., 2005 |
| GrammistinGsE | <i>Grammistes sexlineatus</i> | 13 | H, G-, G+ | Kaji et al., 2006 |
| Grammistin Gs D | <i>Grammistes sexlineatus</i> | 13 | H, G-, G+ | Kaji et al., 2006 |
| Grammistin Gs B | <i>Grammistes sexlineatus</i> | 12 | H, G-, G+ | Sugiyama et al., 2005 |
| Chrysofins | | | | |
| Chrysofinsin-1 | <i>Pagrus major</i> | 25 | G-, G+ | Iijima et al., 2003 |
| Chrysofinsin-2 | <i>Pagrus major</i> | 25 | G-, G+ | Iijima et al., 2003 |
| Chrysofinsin-3 | <i>Pagrus major</i> | 20 | G-, G+ | Iijima et al., 2003 |

Note: F, Fungus; G-, Gram-; G+, Gram+; H, Hemolytic; V, Viruses

Modes of antimicrobial peptides actions

The primary sequences of the different classes and sources of antimicrobial peptides show little homology, differing in peptide length, amino acid composition, charge, hydrophobicity, and secondary structure. Nevertheless, most AMPs are cationic and amphipathic. Indeed, these two structural features play key roles in the antimicrobial actions exerted by these peptides (Leeson, 2001).

Membrane interaction

According to the report of Leeson (2001), before reaching the phospholipid membrane, peptides must traverse the negatively charged outer wall of Gram-negative bacteria, which contains lipopolysaccharides, or through the outer cell wall of Gram-positive bacteria which contains acidic polysaccharides (teichoic acids) (Vorland et al., 1999). In this mechanism, the cationic peptides initially interact with the surface lipopolysaccharides, competitively displacing divalent cations that bridge and partly neutralize the lipopolysaccharides. This causes disruption of the outer membrane that appears as blebs when observed under the microscope (Ulvatne et al., 2001). Studies with several antimicrobial peptides of different lengths hydrophobicities and structures revealed that these blebs are formed only below the minimal inhibitory concentration. At or above the minimal inhibitory concentration, however, bacteria are partially lysed and disintegrated (Ramanathan et al., 2002).

Membrane penetration

Basing on the report of Leeson (2001), the initial interaction of cationic antimicrobial peptides with the cytoplasmic membrane involves the insertion of the peptides parallel to the membrane surface into the interface between the phospholipid head groups and fatty acid chains of the outer monolayer of this membrane. Consequently, the membrane can be rendered permeable through

the formation of transmembrane pores, causing cell lysis and leading cell death (Benitez et al., 2003). Two major models, the barrel-stave "model and the "carpet-like" model, have been proposed to describe how the peptides interact with the membrane (Huang, 2000; Shai and Oren, 2001).

In the barrel-stave "model, as few as three membrane-bound peptides (amphipathic α -helix, hydrophobic α -helix, β -sheet, or both α -helix, β -sheet structures) recognize each other on the membrane surface, oligomerize, insert themselves into the hydrophilic membrane bilayer, and form transmembrane pores. Hence, amphipathic peptides align perpendicular to the membrane to form the staves of a transient barrel of various sizes, forming a hydrophilic pore in its center traversing the cytoplasmic membrane. This would then lead to leakage of the cytoplasmic contents and, subsequently, death (Huang, 2000).

In the carpet-like "model, antimicrobial peptides penetrate into the membrane using the following sequence: (1) binding of peptide monomers to the phospholipid head groups and alignment of the positively charged amino acids of the peptide monomers on the surface of the membrane so that their hydrophilic surface is facing the phospholipid headgroups or water molecules; (2) rotation of the molecule leading to reorientation of the hydrophobic residues toward the hydrophobic core of the membrane; and (3) once a threshold concentration is reached, the bilayer curvature is disrupted, leading to permeability and disintegration of the membrane (Shai and Oren, 2001). Unlike the "barrel-stave "model, no specific peptide structure is needed in the "carpet-like "model.

Interaction with cellular components

To acting at the cell membrane, antimicrobial peptides may also exhibit their activity against multiple potential targets such as cell division, DNA, ribonucleic acid (RNA) for protein synthesis, and autolysin activation (Cudic and Otvos, 2002).

Application of antimicrobial peptides in weaning pigs

Antimicrobial peptides usage in swine to improve performance

Weaned pigs often face post-weaning challenges, including diarrhea, impaired growth rate, low feed intake, and mortality (Yin et al., 2010). Antimicrobial peptides are considered as feed additive to maintain the performance and health status of weaned piglets. It is indicated that the growth-promoting effects of the AMPs were thanks to the improvements in the intestinal morphology (Wang et al., 2006; Wang et al., 2007; Yoon et al., 2013; Xiong et al., 2014), PR-39 and protegrin-1 gene expression to some extent, that promotes the nutrition digestion and absorption, regulates and enhances the immunity of mucosa (Wang et al., 2006). In addition, the digestibility of nutrients in pigs fed diets supplemented with the AMPs might be due to modulation of gut environment, improvement of intestine microbial balance (Wang et al., 2007; Jin et al., 2008a,b; Tang et al., 2008).

Other researchers also demonstrated positive influence of the dietary AMPs administration on the growth performance and nutrient digestibility in weaning pigs (Table 7).

Table 7. Effect of antimicrobial peptides on growth performance and nutrient digestibility in weaning pigs.

| Composition of AMPs | Dose (g/kg feed) | Growth performance | | | References |
|--|------------------|------------------------|------|-----|---------------------|
| | | ADG | ADFI | G:F | |
| Lactoferrin, cecropin, defensin, and plectasin | 0.2; 0.3 | * | * | * | Xiong et al., 2014 |
| Lactoferrin | 1 | * | * | * | Wang et al., 2006 |
| Lactoferrin | 1 | * | * | * | Wang et al., 2007 |
| AMP-P5 | 0.04; 0.06 | * | * | * | Yoon et al., 2012 |
| AMP-A3 | 0.06; 0.09 | * | Ns | Ns | Yoon et al., 2013 |
| Refined potato protein | 0.2; 0.4; 0.6 | * | Ns | * | Jin et al., 2009 |
| Antibacterial peptide | 0.01 | * | * | Ns | Wang and Feng, 2011 |
| Lactoferricin-lactoferrampin | 0.1 | * | * | Ns | Tang et al., 2008 |
| Niacin | 0.04 | * | - | - | Feng et al., 2021 |
| WK3 | 0.05 | * | * | Ns | Cao et al., 2021 |
| WK3 | 2 mg/kg BW | * | * | Ns | Zhang et al., 2021 |
| Buforin II | 5 mL | * | * | * | Tang et al., 2013 |
| M. domestica and porcine defensin | 0.4 | * | Ns | - | Shi et al., 2018 |
| Cathelicidin-BF | 0.6 mg/kg BW | * | * | Ns | Feng et al., 2020 |
| Composition of antimicrobial peptides | Dose (g/kg) | Nutrient digestibility | | | References |
| | | DM | CP | GE | |
| AMP-P5 | 0.04; 0.06 | * | * | * | Yoon et al., 2013 |
| AMP-A3 | 0.06; 0.09 | * | * | - | Yoon et al., 2012 |
| M. domestica and porcine defensin | 0.4 | * | Ns | Ns | Shi et al., 2018 |

Note: ADG, average daily gain; ADFI, average daily feed intake; AMPs, Antimicrobial peptides; BW, body weight; CP, crude protein; DM, dry matter; GE, gross energy; G:F, gain to feed ratio; -, no measurement.

Antimicrobial peptides usage in weaning pigs to improve intestinal morphology

Pigs' intestine is home for a dynamic microbial population that forms a complex ecosystem and has a symbiotic relationship with the host. The population of gut microbes, or microbiota, plays key roles in maintaining nutritional, physiological, and immunological functions of the pigs (Lee and Mazmanian, 2010; Brestoff and Artis, 2013). A toxin produced by pathogenic bacteria in the gut can cause inflammation of the intestinal mucosa and diarrhea associated with morphological changes in the small intestine, such as shortening of the villi and an increase in crypt depth (Xiao et al., 2015), and these issues normally happens in piglets after weaning and lead to the reduce of feed intake and increase risk of disease. Previous studies reported that the antibacterial action of AMPs provides an effective support for normal intestinal morphology and gut microflora of animal (Table 8).

Table 8. Effects of antimicrobial peptides on intestinal morphology and gut microflora in weaning pigs.

| Composition of AMPs | Dose (g/kg feed) | Intestinal morphology | | Gut microflora | References |
|-----------------------------------|------------------|-----------------------|-------------|---|--------------------|
| | | Villus height | Crypt depth | | |
| Lactoferrin | 1 | * | * | - | Wang et al., 2014 |
| Lactoferrin | 1 | * | * | Reduced the total viable counts of E. coli and Salmonella in the small intestine Increased the colonic Lactobacillus and Bifidobacterium | Wang et al., 2007 |
| AMP-P5 | 0.04 | - | - | Decreased the total anaerobic bacteria, coliforms | Yoon et al., 2013 |
| | 0.06 | | | | |
| AMP-A3 | 0.06 | * | * | Decreased the total anaerobic bacteria, coliforms and Clostridium spp. | Yoon et al., 2012 |
| | 0.09 | | | | |
| Refined potato protein | 0.2 | - | - | Decreased total bacteria, Coliform bacteria, Staphylococcus spp. | Jin et al., 2009 |
| | 0.4 | | | | |
| | 0.6 | | | | |
| lactoferricin-lactoferrampin | 0.1 | * | Ns | Decreased the concentration of E.coli Increased the concentration of Lactobacilli and Bafidobacteria | Tang et al., 2008 |
| Niacin | 0.04 | * | - | - | Feng et al., 2021 |
| WK3 | 0.05 | * | * | Decreased the Enterobacterium spp. concentration Increased the concentration of Lactobacillus spp. and Bifidobacteria spp. | Cao et al., 2021 |
| | | | | Decreased the Enterococcus spp. concentration | |
| WK3 | 2 mg/kg BW | * | Ns | - | Zhang et al., 2021 |
| Buforin II | 5 mL | * | Ns | - | Tang et al., 2013 |
| M. domestica and porcine defensin | 0.4 | - | - | Decreased the E.coli concentration Increased the concentration of Lactobacillus spp. and Bifidobacteria spp. | Shi et al., 2018 |
| | | | | - | |
| Cathelicidin-BF | 0.6 mg/kg BW | * | Ns | - | Feng et al., 2020 |

Note: AMPs, Antimicrobial peptides; BW, body weight; Ns, no significant; -, no measurement.

Antimicrobial peptides usage in weaning pigs to enhance the immune

Antimicrobial peptides are gene-encoded natural antibiotics with potent and broad antimicrobial capabilities that function as a first line of defense in the innate immunity of the host (Ganz, 2002; Lehrer and Ganz, 2002). The action of cationic AMPs is not limited to their effect on microorganism. Antimicrobial peptides may serve as a bridge between the innate and adaptive immune systems (Gudmundsson and Agerberth, 1999; Hancock and Diamond, 2000; Hancock, 2001). More detailed studies are performed in weaning pigs in Table 9.

Table 9. Effects of antimicrobial peptides on immune response in weaning pigs.

| Composition of AMPs | Dose (g/kg feed) | Immune response | References |
|------------------------------|------------------|---|--------------------|
| Lactoferricin–lactoferrampin | 0.1 | Increased serum IgA, IgG and IgM levels | Tang et al., 2008 |
| AMP-A3 | 0.06 | Had no effect on serum immunoglobulins (IgG, IgA and IgM) concentration | Yoon et al., 2012 |
| | 0.09 | | |
| Lactoferrin | | Increased in serum IgG, IgA, (d 15 and 30) and IgM (d 15) concentration | Shan et al., 2007 |
| Cecropin A and Cecropin D | | Increased levels of secretory IgA in jejunum and serum IgA, IgG, interleukin-1 β and interleukin-6 | Wu et al., 2012 |
| WK3 | 0.05 | Inhibited intestinal inflammation by down regulating the mRNA expression of IL-1 α and TLR-4 in the jejunal mucosa | Cao et al., 2021 |
| Cathelicidin-BF | 0.6 mg/kg BW | Decreases the expression of IL-6, IL-8 and IL-22 | Yi et al., 2015 |
| APB | 0.25 | Enhanced the proliferation of T blood T cell subsets (the percentages of CD3+, CD3+CD4+, and CD3+CD8+) | Ren et al., 2015 |
| | 0.5 | Decreased the percentages of apoptotic spleen cells significantly | |
| | 1 | | |
| WK3 | 2 mg/kg BW | Downregulated the mRNA expression of IL-1 α , TLR-4 and MyD88 in the jejunal mucosa | Zhang et al., 2021 |
| APB | 0.25; 0.5; | Increased on the immunoglobulin levels (IgG, IgM, and IgA) | Yuan et al., 2015 |
| | 1 | | |
| Buforin II | 5 mL | Increased goblet cell amount, and the expression | Tang et al., 2013 |
| | | level of HGF, Reg-3 γ , TGF- β 1 and TFF-3 in the jejunum and the ileum | |
| Cathelicidin-BF | 0.6 mg/kg BW | Increased in serum IgG, IgA concentration and the expression levels of ZO-1, Occludin and Claudin-1 in the jejunum and colon. | Feng et al., 2020 |
| | | Decreased serum TNF- α , IL-6, IL-8, IL-10 and TGF- β production | |

Note: AMPs, Antimicrobial peptides; BW, body weight.

Conclusions

From the above studies it is understood that, antimicrobial peptides are an important component of the first line defence in wide range of organisms, from insects to plants to bacteria, animals as well as in humans in order to against invading pathogens thanks to the widespread distribution of potent, broad spectrum antimicrobial peptides in multicellular organisms that have been suggested to use to resist a wide range of microbes, including bacteria, fungi, viruses, and protozoa. However, the effect of antimicrobial peptides in practice is not always consistent due to the wide variety of available antimicrobial peptides, the type composition, dosage, animal species, animal age, and health status of animals. The available documents to date in feeding such compounds to weaning pigs seem to justify the assumption that antimicrobial peptides have the potential to prevent the growth of pathogens, improve the intestinal mucosal function, the immune system, digestion, and absorption capacity, as well as useful intestinal flora, and decrease animal diarrhea rate, keep the weanling pig health, and eventually improve the growth performance, and potential alternatives to replace antibiotics in the diets of animals.

List of abbreviations

| | | | |
|---------------------------------|-------------------|-------------------------|---------------------|
| ADG: Average daily gain | BW: body weight | G+: Gram positive | Ns: no significance |
| ADFI: Average daily feed intake | F: Fungus | GE: Gross energy | V: Viruses |
| AMPs: Antimicrobial peptides | FI: Feed intake | G:F: Gain to feed ratio | Y: Yeast |
| B: Bacteria | G-: Gram negative | H: Hemolytic | |

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