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Brief Communication

Thiopeptide Biosynthesis Featuring Ribosomally Synthesized Precursor Peptides and Conserved Posttranslational Modifications

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SUMMARY

Thiopeptides, with potent activity against various drug-resistant pathogens, contain a characteristic macrocyclic core consisting of multiple thiazoles, dehydroamino acids, and a 6-membered nitrogen heterocycle. Their biosynthetic pathways remain elusive, in spite of great efforts by in vivo feeding experiments. Here, cloning, sequencing, and characterization of the thiostrepton and siomycin A gene clusters unveiled a biosynthetic paradigm for the thiopeptide specific core formation, featuring ribosomally synthesized precursor peptides and conserved posttranslational modifications. The paradigm generality for thiopeptide biosynthesis was supported by genome mining and ultimate confirmation of the thiocillin I production in *Bacillus cereus* ATCC 14579, a strain that was previously unknown as a thiopeptide producer. These findings set the stage to accelerate the discovery of thiopeptides by prediction at the genetic level and to generate structural diversity by applying combinatorial biosynthesis methods.

INTRODUCTION

Thiopeptides are a class of polythiazolyl antibiotics (Bagley et al., 2005). The clinical interest in this family was recently renewed, since many members show potent activity against various drug-resistant pathogens, including methicillin-resistant *Staphylococcus aureus* (MRSA), penicillin-resistant *Streptococcus pneumoniae* (PRSP), and vancomycin-resistant enterococci (VRE). Thiopeptides share a characteristic macrocyclic core, consisting of multiple thiazoles, dehydroamino acids, and a 6-membered, tri- or tetra-substituted nitrogen heterocycle, with side chain(s) appending additional structural diversity (Figure 1; see Figure S1 available online). The complex architectures pose a tremendous challenge to chemical synthesis (Nicolaou et al., 2005a, 2005b; Hughes and Moody, 2007). Although previous isotope-labeled experiments, which aimed at the elucidation of the biosynthetic origins of a few members, established that all moieties exclusively derive from proteinogenic amino acids (Frenzel et al., 1990; Mocek et al., 1993; Smith et al., 1993; Priestley et al., 1996), the biosynthetic pathways of thiopeptides remain elusive. Here, we set out to investigate their biosynthesis by exploiting the genetic basis. Cloning, sequencing, and characterization of the thiostrepton and siomycin A gene clusters unveiled a new biosynthetic paradigm for the thiopeptide specific core formation, featuring ribosomally synthesized precursor peptides and conserved posttranslational modifications. Genome mining and ultimate confirmation of the thiocillin I production in *Bacillus cereus* ATCC 14579, a strain that was previously unknown as a thiopeptide producer, validated that this paradigm is common in thiopeptide biosynthesis.

RESULTS AND DISCUSSION

Cloning, Sequencing and Characterization of the Thiostrepton Biosynthetic Gene Cluster

Thiostrepton (Donovick et al., 1955; Dutcher and Vandeputte, 1955; Jambor et al., 1955) (Figure 1), often referred to as the parent compound in this family, was chosen to be the model molecule for accessing the genetic basis of thiopeptide biosynthesis. Cloning and sequencing of the *tsr* gene cluster (deposited into GenBank under the accession number FJ436358) from *Streptomyces laurentii* ATCC 31255 revealed 21 open reading frames (orfs), whose deduced gene products supported a new paradigm for thiopeptide biosynthesis featuring a ribosomally synthesized precursor pepetide and conserved posttranslational modifications (Figure 2A and Table 1). The 58-aa precursor peptide TsrH contains a 41-aa leading peptide (LP) and a 17-aa structural peptide (SP). The SP sequence IASASCTTCI CTCSCSS is in perfect agreement with the amino acids constituting the thiostrepton peptide backbone, unveiling for the first time the ribosomal origin of thiostrepton (Figure 3A). Central to the *tsr* gene cluster are the seven orfs, *tsrJKLMNOS*, the deduced products of which presumably act on the precursor peptide TsrH to afford the characteristic thiostrepton macrocyclic core structure (Figures 2B and 3B). TsrO, with sequence

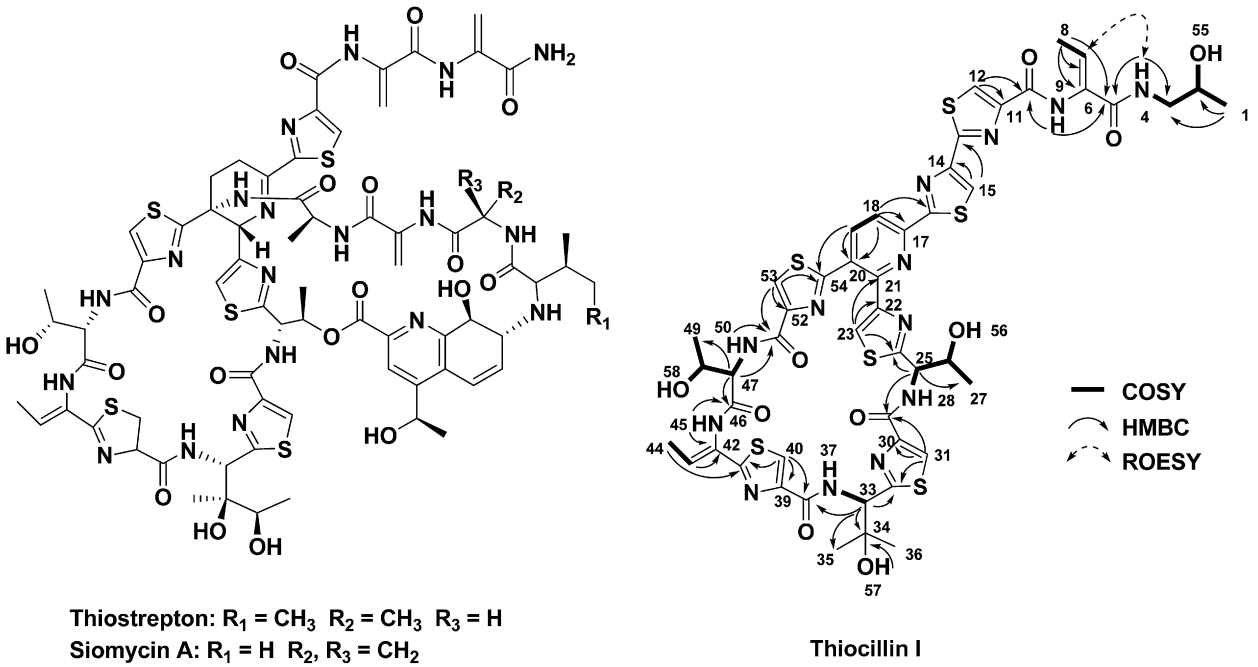

Figure 1. Structures of Thiostrepton, Siomycin A and Thiocillin I
^{1}H-^{1}H COSY, HMBC, and selected ROESY correlations in this study were labeled.

similarity to the cyclodehydratase PatD (38% similarity and 22% identity) in the patellamide biosynthesis (Schmidt et al., 2005), might be functionally associated with the putative dehydrogenase TsrM and able to catalyze the nucleophilic attack of each Cys side chain onto the proceeding carbonyl group, followed by dehydration and optional dehydrogenation to afford the thiazoline and thiazole moieties characteristic to **1**. TsrJ and TsrK, homologous to the N- (25% similarity and 11% identity) and C-terminal (30% similarity and 15% identity) sequences of SpaB in the subtilin biosynthesis (Xie et al., 2002), respectively, presumably are responsible for multiple dehydrations of Ser or Thr residues, yielding the dehydroamino acids featured in **2** as those in lantibiotics. The existence of the additional dehydratase TsrS (also homologous to the N-terminal SpaB[24% similarity and 11% identity]) suggests a putative residue or region-dependent dehydration pattern in the thiostrepton biosynthesis. The resultant linear intermediate **2** might then be forced into a conformation that can readily undergo an intramolecular [4 + 2] cycloaddition reaction to afford the 6-membered heterocyclic ring and complete the biosynthesis of the 26-membered macrocyclic system, giving the intermediate **3** for further modifications. TsrN and TsrL, showing no significant sequence homology to any proteins of known functions, could serve as candidates to catalyze this process. To provide experimental evidence supporting the above bioinformatics-based proposal, selected genes were inactivated to validate their indispensability. As exemplified by the in-frame deletion of *tsrJ*, the resulting mutant strain completely lost the ability to produce thiostrepton (Figure 3C, II), clearly confirming its involvement in the thiostrepton biosynthesis.

Functional assignment of the remaining orfs within the *tsr* cluster allowed the proposal for tailoring intermediate **3** into thiostrepton. Nine genes, *tsrFAEBDUPQI*, serve as candidates, encoding enzymes responsible for the quinaldic acid formation and affording the 27-membered side ring moiety (Figure 2B; Figure S2). They encode a methyltransferase (TsrF), a pyridoxal phosphate (PLP)-dependent aminotransferase (TsrA), an acyl-CoA α/β dehydrogenase-like protein (TsrE), a hydrolase (TsrB), a polyketide cyclase-like enzyme (TsrD), a dehydrogenase/reductase (TsrU), a P450 epoxidase (TsrP), an acyl-CoA synthetase (TsrQ), and a hydrolase/esterase (TsrI). Together, these enzyme functions are consistent with the previously proposed pathway for the quinaldic acid moiety (**4**) formation from Trp (Mocek et al., 1993; Smith et al., 1993; Priestley et al., 1996); the biosynthetic process may require methylation, desamination, and oxidation, followed by imine ring opening and recyclization, epoxidation, and carboxyl group activation. The attachment of **4** onto Ile42 (via amination) and Thr53 (via esterification) may lead to the closure of the side macrocyclic ring with the concomitant release of the 41-aa LP. Finally, *tsrR* and *tsrC* encode a putative P450 hydroxylase (TsrR) and an asparagine synthase-like protein (TsrC), respectively, serving as candidates for the oxidations of Ile51 and C-terminal amide bond formation to furnish thiostrepton (Figure 2B). While the precise timing for many steps remains to be determined, the available *tsr* gene cluster and proposed pathway for thiostrepton biosynthesis have now set the stage for experimental validation.

Cloning, Sequencing and Characterization of the Siomycin A Biosynthetic Gene Cluster

To examine if the newly unveiled thiostrepton pathway is common for the thiopeptide biosynthesis in general, we next cloned and sequenced the biosynthetic gene cluster of siomycin A (deposited into GenBank under the accession number

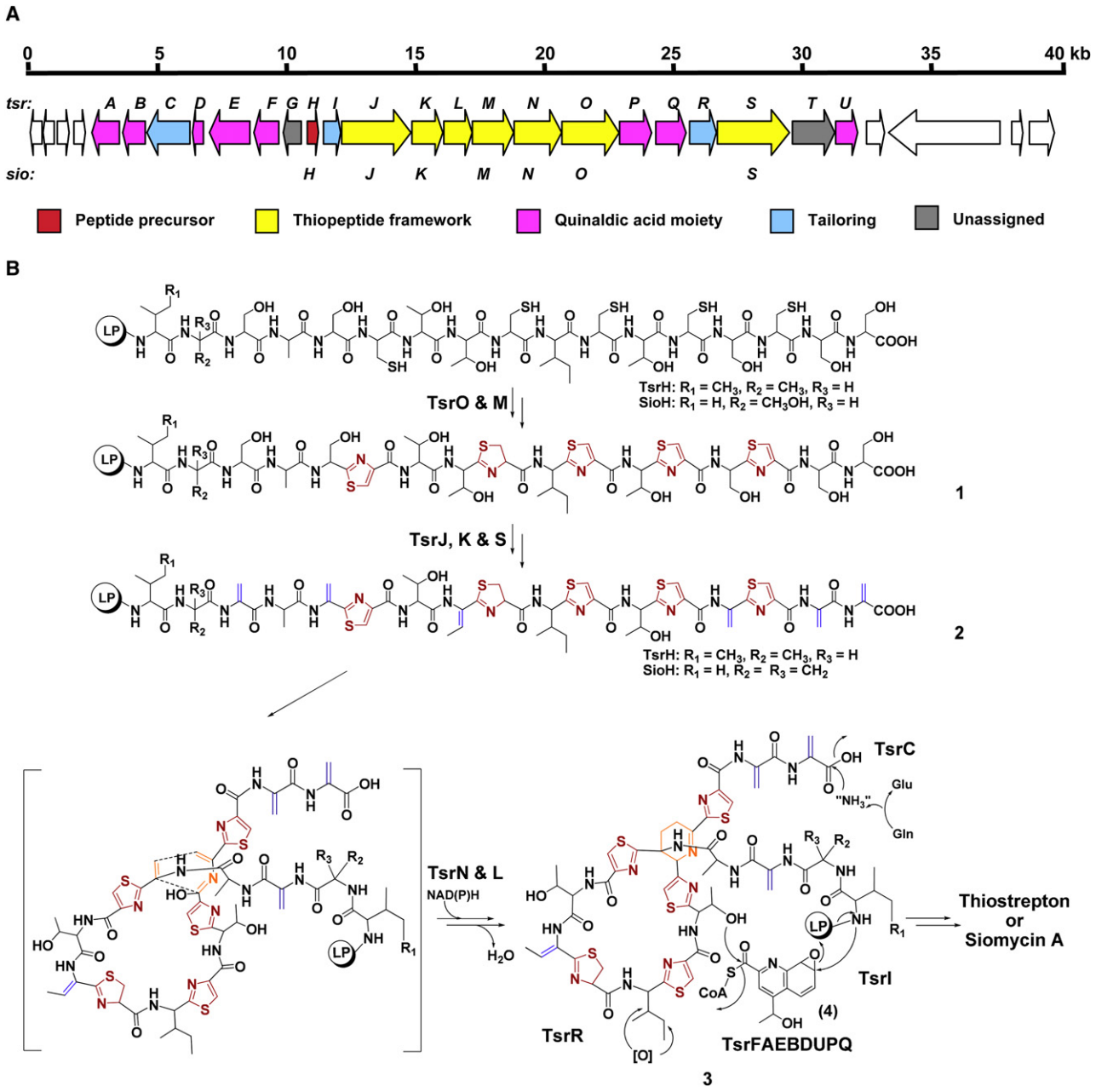

Figure 2. Gene Cluster and Proposed Biosynthetic Pathway

(A) Organization of the *tsr* biosynthetic genes, the deduced functions of which are labeled in color and summarized in Table 1.

(B) Biosynthetic hypothesis for the thiostrepton (or siomycin A) framework and modifications. Color coding indicates the thiazole/thiazoline (red), dehydroamino acids (blue), and 6-membered nitrogen heterocycle (orange).

FJ436355), a naturally occurring analog of thiostrepton (Ebata et al., 1969; Tori et al., 1979) (Figure 1), from *S. sioyaensis* ATCC 13989 for comparative analysis. Remarkably, within the *sio* gene cluster, *sioH* encodes a 61-aa precursor peptide SioH containing a 17-aa SP that is nearly identical to that of TsrH (Figure 3A). The only exception is the N-terminal Val45-Ser46 residues, which is consistent with their structural difference in a Val-dehydroalanine unit of siomycin A in place of an Ile-Ala unit of thiostrepton. The seven genes, *sioJKLMNOS*, highly conserved relatives to *tsrJKLMNOS* in both sequence and organization (Figure 3B), were proposed to encode the comparable enzymatic activities for the similar thiopeptide core formation as that in thiostrepton biosynthesis (Figures 2 and 3). The inactivation of the putative cyclodehydratase gene *sioO* completely abolished the production (Figure 3C, IV), confirming its indispensability to the siomycin A biosynthesis. These findings support a common paradigm for the thiopeptide biosynthesis. Thus, a bacterial thiopeptide biosynthetic machinery should minimally

Table 1. Deduced Functions of Orfs in the Thiostrepton Biosynthetic Gene Cluster

Gene	Size[a]	Protein Homolog[b] and Origin	Identity/Simiarity (%)	Proposed Function	*sio* Homolog	*tcl* Homolog
orf1[c]	193	Upp (NP_628223), from *Streptomyces coelicolor* A3(2)	91/97	uracil phosphoribosyl-transferase		
orf2[c]	208	SGR_3903 (YP_001825415), from *S. griseus subsp. griseus* NBRC 13350	41/53	hypothetical protein		
orf3[c]	177	SSCG_02932 (YP_002192918), from *S. clavuligerus* ATCC 27064	68/84	hypothetical protein		
orf4[c]	142	MesJ (NP_696675), from *Bifidobacterium longum* NCC2705	57/68	cytidine and deoxycytidylate deaminase		
tsrA	362	HisC2 (YP_001853585), from *Mycobacterium marinum* M	44/60	histidinol-phosphate aminotransferase		
tsrB	276	SSEG_03719 (YP_002206063), from *S. sviceus* ATCC 29083	50/65	predicted hydrolase of the alpha/beta superfamily		
tsrC	618	OxyD (AAZ78328), from *S. rimosus*	54/65	amidotransferase		
tsrD	135	SnoaL (AAF01813), from *S. nogalater*	32/54	polyketide clyclase-like enzyme		
tsrE	428	STH2357 (YP_076186), from *Symbiobacterium thermophilum* IAM 14863	35/51	acyl-CoA dehydrogenase-like protein		
tsrF	311	Sare_0495 (YP_001535415), from *Salinispora arenicola CNS-205*	41/57	putative methyltransferase		
tsrG	213	Mext_1123 (YP_001638598), from *Methylobacterium extorquens PA1*	28/46	hypothetical protein		
tsrH	58	———	–/–	thiostrepton precursor peptide	*sioH*	$tclB_{1-4}$
tsrI	197	Bm1_20485 (XP_001895551), from *Brugia malayi*	29/42	hydrolase/esterase		
tsrJ	933	SpaB (AAL15564), from *Bacillus subtilis*	11/24	dehydratase	*sioJ*	*tclE*
tsrK	346	SpaB (AAL15564), from *B. subtilis*	12/29	dehydratase	*sioK*	*tclF*
tsrL	368	BC5082 (NP_834750), from *B. cereus* ATCC 14579	21/41	hypothetical protein	*sioL*	*tclG*
tsrM	589	BAT_3535 (ZP_03054696), from *B. pumilus* ATCC 7061	24/40	dehydrogenase	*sioM*	*tclH*
tsrN	612	BL02837 (YP_078248), from *B. licheniformis* ATCC 14580	25/39	hypothetical protein	*sioN*	*tclK*
tsrO	681	PatD (AAY21153), from *Prochloron didemni*	22/35	cyclodehydratase	*sioO*	*tclD*
tsrP	474	PimD (CAC20932), from *S. natalasis*	26/42	P450 epoxidase		
tsrQ	424	PstD (CAM56771), from *Actinoplanes friuliensis*	29/39	acyl-CoA synthetase		
tsrR	396	RubU (AAM97370), from *S. collinu*	30/44	cytochrome P450 monoxygenase		
tsrS	936	SpaB (AAL15564), from *B. subtilis*	11/23	dehydratase	*sioS*	
tsrT	599	Gura_3608 (YP_001232335), from *Geobacter uraniireducens* Rf4	27/39	radical SAM domain-containing protein		
tsrU	272	FabG (YP_177255), from *B. clausii* KSM-K16	36/51	dehydrogenase/reductase		
orf5[c]	247	orf_L7 (CAN89623), from *S. collinus*	39/60	hypothetical protein		
orf6[c]	1447	SsviA_010100017073 (ZP_03195299), from *S. sviceus* ATCC 29083	38/51	WD-40 repeat protein		
orf7[c]	99	SCO4036 (NP_628218), from *S. coelicolor* A3(2)	82/91	hypothetical protein		
orf8[c]	336	SclaA_010100013725 (ZP_03183088), from *S. clavuligerus* ATCC 27064	79/81	RNA polymerase sigma factor, sigma F		

[a] Numbers are in amino acids.
[b] NCBI accession numbers are given in parentheses.
[c] orfs beyond the *tsr* gene cluster.

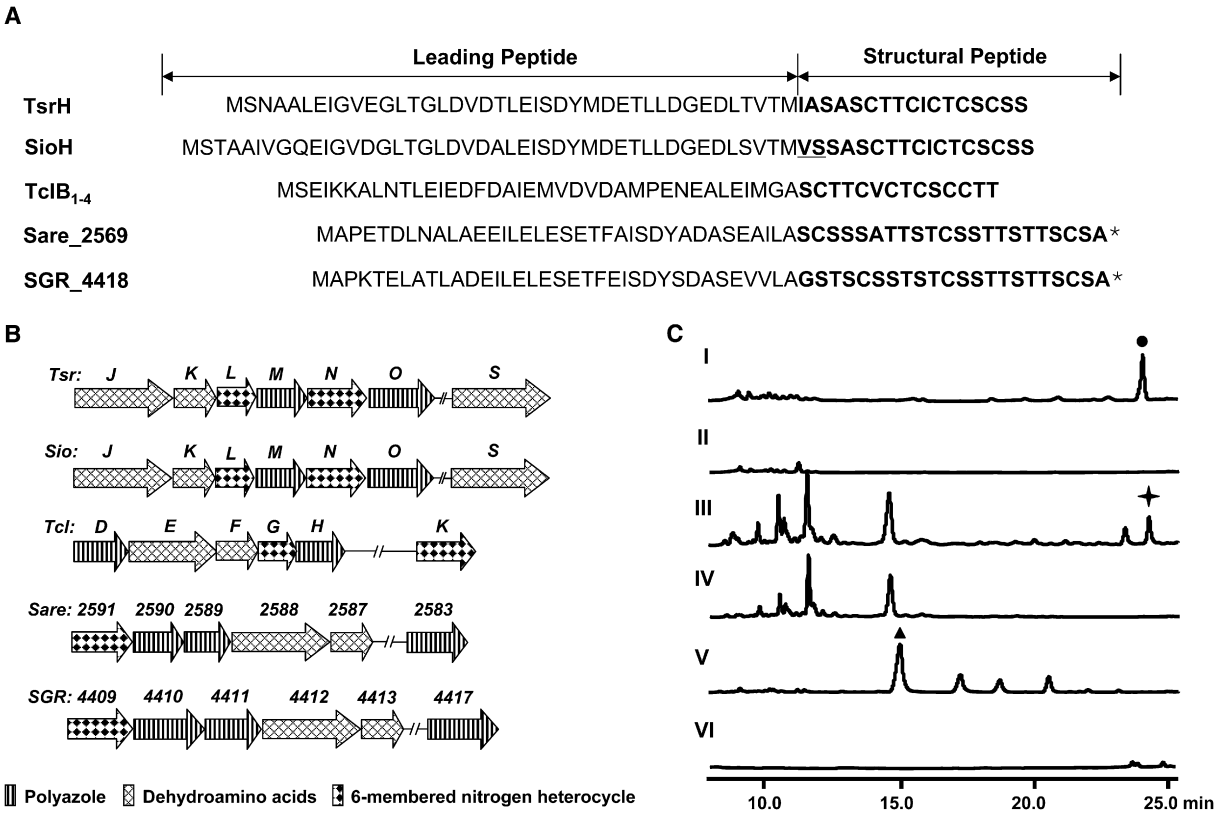

Figure 3. Comparison and Validation of the Thiopeptide Framework Formation

(A) Peptide precursors for thiostrepton (TsrH), siomycin A (SioH), thiocillin I ($TclB_{1-4}$), and two putative thiopeptides (Sare_2569 and SGR_4418). The SP sequences are labeled in bold (asterisk indicates the proposed SPs). The SP amino acids difference of SioH from TsrH is underlined.

(B) Organization of the thiopeptide framework-forming genes identified from the producers of thiostrepton (*tsr*), siomycin A (*sio*), and thiocillin I (*tcl*), and two uncharacterized producers *Salinispora arenicola* CNS-205 (*sare*) and *S. griseus subsp. griseus* NBRC 13350 (*sgr*).

(C) HPLC analysis of the thiopeptide production in the wild-type strain of the thiostrepton (solid dot) producer *S. laurentii* ATCC 31255 (I), *tsrJ* mutant *S. laurentii* strain SL1001 (II), wild-type strain of the siomycin A (solid star) producer *S. sioyaensis* ATCC 13989 (III), *sioO* mutant *S. sioyaensis* strain SL2001 (IV), wild-type strain of the thiocillin I (solid triangle) producer *B. cereus* ATCC 14579 (V), and *tclE* mutant *B. cereus* strain SL3001 (VI).

be characterized by: (1) a ribosomally synthesized precursor peptide whose SP is Cys and Ser/Thr-rich, matching the aa sequence of the resultant thiopeptide backbone (Figure 3A); (2) a cyclodehydratase/dehydrogenase complex (e.g., TsrOM and SioOM) to catalyze the formation of the multiple thiazole and thiazoline rings; (3) a dehydratase pair (e.g., TsrJK and SioJK) to generate the dehydroamino acid residues; and (4) at least a TsrN or SioN-like protein to furnish the 6-membered nitrogen heterocycle via putative [4 + 2] cycloaddition. These enzymes are unique to thiopeptide biosynthesis. As exemplified by phylogenetic analysis of the thiopeptide cyclodehydratases, they are distinct from the polythiazole synthetases in both bacteriocin and cyanobactin biosynthesis (Li et al., 1996; Donia et al., 2006; Lee et al., 2008; Walsh and Nolan, 2008) (Figure S3).

Genome Mining and Confirmation of the Thiocillin I Production in a Previously Unknown Producer

To demonstrate the generality of the newly emerged thiopeptide biosynthetic paradigm, we further carried out a comprehensive survey of published sequence data of microbial origins, focusing on mining the genomes for the Cys and Ser/Thr-rich precursor peptide and the conserved posttranslational modification enzymes. The characteristic genetic loci were indeed identified from several bacterial genomes, as exemplified by *Bacillus cereus* ATCC 14579 (NC_004722) (Ivanova et al., 2003), *Salinispora arenicola* CNS-205 (NC_009953), and *S. griseus subsp. griseus* NBRC 13350 (NC_010572), none of which, to our knowledge, was previously known as a thiopeptide producer. In the case of *B. cereus* ATCC 14579, there are four tandem genes, namely $tclB_1$, B_2, B_3 and B_4, which encode an identical 52-aa precursor peptide (Figure 3A). Intriguingly, the 14-aa SP sequence completely matches the aa sequence predicted for micrococcins or thiocillins (Shoji et al., 1981; Bagley et al., 2005) (Figure 1; Figure S1), a group of thiopeptides that have previously isolated from *Bacillus* strains. For the remaining two bacterial strains, the deduced peptide precursors (Sare_2569 from *S. arenicola* CNS-205, and SGR_4418 from *S. griseus subsp. griseus* NBRC 13350) (Figure 3A) share high similarity (74% identity) to each other and likely serve as the substrates for the conserved posttranslational modification enzymes to synthesize structurally related but new thiopeptides, since their C-terminal SP sequences do not fit any peptide backbone of structurally characterized thiopeptides.

Inspired by the genome mining findings, we fermented *B. cereus* ATCC 14579 and isolated the product to validate

thiopeptide production. HPLC-ESI-MS analysis of the crude extract from 12 l of fermentation revealed one major product (Figure 3C, V), which was further purified for structural elucidation (Supplemental Data). HR-ESI-MS analysis showed its positive $[M + Na]^+$ ion at *m/z* 1182.19996, establishing the molecular formula as $C_{48}H_{49}N_{13}O_{10}S_6$. Taking the ultraviolet absorptions at λ_{max} 225 nm, 280 nm, and 350 nm into account, this compound was deduced to be a highly unsaturated molecule rich in sulfur, amide bonds, and aromatic rings. The ^1H, ^{13}C, and 2D NMR analyses (including ^1H-^1H COSY, HSQC, HMBC, and ROESY spectra) eventually confirmed its identity as thiocillin I (Figure 1; Table S2 and Figure S4), which has been previously isolated from *B. cereus* G-15 (Shoji et al., 1976). Finally, the dehydratase gene *tclE* was inactivated in *B. cereus* ATCC 14579, and, as expected, the resulting mutant strain completely lost its ability to produce thiocillin (Figure 3B, VI), unambiguously establishing the predicted thiopeptide genetic locus as responsible for thiocillin production.

SIGNIFICANCE

In this study, we have uncovered a common paradigm for thiopeptide biosynthesis that features ribosomally synthesized precursor peptides and conserved posttranslational modifications. We discovered this pathway by first cloning, sequencing, and characterizing the thiostrepton biosynthetic gene cluster from *S. laurentii* ATCC 31255, subsequently validating its generality by cloning, sequencing, and characterizing the siomycin A biosynthetic gene cluster from *S. sioyaensis* ATCC 13989, and finally demonstrating its applicability as a new paradigm for thiopeptide biosynthesis by genome mining and ultimate confirmation of thiocillin I production in *B. cereus* ATCC 14579, a strain that was previously unknown as a thiopeptide producer. The newly discovered pathway is remarkably concise and efficient, in contrast to the heroic efforts of chemical synthesis of these natural products. Sequence permutations to the precursor peptides followed by the diverse tailoring modifications on the resulting thiopeptide scaffold could be a very attractive strategy to access thiopeptide structural diversity. The findings reported here now set the stage to accelerate the discovery of thiopeptides by genome mining and to generate structural diversity by applying combinatorial biosynthesis methods.

ACCESSION NUMBERS

The biosynthetic gene clusters of thiostrepton and siomycin A have been deposited in the GenBank with accession codes FJ436358 and FJ436355, respectively.

SUPPLEMENTAL DATA

Supplemental Data include Supplemental Experimental Procedures, Supplemental References, two tables, and five figures and can be found with this article online at http://www.cell.com/chemistry-biology/supplemental/S1074-5521(09)00031-3.

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