

David Andreu¹

Luis Rivas²

¹ Universitat de Barcelona,
Barcelona, Spain

² Centro de Investigaciones
Biológicas (CSIC),
Madrid, Spain

Animal Antimicrobial Peptides: An Overview

Abstract: Antibiotic peptides are a key component of the innate immune systems of most multicellular organisms. Despite broad divergences in sequence and taxonomy, most antibiotic peptides share a common mechanism of action, i.e., membrane permeabilization of the pathogen. This review provides a general introduction to the subject, with emphasis on aspects such as structural types, post-translational modifications, mode of action or mechanisms of resistance. Some of these questions are treated in depth in other reviews in this issue. The review also discusses the role of antimicrobial peptides in nature, including several pathological conditions, as well as recent accounts of their application at the preclinical level. © 1999 John Wiley & Sons, Inc. Biopoly 47: 415–433, 1998

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INTRODUCTION

Despite their structural and functional diversity, multicellular organisms have certain common features in their defense-and-surveillance systems against pathogens. Early concepts of nonspecific and specific defense systems for plants and animals, respectively, are being reevaluated and expanded in the light of growing evidence that plants are endowed with certain specific defense systems, while on the other hand innate (nonadaptive) immunity in animals largely depends on nonspecific effectors.^{1–6} In particular, gene-encoded antimicrobial peptides are now clearly established as key players in both plant and animal defense systems. In the last two decades, a considerable num-

ber of peptides, either inducible or constitutive, and with activity against different types of microorganisms, have been found in almost all groups of animals. These discoveries were preceded by the finding of thionins in plants,⁷ the earliest example of antimicrobial peptides related to host defense. At the moment of this writing, several hundreds of structures with some type of antimicrobial activity have been described. A quite comprehensive, periodically updated data base can be found on the Internet at <http://www.bbcm.univ.tries.it/~tossi>. The present chapter is meant to provide a general overview of the main families of animal host defense peptides, as well as selected details on their biological action, including

Correspondence to: David Andreu, Department of Organic Chemistry, Universitat de Barcelona, Martí i Franquès 1-11, E-08028 Barcelona, Spain; email: andreu@admin.qo.ub.es

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also relevant synthetic analogues. A number of significant aspects of this emerging field have been covered by recent reviews^{8–23} and by the accompanying articles in this issue.

STRUCTURAL ASPECTS

A considerable variety of peptide sizes and structures are associated to antimicrobial activity in eukaryotic hosts. The early classification of antimicrobial peptides on a taxonomical basis has been increasingly found inadequate, in view of the fact that very similar structural patterns are shared by peptides from widely different organisms. In contrast, the alternative classification based on chemical-structural criteria¹ is still quite useful for cataloging the different families of antimicrobial peptides. This classification defines two broad groups, corresponding to linear and cyclic structures, respectively. Within the first group, two subgroups can be distinguished (a) linear peptides tending to adopt α -helical amphipathic conformation (Table I); and (b) linear peptides of unusual composition, rich in amino acids such as Pro, Arg, or (occasionally) Trp (Table II). The second group, encompassing all cystine-containing peptides, can also be divided into two subgroups corresponding to single or multiple disulfide structures (Tables III and IV), respectively. Tables I–IV include sequences of some the earliest reported antimicrobial structures, as well as recent noteworthy additions, with no pretense to be exhaustive. Readers looking for additional structures are directed to the above Internet address and other general reviews of this field.^{1–23}

A number of secondary structures of antimicrobial peptides, broadly representative of the above structural groups, have been determined by two-dimensional nmr, either in solution or in model membrane environments. They include cecropins,^{89–92} magainins,^{93–95} PGLa,⁹⁶ sarcotoxin,⁹⁷ buforin,⁹⁸ caerin,⁹⁹ bactenecins,¹⁰⁰ enkelytin,¹⁰¹ histatin,¹⁰² ranalexin,¹⁰³ thanatin,¹⁰⁴ protegrin,¹⁰⁵ tachyplesin,¹⁰⁶ different types of defensins,^{107–115} and drosomycin.¹¹⁶

POSTTRANSLATIONAL MODIFICATIONS

Antimicrobial peptides display different types of post-translational modifications that can modify their activity in a significant way. The following are among the most frequent.

Glycosylation

Glycosylation has been described in five antimicrobial peptides from insects, all of them belonging to the proline-rich structural subgroup: diptericin,⁵⁰ drosocin,⁵¹ formaecin,⁵³ lebocin,⁵⁶ and pyrrhocoricin.⁶⁰ Occurrence of glycosylation is probably underestimated; for instance, a diptericin-like peptide from *Sarcophaga peregrina*¹¹⁷ reported before the first report on drosocin glycosylation⁵¹ has not been further investigated in this respect. Only *O*-glycosylation has been described to date in insects, with the oligosaccharide chain linked to the peptide backbone through a threonine residue. Although a common requirement for *O*-glycosylation seems to be the presence of nearby proline residues, especially in positions –1 and +3 from the glycosylated threonine,¹¹⁸ one of the oligosaccharide chains of diptericin occurs in a glycine-rich region.⁵⁰ *O*-oligosaccharide chains are short and often microheterogeneous. Glycosylations with only one (GalNAc → Thr), two (Gal → GalNAc → Thr), or three (Glc → Gal → GalNAc → Thr) glycan residues have been described.^{50,51,53,56,60} As a general rule, integrity of the oligosaccharide chain is necessary for optimal antimicrobial activity. Thus, treatment of diptericin with *O*-glycosidase abolished the antibacterial activity of diptericin against most bacteria tested⁵⁰ and the antibacterial activity of a nonglycosylated synthetic drosocin is several times lower than the native compound.⁵⁶

Aside from its important role in antimicrobial activity, little is known about other roles of glycosylation in the lethal mechanisms of the corresponding peptides, though some ideas have been advanced, such as protection against proteinases, modification of secondary structure inhibition of enzymes involved in peptidoglycan biosynthesis or specific recognition between pathogen and peptide.^{50,51,53,119} It is noteworthy that glycosylated peptides do not seem to have membrane permeabilization as their main mechanism of action. Evidence for nonmembrane mechanisms are as follows: (a) Deglycosylated all-*D*-diptericin is much less active than the deglycosylated natural form.¹²⁰ (b) Kinetics of the lethal process is usually quite slow for membrane permeabilization; long contact periods (usually hours) between peptide and microorganism are required for pyrrhocoricin, drosocin, and formaecins to produce a bactericidal effect.^{50,51,53}

Disulfide Bonds

Intramolecular disulfide bonds are relatively common in antimicrobial peptides. Structures ranging from one to five disulfides have been reported (Tables III and

Table I Linear Antimicrobial Peptides with Helical Conformation

Peptide	Sequence	Source	Reference
Andropin	VFIDILDVKVNAIHNAAQVGVGIGFAKPFEKLJINPK	Fruit fly (<i>Drosophila melanogaster</i>)	24
BLP-1	GIGASILSAGKSALKGLAKGLAHEHFAN ^a	Asian toad (<i>Bombina orientalis</i>)	25
Bombinin	GIGALSAKGALKGLAKGLAHEHFAN ^a	Yellow-bellied toad (<i>Bombina variegata</i>)	26
Bombolitin	IKITTMALAKLGKVLAHV ^a	Bumblebee (<i>Megabombus pennsylvanicus</i>)	27
Cecropin A	KWKLFLFKTIKVKVGQNIRDGIIKAGPAVAVVGOATQIAK	Silk moth (<i>Hyalophora cecropia</i>)	28
Cecropin	RWKIFFKIEKMGGRNIRDGIVKAGPAIEVIGSAKAI ^a	Silk moth (<i>Bombyx mori</i>)	29
Cecropin	WNPFKELLERAGQRVRDAVISAAAPAVATVGGAAAATARG ^a	Tobacco moth (<i>Manduca sexta</i>)	30
Cecropin C	GWLKKLKGKRTERIQHQHTRDATIQQLGLIAQQAAANVAAATARG ^a	Fruit fly (<i>Drosophila melanogaster</i>)	31
Cecropin P1	SWLSKTIKKLENSAKKRISSEGIAIAIQGGF ^a	Pig (<i>Sus scrofa</i>)	32
Ceratoxin A	SIGSALKKALPVAKIKIGKIALPIAKAALP	Mediterranean fruit fly (<i>Ceratitis capitata</i>)	33
Clavanin A	VFQFLGKI IHHVGNFVHGFSHV ^a	Tunicate (<i>Sryela clava</i>)	34
CRAMP	ISRLLAGLLRKGGKEIGEKLKKIGQKIKNFFFQKLVPQPE	Mouse (<i>Mus musculus</i>)	35
Dermaseptin 1	ALWKITMLKKLGTMTMALHAGKAALGAANTISQGTQ	Arboreal frog (<i>Phyllomedusa sauvagii</i>)	36
Enbocin	WNYFKEIERAVARTRDAVISAGPAVATVAAATSVAS ^a	Silk moth (<i>Bombyx mori</i>)	37
FALL-39	FALLGDDFFRKSKKEKIGKEFKRIVQRIKDFLRNLVPRTES	Man (<i>Homo sapiens</i>)	38
Lycotoxin I	IWLTAALKFLGKHAAKHLAKQQQLSKL ^a	Wolf spider (<i>Lycosa carolinensis</i>)	39
Magainin 1	GIGKFLHSAGKFGKAFVGETMKS	South African clawed frog (<i>Xenopus laevis</i>)	40
Melittin	GIGAVLKVLTTTGLPALISWIKRKRQQ ^a	Honeybee (<i>Apis mellifera</i>)	41
Misgurin	RQRVEELSFKFSKKGAAARRRK	Mudfish (<i>Misgurnus anguillicaudatus</i>)	42
PGLa	GMA SKAGAIAGKIAKVALKAL ^a	South African clawed frog (<i>Xenopus laevis</i>)	43
Pleurocidin	GWGSFFKKAHHVGKHVGKAALTHYL	Winter flounder (<i>Pleuronectes americanus</i>)	44
Seminalplasmin	SDEKASPDKHHRFSLSRYAKLANRLANPKLLETFLSKWIGDRGNRSV	Ox (<i>Bos taurus</i>)	45
Styelin	GWFGKAFRSVSNFYKKHKTYIHAGLSAATTLLG	Tunicate (<i>Sryela clava</i>)	46

^a C-terminally amidated sequences.

Table II Linear Antimicrobial Peptides Rich in Certain Amino Acids

Peptide	Sequence	Source	Reference
Abaecin	YVPLNPVPQPGRRPFPTFPQQGPFPNPKIKWPQGY	Honeybee (<i>Apis mellifera</i>)	47
Apidaecin IA	GNNRPVYIPQPRPPHPRI ^a	Honeybee (<i>Apis mellifera</i>)	48
Bactenecin 5	RFRPPIRPPPIRPPFYPPFRPPIRPPFIRPPFIRPPLRFP	Ox (<i>Bos taurus</i>)	49
Diptericin	DEKPKLILPT ^b FAPPNLIPQLVGGGGNKRKGFGVSVDAHQKVW	Black blowfly (<i>Phormia terraenovae</i>)	50
Drosocin	TSDNGRHSIGVT ^b FAPPNLIPQLVGGGGNKRKGFGVSVDAHQKVW	Fruit fly (<i>Drosophila melanogaster</i>)	51
Enkelytin	GKPRPYSPRPT ^b SHPRPITRV	Ox (<i>Bos taurus</i>)	52
Formaecin 1	KRFAEPLPSEEAGES ^c YS ^c KEVPEMEKRYGGM ^a	Australian ant (<i>Myrmecia gulosa</i>)	53
Histatin 1	DS ^c HEKRRHHGYRKFKHEKHSHSKEFPFYGDYGSNYLYDN	Human (<i>Homo sapiens</i>)	54
Indolicidin	ILPWKWPWWPWR ^a	Ox (<i>Bos taurus</i>)	55
Lebocin 1	DLRFLYPRGKLPPVPT ^b PPPFNPKPITYIDMGNRY	Silk moth (<i>Bombyx mori</i>)	56
Metchnikowin	HRHQGPIFDTRPSPPFNQNQPRPGPIY	Fruit fly (<i>Drosophila melanogaster</i>)	57
PR-39	RRRPRPPYLPRPRPPFPFPRLPPRPIPPGFPFPFPFPFP	Pig (<i>Sus scrofa</i>)	58
Prophenin	AFPPPNVPGPR (FPPPNFPGPR) ₃ FPPPNFPGPP	Pig (<i>Sus scrofa</i>)	59
Pyrhocoricin	FPPP IFPGPW FPPPPPFPRP P FFGPPRFP ^a	Sap-sucking bug (<i>Pyrhocoris apterus</i>)	60
Tenezin	VDKGSYLLPRPT ^b PPRPITYNRN	Yellow mealworm (<i>Tenebrio molitor</i>)	61
	HHDGHGLGGHQTGHQQGQQGGHLLGGQQGGHLGGHQQGQPG		
	DGHLGGHQQGIGTGGQQHQHGP GTGAGHQQGYKTHGH		

^a C-terminally amidated sequences.^b Glycosylated Thr.^c Phosphoserine.

Table III Antimicrobial Peptides with a Single Cyclic Disulfide

Peptide	Sequence	Source	Reference
Bovine dodecapeptide	RLCRITVVTRVCR	Ox (<i>Bos taurus</i>)	62
Brevinin-1	ELPVVLAGIAAKVVPALFCKITKC	Japanese frog (<i>Rana brevipoda porosa</i>)	63
Brevinin-1E	ELPLLAGLAANFLPKIFCKITRKC	European frog (<i>Rana esculenta</i>)	64
Esculetin	GIFSKLGRKKIKNLISGLKRNVGKEVGMDFVVRTGIDLAGKIKGEC	European frog (<i>Rana esculenta</i>)	64
Pipinin	ELPQOAGVAAKVFPKFCAISSKKC	Common frog (<i>Rana pipiens</i>)	63
Ranalexin	ELGGGLIKIVPAMICAVTKKC	Bullfrog (<i>Rana catesbeiana</i>)	65
Thanatin	GSKKPPVPIYCNRRTGKQCRM	Hemipteran (<i>Podisus maculiventris</i>)	66
11-kD polypeptide ^a	(GLRKFRKTRKRIQKLGRKIGKTGRKVWKAWEYGQIPYPGRI) ₂	Guinea pig (<i>Cavia porcellus</i>)	67

^a Homodimer, not cyclic disulfide (only structure of this type reported so far).

IV). As with other posttranslational modifications, they do not have a unique function, and in some cases exhibit opposite effects, depending on the peptide and activity assayed. In some instances, reduction of disulfide bonds in native peptides or replacement of cysteine in synthetic analogues shows little or no effect on activity,^{121,122} whereas the same process abrogates almost completely the activity of other structures.^{123,124} Even for related peptides, sharp contrasts can be observed. Thus, reduction cancels the channel-forming activity of insect defensins on *Micrococcus luteus*,¹²⁵ and the antibacterial activity of sapecin,¹²⁶ but not liposome permeabilization by mammalian defensins.¹²⁷ Reduction of both rabbit and human defensins modifies (but does not impair) the mechanism of permeabilization, from an all-or-none mechanism for the native peptides to a gradual leakage in the reduced forms.¹²⁸ Several studies on the relevance of disulfide bonds have been performed on tachyplesins and protegrins, a group of related peptides with predominantly β -sheet structures. While native tachyplesins act upon membranes by channel formation, substantial permeabilization by a detergent-like mechanism is observed for the reduced peptide, which is less antibacterial but still active.^{129,130} Protegrins, in turn, require both disulfide bonds for channel formation but not for antibacterial activity; linear analogues with either free or acetylated thiol groups are less active on gram-negative but maintain lethal activity against gram-positive bacteria.¹³¹

The importance of disulfide bonds for peptide activity and stability is also relevant vis-à-vis the industrial production of antimicrobial peptides. If folding into native-like disulfide pairing can not be achieved spontaneously, either regioselective disulfide formation^{132,133} or production by recombinant technologies must be applied.¹³⁴ Representative examples of antimicrobial peptides with correct disulfide pattern and full biological activity prepared by chemical synthesis are protegrins,^{105,135} α -defensins,¹³⁶ androctonin,⁶⁸ rat cortistatin,¹³⁷ tachyplesin,¹²⁹ and thanatin.⁶⁶ Among those obtained by recombinant techniques are insect defensin,^{112,138} drosomycin,¹³⁹ and α -¹⁴⁰ and β -defensins.^{141,142}

Amidation

Perhaps the most common posttranslational modification of antimicrobial peptides, amidation occurs in a wide variety of peptides, such as melittin,¹⁴³ cecropins,¹⁴⁴ dermaseptins,³⁶ PGLa,¹⁴⁵ clavanin,³⁴ PR-39,⁵⁸ apidaecins,⁴⁸ diptericin,⁵⁰ prophenin,⁵⁹ polyphemusins,⁶⁹ or penaeidins.¹⁴⁶ The process in-

Table IV Antimicrobial Peptides with Several Internal Disulfides

Peptide	Sequence ^a	Cys Pairings	Source	Reference
A. Two disulfide bonds				
Androtonin	RSVCRQIKICRERRGGCCYYKCTNRPY	1–4, 2–3	Scorpion (<i>Androctonus australis</i>)	68
Polyphemusin I	RWCFGFRVCYRGFCYRKCR ^a	1–4, 2–3	Horseshoe crab (<i>Limulus polyphemus</i>)	69
Protegrin I	RGGRLLCYCRRRRFCVCVGR	1–4, 2–3	Pig (<i>Sus scrofa</i>)	70
B. Three disulfide bonds: The α -defensin family				
Cryptdin 1	LRDLVYCYSRSGCKGRERMNGTCRKGHLLYTLLCCR	1–6, 2–4, 3–5	Mouse (<i>Mus musculus</i>)	71
Cryptdin 5	LSKKLICYCRTRGCKRERRVFGTCRNLFLTFVFCC	1–6, 2–4, 3–5	Mouse (<i>Mus musculus</i>)	72
HNP-1 (α -defensin)	ACYCRIPACIAGERRYGTCTYQGRLWAFC	1–6, 2–4, 3–5	Man (<i>Homo sapiens</i>)	73
NP-1 (α -defensin)	VVCACRRALCLPERRRAGFACIRGRRIHPLCCRR	1–6, 2–4, 3–5	Rabbit (<i>Oryctolagus cuniculus</i>)	74
RK-1	MPCSCKKYCDPWEVIDGSCGLFNFSKYICCREK	1–6, 2–4, 3–5	Rabbit (<i>Oryctolagus cuniculus</i>)	75
C. Three disulfide bonds: The β -defensin family				
β -Defensin-1	DFASCHTNGGICLPNRCPGHMIIQIGCIFRPRVKCCRSW	1–5, 2–4, 3–6	Ox (<i>Bos taurus</i>)	76
Big defensin	NPLIPAIYIGATVGP SWAYLVVALVGAAGAATAANIRRASSD NHSAGGNRW/CRSKCFCRHEYVDTYYSAVCGRYFCCRSR	1–5, 2–4, 3–6	Horseshoe crab (<i>Limulus polyphemus</i>)	77
Gallinacin 1	GRKSDCFRKSGFCAFILKCPSSLTLISGKCSRFLYLCCKRIW	1–5, 2–4, 3–6	Chicken (<i>Gallus gallus</i>)	78
LAP	GFTQGVRNQSOSCRNKGICVPIRCPGSMRQIGTCLGAQVKCCRK	1–5, 2–4, 3–6	Ox (<i>Bos taurus</i>)	79
TAP	NPVSCVRNKGICVPIRCPGSMKQIGTCVGRAVKCCRKK	1–5, 2–4, 3–6	Ox (<i>Bos taurus</i>)	80
D. Three disulfide bonds: Insect defensins				
Defensin	GFFGCP LDQM QCHRHCQTITGRSSGGYCSGPKLRLTGTGCR	1–4, 2–5, 3–6	Dragonfly (<i>Aeschna cyanea</i>)	81
Defensin 4K	GFFGCP LNQQGACHRHCRSIRRRGGYCAGEFKQTCTCYRN	1–4, 2–5, 3–6	Scorpion (<i>Leiurus quinquestriatus</i>)	82
Formicin A	ATCDL LSGTG INH SCAA AHCLLRGNRGGYCNGKGVCWCRN	1–4, 2–5, 3–6	Blowfly (<i>Phormia terraenovae</i>)	83
Royalisin	VTCDL LS KFGQVN DSAACA ANCL SLSKGAGGHCEKGVCICRK TSFKDLWMDKYF	1–4, 2–5, 3–6	Royal jelly (<i>Apis mellifera</i>)	84
Sapecin	LTCEIDRSI CLLH CRLKG YLRAYCSQQKV/CRCVQ	1–4, 2–5, 3–6	Flesh fly (<i>Sarcophaga peregrina</i>)	85
E. More than three disulfide bonds				
Drosomycin	DCLSGRYKGP GAVWDNETCRRVCKEEGRSSGHCSPLSLKCWCEGC	1–8, 2–5, 3–6, 4–7	Fruit fly (<i>Drosophila melanogaster</i>)	86
ASABF	AVDFS SCARM DVPL SKVAQ GLC IS SCKF QNC GT GHCEK RGGRPTCV CDR CGR GGG EWP SVPPMPKGRSSRGRHS	Unknown	Roundworm (<i>Ascaris suum</i>)	87
Tachycitin	YLAFRCGRYSPCCLDDGP VNVL YSSCCSFYNCHKCLARLENCPK GLHYNAYLK VCDWPSKAGGTSVNKECHLWKTGRK	1–6, 2–5, 3–9, 4–10, 7–8	Japanese horseshoe crab (<i>Tachypleus tridentatus</i>)	88

volves oxidative decarboxylation of an additional C-terminal glycine residue, in a two-step enzymatic process.¹⁴⁷ Amidation prevents cleavage by carboxypeptidases and provides an extra hydrogen bond for the formation of α -helices. The correlation between amidation and biological activity is not clear: the amidated and nonamidated forms do not differ substantially in a number of cases^{135,148,149}; in other cases, however, activity is significantly impaired.^{145,150} In several cases, synthetic C-terminally amidated analogues of peptides whose native forms are not amidated show increased antimicrobial activity.^{151,152}

Halogenation

Bromination of the indole ring of tryptophan has been described in antibiotic peptides isolated from the hagfish *Mixina glutinosa*.¹⁵³ Mass spectral data also seem to support the presence of chlorine in misgurin from the mudfish *Misgurnus anguillicaudatus*.¹⁵⁴ The role of the halide atom is unclear. Whereas in the *Mixina* peptides it broadens the range of susceptible organisms, in misgurin the antibacterial activity of the synthetic analogue devoid of halogen is undistinguishable from the natural peptide.

D-Amino Acids

The occurrence of D-amino acids in eukaryotic peptides has been reported in several cases.^{155,156} In antimicrobial peptides, the only examples of this modification are bombinin from the frog *Bombina variegata*,¹⁵⁷ which have D-alloisoleucine at position 2. Since no variation in the genetic code or codon use was observed for this residue, its presence was attributed to posttranslational epimerization of the corresponding L-Ile peptide, which is also present in the organism and does not show differences in antibiotic activity. A likely role is protection against aminopeptidases.

Other Modifications

Phosphorylation has been described for histatins,⁵⁴ although absence of phosphate does not preclude candidacidal activity.¹⁵⁸ Chromacin, a fragment from chromogranin A, requires both O-glycosylation and tyrosine phosphorylation for full antibiotic activity; the synthetic nonmodified peptide is completely inactive.¹¹⁹ Enkelytin, an antibacterial peptide derived from proenkephalin A (209–237),⁵² has two phosphoserines and an oxidized methionine required for activity. Other described modifications are hydroxy-

lysine in cecropin B from silkworm⁸³ or methylated tyrosine in clavanins.⁷⁰

MODE OF ACTION OF ANTIMICROBIAL PEPTIDES

Membrane Permeabilization

Studies on both live organisms and model membranes have indicated that most antimicrobial peptides provoke an increase in plasma membrane permeability. A direct correlation between antibiotic effect and permeabilization ability has been found for defensins,^{82,128} magainins,^{159–161} cecropins,^{162–167} bactenecins,¹⁶⁸ or dermaseptins.^{36,169}

A first step in the mechanism of action is the electrostatic interaction between the cationic peptide and the negatively charged components of the membrane of the pathogen; hence, an increase in positive charge of the peptide will increase microbicidal activity. A direct correlation between cationic character and activity has been established for magainin analogues^{130,170–172} and for cecropins, where the less cationic cecropin D also shows the lowest microbicidal activity.¹⁷³ Similar correlations have been established for the interaction of cecropin A–melittin hybrids with either model membranes⁹¹ or anionic lipopolysaccharides,¹⁷⁴ for cryptdins¹⁷⁵ or for rabbit defensins.¹⁷⁶ The correlation between charge and activity is less evident in other cases, such as rat defensins lacking one Arg residue but having the same antibacterial activity¹⁷⁷ or N-terminally acetylated cecropin A–melittin hybrids.¹⁷⁸ On the other hand, many positive charges can lead to a loss of activity. For instance, decreased activity of a highly cationic magainin analogue¹³⁰ has been attributed to either destabilization of the pore due to increased repulsion among peptide monomers, or to strong peptide association with the anionic lipids, which favors fast translocation into the inner leaflet of the membrane. The positive charges also influence specificity of the peptide toward the target membrane; variation in only one charge can lead to dramatic differences in hemolytic and antibacterial properties in pardaxin¹⁷⁹ and indolicidin¹⁸⁰ analogues, or in a seminalplasmin fragment where the Glu for Lys-5 replacement considerably increases microbicidal but not hemolytic activity.¹⁸¹ In contrast, a more positively charged C-terminus of cecropin B decreases microbicidal but increases tumoricidal effects.¹⁸²

While most antibiotic peptides described in the literature are strongly cationic, a few examples of anionic peptides have been reported. Examples in-

clude polyAsp-containing fragments from the ovine pulmonary surfactant¹⁸³ and propieces of ovine trypsinogen and PYLa frog activation peptide.¹⁸⁴ In these cases, the minimal inhibitory concentrations (MICs) against common bacterial strains are much higher than those of typical cationic peptides. On the other hand, Glu-rich enkelytin⁵² shows activity in the submicromolar range against gram-positive organisms. Electron micrographs of bacteria exposed to peptide do not show the typical alterations observed for cationic peptides, suggesting a different mode of action.

An interesting group of antimicrobial peptides are those rich in His, whose net charge is pH dependent within the physiological range. Thus clavanins³⁴ from tunicates and histatins from saliva⁵⁴ show stronger activity at low pHs; the latter case is particularly relevant in view of the pH decrease caused by cariogenic pathogens.¹⁸⁵ Studies with histatin analogues^{186–188} stress the importance of His residues, though the correlation with charge is not fully clarified.

The antimicrobial activity is also affected by membrane characteristics such as phospholipid composition, sterol content, membrane potential, or the presence of polyanions (e.g., LPS, sialic acid residues). For instance, an *Escherichia coli* mutant lacking in cardiolipin is more resistant to sapecin than the wild type.¹⁸⁹ Similarly, resistance of *Serratia* to cecropin A has been related to lower levels of acidic phospholipids, closer to those of higher eukaryotes.¹⁹⁰ Also, the increased susceptibility of tumoral cells to some antibiotic peptides has been ascribed to a higher exposure of phosphatidylserine residues.¹⁹¹ Manipulation of the cholesterol content of erythrocytes resulted in a reverse relationship between sterol levels and peptide susceptibility.¹⁶⁰ Similar results have been observed for cecropins and artificial membranes.¹⁵⁰

Furthermore, the energetic status (membrane potential) of the microorganism contributes to the final outcome of the peptide-pathogen interaction. Thus, depolarized cells tend to be less susceptible to the action of antibiotic peptides.^{192,193} Finally, another relevant but controversial aspect of the mechanism of action is the position of the peptide relative to the membrane, which bears directly on the permeabilization mechanism. Two extreme situations, described respectively as the barrel-stave and carpet models, have been proposed.¹⁹⁴ This question is discussed in detail elsewhere in this issue.

Other Mechanisms

There is substantial evidence that antimicrobial peptides exert their activities through mechanisms other

than membrane permeabilization, though it is not easy to differentiate those other activities from secondary events arising from membrane permeabilization. Several findings point toward this direction. For instance, some peptides have enantio or retronenantio versions significantly less active upon certain organisms than the all-L forms,^{47,57,66,120,195} in contrast with the more general observation of all-D analogues being either equally or more active (due to proteolytic resistance).^{164,170,196,197}

Several pathways alternative to membrane permeabilization have been proposed, including inhibition of synthesis of specific membrane proteins by attacins or gloverin,^{198,199} synthesis of stress proteins,²⁰⁰ arrest of DNA synthesis by PR-39,²⁰¹ breakage of single-strand DNA by defensins,²⁰² interaction with DNA (without arrest of synthesis) by buforins,²⁰³ or production of hydrogen peroxide.²⁰⁴ Antimicrobial peptides can also act by triggering self-destructive mechanisms such as apoptosis in eukaryotic cells or autolysis in bacterial targets. Antimicrobial peptide-induced apoptosis has been described for lactoferricin²⁰⁵ and the cecropin-melittin hybrid CA(1–8)M(1–18).²⁰⁶ Autolysis, based on activation of amidases that degrade the peptidoglycan, has been observed on bacteria exposed to lantibiotics such as nisin and pep5.²⁰⁷

Antimicrobial peptides are also known to act as inhibitors of enzymes produced by pathogenic organisms, either by serving as pseudo-substrates or by tight binding to the active site that disturbs the access of substrate. Thus, histatins at the submicromolar range are capable of inhibiting a trypsin-like proteinase from the oral bacteria *Bacteroides gingivalis*,²⁰⁸ and equine peptide eNAP-2²⁰⁹ inhibits other microbial serine proteases. Alternatively, antimicrobial peptides can serve as a control for proteinases involved in inflammatory processes, such as the inhibition of furin by histatin 3,²¹⁰ which has close sequence homology with the prepropeptide, or proBac5 from bovine neutrophils,²¹¹ which inhibits cathepsin L. That the recognition mechanism is due to the peptide sequence and/or conformation is demonstrated by the specificity of the proteinases and the inactivity of the enantiomers.²¹⁰ Inhibition of thrombin by defensins also helps in the contention of the pathogens, and consequently of the inflammatory process.^{212,213} In contrast, upregulation of the inflammatory process is achieved by induction of IL-8 by defensins.²¹⁴ Other activities described so far for antimicrobial peptides include chemotaxis,^{215,216} induction of syndecan synthesis,²¹⁷ histamine release,^{218–220} and inhibition of steroidogenesis.^{221,222}

MECHANISMS OF RESISTANCE TO ANTIMICROBIAL PEPTIDES

Inactivation and resistance are essential issues for both the understanding of action mechanisms and the potential therapeutic application of antimicrobial peptides. These phenomena have been largely documented on bacterial models through mutant generation and genetic rescue. In many cases, resistance is associated with virulence genes (reviewed in Ref. 223), though not always.²²⁴ The following mechanisms can be distinguished.

Inactivation by the Incubation Media

Serum and its components have been described as inhibitors for different antimicrobial peptides, including LL-37²²⁵ and defensin.²²⁶ Inhibition of defensins by bovine serum albumin,²²⁷ α_2 -macroglobulins,²²⁸ serpins,²²⁹ and complement factor C1q²³⁰ has been reported, though the latter finding is disputed.²³¹ Activated low density lipoproteins are the main inactivator for amphipathic cytolytic peptides C18G and 399.²³² Inactivation of the antimicrobial activity of lactoferricin in cow's milk has been reported.²³³

Inactivation by Oligosaccharide Barriers

Before reaching their final targets, antimicrobial peptides must cross barriers such as bacterial peptidoglycan (discussed below), extracellular matrix in eukaryotic cells, or anionic oligosaccharides bound to different membrane components. Heparin, a major component of the extracellular matrix, inhibits the tumoricidal activity of defensins²²⁶ and the permeabilization activity of cecropin A-melittin hybrid peptides.^{227,228} In the promastigote form of *Leishmania*, a parasitic protozoan, the plasma membrane contains a glycocalyx formed by anionic lipophosphoglycan, which affords partial resistance against these peptides.²²⁸ In erythrocytes, sialic acid residues from membrane glycoproteins induce minor resistance to magainin¹⁶⁰ or melittin; in the latter case resistance increases dramatically by certain substitutions.²³⁶

Inactivation by Bacterial Outer Membrane

In gram-negative bacteria, the main component of the outer leaflet is LPS (reviewed in Refs. 237–239). Any active peptide not recognized by peptide transporters must cross the outer membrane by the so-called self-promoting pathway (a term coined²³⁸ to explain the

bactericidal activity of polymixin), which consists of the displacement of divalent cations that keep LPS together, thus allowing passage of external molecules. The phenomenon has been observed for peptides such as indolicidin and analogues,¹⁸⁰ gloverin,¹⁹⁹ α -defensins,²⁴⁰ bactenecin,²⁴¹ cecropin B,²⁴² or cecropin A-melittin hybrids.^{174,243} Such studies have focused on either the microbicidal activity of the peptides, or on permeabilization to (otherwise excluded) fluorescent probes, hydrophobic antibiotics, or substrates for periplasmic enzymes. As peptide recognition by LPS takes place mainly by electrostatic interaction between cationic residues and phosphate groups, respectively, inactivation at the outer membrane level can be originated by either absence of LPS, such as in bactenecin-resistant *Borrelia burgdorferi*²⁴⁴ or by decrease in overall negative charge, such as resulting from esterification of phosphate groups. This latter phenomenon takes place in naturally resistant bacteria such as *Proteus*²⁴⁵ or *Burkholderia*.^{246,247} Although LPS is the main constituent, other outer membrane components in gram-negative bacteria can play as well a role in this interaction, but their importance relative to LPS is not conclusively established. Thus, pathogenic strains of *Yersinia* are resistant to defensins²⁴⁸ and to polyLys, polyOrn, cecropin P1, melittin, and polymixin B.²⁴⁹ A role for the protein YadA, a main component of the outer membrane, was suggested by the former authors, but not found for the set of peptides tested by the second group.

Proteolysis of the Peptide

This perhaps most obvious of inactivation processes has important bearing on the practical application of antibiotic peptides. The high content in basic residues favors degradation by trypsin-like proteinases. However, pinpointing a given enzyme as responsible for a resistance mechanism is more difficult. Specific cecropin-degrading enzymes produced by pathogens such as *Bacillus larvae* in honeybees²⁵⁰ and entomopathogenic strains of *Pseudomonas aeruginosa*²⁵¹ have been described. Virulence of the pathogenic strains correlates with the level of these proteinases. In *Salmonella*, a protein has been identified²²³ with activity similar to magaininase, a metalloproteinase from the amphibian skin known to be involved in the degradation of magainins as well as other antibacterial peptides.²⁵²

Resistance by Plasma Membrane Components

Several membrane elements, both passive and active, have been described as contributing to resistance.

Lipid Composition. Lower levels of anionic phospholipids are associated to bacterial resistance, either in natural species such as *Serratia*,²⁵³ or in spheroplasts from different gram-negative bacteria.²⁵⁴ Higher activity of sapecin on *S. aureus* than on *E. coli* has been linked to cardiolipin content, since a mutant deficient in its biosynthesis is more resistant.²⁵⁵ Similarly, treatment of erythrocytes with phospholipase D, which raises the phosphatidic acid content, is associated with higher susceptibility to antimicrobial peptides.¹⁶⁰

Membrane Potential. Membrane potential has been associated with a higher permeabilization by antimicrobial peptides in both bacteria and model membranes. The amphipathic peptide H9c2²⁵⁶ shows higher activity on rat embryo myoblasts depending on the cell cycle, in direct correlation to the variation in membrane potential. Similarly, hyperpolarization of erythrocytes increased their susceptibility to magainin but not to melittin¹⁶⁰ and collapse of the potassium gradient in *Leishmania* decreased the activity of cecropin A-melittin hybrids.²³⁵ The *uncA* *E. coli* mutant, which relies on glycolysis rather than on oxidative phosphorylation for viability, and has therefore a lower membrane potential, is more resistant to sarco-toxin I.^{257,258}

Reduction of Disulfide Bonds. Inactivation of NK-lysin is performed by human but not *E. coli* thioredoxin reductase; it was suggested that this system is located at the plasma membrane and partially responsible for the incomplete killing by this peptide.¹²⁴ Related forms of inactivation would be disulfide exchange, as described for thionins,²⁵⁹ or binding of defensins to the activated thiol group of α -2 macroglobulin.²²⁸

Peptide Influx/Efflux Systems. Some transmembrane transport complexes, both in animal²⁶⁰ and plant²⁶¹ pathogens, have been shown to be involved in peptide resistance, operating as intake systems that facilitate intracellular peptide degradation. In contrast, resistance to protegrins and LL-37 in *Neisseria gonorrhoeae* seems to be based on mtr, an efflux peptide system²⁶² working by mechanisms similar to other pumps involved in drug multiresistance. However, mdr1-transfected BRO melanoma cells, which show multiresistance to a variety of antitumoral drugs, do not decrease their susceptibility to magainin 2.²⁶³ Likewise, melittin is not a substrate for protein P, from the same group of efflux pumps, though other peptides such as gramicidin and valinomycin are.^{264,265}

FUNCTION AND PATHOLOGY OF ANTIMICROBIAL PEPTIDES

The variety of defensive mechanisms developed by multicellular organisms in nonspecific immunity raises questions on the role of antibiotic peptides as a deterrent against infection. In insects, specially in the *Drosophila* model, such a role was clearly demonstrated by the study of mutants lacking some of the induction pathways for the antibiotic peptide genes (reviewed in Refs. 3,5,6,19, and 266). For more evolved insects, it was clearly shown that mutations in the different signaling pathways of antimicrobial peptides rendered the organism very susceptible to infection.^{267–269} In organisms endowed with highly developed antigen-specific immunity, the role of antibiotic peptides has been only partially ascertained; still, an increasing body of experimental evidence has accumulated during the last years.

Antibiotic Peptides in Infection and Inflammation Processes

Increased levels of antibiotic peptides have been reported for several animal and human infections: for α -defensin in septicemia and bacterial meningitis,²⁷⁰ for β -defensins in *Mycobacterium*, *Pasteurella*, or *Cryptosporidium* infections,^{271,272} for PR-39 in salmonellosis,²⁷³ for a variety of peptides in blisters and wound fluid,²⁷⁴ or for lingual antibacterial peptide (LAP) in injured tongue.⁷⁹ Inflammatory situations or stimuli are also associated with induction of antibiotic peptides such as LL-37²⁷⁴ TAP or LAP.^{275,276} Levels of NK-lysin, a tumorcidal and antibacterial peptide, increase in NK cells or cytotoxic lymphocytes by stimulation with IL-2.²⁷⁷

Absence or Inactivity of Peptides

Depleted levels of antibiotic peptides are associated to several pathologies. Thus, patients of specific granule-deficiency syndrome, completely lacking in α -defensins,²⁷⁸ suffer from frequent and severe bacterial infections. Low levels of histatins from saliva in a group of HIV patients correlated with a higher incidence of oral candidiasis²⁷⁹ and fungal infection.²⁸⁰ Perhaps the most compelling illustration of the implication of antimicrobial peptides in human pathology comes from cystic fibrosis, a genetic disease associated with recurrent bacterial infections of the airways. The defective chloride channel causing the disease increases salinity of the alveolar fluid, and thus impairs the bactericidal activity of β -defensins, which

are salt sensitive.^{281,282} In diabetic patients, an interesting theory on defensin inactivation proposes binding of the peptide to advanced glycation end products.²⁸³

Pathology Caused by Antibiotic Peptides

As part of the defense reactions or inflammatory stimuli, neutrophils discharge their granule contents, releasing defensins that can damage surrounding tissues and cells. Damage to airway epithelia due to release of α -defensins from neutrophils in both cystic fibrosis²⁸⁴ and respiratory distress syndromes²⁸⁵ has been described. Localization of α -defensins in arterial wall vessels²⁸⁶ can contribute to the inflammation process as well as to the formation of atherosclerotic plaque by favoring lipoprotein deposition in the vessel.²⁸⁷

ANTIBIOTIC PEPTIDES IN CLINICS

A great deal of work has been invested in recent years in localizing new antibiotic peptide sequences and improving their potency and selectivity, with the goal of expanding and/or refining resources against infection in an era of antibiotic resistance. These efforts may appear at first sight unrewarded, in view of the scarce examples of antibiotic peptides at advanced phases of clinical approval. Such a dismissal might be premature, however, especially considering the relative infancy of most research in the field. At present, advances in production (synthetic and recombinant) and development of antibiotic peptides are under way, clearing the way for cost-effective use. Therapeutical applications of antibiotic peptides have been largely envisaged in the treatment of bacterial²⁸⁸ or viral²⁸⁹ infections, and cancer.²⁹⁰ While it must be admitted that most applications so far are confined to treatment of local infections, promising results may be forthcoming. A first step in this direction is a magainin analogue, termed pexiganan acetate, which has obtained approval for the treatment of diabetic foot ulcers.²⁹¹ Other fields where work is advancing are the following.

Buco-Dental Infections

Natural defenses of the oral cavity are based on the His-rich histatins from saliva, with a strong candidal activity,¹⁸⁵ and on antibiotic peptides from the epithelia such as LAP⁷⁹ or from neutrophils in the periodontium.²⁹² Many facultative oral gram-negative bacteria are killed by human defensins²⁹³; others such as *Actinobacillus actinomycetemcomitans* and

Eikenella corrodens are resistant, though not for rabbit NP-1 or the D forms of peptides such as protegrins.^{294,295} Histatins can be adsorbed into polyacrylic material to reduce *Candida* adhesion to the denture.²⁹⁶ C-terminal analogues of histatin C show good activity against oral pathogens other than *Candida*.¹⁸⁸ An additional effect of histatins is the inhibition of a proteinase from *Bacteroides gingivalis*.²⁰⁸ In vivo efficacy of histatins has been assessed in an experimental gingivitis model in dogs.²⁹⁷ A promising development in antimicrobial peptide-based gene therapy is the production of histatin 3 by infection with a histatin recombinant adenovirus, active on *Candida* strains.²⁹⁸

Ocular Infections

Antibiotic peptides such as rabbit (defensin) NP-1,²⁹⁹ magainins,³⁰⁰ cecropin-derived Shiva 11,³⁰¹ or cecropin D5C³⁰² have been proposed as preserving media for cornea storage,³⁰³ contact lens disinfectants,^{300,302} or ocular antiseptics. In vivo experiments have been performed with cecropin A–melittin hybrids on rabbits infected with *Pseudomonas aeruginosa*; the peptides were as effective as gentamycin in the clearance of the infection.³⁰⁴

Spermicidal Agents

The activity of magainins and their analogues on spermatozoids,^{305,306} causing morphological and functional alterations led to propose them as contraceptive agents. The broad-range activity of protegrins against several sexually transmitted pathogens, including HIV virus, has suggested a possible combination of antibiotic and contraceptive activities.³⁰⁷

Antitumoral Activity

A number of studies have shown tumoral cells to be more susceptible to antibiotic peptides than their non-transformed counterparts. The basis for this difference is not fully clarified; changes in membrane potential due to higher metabolism,³⁰⁸ higher exposure of acidic phospholipids in the outer leaflet of membrane,¹⁹¹ or cytoskeleton alteration and possible alterations in the extracellular matrix³⁰⁹ have been proposed as potentially implied in the process. In *ras*-transformed cells more susceptible to melittin action, a Ca^{2+} influx induced by hyperactivation of phospholipase A2 was proposed.^{310,311} Preferential activity toward transformed cells has been described for cecropins and analogues,^{182,309,312} magainin 2 and analogues,³¹³ cecropin A–magainin 2 and cecropin A–melittin hybrids,³¹⁴ and analogues derived from

human platelet factor.³¹⁵ Activity of magainin analogues was unchanged in a panel of human cancer cell lines with a broad range of susceptibility toward typical antitumor drugs,³¹⁶ or when a human melanoma cell line was transfected with the drug efflux transporter mdr1 that provides high resistance against usual antitumor agents.²⁶³ As usual, extrapolation to an *in vivo* situation is hampered by partial inactivation by serum components³¹⁵ or by the increase in proteolytic activity of tumoral cells, a case where all-D analogues were shown to be quite successful.²⁹⁰ Examples of the efficacy of antibiotic peptides against murine tumors include the complete cure of an induced melanoma in athymic nude mice with a single injection of all-D MSI-511 magainin analogue²⁹⁰ or the 100% lifespan increase in mice with induced ascites and spontaneous ovarian tumors by intraperitoneal treatment with the magainin analogue MSI-238.³¹³ Colateral approaches tested *in vitro* for cancer therapy include the targeting of thionin conjugated to a monoclonal antibody toward lymphoma-causing CD5+ lymphocytes,³¹⁷ or the reversion and/or attenuation of the transformed phenotype by the internal expression of either cecropin or melittin inside tumoral cells.³¹⁸

Antiviral Activity

Antibiotic peptides have been described to act upon viruses at three levels. Direct action related to peptide binding to the viral particle has been assessed on herpes virus for α -defensins,^{227,319} modelin-1, an amphipathic model peptide,²⁸⁹ and Hecate, a melittin analogue³²⁰; on HIV virus for polyphemusins and their analogues,³²¹ and on viral stomatitis virus by tachyplesin I.³²²

Secondly, inhibition of virion production has been proposed to account for antiviral activity of melittin or cecropin A^{323,324} on HIV. Virus production was arrested at sublethal peptide concentrations either with the peptide added externally or produced intercellularly by transfection with an expression vector.

Finally, mimicry of viral infective processes is a third mechanism by which antimicrobial peptides exert antiviral activity. Thus, melittin and its subK7I analogue, lacking antibiotic activity, inhibit infectivity of the tobacco mosaic virus by perturbing its assembly due to the similarity of melittin with a virus capsid region involved in RNA interaction.³²⁵ Another interesting example is the T22 [Tyr^{5,12} Lys⁷] analogue of polyphemusin, with EC₅₀ in the nanomolar range against HIV³²⁶ (even AZT-resistant strains). The peptide, which requires intact disulfide bridges and Zn²⁺ for optimal activity,^{321,327} seems to act

through a nonmembrane-related mechanism, since its all-D version is 20-fold less active.³²⁸ Though the molecular basis for T22 activity is not fully understood, it is known to bind gp120 and CD4 molecules^{329–331} and thus to block virus-cell fusion; it also competes with the virus for the coreceptor of chemokines CXCR4 and fusin.³³² Recently, less cytotoxic (i.e., less cationic) analogs of this promising peptide have been developed.³³³

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