Chemical Science

EDGE ARTICLE

View Article Online
View Journal | View Issue

Cite this: *Chem. Sci.*, 2017, **8**, 1607

Activation and characterization of a cryptic gene cluster reveals a cyclization cascade for polycyclic tetramate macrolactams†

Subhasish Saha,‡[a] Wenjun Zhang,‡[a] Guangtao Zhang,‡[a] Yiguang Zhu,[a] Yuchan Chen,[b] Wei Liu,[ac] Chengshan Yuan,[a] Qingbo Zhang,[a] Haibo Zhang,[a] Liping Zhang,[a] Weimin Zhang[b] and Changsheng Zhang[ac]

Polycyclic tetramate macrolactams (PTMs) are a growing class of natural products and are derived from a hybrid polyketide synthase (PKS)/non-ribosomal peptide synthetase (NRPS) pathway. PTM biosynthetic gene clusters are conserved and widely distributed in bacteria, however, most of them remain silent. Herein we report the activation of a PTM gene cluster in marine-derived *Streptomyces pactum* SCSIO 02999 by promoter engineering and heterologous expression, leading to the discovery of six new PTMs, pactamides A–F (**11–16**), with potent cytotoxic activity upon several human cancer cell lines. *In vivo* gene disruption experiments and *in vitro* biochemical assays reveal a reductive cyclization cascade for polycycle formation, with reactions sequentially generating the 5, 5/5 and 5/5/6 carbocyclic ring systems, catalysed by the phytoene dehydrogenase PtmB2, the oxidoreductase PtmB1, and the alcohol dehydrogenase PtmC, respectively. Furthermore, PtmC was demonstrated as a bifunctional cyclase for catalyzing the formation of the inner five-membered ring in ikarugamycin. This study suggests the possibility of finding more bioactive PTMs by genome mining and discloses a general mechanism for the formation of 5/5/6-type carbocyclic rings in PTMs.

Received 30th August 2016
Accepted 21st October 2016

DOI: 10.1039/c6sc03875a

www.rsc.org/chemicalscience

Introduction

Polycyclic tetramate macrolactams (PTMs) feature a tetramate-embedding macrocyclic lactam ring that is fused to a subset of diverse carbocyclic ring systems (Fig. 1),[1] such as the 5/5 ring system in alteramides (**1**, **2**),[2] 5/5/6 ring system in HSAF (heat-stable antifungal factor, **3**), lysobacteramide B (**4**),[3,4] and frontalamides (**5**, **6**),[5] 5/6/5 ring system in ikarugamycin (**7**)[6] and butremycin (**8**),[7] and 5/4/6 ring system in **9**.[8] PTMs exhibit a wide range of antifungal, antibacterial, antiprotozoal, antiulcer, antiviral, cytotoxic, and apoptosis-inducing biological activities.[1] As such, PTMs have shown significant potential in both agricultural and medicinal applications.[1]

The structural complexity of PTMs has greatly hampered efforts towards their total synthesis.[9–12] In sharp contrast, nature has developed a conserved and compact biosynthetic pathway to construct the complex structures of PTMs.[1,13] PTMs were revealed to have originated from a conserved hybrid polyketide synthase (PKS)/non-ribosomal peptide synthetase (NRPS) pathway.[5] The PKS was iteratively used to generate two separate polyketide chains that were respectively condensed to the α- and δ-amino groups of an L-ornithine tethered in the NRPS, leading to a common tetramate-containing polyene precursor **10** (Fig. 1).[8,14–17] The extraordinary simplicity of PTM biosynthesis was exemplified by a three-

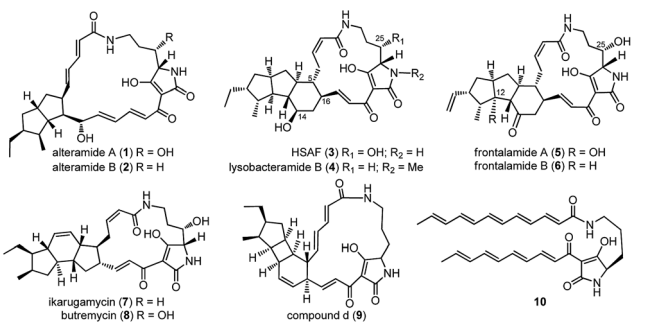

Fig. 1 Representative PTMs (**1–9**) and the key precursor (**10**).

[a]*CAS Key Laboratory of Tropical Marine Bio-resources and Ecology, Guangdong Key Laboratory of Marine Materia Medica, South China Sea Institute of Oceanology, Chinese Academy of Sciences, 164 West Xingang Road, Guangzhou 510301, China. E-mail: czhang2006@gmail.com; czhang@scsio.ac.cn*

[b]*State Key Laboratory of Applied Microbiology Southern China, Guangdong Institute of Microbiology, 100 Central Xianlie Road, Guangzhou 510070, China*

[c]*State Key Laboratory of Applied Microbiology Southern China, South China Sea Resource Exploitation and Protection Collaborative Innovation Center (SCS-REPIC), China*

† Electronic supplementary information (ESI) available: The experimental procedures, materials, and characterization of the compounds. See DOI: 10.1039/c6sc03875a

‡ S. Saha, W. Zhang and G. Zhang contributed equally to this work.

gene cassette (*ikaABC*) mediated production of ikarugamycin (**7**) in a heterologous host.[15,16] However, the enzymatic machinery that dictates the manner of the divergent cyclization cascades that convert **10** into diverse ring systems in PTMs remains mysterious.[1] The only well studied example was the formation of the inner five-membered ring in **7**, which is catalyzed by the alcohol dehydrogenase IkaC in the manner of a Michael addition reaction.[15]

A genomic survey has revealed the wide distribution of conserved PTM biosynthetic gene clusters in phylogenetically diverse bacteria.[5] However, most of them are silent.[1,5] Recently, different strategies were employed to successfully activate silent PTM gene clusters for the production of new PTMs, including promoter engineering[18] and the heterologous expression of a reconstituted PTM gene cluster *via* synthetic biology.[8] The success of these strategies highlights the potential for the discovery of new PTMs by the genome mining-based activation of PTM gene clusters. Herein we report (i) the activation of a cryptic PTM biosynthetic gene cluster in the marine-derived *Streptomyces pactum* SCSIO 02999 *via* promoter engineering; (ii) the isolation, characterization and cytotoxicity determination of six new PTMs, the pactamides A–F; (iii) the discovery of a reductive cyclization cascade to sequentially generate the 5, 5/5 and 5/5/6 ring systems in pactamides by the inactivation of three oxidoreductase-encoding genes (*ptmB2*, *ptmB1* and *ptmC*) and analysis of the corresponding intermediates; (iv) the biochemical demonstration of the alcohol dehydrogenase PtmC as a bifunctional cyclase capable of mediating the formation of both six- and five-membered inner rings in PTMs.

Results and discussion

Identification of a putative PTM gene cluster by genome mining

Deep-sea derived *S. pactum* SCSIO 02999 has been shown to produce xiamycin-related indolosesquiterpenes as major products, and the xiamycin biosynthetic gene cluster (*xia*) was identified by genome sequencing.[19–22] Further genomic analysis reveals the presence of a 14.8 kb biosynthetic gene cluster (GenBank accession number KU569222) composed of five genes (*ptmD*, *ptmA*, *ptmB1*, *ptmB2*, and *ptmC*) that are highly homologous to the PTM biosynthetic genes, immediately neighbouring the *xia* gene cluster (Fig. 2A, Table S1†). The PtmD protein has over 50% identity with those hydroxylases (previously annotated as sterol desaturases[3]) which were established as introducing the hydroxy group at the ornithine moiety of PTMs.[5,23,24] PtmA is predicted to be a typical hybrid PKS/NRPS protein, and shows a high similarity to PTM PKS/NRPS proteins such as IkaA,[15,16] FtdB,[5] and HSAF PKS/NRPS.[3] PtmB1 is highly homologous to FAD-dependent oxidoreductases in other PTM pathways, while PtmB2 is highly similar to a number of phytoene dehydrogenases putatively involved in PTM biosynthesis (Table S1†).[1] PtmC bears a striking resemblance to alcohol dehydrogenases involved in PTM biosynthesis, such as FtdE,[5] OX4,[14] and IkaC.[15]

Activation and characterization of the cryptic PTM gene cluster

The presence of a conserved PTM biosynthetic gene cluster in *S. pactum* SCSIO 02999 suggests its potential for PTM production. However, no PTM-like compounds were detected either in the wild type *S. pactum* SCSIO 02999 (data not shown), or in the mutant 2999XM47i (Table S2†) where the *xiaP* gene (encoding an essential polyprenyl synthetase for xiamycin biosynthesis[19]) was in-frame deleted to abolish the production of xiamycin-type indolosesquiterpenes and hence facilitate the detection of secondary metabolites other than xiamycins (Fig. 2B, trace i). The cosmid pCSG2404 (Table S2†), obtained in our previous work in screening the xiamycin gene cluster,[19] was found to contain the intact PTM gene cluster. However, introduction of the cosmid pCSG2801 (Table S2†), a derivative of pCSG2404 in which the *neo* gene (encoding kanamycin resistance) was replaced by a gene cassette containing *aac(3)IV* (encoding apramycin resistance), *oriT* (for conjugation), and *Int*ϕ*C31* (for specific integration into *Streptomyces* species) from pSET152A′B[25] (Table S2†) into *Streptomyces lividans* TK64, resulted in no observed production of PTM-like compounds (Fig. 2B, trace ii), similar to the control strain *S. lividans* TK64/pSET152 (Fig. 2B, trace iii).

In attempts to activate the PTM gene cluster, the constitutive promoter *ermE**p from pPWW50,[26] was inserted independently in front of *ptmA* and *ptmD* for heterologous expression in *S. lividans* TK64 (Tables S2 and S3; Fig. S1 and S2†). Interestingly, a number of products with UV spectra similar to PTMs, such as **11–15** (Fig. 2B, trace iv), were detected when the *ermE**p promoter was inserted in front of *ptmA*. Surprisingly, no PTMs were observed upon inserting the *ermE**p promoter in front of *ptmD* (Fig. 2B, trace v). For in-frame gene deletion experiments, we subsequently constructed three cosmids, pCSG2809 (Δ*ptmC*), pCSG2811 (Δ*ptmB1*), and pCSG2814 (Δ*ptmB2*), in which the *ermE**p promoter was inserted in front of *ptmA* (Fig. S3–S5†). Compound **13** was found to be the major product upon inactivating *ptmC* (Fig. 2B, trace vi), whereas **15** became the major product when *ptmB1* was inactivated (Fig. 2B, trace vii). When ptmB2 was in-frame deleted, compound **10** was the major product (Fig. 2B, trace viii). The identity of compound **10** (Fig. 1) was deduced from its UV spectrum and mass (*m*/*z* 475.4 $[M + H]^+$, 473.6 $[M - H]^-$) which were almost identical to those of **10** from the Δ*ikaB* mutant in the biosynthesis of **7** (Fig. S6†).[15]

Finally, an attempt was made to *in situ* activate the *ptm*-gene cluster in *S. pactum* 2999XM47i to afford a corresponding mutant 2999PTMp1 (Table S2†), in which the *ermE**p promoter was inserted in front of *ptmA*. The fermentation of 2999PTMp1 also led to the production of a number of PTMs, including **10–16** (Fig. 2B, trace ix).

Isolation, structure elucidation and cytotoxicity determination of new PTMs

Pactamides A–F (**11–16**, Fig. 2C) were isolated from the fermentation extracts of *S. pactum* 2999PTMp1, *S. lividans* TK64/pCSG2809, or *S. lividans* TK64/pCSG2811 (ESI†), and their structures were elucidated by extensive interpretation of the

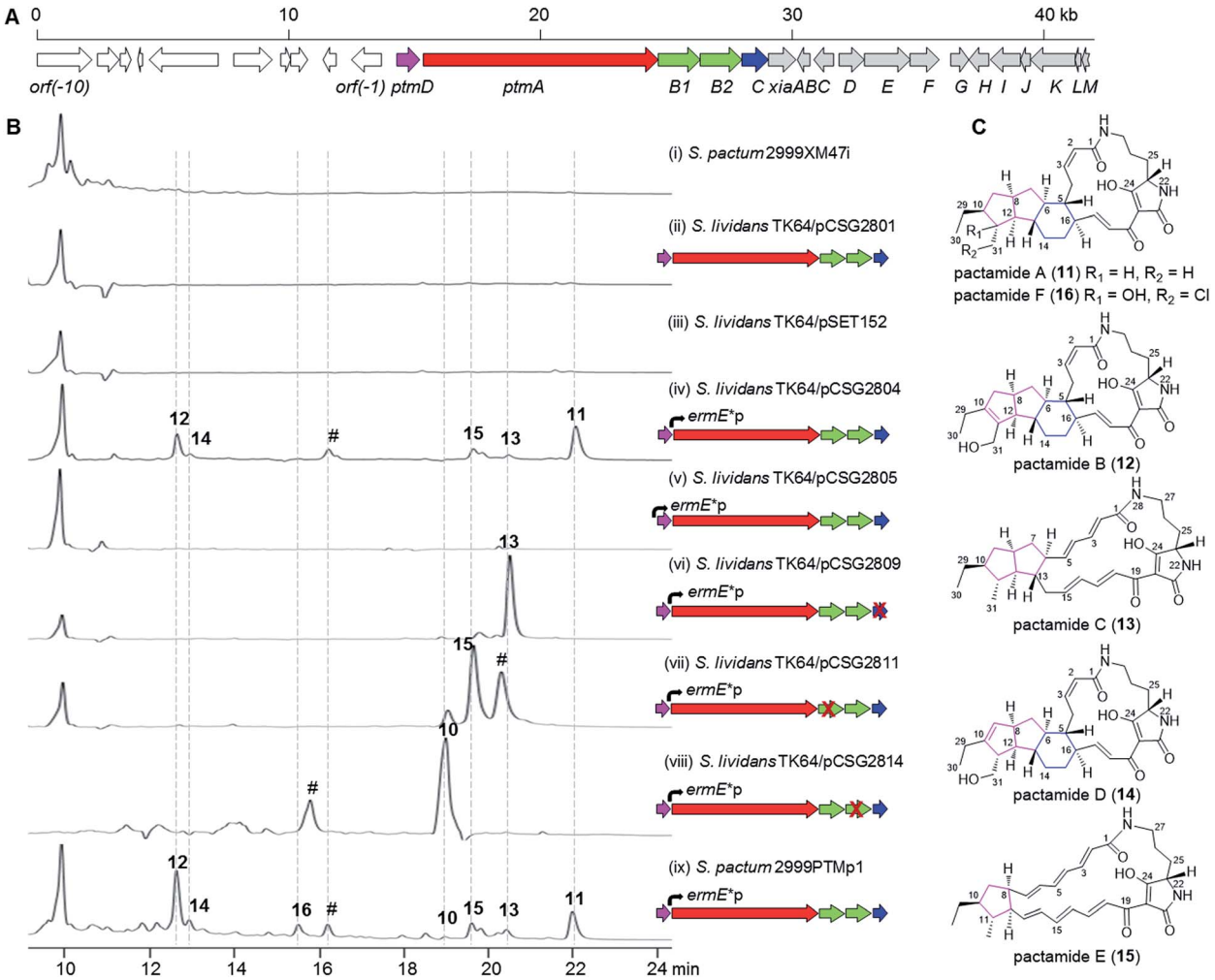

Fig. 2 (A) (A) Genetic organization of the *ptm* gene cluster in pCSG2404 from a genomic library of *S. pactum* SCSIO 02999. (B) HPLC analysis of metabolite profile of different strains: (i) *S. pactum* 2999XM47i, where *xiaP* is in-frame deleted; (ii) *S. lividans* TK64/pCSG2801, no promoter inserted; (iii) *S. lividans* TK64/pSET152; (iv) *S. lividans* TK64/pCSG2804, where *ermE**p is inserted in front of *ptmA*; (v) *S. lividans* TK64/pCSG2805, where *ermE**p is inserted in front of *ptmD*; (vi) *S. lividans* TK64/pCSG2809, where *ermE**p is inserted in front of *ptmA* and *ptmC* is in-frame deleted; (vii) *S. lividans* TK64/pCSG2811, where *ermE**p is inserted in front of *ptmA* and *ptmB1* is in-frame deleted; (viii) S. *lividans* TK64/pCSG2814, where *ermE**p is inserted in front of *ptmA* and *ptmB2* is in-frame deleted; (ix) *S. pactum* 02999PTMp1, where *ermE**p is inserted in front of *ptmA*. (i)–(vii) and (ix), detection at 300 nm; (viii), detection at 360 nm. The "#" symbols denote uncharacterized PTM-like products. (C) Chemical structures of patamides A–F (**11–16**).

spectroscopic/spectrometric data (Tables S4–S7, Fig. S7–S13†) including high resolution electrospray ionization mass spectrometry (HRESIMS), 1D and 2D NMR, and electronic circular dichroism spectroscopy (ECD). The molecular formula of pactamide A (**11**) was established as $C_{29}H_{40}N_2O_4$ by HRESIMS. The planar structure of **11** was elucidated by comparing the NMR spectroscopic data of **11** (Tables S4 and S5, Fig. S7†) and **4** (Fig. 1).[4] The relative configuration of **11** was deduced by the proton coupling constants ($Z\Delta^{2,3}$ $J_{2,3}$ 11.5 Hz; $E\Delta^{17,18}$ $J_{17,18}$ 15.0 Hz, Table S4†) and NOESY correlations (Fig. S7†). The assignment of H-5/H-11/H-13 on the same side of the 5/5/6-tricyclic ring system in **11**, and H-6/H-8/H-10/H-12/H-16/H_3-31 on another side, was supported by the observed NOESY correlations (Fig. S7†). On the basis of the biosynthetic origin of the L-ornithine of PTMs,[1,4] the *S*-configuration was assignable to C-23. Given that **11** and **4** exhibited almost identical ECD spectra (Fig. S8†),[4] the absolute configuration of **11** was deduced as 5*R*, 6*S*, 8*S*, 10*S*, 11*R*, 12*R*, 13*S*, 16*R* and 23*S*. Similarly, the structures of pactamides B–F (**12–16**) were determined (see the ESI† for the structure elucidation). The *trans*-orientation of H-10/H-11 in **11**, **13** and **15** is similar to that in aburatubolactam A.[27] In contrast, a *cis*-orientation of H-10/H-11 was found in other PTMs with determined relative configurations (Fig. 1 and S14†).[1] Pactamide D (**14**) contains a $\Delta^{9,10}$ double bond, similar to that in the marine sponge metabolites cylindramide[28] and geodin A[29] (Fig. S14†), whereas **12** contains a unique $\Delta^{10,11}$ double bond. Pactamide F (**16**) represents the first example of a halogenated PTM. Pactamides A–F (**11–16**) exhibited *in vitro* antiproliferative activity against four cancer cell lines (SF-268, MCF-7, NCI-H460 and Hep-G2) with IC_{50} values ranging from 0.24–26 μM

Table 1 Cytotoxicities of pactamides A–F (**11–16**)

	IC_{50} (μM)			
	SF-268	MCF-7	NCI-H460	Hep-G2
11	0.51 ± 0.01	0.26 ± 0.02	0.24 ± 0.02	0.37 ± 0.03
12	25.47 ± 1.09	24.45 ± 0.53	21.93 ± 0.58	26.15 ± 1.37
13	2.42 ± 0.15	0.71 ± 0.02	0.74 ± 0.02	1.71 ± 1.71
14	19.26 ± 0.69	14.50 ± 1.56	17.41 ± 0.92	17.23 ± 1.18
15	8.70 ± 0.25	5.10 ± 0.43	5.19 ± 0.11	6.88 ± 0.10
16	2.65 ± 0.29	2.66 ± 0.04	2.85 ± 0.22	2.66 ± 0.07
CP[a]	3.99 ± 0.49	9.23 ± 0.41	1.53 ± 0.12	1.39 ± 0.18

[a] Cisplatin, positive control.

(Table 1). Pactamide A (**11**) displayed the best cytotoxic activity with IC_{50} values of 0.24–0.51 μM, and these were better than those of lysobacteramides and HSAF.[4] Notably, the presence of a double bond in **12** and **14** greatly decreased their cytotoxicities.

Biochemical characterization of PtmC

The alcohol dehydrogenase IkaC has been previously shown to catalyse the formation of the inner five-membered ring in ikarugamycin (**7**, Fig. 1). Given the high similarity of PtmC and IkaC, we expected that PtmC should have a similar function to IkaC. To probe its function *in vitro*, PtmC was overproduced in *E. coli* BL21(DE3) as a soluble *N*-His_6-tagged protein (Fig. S15†). *In vitro* assays showed that **13** was converted to **11** by PtmC in the presence of NADPH or NADH (Fig. 3A, traces i–iii), while no conversion of **13** to **11** was observed in the absence of PtmC or NAD(P)H (Fig. 3A, traces iv & v), or upon replacing PtmC with IkaC (Fig. 3A, trace vi). These data unequivocally established that PtmC was able to catalyse the conversion of **13** to **11**.

We have previously established that the inner five-membered ring in ikarugamycin (**7**, Fig. 1) was formed through an IkaC-catalyzed 1,6-Michael addition reaction,[15] by deuterium incorporation experiments in coupling assays with glucose dehydrogenases (GDH), providing either (*S*)-[4-^{2}H]NADPH by BmGDH from *Bacillus megaterium* DSM 2894,[30] or (*R*)-[4-^{2}H]NADPH by TaGDH from *Thermoplasma acidophilum* ATCC 25905.[31]

The same strategy was employed to probe the reaction mechanism of PtmC. The LC-HRESIMS analyses of the reaction product (**11**) in the PtmC/GDH coupling assays, in buffers either prepared with H_2O or ^2H_2O (Fig. S16†), revealed the incorporation of two protons, one from (*R*)-[4-H]NADPH and another from H_2O, into the product **11**. These observations revealed a similar 1,6-Michael addition reaction for the PtmC-catalysed formation of the six-membered ring in **11** from **13** (Fig. 3B). Similarly to IkaC catalysis, an isomerization from species **13a** to **13b** (Fig. 3B) was proposed to change $Z\Delta^{2,3}$ in the substrate **13** to $E\Delta^{2,3}$ in the product **11** during PtmC catalysis (Fig. 3B). Interestingly, PtmC could catalyse the conversion of **17** (the native substrate of IkaC[15]) into two products (Fig. 3A, traces vii & viii), one of which was identical to **7** by comparison with authentic **7** (Fig. 3A, trace ix). Another product **18** (1.7 mg) was isolated from a preparative PtmC enzyme reaction and was structurally

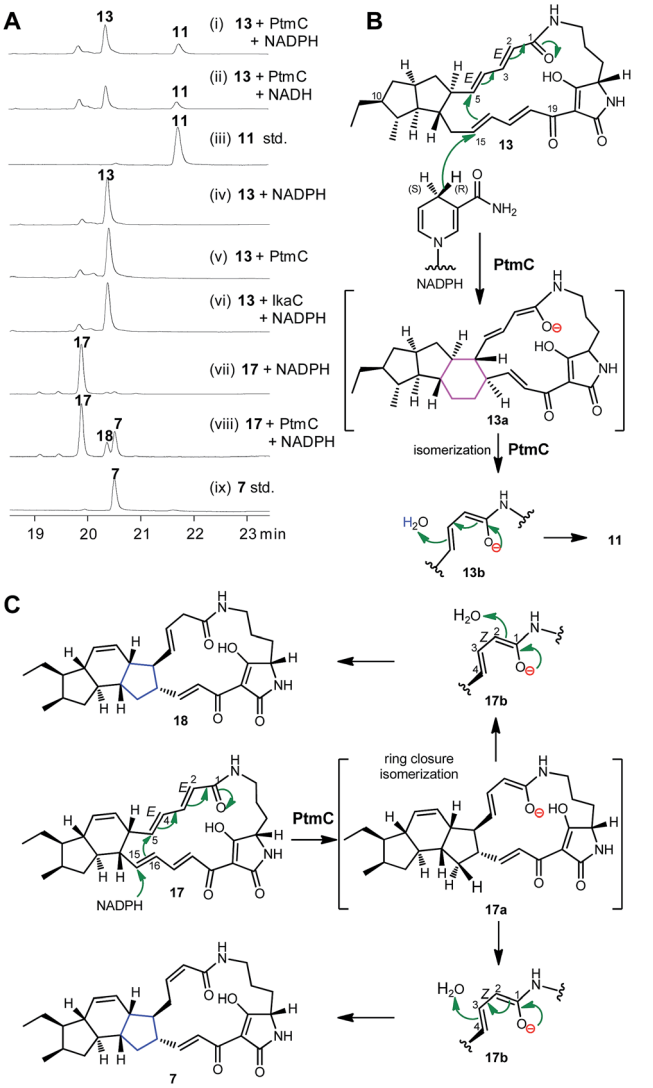

Fig. 3 Biochemical characterization of PtmC and the proposed reaction mechanism. (A) HPLC analysis of the enzyme assays. (i) **13** + PtmC + NADPH; (ii) **13** + PtmC + NADH; (iii) standard **11**; (iv) **13** + NADPH; (v) **13** + PtmC; (vi) **13** + IkaC + NADPH; (vii) **17** + NADPH; (viii) **17** + PtmC + NADPH; (ix) standard **7**. (B) The proposed mechanism of PtmC catalysis. (C) The proposed PtmC mechanism to convert **17** to **7** and **18**.

elucidated as isoikarugamycin by comparing its ^{1}H and ^{13}C NMR data (Table S8, Fig. S17†) with the reported data.[32] In contrast, IkaC was unable to convert **13** to **11** (Fig. 3B, trace vi), although IkaC has 65% identity with and 76% similarity to PtmC. The formation of **7** and **18** by PtmC catalysis was also consistent with a 1,6-Michael addition reaction (Fig. 3C).[32] These data revealed that PtmC was a bifunctional enzyme capable of catalysing the formation of both six- and five-membered rings *via* a common Michael addition mechanism.

Implications of a reductive cyclization cascade in constructing a 5/5/6 ring system in PTMs

A substantial understanding of PTM biosynthesis has been gained for HSAF (**3**),[3,14,17,23,33] frontalamides (**5**, **6**),[5] and

ikarugamycin (7).[1,15,16] The simplicity of PTM biosynthesis lies mainly in the beauty of synthesizing the polyene tetramate precursor **10** by a single PTM PKS/NRPS enzyme due to the functional iteration of PTM PKSs (Fig. 4).[1] This study provides further support with **10** (generated by PtmA alone, Fig. 4) as a common biosynthetic intermediate in the PTM pathway. The in-frame deletion of *ptmB2*, *ptmB1*, and *ptmC* led to the accumulation of **10**, **15**, and **13**, respectively, providing convincing evidence for a cascade of three reductive cyclization reactions to form the 5/5/6 ring system in **11** (Fig. 4). The phytoene dehydrogenase PtmB2 catalyses the first cyclization reaction, converting **10** to **15**, in a not yet understood manner. Next, the oxidoreductase PtmB1 performs the second reductive cyclization to convert **15** to **13**, probably undergoing a 1,8-Michael addition like reaction. Finally, the third reductive cyclization, mediated by the dehydrogenase PtmC, transforms **13** into **11** to furnish the 5/5/6 ring system (Fig. 4).

In accordance with these hypotheses, feeding **15** into *S. lividans* TK64/pCSG2814 (where *ptmB2* is in-frame deleted and *ptmB1* and *ptmC* are intact) clearly led to the detection of compounds **13** and **11** (Fig. S18†), confirming that **15** is a biosynthetic intermediate *en route* to **11**. PtmD displays high similarity to the hydroxylases involved in the hydroxylation at C-25 of the ornithine moiety (Fig. S19†),[5,8,23,24] however, the absence of a C-25 hydroxy group in **11–16** suggests that PtmD might function as a C-31 hydroxylase in the biosynthesis of **12** and **14** (Fig. 4). The enzymes to generate the double bonds in **12** and **14** are still unknown, but should be encoded by genes shown in Fig. 2A, since **12** and **14** were also produced in *S. lividans*/pCSG2804 (Fig. 2B, trace v). Pactamide F (**16**) was only detected in *S. pactum* 2999PTMp1, but not in *S. lividans* TK64/pCSG2804 (Fig. 2B), indicating that the required tailoring enzymes, a halogenase and a C-11 hydroxylase, might be encoded by genes outside of the *ptm*-gene cluster.

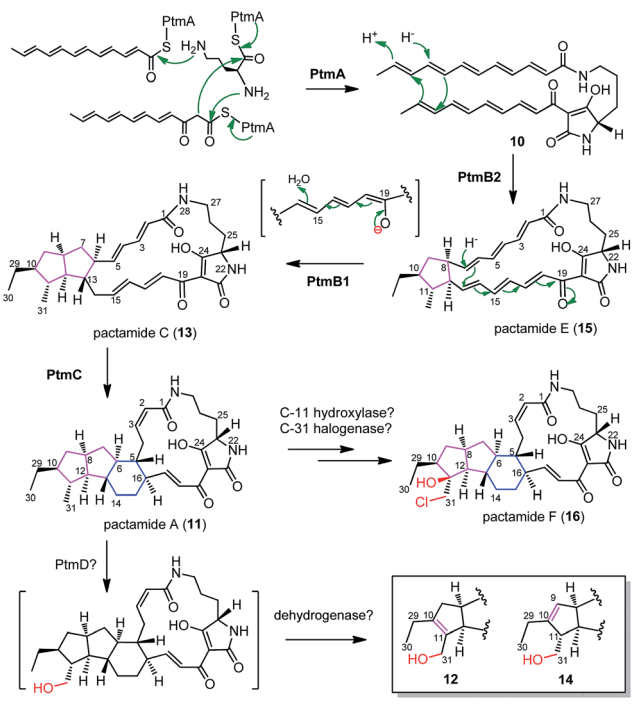

Fig. 4 Proposed biosynthetic pathway for pactamides A–F (**11–16**).

Conclusions

Six new PTMs, pactamides A–F (**11–16**), have been discovered by the successful activation of a cryptic PTM gene cluster *via* promoter engineering in marine-derived *S. pactum* SCSIO 02999. The PTM gene clusters in *S. pactum* SCSIO 02999, *S. albus* J1074 (activated by promoter engineering[18]) and *S. griseus* IFO 13350 (activated by synthetic biology[8]) share the same genetic organization and have high sequence similarity in their encoded proteins, however, the activation of each cluster led to structurally distinct PTMs (Fig. S20†). This indicates a great potential to discover more new bioactive PTMs by activating the hundreds of conserved and silent PTM gene clusters in phylogenetically diverse bacteria.[1,5] Furthermore, the discovery of the major products of the Δ*ptmB2* mutant (**10**), the Δ*ptmB1* mutant (**15**), and the Δ*ptmC* mutant (**13**), provided solid evidence for three consecutive reductive cyclizations, in a stepwise manner, to generate the 5 (in **15** by PtmB2), 5/5 (in **13** by PtmB1) and 5/5/6 (in **11** by PtmC) carbocyclic ring systems in pactamides. This discovery highlights a general strategy for the formation of a subset of 5/5/6 ring systems in other PTMs, such as in **3** and **5**. In contrast to the single enzyme IkaB-catalysed formation of the 5/6 ring system in **17**,[15] two oxidoreductases (PtmB2/B1) are required to generate the 5/5 ring system in **13**. This discrepancy may serve as a general predictor for divergence dictating the 5/5/6 or 5/6/5 ring systems in PTM biosynthesis, and serve to guide the genome mining approach for predicting the anticipated PTM structures. Finally, PtmC was demonstrated herein as a bifunctional cyclase to mediate the formation of both six- and five-membered rings, *via* a common Michael addition reaction mechanism .

Acknowledgements

This work is supported in part by the National Natural Science Foundation of China (31630004, 31290233, 31125001), the Chinese Academy of Sciences (XDA11030403, QYZDJ-SSW-DQC004), and the Administration of Ocean and Fisheries of Guangdong Province (A201601C03, GD2012-D01-002). Q. Z. is a "Pearl New Star" scholar and is supported by the Science and Technology Program of Guangzhou. We thank Prof. Hanjie Ying in Nanjing University of Technology for providing the plasmid pRSF-BmGDH and Prof. Lichuan Gu in Shandong University for providing genomic DNA of the strain *Thermoplasma acidophilum* ATCC 25905. We are grateful for the use of the analytical facilities at the SCSIO.

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