Siderophore-mediated iron acquisition in *Bacillus anthracis* and related strains

Kinya Hotta,1 Chu-Young Kim,1 David T. Fox2 and Andrew T. Koppisch2

1Department of Biological Sciences, National University of Singapore, Singapore
2Bioscience Division, Los Alamos National Laboratory, Los Alamos, NM 87545, USA

Recent observations have shed light on some of the endogenous iron-acquisition mechanisms of members of the *Bacillus cereus sensu lato* group. In particular, pathogens in the *B. cereus* group use siderophores with both unique chemical structures and biological roles. This review will focus on recent discoveries in siderophore biosynthesis and biology in this group, which contains numerous human pathogens, most notably the causative agent of anthrax, *Bacillus anthracis*.

**Introduction**

Iron is a requisite nutrient for the growth and proliferation of bacteria. Unlike higher organisms, which may obtain bioavailable iron from the diet, bacteria must acquire iron from their environment. This presents a challenging problem, as soluble Fe\(^{3+}\) in aqueous oxic environments typically exists at attomolar (10\(^{-18}\)) concentrations (Harris, 2002). Iron homeostasis in a mammalian host is also tightly regulated; virtually no iron exists in serum that is not bound to haem, iron-storage proteins (ferritin, transferrin, etc.) or as cofactors for various enzymes. Rigorous control of iron availability in mammals is known to serve as a barrier against infection (Andrews et al., 2003; Bullen & Griffiths, 1999). The paucity of iron in serum has driven many pathogenic bacteria to evolve sophisticated means to acquire iron from the host, including the use of high-affinity iron chelates termed siderophores (Boukhalfa & Crumbliss, 2002; Miethke & Marahiel, 2007; Neilands, 1974; Payne & Crosa, 2004; Raymond & Carrano, 1979; Winkelmann, 2002). The efficiency with which this is accomplished by pathogenic bacteria generally parallels their virulence (Byers & Arceneaux, 1998; Griffiths, 1999; Koehler, 2000). As such, the interplay between iron sequestration by the host and acquisition by the pathogen is an important determinant in the establishment of infection. Siderophore biosynthesis by itself is not a *de facto* determinant of virulence but can certainly play a pivotal role in augmenting the pathogenicity of a given microbe (Cendrowski et al., 2004; Dale et al., 2004; De Voss et al., 2000).

**Siderophores of the Bacillus cereus sensu lato group**

Members of the *B. cereus sensu lato* group are known to produce and utilize two siderophores, bacillibactin (Fig. 1a, boxed structure) and petrobactin (Fig. 2a, boxed structure) (Koppisch et al., 2005; Wilson et al., 2006). Both are considered catechol-based siderophores, in that the metal is bound in the holo-siderophore either partially (petrobactin) or entirely (bacillibactin) by dihydroxybenzoate (DHB) units. Although both molecules are chemically capable of binding and solubilizing iron, genetic, biochemical and virulence studies indicate that they play markedly different biological functions in the bacteria.

**Bacillibactin: structure, biochemistry and iron-binding properties**

As its name suggests, bacillibactin was identified in culture extracts of *Bacillus subtilis* (May et al., 2001). The siderophore is a cyclic trimer consisting of threonine, glycine and DHB moieties. Like most characterized catecholate siderophores, bacillibactin harbours 2,3-dihydroxylated benzoyl units (2,3-DHB) for efficient chelation of the metal. Typical of most macrolactone siderophores, bacillibactin is biosynthesized via non-ribosomal peptide synthetases (NRPSs), and Marahiel and co-workers have thoroughly characterized the enzymes responsible for its synthesis (Fig. 1a) (May et al., 2001).

The bacillibactin biosynthetic gene cluster is organized in an apparent single operon under Fur regulation (Fig. 1b 1). The cluster also contains an *mtbH*-like gene whose function remains ambiguous but is frequently associated with NRPS-assisted biosynthesis of aroyl-containing natural products (Drake et al., 2007). It also includes an *sfp* gene encoding a 4′-phosphopantetheinylation transferase, essential for proper post-translational phosphopantetheinylation of enzymic domains, a major facilitator superfamily (MFS)-type efflux...
transporter and a homologue of *ubiC* which encodes chorismate pyruvate lyase (Siebert et al., 1994), although the role of this gene in bacillibactin biosynthesis remains unclear. Bacillibactin, like related tris-catecholate siderophores, binds iron with an affinity ($K_f \approx 10^{7.6}$) (Dertz et al., 2006) that is markedly greater than that of the mammalian iron-storage proteins transferrin and ferritin (Dhungana et al., 2004, 2005; Ratledge & Dover, 2000).

Bacillibactin production, uptake and export

Bacillibactin is produced by all examined strains of *Bacillus anthracis* and presumably throughout the *B. cereus sensu lato* group (Koppisch et al., 2008b). While the synthesis of this molecule is widely conserved among *Bacillus* strains, it is not required for the viability of all strains (Cendrowski et al., 2004).

Siderophore uptake in Gram-positive bacteria is facilitated by both membrane-bound substrate-binding proteins and membrane-spanning ABC transporters (Heinrichs et al., 2004). The uptake of bacillibactin in members of the *B. cereus sensu lato* group likely involves FeuA, B and C (Ollinger et al., 2006) as well as the trilactone hydrolase YuiI (BesA) (Miethke et al., 2006, 2008). Genes encoding these four genes in addition to *feuD*, which encodes an ATPase component of an ABC-type iron-compound transporter, are organized in an operon with a Fur box at its 5’ end (Fig. 1b 2.). The FeuABC system has been implicated in the uptake of ferric-bacillibactin in *B. subtilis*, and FeuA has been shown to exhibit nanomolar binding affinity for the ferric-siderophore. YuiI, on the other hand, has been shown to hydrolyse both bacillibactin and ferric-bacillibactin, although it hydrolyses the latter with a 25-fold greater catalytic efficiency. Thus, it has been postulated that YuiI is responsible for liberating iron from its bacillibactin chelate in the cytosol. All of these proteins are conserved in strains within the *B. cereus sensu lato* group (Table 1), and presumably play similar roles in the different strains. Bacillibactin export by these strains likely occurs using the same enzymic machinery as that used by *B. subtilis*, namely the MFS-type transporter YmfD (Fig. 1b 3.) and the transcriptional regulator Mta (Miethke et al., 2008).

Petrobactin: structure, biochemistry and iron-binding properties

Although petrobactin contains catecholate (in addition to an $\alpha$-hydroxy carboxylate) iron-coordinating moieties, it differs from bacillibactin (as well as all other catechol siderophores) in the hydroxylation pattern of the DHB moieties (Fig. 2a, boxed structure). Petrobactin uses 3,4-
DHB ligands, whereas the overwhelming majority of catechol siderophores identified to date utilize the 2,3-DHB structural isomer.

Currently, petrobactin and its sulfonated derivatives are the only known siderophores that use this unusual ligand (although free 3,4-DHB is produced by some strains of *B. anthracis* and *Magnetospirillum magneticum* (Barbeau et al., 2002; Calugay et al., 2006; Gardner et al., 2004; Garner et al., 2004; Hickford et al., 2004; Homann et al., 2009). Petrobactin was initially identified as a siderophore of the petroleum-degrading marine bacterium *Marinobacter hydrocarbonoclasticus* (Barbeau et al., 2002). The first evidence of the production of a 3,4-DHB-containing siderophore by *B. anthracis* was reported by Garner et al. (2004), and identification of this molecule as petrobactin was first reported in 2005 (Koppisch et al., 2005). The 3,4-DHB moieties are not only a chemical anomaly in the siderophore world, but have been found to have a significant biological role in organismal development (discussed below).

Petrobactin is a linear molecule composed of citrate, spermidine and DHB moieties, and its biosynthetic enzymes are distinct from those responsible for cyclic siderophores, and are thus termed NRPS-independent siderophore synthases (NIS synthases). Siderophore production by NIS synthases in other bacteria is relatively widespread. As is the case with petrobactin, NIS synthase-produced siderophores seemingly play a significant role in the virulence of their producers.

Assembly of the three molecular building blocks into petrobactin requires the action of six enzymes, encoded by the *asbABCDEF* cluster (Fig. 2a, Table 1) (Cendrowski et al., 2004; Lee et al., 2007; Pfleger et al., 2007). Petrobactin biosynthesis is unusual in that two distinct classes of enzymes, the NRPSs and the NIS synthases, work in concert to provide the final product. Challis and co-

![Fig. 2. Metabolic route for the biosynthesis of petrobactin (boxed), and organization of the gene clusters involved in the biosynthesis and uptake of petrobactin. (a) The DHB ligand is formed from DHS, which in turn is from the endogenous pentose phosphate pathway (yellow box). (b) (1) Enzymes involved in the assembly of petrobactin are encoded by the genes from the *asbABCDEF* cluster. (2, 3) Genes involved in the uptake of petrobactin and 3,4-DHB originate from the *fpuA/fhuB* and *fatBCD/fhuC* gene clusters. (c) Genes homologous to iron compound-uptake transporters of unknown substrate specificity.](image-url)
workers have provided compelling biochemical evidence for the functions of both of the NIS synthases, AsbA and AsbB (Oves-Costales et al., 2007, 2008). Importantly, they have clearly demonstrated that the type A NIS synthase, AsbA, specifically catalyses the stereospecific addition of spermidine onto one of the prochiral carboxylates of citrate to yield (3S)-N8-citryl-spermidine (Fig. 2a, 1) (Oves-Costales et al., 2009). The petrobactin biosynthetic pathway

*Genes with potentially misassigned GenBank annotations.

Table 1. Genes found in five representative members of the *B. cereus sensu lato* group that are involved in bacillibactin biosynthesis, uptake and export; petrobactin biosynthesis and export; and uptake of iron compounds of unknown specificity

<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Bacillibactin-associated genes</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MFS for BB export</td>
<td>GBA_1988*</td>
<td>BAS1845–7*</td>
<td>BT9727_1819</td>
<td>BC_1985*</td>
<td>BCE_2066*</td>
<td>YmID</td>
</tr>
<tr>
<td><em>dhb</em> cluster for BB biosynthesis</td>
<td>GBA_2368</td>
<td>BAS2204</td>
<td>BT9727_2143</td>
<td>BC_2302</td>
<td>BCE_2398</td>
<td>EntA</td>
</tr>
<tr>
<td></td>
<td>GBA_2369</td>
<td>BAS2205</td>
<td>BT9727_2144</td>
<td>BC_2303</td>
<td>BCE_2399</td>
<td>DhbC</td>
</tr>
<tr>
<td></td>
<td>GBA_2370</td>
<td>BAS2206</td>
<td>BT9727_2145</td>
<td>BC_2304</td>
<td>BCE_2400</td>
<td>DhbE</td>
</tr>
<tr>
<td></td>
<td>GBA_2371</td>
<td>BAS2207</td>
<td>BT9727_2146</td>
<td>BC_2305</td>
<td>BCE_2401</td>
<td>DhbB</td>
</tr>
<tr>
<td></td>
<td>GBA_2372</td>
<td>BAS2208</td>
<td>BT9727_2147</td>
<td>BC_2306–8*</td>
<td>BCE_2402</td>
<td>DhbF</td>
</tr>
<tr>
<td></td>
<td>GBA_2373</td>
<td>BAS2209</td>
<td>BT9727_2148</td>
<td>BC_2309</td>
<td>BCE_2403</td>
<td>MbtH</td>
</tr>
<tr>
<td></td>
<td>GBA_2374</td>
<td>BAS2210</td>
<td>BT9727_2149</td>
<td>BC_2310</td>
<td>BCE_2404</td>
<td>MFS</td>
</tr>
<tr>
<td></td>
<td>GBA_2375</td>
<td>BAS2211</td>
<td>BT9727_2150</td>
<td>BC_2311</td>
<td>BCE_2405</td>
<td>Sp</td>
</tr>
<tr>
<td><em>feuABCD/yuiI</em> cluster for BB uptake</td>
<td>GBA_3863</td>
<td>BAS3579</td>
<td>BT9727_3479</td>
<td>BC_3734</td>
<td>BCE_3576</td>
<td>Yuil</td>
</tr>
<tr>
<td></td>
<td>GBA_3864</td>
<td>BAS3580</td>
<td>BT9727_3480</td>
<td>BC_3735</td>
<td>BCE_3578</td>
<td>FeuD</td>
</tr>
<tr>
<td></td>
<td>GBA_3865</td>
<td>BAS3581</td>
<td>BT9727_3481</td>
<td>BC_3736</td>
<td>BCE_3579</td>
<td>FeuC</td>
</tr>
<tr>
<td></td>
<td>GBA_3866</td>
<td>BAS3582</td>
<td>BT9727_3482</td>
<td>BC_3737</td>
<td>BCE_3770</td>
<td>FeuB</td>
</tr>
<tr>
<td></td>
<td>GBA_3867*</td>
<td>BAS3583</td>
<td>BT9727_3483</td>
<td>BC_3738</td>
<td>BCE_3771</td>
<td>FeuA</td>
</tr>
<tr>
<td>Petrobactin-associated genes</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>asb</em> cluster for PB biosynthesis</td>
<td>GBA_1981</td>
<td>BAS1838</td>
<td>BT9727_1812</td>
<td>BC_1978</td>
<td>Absent</td>
<td>AsbA</td>
</tr>
<tr>
<td></td>
<td>GBA_1982</td>
<td>BAS1839</td>
<td>BT9727_1813</td>
<td>BC_1979</td>
<td>Absent</td>
<td>AsbB</td>
</tr>
<tr>
<td></td>
<td>GBA_1983</td>
<td>BAS1840</td>
<td>BT9727_1814</td>
<td>BC_1980</td>
<td>Absent</td>
<td>AsbC</td>
</tr>
<tr>
<td></td>
<td>GBA_1984</td>
<td>BAS1841</td>
<td>BT9727_1815</td>
<td>BC_1981</td>
<td>Absent</td>
<td>AsbD</td>
</tr>
<tr>
<td></td>
<td>GBA_1985</td>
<td>BAS1842</td>
<td>BT9727_1816</td>
<td>BC_1982</td>
<td>Absent</td>
<td>AsbE</td>
</tr>
<tr>
<td></td>
<td>GBA_1986</td>
<td>BAS1843</td>
<td>BT9727_1817</td>
<td>BC_1983</td>
<td>Absent</td>
<td>AsbF</td>
</tr>
<tr>
<td><em>fpuA/fhuB</em> cluster for PB uptake</td>
<td>GBA_4766</td>
<td>BAS4424</td>
<td>BT9727_4264</td>
<td>BC_4528</td>
<td>Absent</td>
<td>FpuA</td>
</tr>
<tr>
<td></td>
<td>GBA_4767</td>
<td>BAS4425</td>
<td>BT9727_4265</td>
<td>BC_4529*</td>
<td>Absent</td>
<td>FhuB-like</td>
</tr>
<tr>
<td><em>fatBCD/fhuC</em> cluster for PB uptake</td>
<td>GBA_5327</td>
<td>BAS4949</td>
<td>BT9727_4792</td>
<td>BC_5103</td>
<td>BCE_5223</td>
<td>FhuC-like</td>
</tr>
<tr>
<td></td>
<td>GBA_5328</td>
<td>BAS4951</td>
<td>BT9727_4793</td>
<td>BC_5104</td>
<td>BCE_5224</td>
<td>FatC</td>
</tr>
<tr>
<td></td>
<td>GBA_5329</td>
<td>BAS4952</td>
<td>BT9727_4794</td>
<td>BC_5105</td>
<td>BCE_5225</td>
<td>FatD</td>
</tr>
<tr>
<td></td>
<td>GBA_5330</td>
<td>BAS4953</td>
<td>BT9727_4795</td>
<td>BC_5106</td>
<td>BCE_5226</td>
<td>FatB</td>
</tr>
<tr>
<td>Unassigned iron compound-transporter genes</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Lone <em>yfiY</em></td>
<td>GBA_2255</td>
<td>BAS2099</td>
<td>BT9727_2038</td>
<td>BC_2208</td>
<td>BCE_2283</td>
<td>YfiY (FhuD-like)</td>
</tr>
<tr>
<td><em>feuA/fhuGB</em> cluster</td>
<td>GBA_3532*</td>
<td>BAS3273</td>
<td>BT9727_3245</td>
<td>BC_3466</td>
<td>BCE_3485</td>
<td>FeuA-like</td>
</tr>
<tr>
<td></td>
<td>GBA_3533</td>
<td>BAS3276</td>
<td>BT9727_3246</td>
<td>BC_3467</td>
<td>BCE_3486</td>
<td>FhuG-like</td>
</tr>
<tr>
<td></td>
<td>GBA_3534</td>
<td>BAS3277</td>
<td>BT9727_3247</td>
<td>BC_3468</td>
<td>BCE_3487</td>
<td>FhuB-like</td>
</tr>
<tr>
<td><em>fepC/fhuGD</em> cluster</td>
<td>GBA_4595</td>
<td>BAS4263</td>
<td>BT9727_4100</td>
<td>BC_4361</td>
<td>BCE_4448</td>
<td>FepC-like</td>
</tr>
<tr>
<td></td>
<td>GBA_4596</td>
<td>BAS4264</td>
<td>BT9727_4101</td>
<td>BC_4362</td>
<td>BCE_4449</td>
<td>FhuG-like</td>
</tr>
<tr>
<td></td>
<td>GBA_4597</td>
<td>BAS4265</td>
<td>BT9727_4102</td>
<td>BC_4363</td>
<td>BCE_4450</td>
<td>FhuD-like</td>
</tr>
<tr>
<td>Lone <em>fhuD</em></td>
<td>GBA_4652</td>
<td>BAS4317</td>
<td>BT9727_4155</td>
<td>BC_4416</td>
<td>Absent</td>
<td>FhuD-like</td>
</tr>
<tr>
<td><em>fepBC/fhuGB</em> cluster</td>
<td>GBA_5628</td>
<td>BAS5529</td>
<td>BT9727_5060</td>
<td>BC_5380</td>
<td>BCE_5909</td>
<td>FepB-like</td>
</tr>
<tr>
<td></td>
<td>GBA_5629</td>
<td>BAS5530</td>
<td>BT9727_5061</td>
<td>BC_5381</td>
<td>BCE_5910</td>
<td>FepC-like</td>
</tr>
<tr>
<td></td>
<td>GBA_5630</td>
<td>BAS5531</td>
<td>BT9727_5062</td>
<td>BC_5382</td>
<td>BCE_5911</td>
<td>FhuG-like</td>
</tr>
<tr>
<td></td>
<td>GBA_5631*</td>
<td>BAS5532/3*</td>
<td>BT9727_5063</td>
<td>BC_5383</td>
<td>BCE_5912</td>
<td>FhuB-like</td>
</tr>
</tbody>
</table>
apparently bifurcates at this point by the action of either the NRPS-type protein AsbE, transferring 3,4-DHB from AsbD onto 1 to provide N\(^4\)-(3,4-dihydroxybenzoyl)-N\(^8\)-citryl-spermidine (2), or the type C NIS synthase AsbB to afford the bis-amide 3. Intermediates 2 and 3 converge to 4 by the actions of AsbB and AsbE, respectively, and the biosynthesis of petrobactin is completed by AsbE adding the second molecule of 3,4-DHB to 4.

Whereas the functions of the AsbABCDE petrobactin biosynthetic enzymes were clearly demonstrated through both in vivo and in vitro studies, the role of AsbF remained enigmatic. We provided an initial insight into the major metabolic pathway to 3,4-DHB through feeding studies with \([U^{13}C]\)glucose. Based on examination of isotopic enrichment in the catecholate moiety of isolated petrobactin, the early steps of the shikimate pathway were identified as the primary source for 3,4-DHB production (Koppisch et al., 2008a). Shortly thereafter, we and Sherman and co-workers independently characterized AsbF as a dehydroshikimate dehydratase (DHSase) (Fox et al., 2008; Pfleger et al., 2008) for direct conversion of 3-dehydroshikimic acid (DHS) to 3,4-DHB. The action of the NRPS-like enzymes AsbCD is ultimately responsible for the activation of 3,4-DHB for transfer onto the citryl-spermidine framework to complete the assembly into petrobactin.

Although bacillibactin displays a much greater affinity for ferric iron than does petrobactin (\(K_{f}^{bac}=10^{67.6}\) vs \(K_{f}^{pet}=10^{23}\)) (Abergel et al., 2008; Zhang et al., 2009), both have greater affinities towards Fe\(^{3+}\) than does transferrin (\(K_{f}=10^{5}\)). Hence, transferrin is the primary source of iron for pathogenic Bacillus species during infection. Furthermore, petrobactin removes iron from transferrin at faster rates and with greater efficiency than either enterobactin or aerobactin (Abergel et al., 2008). Undoubtedly, the ability of petrobactin to rapidly extract and solubilize iron from this protein in a microbiologically accessible manner plays a major role in the infectivity of the organism (which can reach a cellular density of \(1 \times 10^{6}\) cells ml\(^{-1}\) in the mammalian blood stream) (Koehler, 2000). Interestingly, Fe–petrobactin complexes are known to decarboxylate upon prolonged exposure to light (Barbeau et al., 2002), and the photoproduct itself has a greater affinity for Fe\(^{3+}\) (\(K_{d}=10^{24.4}\)) than petrobactin itself (Abergel et al., 2008). While this has been postulated to play a role in the life cycle of petrobactin-producing marine bacteria, it presumably does not play an analogous role for the soil-dwelling Bacillus strains. Nevertheless, both petrobactin and its photoproduct may be used as xenosiderophores by other members of this species (Abergel et al., 2008).

**Petrobactin production and uptake**

The production of petrobactin in the *B. cereus sensu lato* group is not exclusive to pathogenic strains (Table 1) (Koppisch et al., 2008b). However, all of the strains that are known to be capable of developing potentially lethal infections in humans do produce petrobactin as their main siderophore. Thus, while petrobactin production by itself is not a biomarker of virulence in this group, it is a trait that is required for the pathogenesis of this species in mammals (Casadevall, 2006).

Petrobactin uptake is believed to be facilitated by membrane-associated substrate-binding proteins and transporters. Zawadzka and co-workers demonstrated that the substrate-binding proteins FpuA and FatB exhibit a tight binding affinity to both petrobactin (or its photoproduct) and Fe–petrobactin (or its photoproduct), with the latter also exhibiting an ability to bind 3,4-DHB and its bis-ligated ferric iron congener (Zawadzka et al., 2009a). The aforementioned siderophores are also tightly bound by YclQ, a FatB homologue in *B. subtilis*, and orthologues of this protein are found throughout the *B. cereus sensu lato* group (Zawadzka et al., 2009b). Similarly, a survey of the genomes of representative strains from the *B. cereus sensu lato* group reveals the presence of a number of iron-compound transporters whose substrate specificity and function remain unknown (Table 1, Fig. 2c). Thus, it is possible that a number of potential petrobactin-uptake mechanisms exist within any given strain. Despite multiple transporters capable of binding petrobactin, studies by Carlson and co-workers have demonstrated that in *B. anthracis* str. Sterne, FpuA plays a more significant role in petrobactin uptake than FatB in in vivo studies (Carlson et al., 2010). Genetic deletion strains of *fpuA* grow more slowly and accumulate petrobactin in the medium to a greater extent than wild-type or *fatB*-deficient strains. Most significantly, spores of the *fpuA*-deficient strain exhibit reduced virulence in a murine model, despite the fact that petrobactin synthesis is not attenuated in this strain. The LD\(_{50}\) of the spores of the *fpuA*-deficient strain is over three orders of magnitude higher than that of wild-type spores, and 10-fold higher than that of a strain deficient in petrobactin production. Some avirulent strains, such as *B. cereus* ATCC 10987 (Table 1), lack petrobactin-synthesis machinery and *fpuA*. Also, an exhaustive comparative analysis of genomes within the *B. cereus sensu lato* group reveals that most non-pathogenic strains lack *fpuA* or *fatB*, with few exceptions (see Supplementary Information). While FpuA seemingly plays a significant role in the virulence of its host strains, the role of FatB is less well understood. However, given that the growth of *fpuA/fatB* deletion strains in iron-deficient media is slowed relative to *fpuA* deletion strains (Carlson et al., 2010), FatB likely plays an auxiliary role in iron acquisition. It is conceivable that the primary role of FatB lies in the transport of 3,4-DHB-ligated iron itself, which is consistent with the observation that the \(K_{d}\) for the substrate [Fe\(^{III}\)(3,4-DHB)\(^{2+}\)]\(^{-}\) is roughly 100-fold lower than that for [Fe\(^{III}\)(PB)]\(^{-}\) (Zawadzka et al., 2009a). Additionally, unlike the *fat* gene cluster, neither the *asb* nor the *fpu* gene cluster contains a Fur regulatory element, suggesting a closer functional linkage between petrobactin biosynthesis and FpuA-mediated petrobactin uptake (Fig. 2b). Further studies on
Microbiological roles of bacillibactin and petrobactin

While both petrobactin and bacillibactin solubilize and sequester iron, there is a growing body of evidence which suggests that the two siderophores have distinct biological roles in the bacteria that produce them. The production of petrobactin plays a crucial role in the establishment of *B. anthracis* infection in the mammalian host, while the production of bacillibactin is seemingly far less important in this regard to pathogenic *Bacillus* strains. Genetic deletions of the bacillibactin biosynthetic gene cluster in *B. anthracis* str. Sterne do not affect the growth of the organism in iron-deficient media, nor its observed virulence in a mouse model (Cendrowski et al., 2004). This is partially explained by the observation that the siderophores of *B. anthracis* are produced and accumulate in culture media in a temporally distinct manner (Wilson et al., 2010). Petrobactin accumulates in culture media after 5 h of bacterial outgrowth from spores, which is less than half the time required for bacillibactin accumulation under identical conditions. These studies indicate that petrobactin is used by the bacterium in the early growth stages, such as spore outgrowth, while bacillibactin is not. A petrobactin-deficient mutant strain of *B. anthracis* only grows from spores supplemented with exogenous petrobactin or other iron sources, which is consistent with this hypothesis. Additionally, bacillibactin production by the organism at 37 °C in a CO_{2}-enriched atmosphere is markedly reduced relative to growth under environmental conditions (Koppisch et al., 2005; Wilson et al., 2010). Wilson and co-workers have reported that growth of vegetative *B. anthracis* str. Sterne at 37 °C without CO_{2} supplementation affords a twofold decrease in bacillibactin production relative to cultures grown at 23 °C (10 vs 20 μM, respectively). Bacillibactin is not found to accumulate to a quantifiable amount in cultures amended with 0.4–0.8 % bicarbonate, which is consistent with other CO_{2}-supplementation analyses (Koppisch et al., 2005). The elevated temperature and carbon dioxide mimic some conditions found in the mammalian circulatory system, and conditions found in the host are known to influence the expression of a number of bacterial virulence traits (Caparon et al., 1992; Koehler et al., 1994; Okada et al., 1993; Shimamura et al., 1985). The suppression of bacillibactin production may reflect an attempt by the organism to conserve metabolic resources from being spent on a molecule that is sequestered by host defences (see below), and thus does not provide a biological advantage under these conditions. Both the temporal production of the two siderophores and the suppression of bacillibactin production by host factors provide intriguing evidence that the siderophores play discrete biological roles in the life cycle of *B. anthracis*, and presumably other related *Bacillus* strains. While petrobactin is clearly the siderophore that is used by the organism in the outgrowth process and throughout the manifestation of infection, it is postulated that bacillibactin is employed in the later stages of infections when CO_{2} concentrations and temperature vary, or in the transition of the vegetative cells back to spores (Wilson et al., 2010).

Siderophores and human health: the role of siderocalin

In general, there is increasing evidence that some siderophores may be considered virulence mediators in the bacterial pathogens that secrete them. Petrobactin synthesis in pathogenic *Bacillus* strains is one of the best illustrations of this concept in microbiology. It has been known for some time that *B. anthracis* strains incapable of producing this siderophore are non-pathogenic, due to the seminal work of Cendrowski et al. (2004). While growth of the organism is facilitated by the ability of petrobactin to extract iron from host proteins, growth within the host is further facilitated by the unique ability of the siderophore to evade the endogenous siderophore sequestration protein found in the mammalian immune system, siderocalin (Clifton et al., 2009). Siderocalin has a high affinity for tris-catecholate siderophores, including bacillibactin, but has negligible affinity for petrobactin (Abergel et al., 2006). Further, a subsequent crystal structure of the enzyme bound to bacillibactin suggests that the 3,4-DHB groups of petrobactin may themselves play a role in the occlusion of...
the siderophore from the binding pocket of siderocalin (Fig. 3) (Abergel et al., 2008, 2006). This dichotomy in siderophore binding plays a unique role in the ecology of infection of this organism.

The inability of siderocalin to bind petrobactin allows the siderophore to persist in the bloodstream and to provide a more favourable environment for bacterial growth. Due to its ability to evade siderocalin, petrobactin has been termed a ‘stealth’ siderophore, and is a critical enabler of virulence in the host. More importantly, the abolition of its production in pathogenic strains has been demonstrated to abolish virulence. To this end, the development of therapeutics that target petrobactin biosynthesis is expected to afford novel means of anti-anthrax treatment and prophylaxis.

Conclusion

Siderophores have long been recognized to be both critically important metabolites and compounds with intriguing metal-binding abilities. In pathogenic bacteria, siderophores themselves are often key virulence mediators. Bacillibactin and petrobactin together provide an interesting example of how iron acquisition not only mediates virulence in a family of pathogens but also influences the development of the organism through its life cycle. With a more thorough understanding of bacterial iron-acquisition strategies, ideally we may garner not only an understanding of the biology of these organisms but also a new insight into how the infections that they cause may be combated.

Acknowledgements

We would like to thank Katherine Lovejoy for critical reading of this manuscript.

References


