Arixanthomycins A–C: Phylogeny-Guided Discovery of Biologically Active eDNA-Derived Pentangular Polyphenols

Hahk-Soo Kang and Sean F. Brady*

Howard Hughes Medical Institute, Laboratory of Genetically Encoded Small Molecules, The Rockefeller University, 1230 York Avenue, New York, New York 10065, United States

Supporting Information

ABSTRACT: Soil microbiomes are a rich source of uncharacterized natural product biosynthetic gene clusters. Here we use short conserved biosynthetic gene sequences (natural product sequence tags) amplified from soil microbiomes as phylogenetic markers to correlate genotype to chemotype and target the discovery of novel bioactive pentangular polyphenols from the environment. The heterologous expression of an environmental DNA-derived gene cluster (the ARX cluster), whose ketosynthase beta (KSβ) sequence tag was phylogenetically distinct from any known KSβ sequence, led to the discovery of the arixanthomycins. Arixanthomycin A (1) exhibits potent antiproliferative activity against human cancer cell lines.

Microbially based natural products discovery programs have traditionally relied on the random screening of a pool of novel biodiversity (i.e., new microbial species) to secure a source of structurally novel small molecules.1 As most bacteria in the environment have not yet been cultured, libraries of DNA extracted directly from environmental samples (environmental DNA, eDNA) represent large reservoirs of unexplored natural product biosynthetic gene clusters that could serve as new sources of additional bioactive small molecules.2,3 Advances in modern sequencing technologies, bioinformatics analysis tools, and environmental DNA cloning methods should allow for a movement in natural products discovery away from a random microbe screening approach to a more systematic sequence-based screening approach that will allow for the functional examination of gene clusters that remain hidden in the environment.4,5 In its simplest version, we envision that this sequence-based approach will use highly conserved biosynthetic genes as phylogenetic markers to identify novel gene clusters that can serve as starting points for the discovery of novel bioactive natural products. Here, we report the use of a single gene phylogeny-based mining approach to guide the discovery of arixanthomycins A–C (1–3, Chart 1), new pentangular polyphenols that exhibit potent in vitro antiproliferative activity.

Pentangular polyphenols are a subfamily of aromatic polyketides (PK) that use C24 to C30 polyacetate precursors.6 Among characterized biosynthetic pathways, these are the longest polyketide chains to be generated by minimal type II polyketide synthases (min-PKSs).7 Known pentangular polyphenols exhibit a wide range of biological activities, including antibacterial, antiproliferative, and antifungal activities.8,9 In comparison to the structural diversity reported for many other aromatic PK subfamilies, pentangular polyphenols appear to be underrepresented among known natural products. Their larger size should theoretically afford the ability to generate more diverse folding patterns, skeletal rearrangements, and tailoring modifications than is seen in the biosynthesis of the smaller aromatic PKs. We reasoned that the relative dearth of known pentangular structures, yet high structural potential of this biosynthetic subgroup, would make pentangular polyphenols a rewarding target for phylogeny-guided natural product discovery approaches.

Our search for novel pentangular polyphenols began by PCR amplifying and sequencing ketosynthase beta (KSβ) genes from archived soil eDNA libraries. The KSβ gene encodes a subunit of the min-PKS that is responsible for producing the nonreduced polyketide, which is used as an intermediate in aromatic polyketide biosynthesis. KSβ genes have been shown to be robust phylogenetic markers for structural differences in the natural products encoded by type II PKS gene clusters.5,10 When eDNA-derived KSβ amplicons were mapped onto a phylogenetic tree of functionally characterized KSβ genes, a

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Chart 1

1

2 R = CH₃
3 R = H

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number of amplicons were found to fall into the well-defined pentangular polyphe

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Figure 1. Maximum likelihood subtree (1,000 bootstrap replicates) of KSβ genes that clade with known pentangular polyphe

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Figure 2. TAR reassembly of three overlapping eDNA clones carrying the ARX pentangular polyphe

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AZ1076/33/378 by transformation-associated recombination (TAR) in yeast (Figure 2). The correct assembly of the AZ33 cluster was confirmed by de novo sequencing of BAC-AZ1076/33/378. This BAC construct was then transferred into Streptomyces albus via intergenic conjugation and integrated into the genome by ΦC31 integrase to generate the strain S. albus BAC-AZ1076/33/378. For natural product isolation studies, this strain was grown at 30 °C in R5A media for 7 days with shaking, and the resulting cultures were extracted with ethyl acetate. S. albus BAC-AZ1076/33/378 culture broth extract showed a potent antiproliferative activity against human carcinoma cell lines (Table 1), and LC–MS analysis of the extract showed the presence of three gene cluster-specific molecules. Each molecule was predicted by HRMS to have a
molecular formula that was distinct from any previously isolated pentangular polyphenol natural product (Figure 2). On the basis of the potent crude extract bioactivity, the bioinformatics, and chemical novelty, we chose to carry out a detailed structure analysis of the clone specific metabolites produced by S. albus BAC-AZ1076/33/378.

The three clone specific metabolites were purified from large-scale cultures (1 L) broth extracts using C18 reversed-phase HPLC to yield compounds 1 (1.9 mg L−1), 2 (4.6 mg L−1), and 3 (4.0 mg L−1). Compounds 1–3 were named arixanthomycins A, B, and C, respectively. The planar structures and relative configurations shown for the oxazolidine ring (Figure 3, red) that is predicted to arise from a Baeyer–Villiger oxidative rearrangement of a pentangular polyphenol precursor as would be expected from the position of the AZ33 KSβ gene sequence in the KSβ phylogenetic tree. However, as we anticipated from the position of the AZ33 KSβ gene sequence on a new branch in the phylogenetic tree, the arixanthomycins differ from known members of the xanthone family pentangular polyphenols by a number of key features. These differences include the presence of the carboxylated oxazolidine ring (Figure 4, G ring), the oxidation state of the D ring, the oxidation state of the F ring, and the glycosylation at C-13 (Figure 4, green). The oxazolidine ring likely arises from the coupling of a serine to the terminal polyketide carboxylic acid (Figure 4). The kigamicins and cervinomycins are the only members of the pentangular polyphenol family that possess an oxazolidine G ring.21–23 In these known metabolites, the oxazolidine rings would appear to arise from the incorporation of an ethanolamine and therefore the carboxylate is not present. While sugars are seen on some pentagonal polyphenols,23–25 no previous reports of a C-13 glycosylation appear in the literature.

Arixanthomycins A–C (1–3) were assayed for antiproliferative, antibacterial, and antifungal activities. The arixanthomycins were found to be most active in antiproliferative assays (Table 1). Arixanthomycin A (1) shows a particularly potent antiproliferative activity against colon (HCT-116 and WiDr) and breast (MDA-MB-231) cancer cell lines (Table 1). Arixanthomycin A (1) has a distinct mode of action from other pentangular polyphenols or that the sugar moiety is important in light of the potent activity in the absence of a sugar moiety.25 Whether this is an indication that arixanthomycin A (1) has a distinct mode of action from other pentangular polyphenols or that the sugar is needed to improve the bioavailability of 1 in light of the new carboxylate remains to be determined.

The biosynthesis of the arixanthomycins can be rationalized on the basis of the predicted function of the genes found within BAC-AZ1076/33/378 (Figure 4). The predicted ARX gene cluster spans 33 kb and contains 35 genes predicted to be involved in the biosynthesis, regulation, and resistance of the

### Table 1. Anticancer, Antifungal, and Antibacterial Activities of 1–3

|               | crude | 1   | 2   | 3   |
|---------------|-------|-----|-----|-----|
| anticancerb   | HCT-116 | 1.1 | 0.15| 5.14| 25.42|
|               | WiDr  | 2.5 | 0.83| >50 | >50 |
|               | MDA-MB-231 | 1.4 | 0.25| 9.36| >50 |
| antifungalc   | S. cerevisiae | >50 | >50 | >50 | >50 |
| antibacterialc| MRSA USA300 | 1.6 | 25  | >50 | >50 |
|               | B. subtilis RM125 | 3.1 | 12.5| >50 | >50 |
|               | VRE EF16  | 50  | >50 | >50 | >50 |
|               | E. coli DRC39 | >50 | >50 | >50 | >50 |

*aIC50 in μg/mL. bIC50 in μM. cMIC in μg/mL.

The arixanthomycins feature a hexacyclic xanthone core (Figure 3, red) that is predicted to arise from a Baeyer–Villiger oxidative rearrangement of a pentangular polyphenol precursor as would be expected from the position of the AZ33 KSβ gene sequence in the KSβ phylogenetic tree. However, as we anticipated from the position of the AZ33 KSβ gene sequence on a new branch in the phylogenetic tree, the arixanthomycins differ from known members of the xanthone family pentangular polyphenols by a number of key features. These differences include the presence of the carboxylated oxazolidine ring (Figure 4, G ring), the oxidation state of the D ring, the oxidation state of the F ring, and the glycosylation at C-13 (Figure 4, green). The oxazolidine ring likely arises from the coupling of a serine to the terminal polyketide carboxylic acid (Figure 4). The kigamicins and cervinomycins are the only members of the pentangular polyphenol family that possess an oxazolidine G ring.21–23 In these known metabolites, the oxazolidine rings would appear to arise from the incorporation of an ethanolamine and therefore the carboxylate is not present. While sugars are seen on some pentagonal polyphenols,23–25 no previous reports of a C-13 glycosylation appear in the literature.

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Arixanthomycins. The structure of arixanthomycin A (1) can be divided into three parts, the naphthaxanthone core, the oxazolidine ring, and the quinovose sugar moiety. Key ARX enzymes that are predicted to be involved in the biosynthesis of each of these substructures are shown in Figure 4. The hexachry nephthaxanthone core is predicted to arise from a pradimcin-type anthraquinone intermediate by a Baeyer–Villiger oxidation catalyzed by Arx30 (62% identity to llpOVIII and 61% identity to xenO). Stereospecific formation of the oxazolidine (G ring) is likely to occur spontaneously upon incorporation of serine into the terminal carbocyclic by the predicted amidotransferase Arx5. The addition of the trimethylated quinovose sugar moiety is predicted to occur through the action of the glycosyltransferase Arx9. A detailed biosynthetic proposal appears in the Supporting Information (Figure S3).

This work demonstrates the power of using single gene sequence tags to rapidly and economically bridge the gap between genotype and chemotype in complex microbiomes. This methodology is easy to scale using high throughput sequencing technology and archived eDNA libraries. Sequence-based eDNA mining approaches like those used here should allow for the movement away from the traditional new species-based natural product discovery paradigm to a new bioinformatics-driven, clade-based, natural products discovery paradigm. Using this general approach, it should be possible to systematically access untapped chemical diversity encoded within diverse natural microbiomes.

**METHODS**

**Clone Recovery and Bioinformatics Analysis.** eDNA clone AZ33 was recovered from the AZ eDNA library by serial dilution of the 5,000-member subpool from which the AZ33 amplicon was originally amplified. To do this, an overnight culture of the AZ33 subpool was inoculated into 96-well microtiter plates at a dilution of 10⁻⁵. After 18 h of shaking at 37 °C, the diluted cultures were screened by whole-cell PCR using the KS₅ screening primers and touchdown PCR protocol. PCR positive wells were plated onto solid media (LB agar) to yield distinct colonies that were screened individually in a second round of whole-cell PCR. Overlapping clones for AZ33 were subsequently identified in the AZ library using clone-specific primers designed to recognize the sequence at each end of AZ33 (AZ33F_FW: CAGGAACTCGAGTCCATCTC, AZ33F_RV: ACTTCACCAGTAGCACTGCC, AZ33B_FW: CACATGAAGCTGATGACTC, and AZ33B_RV: GCCATTCGATCTCGATAC). The PCR protocol used was as follows: denaturation (95 °C, 5 min), 36 standard cycles (95 °C, 30 s; 55 °C, 30 s; 72 °C, 40 s), and a final extension step (72 °C, 7 min). Hits were identified in subpools AZ1076 and AZ378. Overlapping eDNA cosmids (designated AZ1076 and AZ378) were recovered from these pools using the serial dilution method outlined above. All three cosmids were sequenced by 454 pyrosequencing. ORFs (open reading frames) were predicted using MetaGeneMark,30 and predicted ORFs were annotated by Blast search and Pfam domain analysis.

**TAR Assembly of Overlapping eDNA Clones.** The three overlapping eDNA cosmids clones that are predicted to contain the AZ33 gene cluster (AZ1076, AZ33 and AZ378) were assembled into a single bacterial artificial chromosome (BAC) clone using transformation-associated recombination (TAR) in yeast and the pTARa baculagene shuttle vector.19,20 The pathway-specific TAR capture vector was constructed using InFusion cloning methodology (Clontech). Five hundred bases upstream and downstream homology arms were amplified from the AZ1076 and AZ378 cosmids, respectively, using the following primers:

AZ1076UPS_FW (5′-GGTCCACCTGTTAACCTCAACCTCCATCCTCACCT-3′),
AZ378DWS_FW (5′-GTTTACGGCAGCTGTCGTTCTT-3′),
AZ378DWS_RV (5′-CCCTGAGAGACCTCGTCTCTTTTCTGACCTGGTG-3′)

Primer AZ1076UPS_FW and AZ1076DWS_RV include 15 bp sequences (underlined) that overlap with BmtI/SphI linearized pTARa capture vector. Primer AZ1076UPS_FW was designed to contain a 15 bp overlap (underlined) with the AZ378DWS_FW primer and an HpaI site (bold), which was added to facilitate the subsequent linearization of the pathway-specific pTARa capture vector. Gel-purified amplicons (Qiagen) and BmtI/SphI linearized pTARa were combined in a standard InFusion cloning reaction (Clontech) to yield the pathway-specific capture vector.

For TAR assembly, 200 ng of DraI-digested AZ1076, AZ33, and AZ378 were mixed with 100 ng of the HpaI-cut pathway-specific capture vector and then transformed into 200 μL of Saccharomyces cerevisiae CRY1-2 spheroplasts prepared according to published protocols.19,20 Transformed spheroplasts were mixed with synthetic complete (SC) top agar (1 M sorbitol, 1.92 g/L synthetic complete uracil dropout supplement, 6.7 g/L yeast nitrogen base, 2% glucose, and 2.5% agar) and overlaid onto SC uracil dropout plates. Plates were incubated at 30 °C for 72 h. DNA was prepared from 12 yeast colonies using a zymolase lysis protocol (ZYM RESEARCH) and screened by PCR with primers designed to recognize sequences from AZ1076, AZ33, and AZ378. A BAC clone that was “PCR positive” with all the primer sets was electroporated into E. coli EP1300. DNA isolated from the resulting E. coli was PGM (Ion Torrent Personal Genome Machine) sequenced to confirm the correct reassembly of the three overlapping cosmids into a 80 kb insert BAC clone (BAC-AZ1076/33/378).

**Heterologous Expression.** BAC-AZ1076/33/378 was transformed into E. coli S17-1 and conjugated into S. albus to generate S. albus BAC-AZ1076/33/378 (apramycin selection). This strain was cultured in RSA5 liquid medium for 7 days (200 rpm at 30 °C) and then extracted with ethyl acetate (1/3 volume to the culture broth). The resulting ethyl acetate extract was compared by HPLC to the extract from a similarly grown culture of S. albus transformed with a pTARa empty vector control (HPLC conditions: 30 min gradient from 5% to 100% aqueous methanol containing 0.1% trifluoroacetic acid, C₁₈ 4.6 mm × 150 mm, 1 mL/min).

**Extraction and Isolation.** Compounds 1–3 were isolated from cultures of S. albus BAC-AZ1076/33/378 grown (200 rpm at 30 °C) in 125 mL baffled flasks containing 50 mL of RSA media. Seven-day-old cultures were extracted with ethyl acetate (1/3, v/v, to the culture broth), and the ethyl acetate was dried in vacuo. Arixanthomycins A (1), B (2), and C (3) were isolated from the resulting ethyl acetate extract using two rounds of reversed-phase HPLC (C₁₈ column, 10 mm × 250 mm, 3.5 mL/min). The first round of HPLC (isocratic, 55% acetonitrile containing 0.1% trifluoroacetic acid) yielded three crude compounds 1 (17.9 min), 2 (18.8 min), and 3 (6.6 min), which were repurified by a second round of HPLC using 80%, 72%, and 70% aqueous methanol with 0.1% trifluoroacetic acid to yield arixanthomycins A (1, 1.6 mg L⁻¹), B (2, 4.6 mg L⁻¹), and C (3.4 mg L⁻¹), respectively.

**Arixanthomycin A (1).** Yellowish powder; [α]DOhio = −197; UV (MeOH) λmax (log ε) 287 (4.24), 327 (shoulder; 4.13), 346 (shoulder; 3.98), 403 (3.57) nm; IR (neat) νmax 3375, 2981, 2945, 2912, 2835, 1680, 1641, 1631, 1606, 1548, 1529, 1492, 1462, 1431 cm⁻¹; H and ¹³C NMR, COSY, and HMBC data, see Supplementary Table 1; HRESIMS m/z 720.2300 [M + H]⁺ (calcd for C₃₉H₃₈NO₁₄, 720.2292).

**Arixanthomycin B (2).** Greenish powder; [α]DOhio = −127; UV (MeOH) λmax (log ε) 285 (4.42), 331 (shoulder; 4.12), 399 (3.47) nm; IR (neat) νmax 3110, 2980, 2891, 2846, 1681, 1614, 1586 1488, 1467, 1437 cm⁻¹; H and ¹³C NMR data, see Supplementary Table 2; HRESIMS m/z 546.1379 [M + H]⁺ (calcd for C₂₅H₂₅NO₁₀, 546.1400).

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ARKANTHOXYMVIC C (3). Yellowish powder; [α]25D −351; UV (MeOH) λmax (log ε) 287 (4.74), 324 (shoulder; 4.55), 347 (shoulder; 4.40), 399 (3.90) nm; IR (neat) νmax 3429, 2982, 2940, 2893, 2837, 1679, 1640, 1610, 1590, 1492, 1440 cm−1; 1H and 13C NMR data, see Supplementary Table 2; HRESIMS m/z 532.1246 [M + H]+ (calcd for C32H23NO16, 532.1244).

ASSOCIATED CONTENT

Supporting Information
Methods for library construction, library screening, and bioassays and discussions for structure determination. NMR data table, gene annotation table and NMR spectra. This material is available free of charge via the Internet at http://pubs.acs.org.

AUTHOR INFORMATION

Corresponding Author
*E-mail: sbrady@rockefeller.edu.

Notes
The authors declare no competing financial interest.

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