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Host Defense Peptides and Their Potential as Therapeutic Agents

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Chapter 12

Host Defense Peptides and Their Advancements in Translational *Staphylococcus aureus* Research

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Abstract *Staphylococcus aureus* is responsible for a multitude of infections ranging from skin and soft tissue infections to more severe invasive diseases. In response to *S. aureus*, host defense peptides (HDPs) are produced as nature's own sentinel effector molecules. HDPs are small, often cationic, molecules that possess numerous biological activities, such as antimicrobial activity, cellular recruitment, anti-inflammatory properties, and wound healing, all of which play a role in controlling *S. aureus* infections. In hopes of capitalizing on the powerful anti-infective functions of HDPs, there has been a considerable amount of interest in deriving HDP-based therapeutics. Here, we highlight current advancements in HDP research, constraints to commercial development, and solutions for safer and more feasible HDP-based therapies against *S. aureus*.

12.1 Staphylococcal Species and Colonization

Staphylococci are the most abundant bacterial inhabitants of the human skin microbiome. Humans are generally colonized with many different Staphylococcal species, with *S. epidermidis*, a coagulase-negative *Staphylococcus* (CoNS), being the most universal and dominant colonizer. The skin is colonized with many other CoNS species including *S. haemolyticus*, *S. saprophyticus*, *S. capitis*, *S. hominis*, *S. warneri*, *S. cohnii*, and *S. simulans* (Coates et al. 2014). Staphylococcal species differ in their ability to cause disease. Most CoNS are commensal, causing opportunistic infections in immune-compromised individuals (Otto 2010).

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Coagulase-positive *S. aureus*, however, has received considerable attention for its ability to cause disease even in healthy individuals. Colonization is known to be a risk factor for *S. aureus* infection and 20 % of the population is persistently colonized while 30 % carry *S. aureus* transiently. *S. aureus* causes a wide spectrum of diseases ranging from mild skin and soft tissue infections (boils, abscess, impetigo) to life-threatening diseases, such as severe sepsis, pneumonia, toxic shock syndrome, and endocarditis. *S. aureus* is also capable of forming multicellular communities or recalcitrant biofilms, resulting in a high incidence of indwelling device and catheter-related infections.

Adding to its severity, *S. aureus* is a highly adaptable human pathogen. In fact, resistance to methicillin was reported in 1961, only 1 year after it was first introduced. Initially confined to hospitals and other health care facilities, methicillin-resistant *Staphylococcus aureus* (MRSA) affected mainly immune-compromised individuals. Since the mid 1990s, however, there has been an explosion in the number of MRSA cases reported in the community, affecting healthy individuals that may have not been previously exposed to the healthcare environment (Herold et al. 1998, David and Daum 2010). Moreover, the incidence of vancomycin-intermediate and vancomycin-resistant *S. aureus* (VISA and VRSA, respectively) have increased (Tiwari and Sen 2006). Alarming, resistance to almost all clinically available antibiotics has emerged (Waldvogel 1999; Levin et al. 2005; Gu et al. 2013).

During the past half-century, very few new antibiotic classes have been developed that can effectively target *S. aureus*. To highlight this urgency, MRSA infections have claimed more lives than human immunodeficiency virus/acquired immune deficiency syndrome (HIV/AIDS) in the western world (Klevens et al. 2007). With the antibiotic pipeline running dry and multi-drug resistance on the rise, there has been considerable interest to exploit HDPs for the treatment of *S. aureus* infections. In this chapter, we will explore advancements in anti-*S. aureus* HDP research and HDP-directed translational breakthroughs.

12.2 Important Anti-staphylococcal HDPs

Host defense peptides (HDPs; also often referred to as antimicrobial peptides, AMPs) are an essential part of the innate defense response against *S. aureus*. HDPs are generally cationic and range in size from 12 to 50 amino acids, roughly 50 % of which are hydrophobic resulting in an overall amphipathic structure. In vitro, the bactericidal activity exhibited by HDPs is mediated by integration within the cytoplasmic membrane, resulting in pore formation and subsequent lysis.

HDPs are produced by a variety of cell types, either constitutively as a constant line of defense, or inducibly upon infection. Generally speaking, two major classes of HDPs, cathelicidins and defensins, have been described. However, other HDPs

such as RNase7 and dermcidin are important members of the constitutive cutaneous defense mechanism protecting us against initial *S. aureus* colonization.

12.2.1 Defensins

Humans express α - and β -defensins, small cysteine-rich amphipathic peptides that are 18-45 amino acid residues long and stabilized by three disulfide bonds. All defensins are initially synthesized as prepropeptides and become propeptides after cleavage of a signal peptide. Proper folding and activation of the defensin requires proteolytic cleavage of the anionic propeptide, a segment of the peptide considered important for maintaining charge balance and minimizing host toxicity.

Four α -defensins (HNP1-4) are produced in the azurophilic granules of human neutrophils as well as epithelial and certain hematopoietic cells (natural killer cells and monocytes). Despite accounting for almost half of the degranulating neutrophil proteins, α -defensins do not effectively kill *S. aureus* (Lehrer 2007). Instead, certain HNPs have shown to neutralize *S. aureus* toxins. For example, HNP3 was shown to bind to both Pantone-Valentine leukocidin subunits, LukS-PV, and Luk-PV, partially reducing pore formation and neutrophil lysis (Cardot-Martin et al. 2015).

In humans, four types of β -defensins have been characterized (h β D1-4), and are subcategorized based on the number and location of their disulfide bridges. h β D1 was first isolated from human plasma; and h β D2 and h β D3 were subsequently isolated from psoriatic scale extracts (Harder et al. 1997, 2001). h β D4 has been identified in lung tissue and is produced by bronchial and bronchiolar epithelium (Yanagi et al. 2005). β -defensins are expressed broadly by epithelial cells such as keratinocytes as well as certain leukocytes. In most tissues, h β D1 is expressed constitutively, while expression of h β D2 and h β D3 is induced upon pro-inflammatory stimuli with cytokines, various microorganisms and microbial products as well as upon tissue injury (Menzies and Kenoyer 2006). Of all the β -defensins, h β D-3 represents the most potent anti-staphylococcal peptide, retaining the highest antimicrobial activity in vivo (Kisich et al. 2007).

β -defensin expression is mediated by recognition of pathogen-associated molecular patterns (PAMPs) by toll like receptors (TLRs). TLR2 recognizes common cell wall constituents from *S. aureus* such as peptidoglycan, lipopeptides and lipoteichoic acid, and instigates a number of pro-inflammatory intracellular signaling events. Specifically, *S. aureus* activates the TLR2-mediated p38 MAPK signaling cascade, which regulates the expression of a number of inflammatory mediators (through AP-1 transcription factors) such as cytokines, chemokines and certain HDPs such as h β D2 and h β D3 (Menzies and Kenoyer 2006). Moreover, internalized *S. aureus* has shown to activate the nucleotide-binding oligomerization domain 2 (NOD-2), an intracellular receptor that recognizes muramyl dipeptide in

peptidoglycan, and may be responsible for h β D2 production by keratinocytes (Voss et al. 2006). Lastly, wounding of human skin results in the activation of the epidermal growth factor receptor, which leads to the enhanced production of h β D3 (Sorensen et al. 2006).

12.2.2 Cathelicidin

The human cathelicidin (hCAP-18) is an α -helical amphipathic cationic peptide constitutively expressed in the phagosomes of neutrophils, and inducibly in the mucosal epithelia and keratinocytes. Recent studies by Zhang et al. have shown that dermal adipocytes are also an important source of cathelicidin during cutaneous *S. aureus* infection, as mice defective in adipogenesis produced lower levels of this HDP (Zhang et al. 2015).

Upon release, hCAP-18 becomes proteolytically cleaved by proteinase 3, releasing the inactive N-terminal cathelin domain and generating the active peptide LL-37. LL-37 is 37 amino acid residues in length and is produced in a vitamin D-dependent manner. Moreover, two other cleavage products, RK-31 and KS-30 have been identified, and demonstrates even greater antimicrobial activity compared to LL-37 (Murakami et al. 2002).

12.2.3 RNase 7

In 2002, RNase7 was first characterized in human skin as a peptide that exhibits broad-spectrum antimicrobial activity (Harder and Schroder 2002). RNase7 is constitutively expressed in epidermis and in the stratum corneum of healthy skin, however, can be further induced upon bacterial challenge as well as stimulation by IL-1 β and IFN- γ (Harder and Schroder 2002). Importantly, RNase7 is considered an important part of the constitutive host defense, preventing colonization and infection. For example, after 2 h of *S. aureus* bacterial challenge, RNase7 levels in the stratum corneum of human skin explants are significantly up-regulated at levels high enough to prevent *S. aureus* colonization (Simanski et al. 2010).

12.2.4 Dermcidin

Dermcidin is expressed constitutively in eccrine sweat glands and secreted into sweat onto the epidermal surface, preventing bacterial colonization and serving as an integral cutaneous defense mechanism (Schitteck et al. 2001). Post-secretory

proteolytic processing of dermcidin protein (110 amino acid long) in sweat, results in the 47-aa peptide (DCD-1), 48-aa peptide (DCD-IL) or truncated peptide SSL-46, which all display broad-spectrum activity against *Escherichia coli*, *Enterococcus faecalis*, *Candida albicans* and *S. aureus* (Flad et al. 2002). Within human sweat, DCD-1 is found at concentrations (1–10 µg/mL) sufficiently high to kill microorganisms, and its activity is retained in pH and salt conditions that are characteristic of sweat (Schitteck et al. 2001). Interestingly, dermcidin does not possess any homology to known HDPs. Notably, in contrast to most AMPs, it possesses a net negative charge. This suggests that the mode of action of dermcidin might be different from other HDPs that rely on electrostatic interactions. While the mode of action of dermcidin remained obscure for a long time, it has recently been shown to form pores (Song et al. 2013).

12.3 HDP-Related Diseases

A growing body of evidence has demonstrated that deficiency of certain HDPs predisposes individuals to *S. aureus* infection. For example, lower induction of hβD-3 in *S. aureus*-infected human skin explants, has been correlated to more severe *S. aureus* skin infection as well as greater susceptibility to reoccurring infection (Zanger et al. 2010). Moreover, lesions taken from individuals with atopic dermatitis (AD), a skin disease that is correlated to increased susceptibility to *S. aureus*, produced significantly lower levels of hβD-2, hβD-3 and LL-37 (Ong et al. 2002). Furthermore, reduced production of dermcidin has been shown to contribute to the propensity of AD patients to recurrent bacterial skin infections (Rieg et al. 2005). This deficiency of dermcidin in sweat is correlated to reduced antimicrobial activity against *S. aureus* in vivo (Flad et al. 2002). Interestingly, A/J mice, which are more susceptible to *S. aureus* bacteremia compared to C57BL6 mice, have polymorphisms in their defensin genes (Ahn et al. 2010). Furthermore, mice deficient of cathelicidin-related antimicrobial peptide (CRAMP) produced larger lesions when injected with Group A *Streptococcus* compared to normal littermates (Nizet et al. 2001).

Conversely, elevated levels of certain HDPs have been linked with increased resistance to *S. aureus*. For example, elevated levels of hβD-2 and LL-37 found in psoriatic lesions prevent *S. aureus* colonization (Ong et al. 2002). Moreover, high baseline levels of RNase7 expression in the healthy skin confer protection against *S. aureus* skin infections (Zanger et al. 2009).

HDP deficiency can be attributed to an impairment of particular T cell responses. T cell responses, specifically those associated with Th17 cells, are especially important for HDP production. Th17 cytokines IL-17A and IL-22 were shown to up-regulate antimicrobial peptide expression namely, hβD-2, hβD-3 and cathelicidin, in keratinocytes (Liang et al. 2006). Further evidence that supports a role of

Th17 cells in cutaneous immunity is derived from studies, in which mice deficient in IL-17-producing epidermal $\gamma\delta$ T cells demonstrated higher susceptibility to *S. aureus* skin infection (Cho et al. 2010). In patients with autosomal dominant hyper-IgE syndrome, impaired Th17 cell differentiation, caused by a mutation in signal transducer and activator of transcription 3 (STAT3) (Renner et al. 2008), was linked to a variety of recurrent bacterial including *S. aureus* infections (Milner et al. 2008).

Furthermore, a predominance of Th2 cytokines can specifically impair the production of h β D-2 and h β D-3 (Nomura et al. 2003). Elevated levels of Th2 cytokines in skin lesions from AD patients are thought to promote *S. aureus* colonization by enhancing *S. aureus* binding to fibronectin and fibrinogen (Cho et al. 2001). Moreover, specific *S. aureus*-secreted super antigens such as enterotoxins A and B as well as toxic shock syndrome toxin-1 (TSST-1) elicit dermal infiltration of eosinophils and mononuclear cells, which skews the immune response toward a Th2 environment, exacerbating *S. aureus*-infected skin lesions in AD patients (Laouini et al. 2003).

12.4 Immune-Regulatory Roles of HDPs

Over the years, the immune-regulatory roles of HDPs have become more appreciated. HDPs exert a broad range of activities that refine host defenses to respond to infection, such as chemoattraction, suppression of pro-inflammatory mediators, and wound healing (Mansour et al. 2014). As the antimicrobial activities of many HDPs are significantly dampened at physiological conditions, some would argue that the immune-modulatory activities of HDPs are comparatively more relevant.

In fact, many of the studies highlighting antimicrobial activity are based on *in vitro* experiments using purified HDP extracts. Moreover, many experiments are performed under conditions (i.e., low ionic strength, neutral pH) that allow for optimal killing, while conditions that would better represent the physiological situation, such as by inclusion of divalent cations, anions, serum components, glycosaminoglycans, mucin and 150 mM NaCl, antagonize peptide activity. For example, when minimal inhibitory concentrations (MIC) assays are conducted on LL-37 under low salt conditions (often ≤ 20 mM NaCl), the MIC against a number of common bacteria is between 1 and 30 $\mu\text{g/ml}$. However, in the presence of more relevant ionic conditions (100 mM NaCl), the antimicrobial activity of LL-37 is 2–8 fold lower (Turner et al. 1998) with essentially no activity against *S. aureus* at concentrations as high as 100 $\mu\text{g/ml}$. Moreover, under these same conditions, the antimicrobial activity of h β D-1 and h β D-2 is completely lost. However, the importance of HDPs has been validated in the aforementioned human and animal studies (See Sect. 12.3). These findings have led many to believe that the most

important function of HDPs is to refine the host responses. Here we will highlight the diverse immune-modulatory roles of HDPs that enhance host defenses against *S. aureus*.

12.4.1 Chemoattraction

Interestingly, certain HDPs and chemokines share similar structure as they are both amphipathic and cationic. In fact, an evolutionary relationship between chemokines and HDPs have been inferred based on their strong involvement in the host innate immune response (Yount and Yeaman 2006). Specifically, HDPs were shown to possess a number of chemoattractant capabilities, assisting in the recruitment of immune cells that are important for resolving infection. When produced at sufficiently high concentrations, HDPs can directly act as chemokines, whereas at lower concentrations, they can promote the release of cytokines from other leukocytes (Mansour et al. 2014). For instance, if induced at high enough concentrations, LL-37 can directly attract neutrophils and eosinophils via interactions with formyl-peptide receptors (Tjabringa et al. 2006). However, since these activities are only promoted at LL-37 concentrations above physiological conditions, it is unlikely they possess this direct activity in vivo. On the other hand, LL-37 can indirectly promote chemoattraction by stimulating epithelial cells to release IL-8, an important chemokine for neutrophils and monocytes. Similarly, when human peripheral blood mononuclear cells (PBMCs) are stimulated by LL-37 in culture, they produce neutrophil chemokine IL-8, as well as monocyte chemoattractant protein-1 (MCP-1) and MCP-3 (Davidson et al. 2004). In mice, injection of cathelicidin-related antimicrobial peptide (CRAMP) results in the recruitment of neutrophils and monocytes (Kurosaka et al. 2005). This enhanced chemokine production may have important therapeutic implications, as local application of MCP-1 has been shown to reduce *S. aureus* infection in an osteomyelitis rat model by increasing the number of neutrophils, the first responders to *S. aureus* infection (Li et al. 2010).

Human defensins display a variety of chemotactic roles inducing the migration of immature dendritic cells and lymphocytes, promoting adaptive immunity. For example, h β D2 is capable of enhancing mobility of immature dendritic and memory T cells via interactions with chemokine CCL-20 receptor CCR6 (Yang et al. 1999). Along with CCR6, β -defensins bind to chemokine receptor CCR2 expressed on monocytes, dendritic cells, and certain macrophage subsets. Importantly, CCR2-mediated recruitment of monocytes is essential for innate immune defense and clearance of bacteria in vivo (Kurihara et al. 1997; Jia et al. 2008). Moreover, HNP1 and HNP2 have been shown to serve as a chemotactic for CD4 and CD8 T cells as well as immature dendritic cells via unidentified receptors (Yang et al. 2000).

12.4.2 Wound Healing

LL-37 plays a role in the re-epithelialization of skin wounds and wound closure. Upon skin injury, high levels of LL-37 precursor protein, hCAP18, is produced in the wound bed and it has been suggested that LL-37 plays a role in epithelial cell proliferation. Similarly, low levels of LL-37 precursor protein hCAP18, have been correlated with delayed wound closure and chronic ulcers. Moreover, treatment of anti-LL-37 antibodies inhibited epithelial healing in an ex vivo wound healing model in a dose-dependent manner (Heilborn et al. 2010). Furthermore, h β D3 accelerated wound healing in an *S. aureus*-infected porcine diabetic wound.

12.4.3 Anti-inflammatory

Certain HDPs are important for protecting the host from a harmful cytokine storm that is imposed during bacterial infection. For example, LL-37 has shown to attenuate the production of pro-inflammatory mediators (IL-1 β , IL-6, IL-8, and TNF- α) in neutrophils when subjected to *S. aureus* (Alalwani et al. 2010). Likewise, in PBMCs, production of anti-inflammatory IL-10 is up-regulated. This effect on cytokine release is mediated by LL-37 binding directly to an internal signaling molecule, GAPDH, impairing p38 MAPK signaling and subsequent transcription of chemokines and cytokines (Mookherjee et al. 2009). As inflammation has shown to exacerbate conditions such as pneumonia and early stage sepsis, anti-inflammatory activities of HDPs can be considered an asset provided bacterial clearance is not compromised. Fortunately, certain HDPs such as LL-37 enhance neutrophil-killing capacity by increasing *S. aureus* phagocytosis and enhancing ROS production (Alalwani et al. 2010). Similarly, mice deficient in cathelicidin-related antimicrobial peptide (CRAMP) or murine cathelicidin showed significantly less bactericidal activity against *S. aureus*.

12.5 *S. aureus* HDP Evasion Techniques

Despite the numerous anti-infective roles of HDPs, *S. aureus* can tolerate relatively high concentrations of these peptides (Peschel et al. 1999). As with other innate and adaptive immune responses, *S. aureus* has developed multiple HDP evasion mechanisms (summarized in Fig. 12.1). It is thought that cationic HDPs and HDP-resistance mechanisms have co-evolved to allow *S. aureus* to quickly adapt to these integral and ancient host defense components (Peschel et al. 1999).

S. aureus can recognize challenges by various HDPs using the antimicrobial peptide sensor (Aps) system, which induces several resistance mechanisms (Li et al. 2007a, b). One major Aps-regulated mechanism is the activation of the *dltABCD*

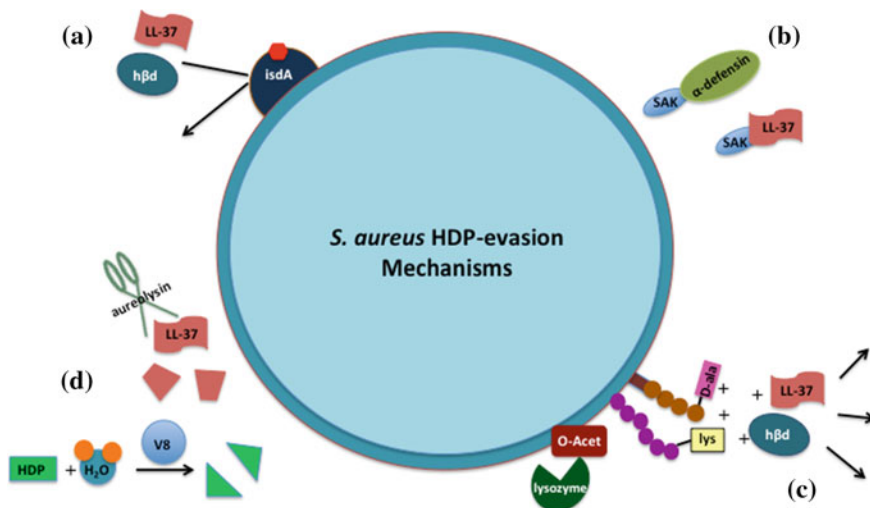


Fig. 12.1 *S. aureus* HDP immune evasion mechanisms. **a.** HDP repulsion via hydrophobic surface molecules. Cell-wall bound proteins such as IsdA, decrease bacterial hydrophobicity, resulting in increased resistance to certain HDPs. **b.** HDP inactivity via staphylokinase (SAK) interference. SAK has shown to form a complex with alpha-defensins, abrogating their activity. Also, SAK binds directly to cathelicidin, enhancing SAK-dependent plasminogen activation, fibrinolysis and bacterial dissemination. **c.** Cell surface modifications repel HDPs. Activation of the *dltABCD* operon and expression of MprF, incorporate positively charged amino acids to cell surface constituents, causing repulsion of positively charged HDPs. Steric hindrance is created via the O-acetylation of peptidoglycan muramic acid preventing lysozyme from targeting *S. aureus*. **d.** Degradation of HDPs by secreted enzymes. Aureolysin and V8 protease are two major *S. aureus*-secreted proteases that cleave and inactivate HDPs

operon, which incorporates positively charged D-alanine onto *S. aureus* anionic teichoic acids, conferring a greater positive charge and ultimately repelling HDPs such as defensins and LL-37 (Peschel et al. 1999). Moreover, to reduce anionic charge, *S. aureus* expresses multiple peptide resistance factor, MprF, which transfers lysine to anionic membrane lipid phosphatidylglycerol (PG), and translocates the lysyl-PG to the outer membrane leaflet conferring a net +1 charge and resulting in α -defensins and LL-37 repulsion (Peschel et al. 2001). Indeed, MprF contributes to clinical failures of daptomycin, the only currently available AMP therapy used to combat *S. aureus* infections (Jones et al. 2008). Interestingly, MRSA strains are more resistant to LL-37 compared to less positively net-charged methicillin-susceptible *S. aureus* (MSSA) isolates, verifying electrostatic repulsion as a major resistance mechanism (Ouhara et al. 2008).

S. aureus secretes an array of factors that contribute to resistance against the innate immune system and HDPs. LL-37 is susceptible to proteolytic degradation by two major *S. aureus*-secreted proteases, aureolysin and V8 protease. Specifically, V8 protease is involved in hydrolyzing particular peptide bonds, while aureolysin cleaves LL-37, abolishing its antimicrobial activity (Sieprawska-Lupa et al. 2004).

Furthermore, the exoprotein staphylokinase (SAK) has been shown to form a complex with alpha-defensins, abrogating the effect of these peptides in vitro and in vivo (Jin et al. 2004). *S. aureus* also exploits the production of cathelicidin as it binds directly to staphylokinase, which enhances SAK-dependent plasminogen activation and fibrinolysis, resulting in bacterial dissemination and enhanced virulence (Braff et al. 2007). Dermcidin has also been shown to induce global regulatory changes, resulting in the expression of dermcidin-degrading proteases in *S. epidermidis* and *S. aureus* (Lai et al. 2007). Furthermore, *S. aureus* expresses IsdA, a cell-wall bound heme-binding protein that decreases bacterial hydrophobicity, resulting in increased resistance to bactericidal human skin fatty acids as well as cathelicidins and β -defensins (Clarke et al. 2007).

Growth states have also been associated with increased resistance to HDPs. For example, *S. aureus* small colony variants (SCVs), which have been associated with slow growth and complex physiological and metabolic changes, are less susceptible to RNase 7, h β D2, h β D3, and LL-37 (Glaser et al. 2014).

Finally, peptidoglycan O-acetyltransferase OatO, is a major determinant of lysozyme resistance in *S. aureus*. The enzymatic activity of OatA results in the O-acetylation of the C6 hydroxyl group of muramic acid found in peptidoglycan, creating steric hindrance and preventing lysozyme binding to peptidoglycan (Bera et al. 2005).

12.6 Therapeutics

HDPs demonstrate modest direct antimicrobial activity with concomitant immune-modulatory activities, making them ideal starting points for deriving new therapies to treat multi-drug resistant *S. aureus* infections. Furthermore, while antibiotics typically impair a specific and essential bacterial process, HDPs target multiple hydrophobic and anionic bacterial targets, making it more difficult for bacteria to develop resistance. Much work has been performed to exploit the powerful activities of natural HDPs through the creation of synthetic mimetics. This has led to the creation of peptides with improved anti-infective and anti-inflammatory activities. For example, innate defense regulator-1 (IDR-1) was derived conceptually from the bovine AMP, bactenecin. In an invasive peritonitis model, IDR-1 was protective against MRSA by enhancing levels of monocyte chemokines, thereby recruiting monocytes and macrophages to combat infection. Moreover, IDR-1 reduced levels of harmful pro-inflammatory cytokine responses, which also aided in resolving the infection (Scott et al. 2007). High-throughput screening of bactenecin derivatives led to the identification of IDR-1002, a peptide that demonstrated enhanced chemokine induction and greater protection compared to IDR-1 in an *S. aureus* peritonitis murine infection model (Nijnik et al. 2010). This heightened anti-infective activity was attributed to increased recruitment of neutrophils and monocytes to the site of the infection. Synergistic therapy combining two peptides has also demonstrated efficacy in live infection models. For instance, combining

LL-37 and IDR-1 ameliorated MRSA-induced pneumonia by significantly attenuating anti-inflammatory cytokine release (mainly TNF- α and IL-6) in bronchoalveolar lavage fluid, reducing pulmonary tissue damage. Furthermore, another 12-amino acid bacteriocin derivative, IDR-1018, possessed very potent immune-modulatory properties through the induction of chemokine and suppression of pro-inflammatory responses. Along with these activities, IDR-1018 demonstrated accelerated wound healing in an *S. aureus*-infected porcine wound model compared to LL-37 (Steinstraesser et al. 2012). Interestingly, this activity was not conserved in an immune-compromised infection model, demonstrating the importance of a functional immune state for peptide activity. Furthermore, in an orthopedic implant *S. aureus* murine infection model, IDR-1018 accelerated the clearance of *S. aureus* by enhancing the recruitment of macrophages (Choe et al. 2015). In this model, IDR-1018 also enhanced osseointegration, which is typically impaired with *S. aureus* bone infection.

12.7 Constraints to HDP Therapeutic Development

Their numerous anti-infective roles make HDPs intriguing candidates for *S. aureus* infections. Nevertheless, there are many hurdles that must be overcome before they may become commercially available. Here, we will highlight these issues, which include toxicity, immunogenicity, susceptibility to proteolytic degradation, and cost.

12.7.1 Toxicity

Unfortunately, a major impediment for the pharmaceutical exploitation of HDPs is their toxicity. This toxicity can be due to many reasons, one of which is the potential of HDPs to stimulate immune responses, which can have unforeseen consequences. In fact, high levels of HDPs have been previously linked to diseases. For example, in humans, abnormally high levels of cathelicidin in facial skin have been linked to rosacea (Yamasaki et al. 2007). In mice, injection of LL-37 in mouse skin induced inflammatory hallmarks of rosacea, such as erythema and vascular dilatation (Yamasaki et al. 2007). This coincided with an increase in IL-8 production and neutrophil infiltration. Moreover, significantly elevated levels of LL-37 have been identified in psoriatic lesional skin (Morizane et al. 2012), where heightened levels of LL-37 were shown to increase the expression of TLR9 on keratinocytes. The enhanced TLR9 expression sensitizes keratinocytes to their ligands, CpG or genomic DNA, resulting in the increased production of type I IFNs, which exacerbate psoriasis (Morizane et al. 2012). Furthermore, LL-37 and h β D2 were shown to stimulate histamine release from mast cells (Niyonsaba et al. 2001).

Interestingly, LL-37-induced mast cell activation results in the release of β -tryptase, a LL-37 degrading enzyme (Duplantier and van Hoek 2013).

Hydrophobic cores of HDPs and synthetic mimetics have been shown to self-associate, aggregate, integrate into zwitterionic membranes, and cause hemolysis (Yin et al. 2012). Although not much is known about whether aggregation is responsible for the observed immune-modulatory effects displayed by HDPs, hydrophobicity (within a certain window) is required for bacterial membrane insertion. Therefore, these properties must be tampered with carefully, preventing peptide inactivation or increase of toxicity (Bahar and Ren 2013).

It is thought that since HDPs have been conserved throughout evolution, they should represent feasible anti-infective strategies (Mansour et al. 2014). In addition, HDPs can be altered to reduce toxicity. For instance, judicious formulation such as nanoparticle encapsulations can alter charge distribution and minimize toxic aggregation. Peptide lengths can be adjusted to minimize toxicity. For example, a shortened 15-amino acid derivative of melittin proved to be 300 times less toxic than melittin (Subbalakshmi et al. 1999). Simple high-throughput screening methodologies that measure cytolytic properties can be used to select for new peptide candidates with reduced toxicity (Haney et al. 2015). Moreover, after HDP targets are identified, computer-aided system biology approaches can be used to predict molecular pathways that may be interrupted, preventing undesirable off-targets of new HDP therapies.

12.7.2 Degradation

Another potential constraint that would reduce efficacy of HDP therapy is the risk of proteolytic degradation. As previously indicated, HDPs are inactivated and degraded by *S. aureus*-secreted enzymes and proteases (See Sect. 12.5). Furthermore, endogenous host enzymes readily degrade HDPs. Notably, digestive enzymes such as trypsin and chymotrypsin cleave peptides at basic and hydrophobic residues altering important structural and functional features of HDPs (Kim et al. 2014).

Many measures can be taken to tackle degradation issues of HDP therapy. Since host proteases cleave peptide bonds between naturally occurring residues, incorporating non-proteinogenic amino acids such as ornithine and β -dihydrophenylalanine into HDP structures can potentially improve metabolic stability (Bahar and Ren 2013). Moreover, cyclization of linear peptides has been shown to increase protease resistance of HDPs (Rozek et al. 2003). As host proteases only cleave peptides with L-enantiomeric backbones, the incorporation of D-amino acids in peptides can drastically reduce degradation, as has been shown with LL-37 (Wang et al. 2014). Presumably due to increased stability, D-amino acid peptides demonstrated greater protective activity compared to their L-counterparts against lethal multi-drug resistant bacteria (de la Fuente-Nunez et al. 2015). However, little is known regarding the pharmacokinetics and toxicity surrounding D-peptide

therapies and whether such manipulations would affect immune-modulatory targets. Furthermore, such modifications in peptide structure and composition are likely to increase the costs of peptide synthesis. Kim et al., described a more economical approach to designing peptides with residues that are systemically arranged to avoid protease-targeted sites (Kim et al. 2014). By using this method and maintaining the structural features that are important for HDP activity (amphipathy, cationic character, helicity, etc.), peptides with retained antimicrobial activity but heightened stability against host proteases could be derived.

12.7.3 Immunogenicity

As mentioned, HDPs are capable of interacting with cells of both the innate and adaptive arms of the immune system, eliciting a number of immunomodulatory roles. While these characteristics may serve as the basis for their protection, peptides may also prove to be immunogenic, stimulating an undesirable humoral response.

Immunogenicity, specifically through the development of anti-therapeutic antibodies, has been reported in a number of current FDA-approved antibody and protein-based therapies (Baker et al. 2010). Initially, these events can be triggered when the foreign peptide is recognized by an antigen-presenting cell (APC). For example, scavenging dendritic cells can phagocytose and present the foreign peptides via the exogenous MHC class II processing pathway, ultimately priming T cell responses. Capturing of antigen by dendritic cells is typically mediated by the FcR receptors that can interact with peptide-immune complexes. Indeed, LL-37 and certain defensins have also been shown to interact with TLRs on the surface of dendritic cells. These interactions can further activate the cells, resulting in the maturation and expression of lymphocyte co-stimulatory receptors initiating a T-cell dependent anti-peptide response (Yang et al. 2009). T-cell independent anti-peptide responses are speculated to be triggered by aggregated peptides that effectively cross-link B cell receptors, enabling the activation of B cells. Such responses can result in the generation of neutralizing antibodies or in some cases, antibodies that cross-react with endogenous proteins. Overall, immunogenicity may result in ineffective peptides or occasionally, autoimmune diseases.

Some proof of concept methods for reducing immunogenicity of protein therapies has involved the use of immunosuppressive therapies (Reding 2006) or slowly inducing tolerance to therapies. Furthermore, removal of T cell epitopes through rational sequence design and targeted amino acid substitutions can lower the development of immunogenicity of protein therapies (Jones et al. 2009). Immunogenicity of peptide derivatives can be assayed using various in vitro T cell assays.

12.7.4 Cost

Another constraint that has hindered mass production of HDPs for therapeutic use is the high cost of synthesis. Peptide synthesis using classic fluorenylmethoxycarbonyl (F-moc) chemistry can range between \$50 and \$400 per gram of peptide, making widespread clinical usage unrealistic. As peptides are antagonized by physiological conditions and degraded by host or bacterial proteases, relatively high doses may be required to attain the desired therapeutic effects. Moreover, deriving large peptide libraries (>100 peptides) to screen for optimized peptide candidates can become exorbitantly expensive.

Although cost of peptide synthesis has remained one of the major barriers to use of HDPs, several solutions have been proposed in the literature. For example, deriving synthetic HDP mimetics with shorter sequences can tackle the high cost of production. For example, efforts to re-engineer GF-17, a short and active fragment of LL-37, has led to the development of 17BIPHE2, a peptide with enhanced activity against *S. aureus*, which has also shown anti-biofilm properties in a mouse model of catheter-related *S. aureus* infection (Wang et al. 2014). Importantly, peptides must contain a minimum of 7–8 amino acids to maintain amphipathic structures, and for α -helical AMPs, 22 amino acids are required to completely span the bacterial lipid bilayer (Bahar and Ren 2013). Furthermore, exceptional anti-infective activity of synthetic mimetics can potentially lower dosage and thus cost of peptide therapy. The classical approach to optimize peptide activity is through rational design of large synthetic peptide libraries via systematic single amino acid substitutions of short HDP backbone templates (Haney et al. 2015). High-throughput screening methodologies can then select peptides that are optimized for various biological properties. For example, screening for anti-*S. aureus* biofilm activity, chemokine induction and endotoxin suppression, led to the selection of the optimized peptide IDR-2009 (Haney et al. 2015). Lastly, exploiting biological expression systems to derive recombinant fusion peptides serves as a scalable and low cost alternative for peptide synthesis (Li 2009). However, purification of peptides from prokaryotic systems must be carried out carefully to prevent endotoxin and bacterial contamination.

12.8 The Future of HDP Therapy

12.8.1 Synergistic Cocktails

Many of the aforementioned issues hindering widespread clinical use of HDPs can be tackled by administering synergistic drug cocktails. Indeed, HDPs have previously shown to act synergistically with each other as well as with conventional antibiotics. For example, studies have demonstrated that when β -defensins are combined at sub-effective concentrations with human cathelicidin (LL-37) and

lysozyme, they exhibit additive or synergistic activity, which may be important for retaining *in vivo* activity (Midorikawa et al. 2003; Chen et al. 2005). Likewise, HDPs and synthetic mimetics display strong synergistic interactions with a number of conventional antibiotics (Reffuveille et al. 2014). Presumably, synergistic combination therapy would drastically lower the dosage of peptide and antibiotic required, reducing the overall cost of peptide therapy and toxicity.

12.8.2 Stimulating Natural HDP Production

Enhancing nature's own arsenal may represent a safer and more feasible method for HDP-directed therapies. Studies have demonstrated that inducing LL-37 by stimulating keratinocytes with both butyrate and vitamin D3 increases antimicrobial activity of keratinocytes against *S. aureus* (Schauber et al. 2008). Furthermore, topical treatment with the vitamin D analog, calcipotriol, following acute skin infection enhanced levels of hCAP18/LL-37 in human skin (Heilborn et al. 2010). As LL-37 has been shown to promote re-epithelialization and tissue repair, therapies that promote LL-37 production may serve as effective wound treatments. However, as previously noted (Sect. 12.7.1), LL-37 displays a wide variety of immune-regulatory activities and levels must be carefully tuned to avoid any adverse consequences.

12.8.3 Impairing CAMP Resistance Mechanisms

An interesting and unexplored avenue for HDP-targeted therapy is to inactivate CAMP resistance mechanisms to sensitize *S. aureus* to HDPs. Studies by Li et al. have shown that mutants of the Aps HDP-sensing system are less virulent in an *S. aureus* murine infection model (Li et al. 2007a, b). Likewise, inactivating Dlt reduces the D-alanine addition to teichoic acids, thereby increasing *S. aureus* susceptibility to HDPs (Peschel et al. 1999). Consistent with these findings, mutants lacking *dltA* and *mprF* are more susceptible to HDPs and have attenuated virulence *in vivo* (Peschel et al. 1999; Collins et al. 2002; Kristian et al. 2003; Weidenmaier et al. 2005). Moreover, targeting secreted proteases that degrade HDPs may help to enhance the activity of HDPs.

12.9 Conclusions

HDPs serve as one of the first lines of defense against *S. aureus* infections. Specifically, defensins, cathelicidins, dermcidins, and RNase 7 display potent anti-staphylococcal activity along with a number of immune-modulatory roles.

Despite these various biological activities, *S. aureus* has developed numerous HDP evasion techniques that function for example by repelling positively charged HDPs and abrogating peptide activity. Nevertheless, many HDPs as well as synthetic peptidomimetics have demonstrated exceptional anti-*S. aureus* activity. Scalable and commercial use of HDPs or their synthetic counterparts is, however, constrained by the cost of production, toxicities, immunogenicity and degradation. The future of HDP therapeutic development relies on re-engineering peptides with greater biological activity and reduced toxicities, deriving synergistic cocktails, identifying new HDP-stimulants and sensitizing bacteria to HDPs.

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