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DEFENSINS: A NOVEL APPROACH TO USE PLANT ANTIMICROBIAL PEPTIDES AS AN ALTERNATIVE TO ANTIBIOTICS

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ABSTRACT

Indiscriminate and irrational use of antibiotics has created an unprecedented challenge for human civilization due to microbes development of antimicrobial resistance. It is difficult to treat bacterial infection due to bacteria ability to develop resistance against antimicrobial agents. Antimicrobial agents are categorized according to their mechanism of action, i.e., interference with cell wall synthesis, DNA and RNA synthesis, lysis of the bacterial membrane, inhibition of protein synthesis, inhibition of metabolic pathways, etc. Bacteria may become resistant by antibiotic inactivation, target modification, efflux pump and plasmidic efflux. Currently, the clinically available treatment is not effective against the antibiotic resistance developed by some bacterial species. However, plant-based antimicrobials have immense potential to combat bacterial, fungal, protozoal and viral diseases without any known side effects. Such plant metabolites include quinines, alkaloids, lectins, polypeptides, flavones, flavonoids, flavonols, coumarin, terpenoids, essential oils and tannins. Antimicrobial peptides (AMPs) are ubiquitous, gene-encoded natural antibiotics that have gained recent attention in the search for new antimicrobials to combat infectious disease AMPs are being extensively evaluated as novel antimicrobial drugs. Plant AMPs are predominantly cysteine-rich compounds that have been isolated from different plant species and from different tissues and show specificity towards Gram-negative or Gram-positive bacteria. Many AMPs kill bacteria by disruption of membrane integrity and are thus thought to be less likely to induce resistance, AMPs are being extensively evaluated as novel

antimicrobial drugs. This review summarizes and discusses the antibiotic properties of AMPs highlighting their potential as alternatives to conventional antibiotics.

KEYWORDS: antibiotics, antimicrobial, mechanism of action, defensins, disease.

INTRODUCTION

Since the start of the 90s heaps of cationic plant, cysteine-rich antimicrobial peptides (AMP) have been contemplated. In any case, instituted the expression "plant defensin," after examination of another class of plant antifungal peptides with known creepy crawly defensins.[1] From that point, many plant defensins have been accounted for and thinks about on this class of peptides envelop its action toward microorganisms and sub-atomic components of the system of activity against microscopic organisms and growths. We are presently confronting a period of anti-toxin resistance in our healing facilities and groups. While, in the no so distant past, the weapons store of anti-microbials seemed adequate to adapt to bacterial ailments, we are currently heading towards (and apparently as of now in) an emergency circumstance with anti-infection resistance. Accordingly, a mounting exertion is in progress to distinguish and create novel anti-infection treatments to help manage present and rising safe microorganisms. Be that as it may, while enhanced variations of conventional anti-infection agents have been produced for a considerable length of time, regularly to address issues with resistance in any case prompting alterations of an indistinguishable resistance instruments from seen with the parent intensifies, the advancement of in a general sense new mixes has falled behind. Among the not very many novel treatments in the pipeline, the as of late created cationic antimicrobial peptides have risen up out of their source as nature's antibiotics[2] to wind up plainly encouraging formative and clinical hopefuls.

RELATED WORK

Antimicrobial peptides (AMPs) are ubiquitous and found as host defenses against pathogens and pests in diverse organisms ranging from microbes to animals.[3] AMPs exist in different molecular forms, although the majority of them are linear peptides from insects, animals and plants. Nevertheless, bacteria produce polycyclic peptides such as lantibiotics and all major forms of life produce circular peptides which include bacteriocins from bacteria, cyclotides from plants and theta-defensins from animals.[4-6] In plants, the majority of AMPs are Cys-rich[7], a feature that enables the formation of multiple disulfide bonds (usually two to six) that contribute to a compact structure and resistance to chemical and proteolytic degradation.

Antimicrobial peptides (AMPs) have been described as evolutionarily ancient weapons against microbial infections.[8] The plant defensins were shared structured properties with mammalian and insect defensins. Plant defensins isolated from wheat and barley grains by Mendez and co-workers[9,10] and these peptides named y-thionins have size (5 kD) and same number of disulfide bridges(four)as a –and p-thionins.[11-13] Proteins isolated from seeds of monocot and dicot are found be homologous to "y" thionins[14-17] or identified via the sequencing of cDNA clones.[18]

STRUCTURE AND CHARACTERISTICS OF PLANT DEFENSINS

Plant defensins present a well-conserved three-dimensional structure composed by a cysteine-stabilized α/β (CSαβ) motif, which forms one α-helix followed by three anti-parallel β-sheets. The amino acid sequence is also quite conserved, especially due to the presence of six to eight cysteine residues, which form three to four disulfide bridges in the sequence of Cys1-Cys8, Cys2-Cys5, Cys3-Cys6 and Cys4-Cys7.[20] Nevertheless, plant defensins with five disulfide bonds have been described, such as the peptide from Petunia hybrida (PhD1), whose cysteine residues interact in the following order: Cys1-Cys10, Cys2-Cys5, Cys3-Cys7, Cys4-Cys8 and Cys6-Cys9.[21] The additional disulfide bond does not affect the typical three-dimensional structure of the defensin, which is located after the α-helix and the first β-sheet. Instrument of activity.

Most microbes are possibly vulnerable to cationic antimicrobial peptides, except for certain refractory species, for example, Burkholderia and typically Serratia and Proteus spp.[22] While there are many reports on such peptides in the writing, there are in actuality just a little rate that have been contemplated top to bottom. The instrument of activity of cationic antimicrobial peptides against microscopic organisms has been considered seriously for just a couple select peptides. Discussion with respect to their instruments of activity depends on the convoluted way of their activity. In reality, it has been proposed that cationic antimicrobial peptides are 'messy medications'[23] in that they conceivably have many targets attributable to their amphiphilic nature and cationic charge. Contrasted and customary anti-infection agents, for example, the [beta]-lactams, which have a spotless instrument of activity with a solitary target site, this makes these peptides harder to examine however then again all the more captivating. While the creed for a long time was that the sole instrument of activity for cationic antimicrobial peptides against microbes was to collaborate with and crush the film porousness hindrance of bacterial cells, it has as of late turned out to be evident that option or

potentially extra non layer targets exist. This offers ascend to two practical classes of cationic antimicrobial peptides: film troublesome and layer non problematic[24] despite the fact that the qualification might be somewhat obscured as peptides that assault layers in one animal groups could possibly have non troublesome activities in another species. Despite which class the peptide falls into, all must associate with the film (now and then two) regardless of whether it is disturbed, if just to achieve its last inward target goal.[25] Owing to the basic contrasts in the two fundamental classes of microorganisms, the pathway to the cytoplasmic layer gone by antimicrobial peptides will vary Be that as it may, the underlying association of a cationic antimicrobial peptide with a bacterial cell is through comparative components. Emphatically charged antimicrobial peptides are pulled in to the polyanionic external surfaces of a phone (because of cell divider related teichoic and lipoteichoic acids in Gram-positive and lipopolysaccharides [LPS] in Gram-negative microscopic organisms). The connection of cationic antimicrobial peptides with Gram-negative cells is better comprehended and clarified here. Following the underlying electrostatic fascination between cationic antimicrobial peptides and the external flyer of a Gram-negative cell, the cationic peptides start their own particular entry over the external film through a 'self-advanced take-up' system. These peptides accomplish this since they have a higher liking for adversely charged LPS than local divalent cations, such as Mg2+ and Ca2+ and all things considered, can cause regions of shakiness in the external layer permitting resulting translocation of the cationic antimicrobial peptides over the external film bilayer.

MEMBRANE-DISRUPTIVE CATIONIC ANTIMICROBIAL PEPTIDES

Interactions with the cytoplasmic membrane begin when the cationic antimicrobial peptides associate with the phospholipids. As long as the peptide:lipid ratio is low, the cationic antimicrobial peptides remain associated, parallel to the plane of the membrane inserted at the interface of the hydrophilic lipid head groups and the hydrophobic fatty acyl chains. However, as the peptide:lipid ratio increases, these peptides are able to aggregate and/or reorient in the membrane and disrupt membrane integrity. as described through one of four proposed models: barrel-stave, aggregate, carpet and toroidal pore. While each of these models have been implicated with selected cationic antimicrobial peptides, no single model is more accurate than another, although the aggregate model explains how cationic antimicrobial peptides can affect killing through both membrane permeation and internal target attack.

CONCLUDING REMARKS

Antibacterial peptides have been described in many different plant species. They belong to a wide range of protein families, varying from typical antimicrobial members to newly discovered ones. Some peptides show specificity towards Gram-positive or Gram-negative bacteria, but most of them are able to inhibit the activity of both. Therefore, there is at present no way to predict the specificity of any given antimicrobial peptide. There are few reports describing the tertiary structures of such peptides. However, in silico analyses have shown that plant antibacterial peptides present similarities in their three-dimensional structures, although their primary amino acid sequences vary according to the protein family to which they belong. Knowledge of the tertiary structure could yield new insights into the mechanism of action against pathogenic bacteria. Moreover, the description of the mechanism of action for these antibacterial peptides suggests that it may involve a strong interaction with phospholipids from the pathogen's membrane. Parameters such as molecular volume, aggregation ability and auto assembly onto the membrane surface are essential for activity against bacteria. Indeed, although the mode of action of antibacterial peptides is well-characterized, investigations of the relative importance of specific amino acid residues and their binding with the bacterial cell wall are still in progress.

Compliance with Ethical Standards

Conflict of Interest: The author has no competing interests to declare.

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