Follow the leader: The use of leader peptides to guide natural product biosynthesis

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Abstract

The avalanche of genomic information in the past decade has revealed that natural product biosynthesis using the ribosomal machinery is much more widespread than originally anticipated. Nearly all of these compounds are crafted through posttranslational modifications of a larger precursor peptide that often contains the marching orders for the biosynthetic enzymes. We review here the available information for how the peptide sequences in the precursors govern the posttranslational tailoring processes for several classes of natural products. In addition, we highlight the great potential these leader peptide directed biosynthetic systems offer for engineering conformationally restrained and pharmacophore-rich products with structural diversity that greatly expands the proteinogenic repertoire.

Introduction

The past decade has seen an upsurge in the available genomic information with about 800 fully sequenced bacterial genomes and around 700 unfinished genomes as of August 2009. This explosion of genomic information has provided unparalleled new insights into the genetic capacity of organisms to generate secondary metabolites[1], including a rapid rise in the discovery of natural products that are ribosomally synthesized and posttranslationally modified[2-13]. These tailoring processes release the peptides from the structural and functional constraints imposed on natural ribosomal peptides, while at the same time restricting conformational flexibility to allow better target recognition and increase metabolic and chemical stability. For the vast majority of natural products of ribosomal origin, the initial precursor peptide is much larger than the final product. These precursors typically contain N-terminal leader peptides, and in some cases, C-terminal extensions that are removed in the last step of the maturation process. Interestingly, a recent comprehensive analysis of the structural motifs generated using these pathways concluded that the types of structures accessible through the ribosomal route are remarkably similar to those produced via nonribosomal biosynthesis[14]. This review will discuss the currently available information regarding the roles of these leader peptides as well as the prospects that leader peptide directed biosynthesis (LDB) offers for natural product engineering.

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Proposed Roles for the Leader Peptides

For almost all natural products produced via the ribosome, the precursor genes encode a peptide that contains an N-terminal leader extension in addition to the C-terminal core peptide that is processed to the mature compound (Fig. 1). Many hypotheses have been offered for the function of the leader peptides, but before discussing these proposed roles, we will outline the nomenclature used in this review because the terminology in the literature differs greatly for the various compound classes (see Supplementary Fig. 1 online). The initial ribosomally produced peptides will be referred to as precursor peptides, with the peptide segment that is converted into the mature natural product denoted as the core peptide (Fig. 1). The peptide sequence that is appended to the N-terminus of the core peptide will be termed the leader sequence, and any sequence that is attached to the C-terminus of a core peptide will be referred to as a recognition sequence. For some natural products from higher organisms, an N-terminal signal peptide may also be present that directs the subcellular localization of the peptide.

The role most commonly proposed for the leader peptides is that of a secretion signal. However, the vast majority of leader peptides of natural product biosynthesis have no homology with the peptides of the typical *Sec* and twin-arginine translocation pathways that are used in bacteria, archaea and plants to transport proteins across membranes. A second role that is frequently postulated is that of a recognition motif for the posttranslational modification (PTM) enzymes. It is this role that is most enticing from a natural product engineering perspective as it may allow generation of analogs by attachment of core peptide variants or even very different peptides to the leader peptides. A related proposed task is that of a *cis*-acting chaperone in which the leader actively assists during the PTM process. Taking clues from the roles of leader peptides attached to enzymes[15], they may also assist in folding of the precursor peptide, stabilizing the precursor against degradation, or keeping the precursor peptide inactive during biosynthesis inside the host until the appropriate time for secretion and proteolysis. Indeed, many of the proteases involved in ribosomal natural product biosynthesis are localized on the outside of the producing cells and in some cases the protease is part of the transporter. As discussed in this review, support for almost all of these roles has been reported, but the function of the leader peptide differs for different classes of compounds and sometimes even within a certain natural product group. Further delineating the function of these peptide sequences will offer exciting insights into basic biological processes as well as provide improved opportunities to reprogram natural product structures by utilizing the leader peptide directed biosynthetic enzymes.

Lantibiotics

Lantibiotics are distinguished by the presence of thioether crosslinks called lanthionines and methyllanthionines (Fig. 2a). These thioether linkages are introduced by dehydration of a serine or threonine to generate a dehydroalanine or dehydrobutyrine, respectively, followed by addition of a cysteine thiol as illustrated in Fig. 2b for lacticin 481. Including the thioether crosslinks and dehydro amino acids, an impressive 15 different PTMs have been documented in various family members (Fig. 2a)[16]. Currently, lantibiotics are divided into two classes on the basis of the sequences of their leader peptides and biosynthetic enzymes. The role of the leader peptide has been investigated for both groups using *in vivo* mutagenesis studies and *in vitro* reconstitution of the posttranslational modification reactions.

Class I lantibiotics include nisin (Fig. 1), a compound used for more than 40 years in more than 80 countries as an effective agent to combat food-borne pathogens[17]. The leader peptides of class I lantibiotics are about 25 amino acids in length and are rich in Asp

residues (Supplementary Fig. 2 online). NMR studies on fully processed nisin attached to its leader peptide did not reveal any interactions between the leader and the nisin molecule, both in solution and in micelles[18]. Moreover, none of the investigated lantibiotic leader peptides displayed secondary structure in aqueous solution, although they attain -helical conformations in trifluoroethanol[19] and structure prediction tools anticipate helical character. These observations do not support the hypothesis that the leader peptide acts as a chaperone for folding. However, leader peptides attached to the mature lantibiotics greatly reduce or abolish their antimicrobial activity, consistent with a protective mechanism[20,21]. In addition, ATP-binding cassette transporters clearly use the class I leader peptides for recognition because various engineered non-lantibiotic cargo attached to these leader sequences are secreted[22,23]. Similarly, the leader peptide of nisin is also recognized by the dehydratase and cyclase enzymes as demonstrated by *in vivo* processing of non-lantibiotic therapeutic peptides attached to the nisin leader[24,25], and by *in vitro* studies on the cyclase enzyme[21]. The nisin cyclase, NisC, is made up of an , -barrel that contains the active site and a separate domain proposed to contain the leader peptide binding site[21].

The leader peptides of class II lantibiotics are typically also rich in Asp and Glu residues, contain an ELXXBXG motif (B = V, L, or I), and usually end in a double Gly motif (Fig. 2c and Supplementary Fig. 3 online). Originally defined as consecutive Gly residues preceding the proteolytic cleavage site of non-lantibiotic bacteriocins[26], this motif now also includes GlyAla and GlySer/Thr sequences. Like the leader peptides of class I lantibiotics, the double Gly leader peptides play several roles that include keeping the modified core peptide inactive when still attached to the leader peptide[27]. In addition, *in vitro* studies on lacticin 481 have shown that the leader peptide is important for efficient dehydration and cyclization (Fig. 2b), but not essential. When the leader peptide and the core region of the lacticin 481 precursor peptide were presented *in trans* to lacticin 481 synthetase, dehydration still occurred, albeit with much decreased efficiency[28]. Unexpectedly, even incubation of the synthetase with just the core peptide resulted in dehydration. Hence, the leader peptide is not a compulsory allosteric element for dehydratase activity. Instead, the enzyme has a low level basal activity in the absence of the leader peptide, suggesting that the leader peptide may influence the equilibrium between an inactive and an active form of the enzyme by binding to the latter[29]. Upon binding, lacticin 481 synthetase processes its substrate peptide distributively and directionally, moving from N- to C-terminus[30], whereas in the absence of the leader peptide, no such directionality was observed[28].

Site-directed mutagenesis studies have shown that the double Gly motif is essential for proteolytic processing[31,32], but not for installation of lanthionine rings[29]. Hence, the recognition of the leader peptides is different for the protease and synthetase. It has proven difficult to delineate the exact factors that are essential for recognition by the synthetase as nearly all single point mutants of the lacticin 481 leader peptide were still processed[29]. A similar plasticity was observed for microcin B17 as discussed below. The only clear disruption of processing by the synthetase was observed with a series of mutants that introduced Pro residues, supporting the hypothesis that the leader peptide attains an -helical conformation when bound to the synthetase[29]. Interestingly, leader peptides of the double Gly type with clear homology with lantibiotic leader peptides are also found in many bacteriocins that do not undergo posttranslational modifications (Supplementary Fig. 4 online). Therefore, these leader peptides are thought to only be important for secretion and/ or for reducing the biological activity of the bacteriocin[33]. Hence, the leader peptides of class II lantibiotics may have evolved from a role in secretion to include additional roles in guiding the enzymes involved in lantibiotic biosynthesis. However, the hypothesis that non-conserved amino acids in these leader peptides would convey recognition by the PTM enzymes for each specific lantibiotic is not supported by mutagenesis studies[29].

Microcins

Enterobacteria produce a structurally diverse group of ribosomally produced small peptides (<10 kDa) called the microcins[34]. At present, four kinds of PTMs have been reported for the microcin family. The potent inhibitor of DNA gyrase, microcin B17, contains four oxazole and four thiazole heterocycles (Fig. 3a)[35]. A different type of cyclization is found in microcin J25, the best-studied member of the lasso peptides that inhibit RNA polymerase (Fig. 3a)[36-38]. Microcin C7 (also known as C51)[34] and microcin E492[39] are also posttranslationally modified but without the need of a leader peptide[40,41] and will therefore not be discussed here.

Microcin B17 was the first posttranslationally modified peptide antibiotic for which the biosynthesis was reconstituted *in vitro*[42]. The precursor peptide contains a 24-amino acid leader peptide that does not carry a net charge and does not show homology with the leader peptides of bacteriocins, lantibiotics, or other microcins. Both *in vivo* and *in vitro* studies have shown the requirement of the leader peptide for the installation of the oxazole and thiazole heterocycles[42,43]. On the other hand, the leader peptide appears not to be involved in transport[43,44], an unusual exception to this general role for leader peptides. Furthermore, unlike the observations for the lantibiotic lacticin 481, the leader peptide of microcin B17 cannot act *in trans*[45]. The installation of the heterocycles requires a three-protein complex composed of a cyclodehydratase that generates oxazoline and thiazoline structures from GlySer and GlyCys sequences, respectively, a flavin-dependent dehydrogenase that oxidizes these intermediates to oxazoles and thiazoles, and a third scaffolding protein that is required for catalysis. Photocrosslinking experiments suggest that the leader peptide binds to this scaffolding protein[46]. The first modified residue in the core region of microcin B17 is separated from the end of the leader peptide by an essential[47] Gly-rich spacer peptide that is proposed to ensure the correct register between the two segments of the precursor peptide and allow the core region to reach the active sites for modification. Like the maturation process for the lantibiotic lacticin 481, heterocyclization of the microcin B17 precursor takes place by a distributive and directional process, with the synthetase moving from N- to C-terminus of the core region[48]. Other similarities with the lantibiotic systems are the propensity of the microcin B17 leader peptide to form an amphipathic -helix[45], and the observation that the modified core peptide of microcin B17 with its leader still attached has greatly reduced antimicrobial activity[46]. A final common theme between lantibiotics and microcin B17 is that many residues in the leader peptide can be mutated without abolishing the ability of the biosynthetic enzymes to process the precursor peptide. However, two residues, Phe8 and Leu12 in a FXXXL motif are critical for binding of the leader peptide to the biosynthetic enzymes[45]. These observations further support an -helical conformation as these residues are located on one face of the -helix structure determined by NMR analysis in aqueous trifluoroethanol. In addition, incorporation of proline residues to disrupt the -helical nature precluded processing of the core peptide.

A structurally intriguing collection of compounds are the lasso peptides, such as microcin J25, in which the N-terminal amino group is engaged in a lactam bond with a carboxylate side chain of an Asp/Glu residue at position 8 in a manner that traps the C-terminal peptide chain threaded through the ring (Fig. 3a). Bulky, often aromatic, side chains of the amino acids that flank the ring prevent the tail from slipping out of the lasso. The precursor peptide to microcin J25 contains a 37-amino acid leader peptide and a 21-residue core peptide (Supplementary Fig. 5 online). *In vitro* reconstitution of microcin J25 biosynthesis demonstrated that the leader peptide is required for posttranslational modification by two enzymes[49]. One protein catalyzes the adenylation of the carboxylate side chain of Glu/Asp8. A second protein cleaves off the leader peptide and installs the new lactam amide bond. The leader peptide cleavage site for the lasso peptides found by database mining is not of the

double Gly type[49]. Because synthetic efforts to construct the lasso peptides have not resulted in the threaded structure[37,38], the tail must be held in a near-mature orientation before the lactam is formed. It has been suggested that the leader peptide might be involved in this orienting of the tail[50], but it is equally plausible that the biosynthetic enzymes position the C-terminal segment while the ring is formed around it.

Cytolysins

In the past few years, many systems related to microcin B17 have been discovered in sequenced genomes, demonstrating that the ribosomal pathway to thiazole and oxazole containing natural products is widespread and not limited to Gram-negative enterobacteria[6,7]. Notably, gene clusters encoding the required biosynthetic machinery are found in various human pathogens including *Clostridium botulinum*, *Listeria monocytogenes*, *Staphylococcus aureus*, and *Streptococcus pyogenes*, as well as in cyanobacteria, archaea, and others. Many of these clusters contain genes that suggest these compounds undergo additional posttranslational tailoring processes[6] in much the same way that lantibiotics contain a myriad of structural modifications. Hence, these clusters will be a rich source of novel natural products of great structural diversity. The two systems that have been investigated experimentally are streptolysin S[6] and listeriolysin S[7] produced by similar routes in *S. pyogenes* and *L. monocytogenes*, respectively.

Streptolysin S (SLS) is responsible for the characteristic lysis of red blood cells (- hemolysis) induced by group A *Streptococcus*. The structure of the compound has not yet been determined, in part because its activity is rapidly lost in the absence of bacterial cells or other stabilizing factors. It is made from a 53-amino acid precursor peptide containing a 23-residue leader peptide of the double Gly type and a 30-residue core region[51] (Fig. 3b and Supplementary Fig. 6 online). Its biosynthetic gene cluster contains orthologs of the three enzymes required for microcin B17 maturation. Heterologous expression of these proteins and the precursor peptide and *in vitro* reconstitution of its biosynthesis[6] has further confirmed that SLS contains oxazoles/thiazoles. In contrast to the systems discussed so far, SLS displays hemolytic activity even when the leader peptide is still attached. The importance of residues in the leader peptide for SLS maturation has been investigated by alanine scanning mutagenesis revealing TQV and FXXXB (B = I, V, Fig. 3b) sequences that are key for recognition, with the latter resembling the FXXXL motif discussed above for microcin B17. Although these motifs are important for SLS maturation, they are not uniformly conserved in the cytolysin leader peptides (Fig. 3b), suggesting that substrate recognition is different for the biosynthetic enzymes of different family members. Another interesting observation is that the leader sequence inhibits microcin B17 biosynthesis *in vitro* with a K_i in the micromolar range, similar to the K_m of the precursor peptide[45], but that the leader peptide of the SLS precursor has much higher affinity (K_D = 6.7 nM) for its synthetase[52]. Furthermore, the SLS leader sequence binds to the cyclodehydratase, not the scaffold protein. The relative affinities of the leader peptides of microcin B17 and SLS for their respective biosynthetic enzymes may be a consequence of microcin B17 being inactive with its leader peptide still attached, whereas SLS is very active even before leader peptide removal. Therefore, the tight complex with the cyclodehydratase may protect the producing organism.

Goadsporin is another linear thiazole and oxazole containing natural product that is biosynthesized using similar logic as microcin B17[53]. Like the thiopeptides discussed below, goadsporin contains dehydroamino acids in addition to the five-membered heterocycles. Its biosynthetic cluster contains enzymes with homology to the microcin B17 and lantibiotic tailoring enzymes, but at present, the role of the leader peptide has not yet been investigated.

Cyanobactins, Amatoxins, and Cyclotides

The patellamides (Fig. 4) belong to the cyanobactin family, which includes more than 100 unique cyclic peptides[2]. Members of this group are produced by diverse cyanobacteria including symbionts of marine invertebrates[2,54,55], and several have antitumor activity. In addition to sharing similar structural features such as thiazoles with the microcins and cytolysins, cyanobactins also share similar biosynthetic pathways[2,42,56,57]. The heterocyclic structures are the result of posttranslational tailoring of Ser, Thr, and Cys residues by two enzymes (Fig. 4), a cyclodehydratase (PatD), and a bifunctional enzyme with an oxidase domain (PatG). The final step in cyanobactin maturation is the release of the bioactive product via cleavage of the leader and recognition sequences from the core peptides and concomitant cyclization (Fig. 4).

Most cyanobactin precursors possess a leader peptide, two core peptides, and flanking recognition sequences that direct posttranslational modification (Fig. 4). Interestingly, the precursor peptides contain highly conserved leader peptides and recognition sequence regions, but have highly variable core peptides (Supplementary Fig. 7 online). The high conservation of the leader and recognition sequences may reflect conserved recognition elements for the biosynthetic enzymes, while the hypervariable core peptides enable high chemical diversity in the products. The role of the leader peptide in directing the PTMs has not been extensively studied *in vitro*, but the demonstration that patellamides can be produced heterologously in *E. coli*[54,57] suggests such studies can be carried out.

The C-terminal segment of the cyanobactin precursor peptides harbors two core peptide cassettes (Fig. 4), sandwiched between flanking recognition sequences[2]. The immediate N-terminal flanking sequences typically consist of G(L/V)E(A/P)S, whereas AYDG(E) is observed C-terminal to the cassettes. Both of these recognition sequences play critical roles in the excision and cyclization of the core peptides. A subtilisin-like serine protease (PatA) catalyzes two amide bond hydrolysis reactions in a sequential manner[58], first proteolytically removing cassette II and its C-terminally attached recognition sequence from the full-length precursor, followed by the removal of cassette I from the previously trimmed precursor (Fig. 4). Recent *in vitro* studies showed that the heterocycles are not required for proteolysis[58], further suggesting the protease recognizes the recognition sequences and not the core peptides. Both cleavage reactions result in free N-termini for subsequent cyclization catalyzed by a second subtilisin-like serine protease (PatG) that simultaneously removes the C-terminal recognition sequences through a transamidation mechanism[58]. Cyanobactins do not have the double Gly protease recognition motif.

Like the cyanobactins, the precursor peptides for amatoxins (e.g. -amanitin, Fig. 1) and phallotoxins - the cause of most fatal mushroom poisonings – also display conserved leader and recognition sequences and a variable core region that is excised and cyclized (Supplementary Fig. 8 online)[5]. Proteolytic cleavage at both ends of the core peptide is performed by a Pro oligopeptidase[59]. Cyclotides produced by plants are cyclized in a head-to-tail fashion and contain a threaded knot of three disulfide bonds[60]. Like cyanobactins, their precursor peptides contain core peptides with recognition sequences preceding and following each core region (Supplementary Fig. 9 online)[61]. The presumed helical structure of the precursor peptides[62] and the identification of an Asn peptidase that may be involved in their processing[63] offer hints for further exploration.

Thiopeptides

Another large group of thiazole containing compounds are the thiopeptides comprising more than 80 members, most of which inhibit protein biosynthesis[64]. Known for over 60 years, their ribosomal assembly was only revealed by four independent studies in early 2009[10-13].

Most thiopeptides consist of a macrocyclic core made up of a string of thiazoles/thiazolines that are joined together by a 6-membered heterocycle that can be a pyridine, a hydroxypyridine or a dehydropiperidine (e.g. thiostrepton, Fig. 5). Aided by fully and partially sequenced genomes, the biosynthetic gene clusters were recently reported for thiostrepton[11], thiocillin[10], siomycin[12], thiomuracin[13], and nosiheptide[65]. The common modifications include dehydrations of Ser and Thr by enzymes with homology to lantibiotic dehydratases, thiazole and thiazoline formation by enzymes with homology with the cyanobactin, microcin B17, and SLS biosynthetic enzymes, and proposed cyclizations of two dehydroalanines to produce the central 6-membered heterocycle by as of yet unidentified proteins (Fig. 5). Additional compound-specific modifications complete the maturation process. As in many of the systems discussed thus far, the leader sequences (34-48 residues) are rich in Asp and Glu and contain some highly conserved hydrophobic residues. Several of the leader peptides end in the typical double Gly motif (Supplementary Fig. 10 online). Currently, the role of the leader peptide has not yet been investigated *in vivo* or *in vitro*, but it is likely that it directs at least part of the posttranslational modifications.

Microviridins

Like most natural products discussed in this review, microviridins have a polycyclic architecture. The crosslinks in these tricyclic compounds are formed by lactone and lactam linkages between the carboxyl groups of Asp/Glu and the side chains of Lys and Ser/Thr residues (Fig. 1). They are potent inhibitors of proteases. Depsipeptides such as the microviridins are typically biosynthesized by non-ribosomal peptide synthetases, but using the fully sequenced genome of an *Anabaena* strain and the raw genome of a *Planktothrix agardhii* strain, two groups recently discovered that the microviridins are ribosomally produced[8,9]. The precursor peptides are made up of a 13-17 residue core peptide and a leader peptide of 34-37 amino acids that does not have a double Gly motif but does harbor several very conserved residues. Interestingly, in the *Anabaena* strain, a cryptic cluster contains a precursor peptide that appears to contain a double Gly leader peptide, three core regions, and intervening recognition sequences[8] in a similar architecture as discussed above for the cyanobactins (Supplementary Fig. 11 online). Microviridin B and J from *Microcystis* strains were heterologously produced in *E. coli*[8], and microviridin K from *P. agardhii* was produced *in vitro* using purified heterologously expressed proteins. The amide and ester bonds are installed by two ATP-grasp ligases with the two ester bonds formed first in a strictly ordered process[9,66]. The *in vitro* studies also showed that the leader peptide is required for the tailoring reactions.

Conopeptides

Conopeptides comprise a group of structurally diverse peptides produced by predatory cone snails that target a broad range of ion channels, membrane receptors, and transporters[67]. A single cone snail species can produce up to 200 different toxins in its venom[68] (e.g. bromocontryphan-R, Fig. 1). It is estimated that collectively, 50,000-100,000 different conopeptides may be produced by this genus[67,68]. They have been classified into different gene superfamilies[67,68], and they contain a wide variety of PTMs (Fig. 6a). Conopeptides are translated as precursor peptides of 80-100 residues that are subsequently processed to the mature compound[69]. The N-termini contain a hydrophobic signal peptide of   20 residues that is highly conserved within each gene superfamily (Supplementary Fig. 12 online) and that directs the peptide to the endoplasmic reticulum (ER) where the peptide is modified[70,71]. This N-terminal signal peptide is followed by a 20-60 residue leader sequence that is conserved within each gene superfamily; little or no sequence homology is found for the leader peptides from different families (Supplementary Fig. 12 online). Interestingly the leader peptides of the contryphans (Fig. 6b), the M-superfamily, and the T-superfamily

(Supplementary Fig. 12 online) have several conserved prolines arguing against the helical conformation proposed for most leader peptides discussed in this review. The C-terminal core peptide is typically 11-30 residues in length and, aside from highly conserved Cys residues, shows a remarkably high degree of polymorphism[72] (Supplementary Fig. 12 online).

A range of PTM enzymes have been identified[67,73,74], but at present, the role(s) of the leader peptides have not been fully investigated. Some conopeptide precursors have a leader peptide containing a -carboxylation recognition sequence (-CRS) defined by the (K/R)XXZXXXX(K/R) motif where Z is a hydrophobic amino acid[71,75-77]. –Carboxylation can also be achieved with the leader peptide provided *in trans*[75]. Protein disulfide isomerase (PDI) assisted disulfide formation is also promoted by the leader peptide compared to oxidative folding of just the core peptide alone[77,78]. However, not all modifications are guided by the leader peptide as amidation of the C-terminus of the core peptide is governed by the presence of XG-$(K/R)_n$ ($n = 0$-4) motifs in the C-terminal recognition sequences resulting in amidation of residue X[67]. On the other hand, the sequence (L/X)X(K/X)RX in the leader sequence governs cleavage after the Arg residue in some conopeptides to remove the signal and leader peptide from the modified core region. Proteolysis will not occur when this recognition sequence is found within the core peptide[67,79]. The exact timing and sub-cellular location of proteolytic removal of the N-terminal signal and leader peptide (and C-terminal recognition sequence) is unknown, but this step is essential to yield the biologically active toxin[67]. A major protease proposed to catalyze such activity has been identified in *Conus textile*[79]. Importantly, the molecular recognition for all these transformations may involve both leader peptide binding as well as recognition of initial PTMs by subsequent modification enzymes[80,81]. For instance, -carboxylation of glutamate residues[77] or hydroxylation of proline residues[82] can have a dramatic influence on the oxidative folding of the core peptide.

Other ribosomally synthesized natural products

The past decade has also seen the discovery of several head-to-tail backbone cyclized bacteriocins[83]. They are produced with leader peptides of various lengths, but very little is currently known about their processing. This group of peptides includes subtilosin A that contains unusual thioether bridges in which Cys residues are crosslinked to the -carbons of Thr and Phe residues[84]. The leader peptide for subtilosin A formation is unusually short (7 amino acids)[85] compared to the typical leader length found for all other systems discussed herein. Interestingly, the gene cluster for the spore killing factor (skf) in bacilli encodes a similar precursor peptide as subtilosin[86], suggesting skf may contain similar modifications, but currently its structure is not known. Bacilli also produce a series of structurally related ComX pheromones that are important for inducing competence. They are produced as 55-amino acid precursors that are posttranslationally modified to introduce a prenylated and cyclized Trp[87] into a 10-residue final product. Similarly, the thiolactone quorum sensing peptides produced by staphylococci that function as important virulence factors are ribosomally synthesized. For both groups, the precise role of the leader peptide has not yet been investigated, but for the thiolactones, it appears to be involved in localizing the precursor peptide to the membrane[88]. They have recently been expressed heterologously in *E. coli*[89], setting up future detailed studies.

Reprogramming Leader Peptide Directed Biosynthesis

Although the molecular details of leader peptide recognition by the biosynthetic enzymes are still largely unknown, researchers have already explored the potential of LDB for engineering of natural products as illustrated below.

Lantibiotics

A large number of site-directed mutants of various lantibiotic precursor peptides are correctly processed by the biosynthetic machinery in whole cell studies with homologous and heterologous hosts resulting in lantibiotic variants (for reviews, see[90-92]). The most extensive examples are full alanine scanning of both peptides of the two-peptide lantibiotic lacticin 3147[93] as well as the investigation of all possible single amino acid mutations for mersacidin[94]. Collectively, these *in vivo* studies have illustrated the remarkably promiscuous nature of the biosynthetic enzymes and in some instances, these investigations have resulted in compounds with improved properties[95-97]. *In vitro* engineering studies have also demonstrated that core peptides containing nonproteinogenic amino acids can be modified to lantibiotic analogs with improved antimicrobial activities[98]. Intriguingly, the lantibiotic biosynthetic enzymes have not only been used to prepare analogs, but also to install dehydro amino acids and thioether rings in a large variety of other peptides attached to the leader peptides[24,25,99-101], further highlighting the potential of LDB. In these studies, the nisin dehydratase dehydrated Ser/Thr residues that were located as far as 42 amino acids C-terminal to the end of the leader peptide[24]. Finally, the biosynthetic enzymes involved in haloduracin biosynthesis were still active when a recognition sequence for a commercial protease was engineered at the junction between the leader peptide and the core peptide, allowing leader peptide removal even when the endogenous protease was not available[3].

Microcins and Cytolysins

The microcin B17 biosynthetic pathway has been explored both *in vivo* and *in vitro* for its potential to generate analogs for structure-function relationships[102,103]. These studies have demonstrated that oxazoles can be interchanged for thiazoles and vice versa, or can be eliminated or introduced at non-native positions. On the other hand, the Ser residues involved in oxazole formation could not be replaced by Thr, and the Gly residues that take part in both oxazole and thiazole formation could not be substituted by other amino acids[47], showing some limitations to the substrate promiscuity. Interestingly, *in vitro* the streptolysin S synthetase partially installed oxazoles/thiazoles into the microcin B17 precursor as well as into a related precursor peptide from *C. botulinum* despite the leader peptides of the latter two having only very limited sequence identity with the SLS leader[52]. Moreover, an entirely artificial core peptide was designed and attached to the SLS leader peptide and after *in vitro* synthetase action, a novel cytolytic product was obtained.

Engineering of the lasso peptides has focused so far on *in vivo* whole cell experiments in which the gene for the precursor peptide was mutated. No less than 381 mutants of microcin J25 have been probed in the native *E. coli* host, resulting in 242 mutants that were correctly procesed[104]. Only the residues that form the noose of the lasso (Gly1 and Glu8) and Gly2 were intolerant to substitution, while only conserved substitutions were compatible at the second aromatic amino acid (Tyr20) that prevents slippage of the tail out of the lactam ring.

Patellamides, Microviridins, and Conopeptides

The portable nature of leader peptide directed biosynthesis has also been demonstrated for the cyanobactins. Genetic engineering of the patellamide hypervariable region and heterologous expression in *E. coli* resulted in the production of a novel cyclic peptide[57]. Similarly, co-expression of the machinery involved in production of the hexapeptide patellin 2 and the octapeptide patellin 3 with a precursor peptide for the heptapeptide trunkamide resulted in the production of the latter[56]. The components of the conopeptide biosynthetic machinery that have been investigated for engineering studies have also shown great potential. For instance, appending the leader peptide with the -CRS sequence to either N- or C-terminus of a non-native synthetic peptide resulted in -carboxylation of glutamate residues in the synthetic peptide[71,75]. In contrast, the microviridin biosynthetic machinery so

far has proven less amenable to leader peptide directed engineering. Whereas substitution of Thr with Ser in the lactone generating step was tolerated, efforts to increase or decrease the size of the ring were unsuccessful[66].

Summary and Outlook

Given the remarkable pace at which natural products of ribosomal origin are being discovered, it is likely that new classes of such compounds will be reported in the near future. Furthermore, the number of members of existing classes will rapidly increase through genome database mining exercises that focus on conserved sequences of either the leader peptides or the PTM enzymes. The biosynthetic enzymes for most of the systems discussed here are inherently promiscuous as they perform posttranslational modifications on multiple residues in the core peptide(s) that are in very different sequence contexts. The strategy to bind a leader peptide/recognition sequence in order to modify core peptides with great sequence tolerance offers a very efficient approach for rapid evolution of structural and functional diversity through hypermutation of the core sequences. It may therefore come as no surprise that the leader peptide directed biosynthetic strategy appears to be widespread in nature. As a corollary, most of these systems will likely lend themselves to leader peptide directed bioengineering to produce natural product analogs, and ultimately to provide a toolbox to design and create tailor-made pharmacophore-rich products with structural diversity that greatly exceeds the proteinogenic repertoire.

For these goals to be reached, the role of the leader peptide needs to be investigated in greater detail for all systems discussed here and especially structural information of the leader peptides bound to the posttranslational modification machinery would be extremely valuable. In all investigated cases, the leader peptides adopt an unstructured conformation in aqueous solution but addition of trifluoroethanol readily stabilizes an -helical conformation, Pro mutants abolish correct processing, and key residues identified by mutagenesis tend to cluster on one face of a helix. It is anticipated that the biosynthetic enzymes may also stabilize and bind the helical conformation, but no direct evidence is available for this model. Nevertheless, even in the absence of detailed knowledge of the molecular recognition between the leader peptides and the biosynthetic enzymes, the power of leader peptide directed engineering has already been demonstrated for generating natural product analogs.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

Acknowledgments

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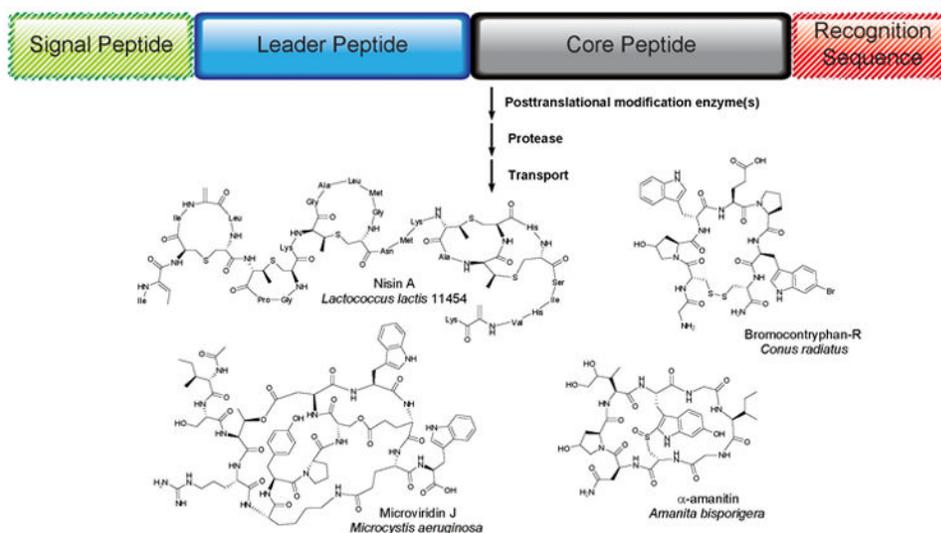
Figure 1. General Scheme and Examples of Leader Peptide Directed Biosynthesis (LDB)
The precursor peptides typically consist of an N-terminal leader and a C-terminal core peptide. A signal peptide governing subcellular localization may be attached to the N-terminus of the leader peptide, and recognition sequences are sometimes found to the C-terminus of the core peptide. The precursor peptides are ribosomally synthesized and posttranslationally modified to their active structures.
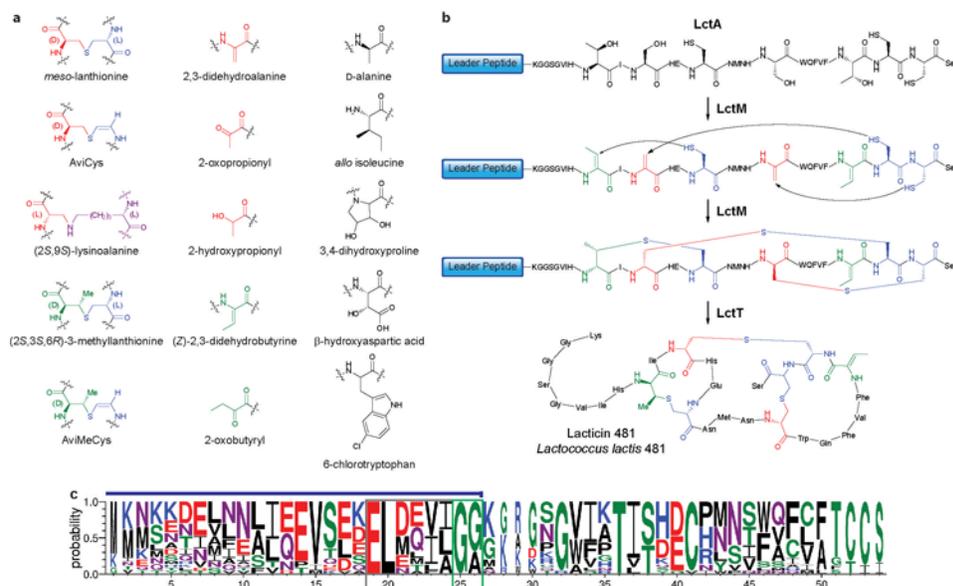
Figure 2. Posttranslational modifications in lantibiotics
a. Different PTMs found in lantibiotics. Colors denote the amino acid origins: red structures are derived from Ser, green from Thr, blue from Cys, and violet from Lys. **b.** Biosynthesis of lacticin 481, a class II lantibiotic. The lacticin 481 precursor peptide (LctA) containing an N-terminal leader and C-terminal core peptide is transformed into a polycyclic thioether product through the action of a bifunctional enzyme (LctM) that dehydrates Ser to dehydroalanine and Thr to dehydrobutyrine, and subsequently catalyzes the Michael-type addition of Cys residues to these unsaturated amino acids. The leader is proteolytically removed from the modified core peptide by a bifunctional protease/transporter enzyme (LctT). Coloring scheme as in Figure 2a. Although the process is drawn as complete dehydration before the commencement of cyclization, recent studies suggest the dehydration and cyclization events may be alternating[30,105]. **c.** Sequence logo representing sequence alignments of selected class II lantibiotic precursor peptides (for alignments, see Supplementary Fig. 3 online). The probability of each amino acid is depicted by the height of the letter and is scaled (width of the letter) according to how many sequences contributed to that position (i.e. narrow letters were generated from a smaller number of sequences than wider letters)[106]. Blue line above the sequence logo indicates the leader peptide, the ELXXBX motif is boxed in grey, and the double Gly motif is boxed in green.

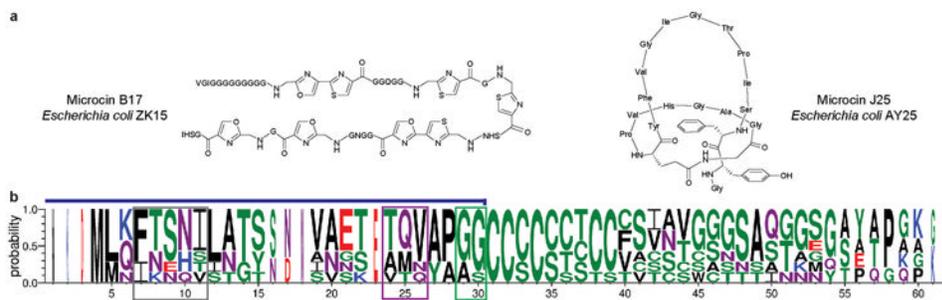**Figure 3. Posttranslational modifications in microcin and cytolysin biosynthesis**
a. Structures of microcin B17 and J25. **b.** Sequence logo representing sequence alignments
of selected cytolysin precursor peptides (for alignments, see Supplementary Fig. 6 online).
See the legend to Fig. 2b for further information about the logo format. The blue line above
the sequence logo indicates the leader peptide, the FXXXB motif is boxed in grey, the TQV
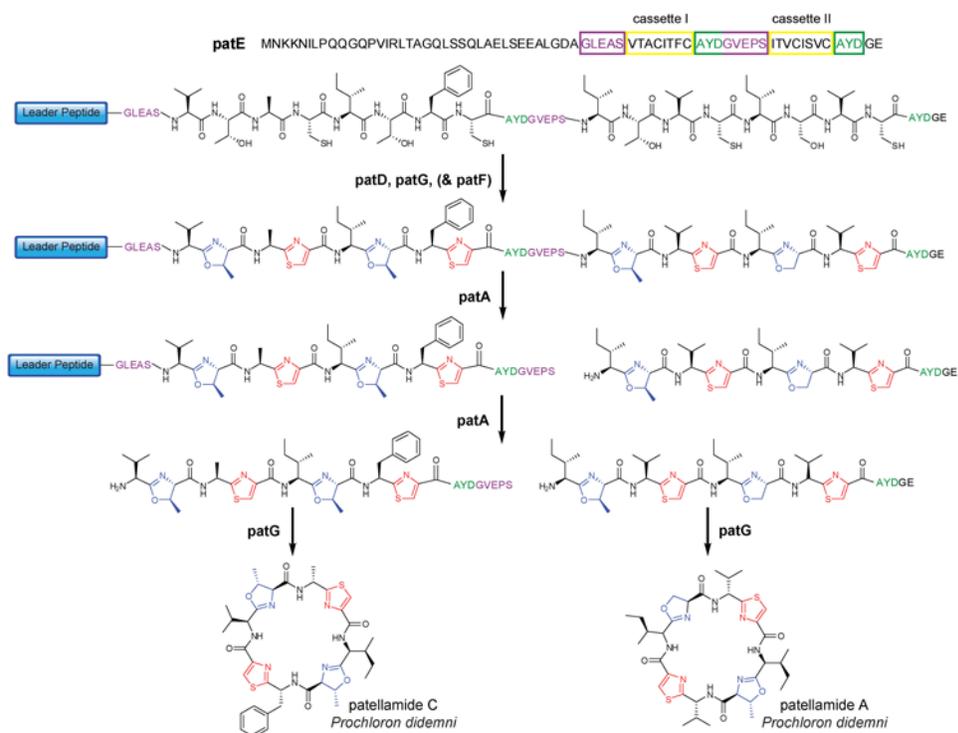motif is boxed in violet, and the double Gly motif is boxed in green.

Figure 4. Proposed biosynthesis of patellamides C and A

The precursor peptide (PatE) consists of an N-terminal leader peptide and two core peptide cassettes, each sandwiched between two recognition sequences (green/violet). It is hypothesized that PatD is responsible for heterocyclization and PatG may be responsible for oxidation of the heterocycles. PatA sequentially removes cassette I and II from the leader peptide and the N-terminal recognition sequences (violet) and PatG removes the remaining recognition sequences (green) and catalyzes cyclization. PatF is essential for patellamide biosynthesis, but its precise role has not been identified[2].
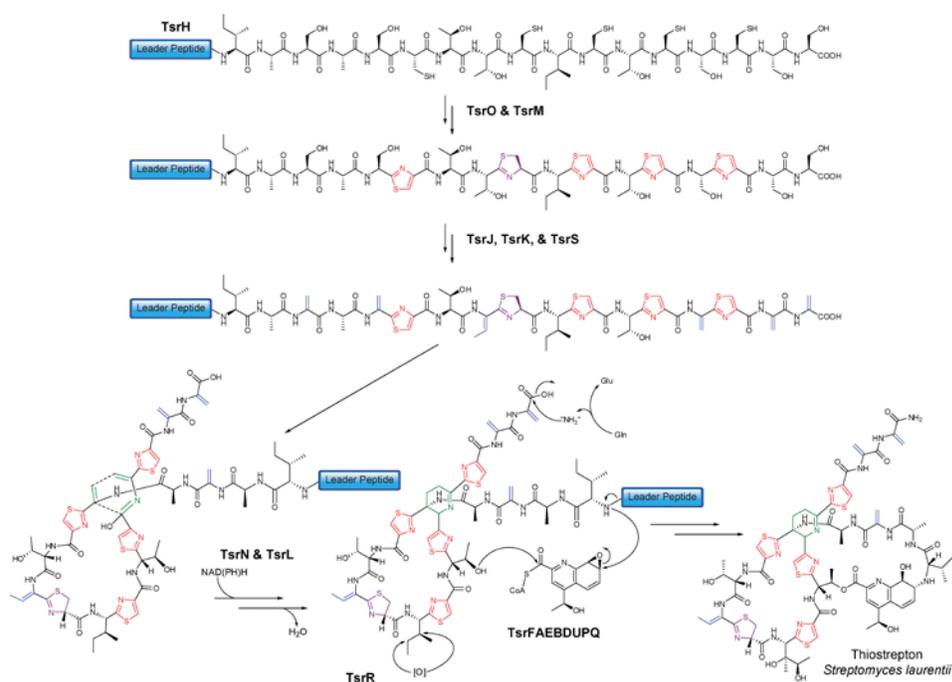
Figure 5. Biosynthesis of thiostrepton
TsrH is ribosomally synthesized as a precursor peptide consisting of an N-terminal leader and C-terminal core peptide. Heterocyclization and dehydration of hydroxyl-amino acids results in a conformationally constrained core peptide, which is further tailored to include a central dehydropiperidine ring, a quinaldic acid moiety, and oxidative modifications. Although the transformations are shown in a particular order, the actual sequence of the modifications is not known. Alphabetical gene nomenclature is used as in [12].
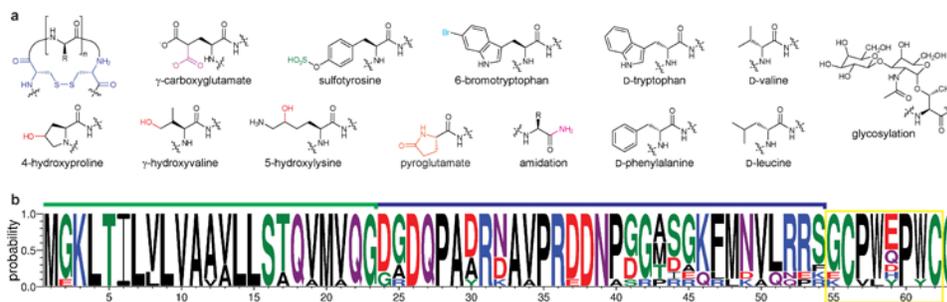
Figure 6. Posttranslational modifications in conopeptides
a. Structures of the PTMs found in conopeptides. **b.** Sequence logo representing sequence alignments of selected contryphan precursor peptides (for alignments, see Supplementary Fig. 12 online). See the legend to Fig. 2b for further information about the logo format. The blue line above the sequence logo indicates the leader peptide, the green line above the sequence logo indicates the signal peptide, and the hypervariable core peptide region is boxed in yellow.