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Malleilactone, a Polyketide Synthase-Derived Virulence Factor Encoded by the Cryptic Secondary Metabolome of Burkholderia pseudomallei Group Pathogens

John B. Biggins, Melinda A. Ternei, and Sean F. Brady*

Laboratory of Genetically Encoded Small Molecules, The Rockefeller University and Howard Hughes Medical Institute, 1230 York Avenue, New York, New York 10068, United States

Supporting Information

ABSTRACT: Sequenced bacterial genomes are routinely found to contain gene clusters that are predicted to encode metabolites not seen in fermentation-based studies. Pseudomallei group *Burkholderia* are emerging pathogens whose genomes are particularly rich in cryptic natural product biosynthetic gene clusters. We systematically probed the influence of the cryptic secondary metabolome on the virulence of these bacteria and found that disruption of the MAL gene cluster, which is natively silent in laboratory fermentation experiments and conserved across this group of pathogens, attenuates virulence in animal models. Using a promoter exchange strategy to activate the MAL cluster, we identified malleilactone, a polyketide synthase-derived cytotoxic siderophore encoded by this gene cluster. Small molecules targeting malleilactone biosynthesis either alone or in conjunction with antibiotics could prove useful as therapeutics to combat melioidosis and glanders.

Pseudomallei group pathogens including *Burkholderia pseudomallei* (BP), *Burkholderia mallei* (BM), and *Burkholderia thailandensis* (BT) are a closely related collection of Gram-negative bacteria.[1] BP is the causative agent of melioidosis in humans, BM is the causative agent of glanders in horses, and while BT is not generally considered to be a human pathogen, it is infectious in a number of model laboratory organisms. Melioidosis is endemic in parts of Southeast Asia and Northern Australia and is the third most frequent cause of mortality from infectious disease after HIV and tuberculosis in Northeast Thailand.[2] Current therapies for this neglected disease are inadequate, as mortality rates from melioidosis have been reported to approach 50%, even with antibiotic treatment.[2] Additionally, these pathogens have been classified as potential bio-terrorism threats by the CDC, and in spite of the considerable attention paid to this group, their virulence determinants are still not well understood.

Small molecules, including signaling molecules, siderophores, and toxins, are known to play important roles in both the establishment and propagation of bacterial infections.[3] Biosynthetic gene clusters to which no small molecule has yet been assigned are frequently encountered in bacterial genome sequencing projects.[4] These cryptic gene clusters represent the pool of biosynthetic pathways from which additional small molecule virulence factors might be characterized. To better understand the virulence factors used by pseudomallei group pathogens, we have investigated the influence of cryptic secondary metabolism on *Burkholderia* pathogenesis by systematically disrupting individual cryptic biosynthetic pathways in BT and assessing these mutants for changes in virulence. Disruption of the polyketide synthase (PKS)-based MAL gene cluster that is conserved across this group of pathogens was found to attenuate virulence. Here we describe the structural and functional characterization of malleilactone (**1**), a MAL gene cluster encoded cytotoxic siderophore and virulence factor.

The pangenome of the pseudomallei group of pathogens[5] is rich in PKS and non-ribosomal peptide synthetase (NRPS) gene clusters, two common biosynthetic systems that are easily identified bioinformatically in sequenced genomes. Many clusters are shared among these three pathogens, and the majority of molecules encoded by these clusters remain cryptic in structure and/or biological function (Figure 1a; Tables S1 and S2). BM and BP are classified as BSL3 level pathogens, and due to their potential use in biological warfare, there are significant regulatory issues governing their genetic manipulation. BT is strikingly similar genetically to BP,[5b,c] possessing the majority of gene clusters found within BP (Table S1), but there are no similar restrictions on its genetic manipulation.

To address the potential role of secondary metabolites in *Burkholderia* pathogenesis, we created a collection of BT mutants wherein individual cryptic PKS/NRPS clusters were disrupted either by suppressing transcription through promoter exchange or by deleting one of the large modular PKS/NRPS genes within the gene cluster itself (Table S1). These strains were then assessed for virulence using a *Caenorhabditis elegans* nematode co-culture model, which has been successfully used to assess pathogenicity and identify virulence factors in bacterial pathogens.[6] In this co-culture virulence model, both BT and BP elicit a rapid toxicity to *C. elegans*, which is thought to arise from specific *in vivo* host−bacteria interactions.[7] In co-culture assays using wild-type BT, worms either display no movement or lack any significant locomotor behavior within 24 h (Figure 1b,c; Video S1). With one exception, *C. elegans* grown on cryptic gene cluster disruption strains were similarly dead or dying within 24 h. The disruption, by either promoter exchange or gene deletion, of a cryptic gene cluster that we have termed the MAL cluster results in worms that uniformly continue to move and forage

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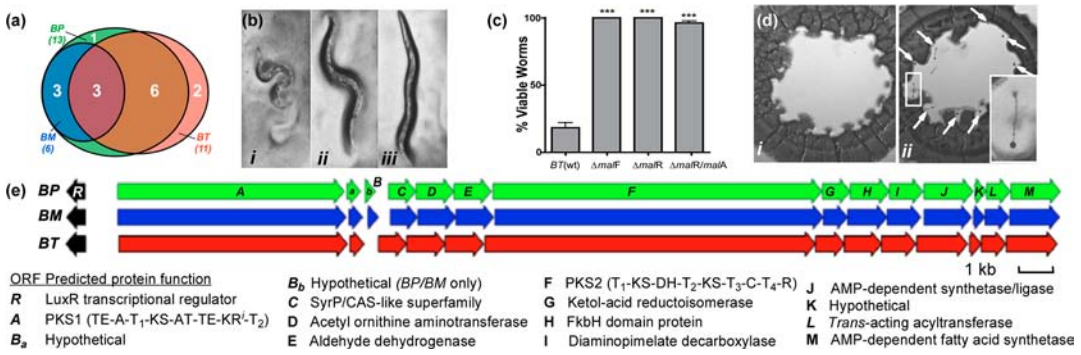

Figure 1. (a) Venn diagram showing the relationship of the number of NRPS/PKS gene clusters shared among pseudomallei group pathogens *B. pseudomallei* K96243, *B. mallei* ATCC 23344, and *B. thailandensis* E264 (BP, BM, and BT, respectively). (b) *C. elegans* after 24 h co-culture with (*i*) wild-type BT (dead), (ii) BT(Δ*malF*), a PKS2 gene deletion mutant, and (iii) BT(Δ*malR*), a transcription factor deletion mutant (40× magnification). (c) *C. elegans* survival after 24 h exposure to wild-type BT, BT(Δ*malF*), BT(Δ*malR*), and BT(Δ*malR*/*malA*), a *malR*-PKS1 double mutant. ***$P < 0.001$, two-tailed *t*-test. (d) *D. discoideum* co-culture at 120 h with (*i*) wild-type BT and (ii) BT(Δ*malF*). Arrows highlight *D. discoideum* aggregation and differentiation into fruiting bodies with MAL cluster disruption (white box: close-up of a fruiting body). (e) MAL clusters from BP, BM, and BT with predicted functions for each MAL protein.

beyond 24 h (Figure 1b,c). Worms feeding upon these MAL knockout strains are larger than worms fed wild-type BT, retain their active feeding and foraging behavior, and grow into adulthood, as evidenced by the accumulation of eggs and hatched larvae on assay plates (Figure 1b,c; Video S1).

To assess the generality of the importance of the MAL gene cluster to pseudomallei group virulence, we also tested MAL disruption mutants in an amoeba co-culture model.[8] The response of the social amoeba *Dictyostelium discoideum* to pathogenic bacteria is hypothesized to closely mimic the response of the mammalian immune system to these organisms.[8,9] In this model, *D. discoideum* cells foraging on pathogenic bacteria often fail to develop past their unicellular state into multicellular aggregates and fruiting bodies. In many instances, this inhibition has been observed to be dependent on the same set of virulence factors that are required for mammalian infections.[8,9] When co-cultured with wild-type BT, amoebae die as unicellular organisms before any observable social coordination. In identical experiments using MAL gene cluster knockout strains, amoebae aggregated as expected and developed completely through the formation of terminal fruiting bodies (Figure 1d). As observed in the *C. elegans* model, the MAL gene cluster appears to be a key component of BT's virulence toward *D. discoideum*.

The MAL gene cluster spans ∼35 kb and is predicted to contain 13 open reading frames, two of which (*malA* and *malF*) encode large modular PKSs (Figure 1e). It is one of only three PKS/NRPS gene clusters that is conserved across the pseudomallei group, making it a conspicuous candidate for encoding a communal virulence factor. MAL gene clusters from all three pathogens have the same gene organization and content (Figure 1e), with the exception of a hypothetical gene ($malB_b$) found in BM and BP but not in BT. Bioinformatics comparisons to previously characterized gene clusters revealed no close relatives that could provide insight into the structure or function of the MAL-encoded metabolite.

Culture broth extracts from MAL gene cluster knockout strains of BT did not show any obvious differences when compared to wild-type control extracts (Figure 2a), indicating that in the laboratory setting this gene cluster is silent. Many secondary metabolite gene clusters are thought to have remained cryptic even after extensive investigation of the organisms in which they reside, because these clusters are expressed only in

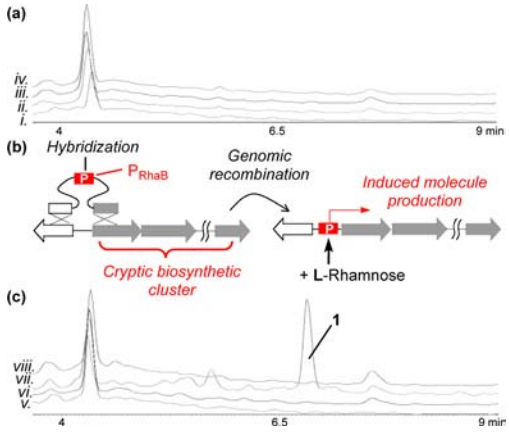

Figure 2. (a) HPLC traces (total diode array: 210−450 nm) of BT culture broth ethyl acetate extracts: (*i*) wild-type BT, (*ii*) BT(Δ*malF*), (*iii*) BT(Δ*malR*), and (*iv*) BT(Δ*malR*/Δ*malA*). (b) Promoter exchange strategy used to induce cryptic gene cluster expression. Small-molecule production is induced with addition of 0.2% L-rhamnose to the culture media. (c) HPLC traces of culture broth extracts, showing that induction of the MAL cluster leads to production of the novel metabolite malleilactone (**1**). Cultures were grown with or without 0.2% L-rhamnose: (*v*) wild-type BT + rhamnose; (*vi*) BT:P_{RhaB}-MAL, no rhamose; (vii) BT:P_{RhaB}-MAL + rhamnose; and (*viii*) BT:P_{RhaB}-MAL(Δ*malF*) + rhamnose.

response to specific environmental cues and therefore silent under standard laboratory fermentation conditions. In previous studies with BT, we found that silent gene clusters could be activated via transcriptional activation strategies.[10] The most universal of such approaches is likely to be promoter exchange, where a native silent promoter governing gene cluster expression is replaced with a model inducible promoter. The MAL gene cluster is predicted to be composed of a set of 13 genes that are unidirectional and potentially organized into a single large operon (Figure 1e). We reasoned that inducing the transcription of this operon could lead to production of detectable levels of the product encoded by the MAL gene cluster. The promoter region in front of the first ORF in the MAL operon (*malA*) was therefore replaced by homologous recombination with the rhamnose-inducible promoter, P_{RhaB},[11] to yield BT:P_{RhaB}-MAL (Figures 2b and S1). Ethyl acetate extracts from cultures of BT:P_{RhaB}-MAL induced with rhamnose contained one major

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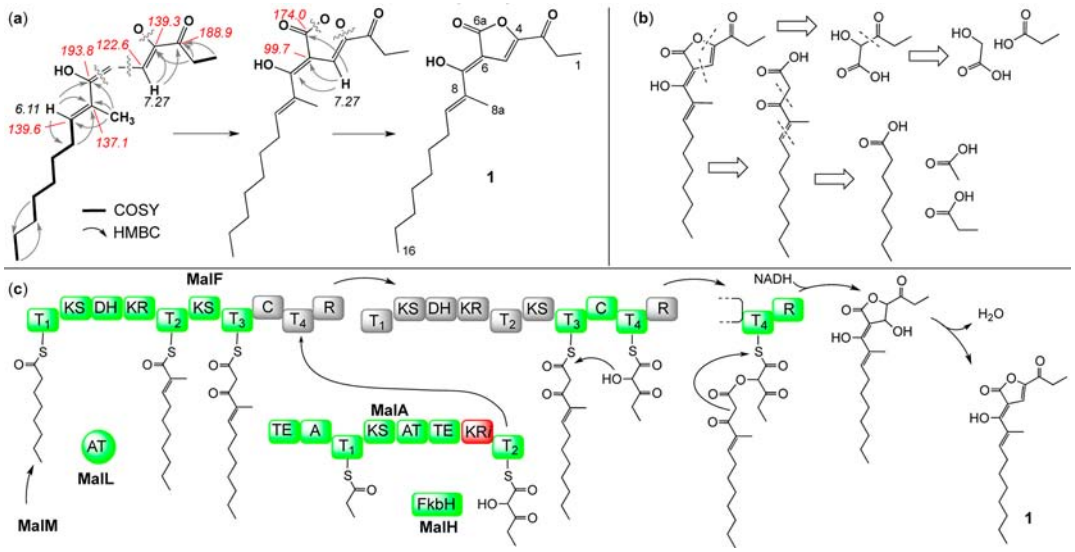

Figure 3. (a) Key NMR arguments used to define the structure of malleilactone (**1**). (b) Retro-biosynthetic analysis of **1**. (c) Biosynthetic proposal for **1**. AT, acyltransferase; KS, ketosynthase; DH, dehydratase; C, condensation; R, reductase; T, thiolation; TE, thioesterase; i, inactive.

metabolite that was not seen in extracts from similarly treated wild-type cultures (**1**, Figure 2c). This peak is not seen in extracts from wild-type BT cultures nor in extracts from rhamnose-induced cultures of BT:P_{RhaB}-MAL(Δ*malF*), a BT:P_{RhaB}-MAL strain where the PKS2 gene (*malF*) is disrupted, thus directly linking MAL operon induction to the production of **1**.

Malleilactone (**1**) was purified from ethyl acetate extracts of large-scale (6 L) cultures of rhamnose-induced BT:P_{RhaB}-MAL using a modified Kupchan scheme followed by three rounds of silica gel chromatography. The structure of **1** was determined through a combination of HRMS (HRMS-TOF *m*/*z*: $[M+H]^+$ calcd for $C_{18}H_{27}O_4$, 307.1910; found 307.1903), NMR, and UV data (Figure 3a). All 18 of the carbons predicted by HRMS to be present in **1** are seen in the ^{13}C NMR spectra. Empirical chemical shift data and $^1H-^{13}C$ HMQC experiments indicated the presence of 2 carbonyl/enol (194, 189 ppm), 5 olefin (140, 139, 137, 123, 100 ppm), 1 ester (174 ppm), 7 methylene, and 3 methyl carbons (Figure 3a). Three spin systems could be resolved in the $^1H-^1H$ COSY spectrum, two of which are joined by HMBC correlations into an unbroken saturated 7-carbon chain that is connected to the methyl-substituted C-8/C-9 olefin through HMBC correlations. The *trans* geometry of this double bond is supported by the chemical shift of the C-8a tertiary methyl (13.9 ppm).[12] HMBC correlations from the C-9 methine proton and the C-8a methyl protons to C-7 connect this substructure to the predicted C-7 enol. At the other end of the molecule, the final 2-carbon $^1H-^1H$ COSY spin system can be connected by HMBC correlations to the C-3 carbonyl and C-4, and HMBC correlations from H-5 to C-3 and C-4 define the position of the C-4/C-5 olefin. These two substructures are linked through C-6, based on the large collection of HMBC correlations involving H-5 (Figure 3a). A final three-bond correlation from H-5 to the C-6a carbonyl yields the complete 18-carbon skeleton of **1**. Based on the unsaturation index and empirical chemical shift data, the final unsaturation is satisfied by closing the γ-butyrolactone ring at C-4 to give **1**. The presence of the conjugated unsaturated system in the final structure of **1** is supported by the UV_{max} observed at 373 nm.[13]

A detailed examination of **1** suggested that it likely arises from the condensation of two separate polyketide chains, one running from the C-16 methyl through the C-6a carbonyl and a second running from the C-1 methyl through the C-4/C-5 olefin (Figure 3b). The formation of two such polyketide precursors and their subsequent condensation into **1** can be rationalized based on the collection of domains found in the MAL PKSs, MalA, and MalF (Figure 3b,c). In our biosynthetic proposal, one polyketide precursor is produced on MalA from propionic acid and a hydroxymalonyl extender unit. Use of the rare oxidized extender unit, which is necessary for subsequent lactone formation, is supported by the presence of an FkbH homologue (MalH) in the MAL cluster. FkbH proteins are predicted to load a glycolytic pathway intermediate onto a thiolation domain (T), which then serves as a substrate for the biosynthesis of oxidized extender units.[14] The second of the two required polyketide precursors is predicted to be synthesized on MalF from a caprylic acid starter unit, followed by two rounds of elongation: one involving incorporation, reduction, and dehydration of a methylmalonyl extender unit and the second involving incorporation of a non-reduced malonyl extender. While MalA contains an acyltransferase (AT) domain, MalF is predicted to be a *trans* AT system that uses the AT activity of MalL. Formation of **1** from these two PKS precursors requires that they be linked through an ester bond and an additional C−C bond to form the central five-membered lactone. A handful of reported NRPS condensation (C) domains are predicted to form esters instead of amides, and MalF contains the conserved "HHXXXDD" active-site motif shared among this set of domains.[15] We therefore propose that the diketide from MalA is transferred to the final T-domain in MalF and linked via a MalF C-domain-catalyzed ester bond. MalA contains two thioesterase (TE) domains, both predicted to be type II ("proofreading") TE domains and therefore not responsible for releasing the polyketide. Release of the polyketide from MalF is predicted to instead occur through the action of the terminal reductase (R) domain, which has increasingly been shown to catalyze the terminal release and cyclization of polyketides.[16] Reductive cleavage of the condensed intermediate found on the T_4 domain of MalF, followed by intramolecular cyclization, provides an intermediate that upon dehydration would yield **1**.

In all three pseudomallei group pathogens, the MAL cluster resides directly adjacent to a predicted LuxR-type transcription

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factor, *malR* (*btaR4*[17]). LuxR homologues function as receptors for *N*-acylhomoserine lactones (AHLs) in quorum sensing circuits and are often responsible for regulating virulence gene expression.[3a] As seen in experiments with the MAL PKS deletion strain BT(Δ*malF*), *C. elegans* and *D. discoideum* co-cultured with *malR* deletion strains show extended life spans (Figure 1b and SI), suggesting that MAL expression is mediated through MalR. A consensus LuxR-like binding element (*lux* box) is present in the promoter region immediately upstream of *malA* (Figure S5). Thus, production of **1**, like that of many virulence factors, appears to be governed by AHL-dependent quorum sensing.

Malleilactone (**1**) was assayed for toxicity against a panel of cell types. It shows low micromolar cytotoxicity to human cell lines (e.g., IC_{50} = 19 μM), and in disk diffusion assays it inhibits the growth of Gram-positive bacteria at as low as 2.5 μg/disk (Table S4). When incorporated in growth media (>100 μg/mL), **1** had no obvious deleterious effects upon *C. elegans*/*E. coli* co-cultures, nor did worms co-cultured with MAL mutants show increased distress upon re-introduction of **1**, suggesting that its bioactivity might extend beyond localized cytotoxicity. The central core of **1** closely resembles a tetronic (or tetramic) acid substructure, and while reported bioactivities for tetronic acids vary widely, they are predicted to share the common phenomenon of chelating cations, in particular iron.[18] Using a chromogenic iron chelation assay, we observed iron-binding activity with **1** (Figure S6). Thus, **1** may serve both as an iron chelator to assist with iron acquisition and as a toxin when secreted at the site of infection. Given that **1** contains a γ-butyrolactone core, a structural motif found in a variety of bacterial signaling molecules including AHLs, it is possible that **1** also functions as a signaling molecule capable of activating downstream virulence factors. It is also possible that *in vivo* **1** serves an additional undetermined role, as so far the MAL cluster has proven recalcitrant to disruption in BP and BM.[19]

As iron is tightly sequestered in eukaryotes, bacterial pathogens have in many cases evolved iron chelation systems to survive in these low iron environments. Two additional PKS/NRPS gene clusters predicted to encode siderophores (malleobactin/ornibactin and pyochelin) are shared between BP and BT genomes (BM lacks pyochelin). It has been theorized that the production of multiple siderophores with different structures and polarities benefits pathogens by providing alternate routes for securing iron and possibly circumventing host defense mechanisms that neutralize conserved microbial siderophores.[20] The therapeutic importance of this class of secondary metabolites as potential anti-infective targets is highlighted by the use of the siderophore (mycobactin) biosynthesis inhibitor, *p*-aminosalicylate, as an anti-tuberculosis drug.[21] Small molecules targeting malleilactone biosynthesis could similarly prove useful as next-generation therapeutics to combat both melioidosis and glanders.

The systematic gene cluster knockout/promoter exchange strategy we used to identify malleilactone is easily generalizable and should permit functional characterization of small-molecule virulence factors encoded by silent gene clusters found in the genomes of a diverse collection of additional bacterial pathogens.

■ ASSOCIATED CONTENT

Supporting Information

Experimental protocols and supplementary data. This material is available free of charge via the Internet at http://pubs.acs.org.

■ AUTHOR INFORMATION

Corresponding Author

sbrady@rockefeller.edu

Notes

The authors declare no competing financial interest.

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