Elucidation of the Burkholderia cenocepacia hopanoid biosynthesis pathway uncovers functions for conserved proteins in hopanoid-producing bacteria


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Elucidation of the *Burkholderia cenocepacia* hopanoid biosynthesis pathway uncovers functions for conserved proteins in hopanoid-producing bacteria

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Summary

Hopanoids are bacterial surrogates of eukaryotic membrane sterols and among earth’s most abundant natural products. Their molecular fossils remain in sediments spanning more than a billion years. However, hopanoid metabolism and function are not fully understood. *Burkholderia* species are environmental opportunistic pathogens that produce hopanoids and also occupy diverse ecological niches. We investigated hopanoids biosynthesis in *B. cenocepacia* by deletion mutagenesis and structural characterization of the hopanoids produced by the mutants. The enzymes encoded by *hpnH* and *hpnG* were essential for production of all C_{35} extended hopanoids, including bacteriohopanetetrol (BHT), BHT glucosamine and BHT cyclitol ether. Deletion of *hpnI* resulted in BHT production, while Δ*hpnJ* produced only BHT glucosamine. Thus, HpnI is required for BHT glucosamine production while HpnJ is responsible for its conversion to the cyclitol ether. The Δ*hpnH* and Δ*hpnG* mutants could not grow under any stress condition tested, whereas Δ*hpnI*, Δ*hpnJ*, and Δ*hpnK* displayed wild type growth rates when exposed to detergent, but varying levels of sensitivity to low pH and polymyxin B. This study not only elucidates the biosynthetic pathway of hopanoids in *B. cenocepacia*, but also uncovers a biosynthetic role for the conserved proteins HpnI, HpnJ, and HpnK in other hopanoid-producing bacteria.

Keywords: hopanoids/*Burkholderia cenocepacia*/membrane permeability
Introduction

Hopanoids are bacterial membrane lipids ubiquitous in modern day environments dominated by microbes and readily preserved in ancient sedimentary rock (Ourisson and Albrecht, 1992), making them ideal tools for reconstructing and understanding microbial ecosystems (Brocks et al., 2004; Summons and Lincoln, 2012). Due to size and structural similarities, hopanoids are considered bacterial surrogates of eukaryotic sterols, possibly regulating the fluidity and permeability of the bacterial membrane (Ourisson et al., 1987; Kannenberg, 1999). Only recently have studies focused on determining the biological function of hopanoids using genetic manipulation and in vivo experimentation. Such studies confirm that hopanoids are involved in enhancing the stability and impermeability of the bacterial membrane, conferring resistance to multiple stress conditions including pH, temperature, and exposure to detergents and antibiotics (Doughty et al., 2009; Welander et al., 2009; Schmerk et al., 2011; Malott et al., 2012). However, it remains unclear what functional importance can be ascribed to particular variations in the hopanoid core and side chain structures.

Hopanoids in lower eukaryotes and bacteria are derived from the direct cyclization of squalene (Rohmer et al., 1984; Ochs et al., 1992), which results in a pentacyclic triterpenoid core commonly modified by unsaturation, methylation and/or the addition of diverse C₅ ribose-derived side chains (Flesch and Rohmer, 1988; Rohmer, 1993). To date, few studies have successfully investigated the genes or proteins involved in modifying the hopanoid core. HpnP and HpnR have been identified as the radical S-adenosylmethionine (SAM) enzymes responsible for production of 2- and 3-methylhopanoids, respectively (Welander et al., 2010; Welander and Summons, 2012). The production of C-3 methylated hopanoids is important for late stationary survival and maintenance of intracytoplasmic membranes in Methylococcus capsulatus (Welander and Summons, 2012), while the production of C-2 methylated hopanoids is important for stress tolerance (Welander and Summons, 2012; Kulkarni et al., 2013). Hopanoids with C₃₅ extended side chains are common among hopanoid producers, but little is known about their biosynthesis or their function(s). The B-12 binding radical SAM protein HpnH and the nucleoside phosphorylase HpnG catalyze the first and second steps in hopanoid side chain biosynthesis, respectively (Bradley et al., 2010; Welander et al., 2012b). In Rhodopseudomonas palustris, the deletion of hpnH resulted in a strain only capable of producing C₃₀
hopanoids, and with compromised integrity of the outer membrane (Welander et al., 2012b). These discoveries have provided much needed insight into the initiation of C_{35} hopanoid production; however, the additional enzymes involved in side chain biosynthesis and the specific role that different functionalized hopanoids play in membrane stability and stress tolerance remain to be elucidated.

*Burkholderia cenocepacia* is one of the 17 species of genetically related bacteria known as the *B. cepacia* complex (Bcc). These bacteria are widely spread in aquatic and soil environments where they play beneficial roles including the promotion of plant growth and the degradation of pollutants (Coenye and Vandamme, 2003). Bcc bacteria are also opportunistic pathogens, causing infections in cystic fibrosis patients and other immune-compromised individuals (Vandamme et al., 1997; Speert, 2002). Given their particular environmental niche, it is not surprising that *Burkholderia* species are intrinsically resistant to most clinically relevant antibiotics and antimicrobial peptides (Waters and Ratjen, 2006; Loutet and Valvano, 2011). Resistance to antimicrobials depends, in part, on the production of hopanoids (Schmerk et al., 2011). The deletion of both squalene-hopene cyclase (Shc) encoding genes in *B. cenocepacia* K56-2 resulted in a strain (Δshc) that could not produce hopanoids and displayed increased sensitivity to low pH, detergent, and various antibiotics. The mutant was also unable to produce flagella, resulting in severely diminished motility (Schmerk et al., 2011). Several *Burkholderia* species produce various C_{35} extended hopanoids, including bacteriohopanetetrol (BHT), BHT glucosamine, and BHT cyclitol ether; however, the functional importance of these individual hopanoids has not been explored (Cvejic et al., 2000; Talbot et al., 2007b).

This study identifies the types of extended hopanoids produced by *B. cenocepacia* and utilizes genetic tools to generate a collection of mutants in predicted hopanoid biosynthetic genes. Environmental stress tests performed with the mutants lead to new suggestions about the biological roles of C_{35} extended hopanoids. Our results are the first to define the biosynthetic pathway of hopanoids in *Burkholderia* and to define a biosynthetic role for the proteins HpnI, HpnJ and HpnK in any hopanoid producing bacterium.

**Results and Discussion**
B. cenocepacia produces a mixture of hopanoids

The biosynthesis of hopanoids requires the cyclization of squalene, a reaction catalyzed by squalene-hopene cyclase (Ochs et al., 1992), followed by the functionalization of the basic hopanoid structure through the addition of various side chains and additional modifications. Previously (Schmerk et al., 2011), we reported the identification and characterization of two paralogs of the squalene-hopene cyclase gene (shc) in B. cenocepacia, which are located on chromosomes 2 (BCAM2831) and 3 (BCAS1067), herein designated as hpnF2 and hpnF3, respectively (Fig. 2). GC analysis of lipid extracts obtained from the deletion mutant lacking both hpnF genes (Δshc) demonstrated that this strain did not produce hopanoids but at the same time accumulated an unidentified compound, which was also produced by the hpnF2 single deletion mutant (Schmerk et al., 2011). This compound was subsequently identified as squalene (Figure S1). We next examined lipid extracts from stationary phase liquid cultures to determine the species of functionalized hopanoids produced by B. cenocepacia. These experiments revealed that B. cenocepacia produces various hopanoid structures including the C30 hydrocarbon diploptene and three functionalized bacteriohopanepolyols: bacteriohopanetetrol (BHT), BHT cyclitol ether, and BHT glucosamine (Figure 1a and Figure S2). B. cenocepacia also produced an unsaturated hopanoid. The mass spectral data was insufficient to distinguish if it is an unsaturated BHT cyclitol ether or BHT glucosamine, and whether the unsaturation is at C-6 or C-11 positions of the ring system (Figure 1a). However, our findings agree with previous studies reporting that a strain of B. cepacia produces these same saturated hopanoid species and also a C-6 unsaturated BHT cyclitol ether (Cvejic et al., 2000; Talbot et al., 2007a).

Characterization of hopanoid biosynthesis genes in B. cenocepacia

The hopanoid biosynthesis associated genes of B. cenocepacia are located in one cluster on chromosome 1 and two clusters on chromosome 2 (Figure 1b). In addition, the second squalene-hopene cyclase gene (hpnF3) is present as a single gene on chromosome 3, as discussed above. Homologs of ispH/lytB (BCAM2738 and BCAL2710), hpnE (BCAM2832) and hpnC (BCAM2833) are required for squalene production (Perzl et al., 1998; Wolff et al., 2003). ispHBCAL2710 and ispHBCAM2738 were deleted in a previous study (Loutet et al., 2011), while hpnC and hpnE could both...
be essential for bacterial viability, as their homologs could not be deleted in *R. palustris* (Welander et al., 2012b). In the present study, we focus on the genes required for the synthesis of the hopanoid chain (Table 1).

The *hpnA* homolog (BCAM2735) could not be deleted; repeated attempts to delete this gene resulted in exconjugants reverting to the wild type background. To confirm whether this gene was essential for bacterial viability, we created a conditional mutant by placing *hpnA* under the control of a rhamnose-inducible promoter (Ortega et al., 2007). The conditional *P_{rhaB}::hpnA* mutant could grow in the presence of rhamnose (permissive condition) and glucose (non-permissive condition), indicating that *hpnA* is not essential for *B. cenocepacia* (data not shown). The reasons why this gene could not be deleted remain unknown. A similar case was encountered when attempting to delete *hpnH* (BCAM2739). To successfully remove *hpnH* from the chromosome the deletion had to be constructed in a Δshc background strain (Schmerk et al., 2011). After *hpnH* was successfully deleted, hopanoid production was restored by introducing pBCAM2831, which encodes the HpnF2 squalene-hopene cyclase.

Chemical analyses of the hopanoids produced by the deletion mutants were performed by gas chromatography-mass spectrometry (GC-MS) and liquid chromatography-mass spectrometry (LC-MS), and demonstrated that five of the ten genes play roles in the production of extended hopanoids (Table 2). The other five genes did not demonstrate a clear role in hopanoid biosynthesis. It is possible that these genes are involved in the regulation of hopanoid production or their transport to specific locations within the bacterial cell envelope, both of which were not evaluated in this study.

*HpnI* and *HpnK* are required for bacteriohopanetetrol glucosamine production

The B-12 binding radical SAM protein HpnH is responsible for the primary step in producing extended hopanoids (Bradley et al., 2010; Welander et al., 2012b). The C$_3$ unit of the extended hopanoid side chain is derived from a ribosugar, whose addition is catalyzed by HpnH (Figure 2) (Bradley et al., 2010). The deletion of *hpnH* (BCAM2739) in *B. cenocepacia* resulted in a similar effect to that observed in *M. extorquens* and *R. palustris*, with only the C$_{30}$ hopanoid diploptene being produced (Figure S3). Deletion of *hpnG* also prevented the production of any functionalized
hopanoids and LC-MS analysis demonstrated the sole accumulation of adenosyl hopane (Figure S4, Figure 2, step 2), an intermediate also found accumulated in *R. palustris* and *M. extorquens* *hpnG* mutants (Bradley et al., 2010; Welander et al., 2012b). With the adenine cleaved off the hopanoid compound by the nucleosidase HpnG (Figure 2, step 3), the resulting intermediate would be free to form bacteriohopanetetrol (BHT; Figure 2, step 4). In earlier studies, the final BHT intermediate has been suggested to be ribosyl hopane or derivatives such as ribonyl hopane and formyl hopane, and also phosphoribohopane rapidly cleaved to form BHT (Duvold and Rohmer, 1999; Seemann et al., 1999; Bradley et al., 2010; Welander et al., 2012b). However, the hopanoid biosynthesis associated gene clusters of *B. cenocepacia* do not encode any enzymes that could catalyze the formation of BHT from such intermediates, despite the common belief that one more enzyme is required for its production. Because monosaccharides such as ribose and glucose naturally exist in both cyclic and open chain forms, it is conceivable that the ribose opens up without the aid of an enzyme (Bradley et al., 2010). Therefore, we propose that the conversion of the ribose hopanoid to BHT occurs nonenzymatically.

LC-MS results revealed that the next enzyme for the formation of extended hopanoids is the glycosyltransferase HpnI (Figure 2, step 5, and Figure 3b). Labelled sugar incorporation experiments previously performed in *Zymomonas mobilis* demonstrated that the cyclopentane group added to the extended hopanoid side chain is derived from *N*-acetyl-*D*-glucosamine (GlcNAc) (Vincent et al., 2003). Bradley *et al.* have proposed that HpnI catalyzes the addition of GlcNAc to the hopanoid side chain (Bradley et al., 2010). Deletion of *hpnI* (BCAL1050) resulted in a mutant that only produced BHT (Figure 3b). However, it is still uncertain whether this enzyme utilizes the ribosylhopane intermediate or BHT as its substrate.

A deacetylation step (Figure 2, step 6), prior to ring contraction, is predicted to follow the glycosylation of the hopanoid side chain (Vincent et al., 2003). HpnK (BCAL1052) contains a YdjC protein motif which is thought to be involved in cellulose metabolism (Lai and Ingram, 1993). In *Citrobacter rodentium* the *hpnK* homolog is annotated as a chitobiose-phosphate hydrolase (*chbG*). A study of *chbG* in *E. coli* demonstrates that this gene encodes a monodeacetylase that acts on chitooligosaccharide substrates similar in structure to acetylglucosamine (Verma and Mahadevan,
BLASTp analysis of *E. coli* ChbG against the *Burkholderia cenocepacia* J2315 protein database identifies HpnK as the polypeptide providing the most significant alignment (E-value 4e\(^{-15}\)).

Deletion of *hpnK* in *B. cenocepacia* resulted in production of BHT glucosamine but not BHT cyclitol ether (Figure 3c), indicating deacetylation is required for the subsequent production of BHT cyclitol ether. Because all lipid samples have to be acetylated as part of the LC-MS analysis protocol we were not able to directly detect the deacetylated BHT glucosamine.

**HpnJ is essential for the production of bacteriohopanetetrol cyclitol ether**

Deletion of *hpnJ* (BCAL1051) resulted in the loss of BHT cyclitol ether production while the production of the other extended hopanoids was maintained (Figure 3d). A ring contraction may be necessary to produce BHT cyclitol ether from BHT glucosamine (Figure 2, step 7), but the exact mechanism of the ring contraction reaction remains unknown (Vincent et al., 2003; Pan and Vincent, 2008). Like HpnH, HpnJ is annotated as a radical SAM protein. This family of enzymes catalyzes a wide range of reactions including RNA modifications and the synthesis of cofactors and antibiotics (Sofia et al., 2001), and utilize an enzyme-bound [4Fe–4S] cluster (Frey et al., 2008; Duschene et al., 2009; Shisler and Broderick, 2012). The iron-sulfur cluster is active in its reduced state and from this state it can transfer an electron to the sulfonium of SAM. This electron transfer promotes the homolytic cleavage of SAM, producing methionine and a 5′-deoxyadenosyl (5′-dAdo) radical intermediate (Nicolet et al., 2009). This highly reactive radical can abstract a hydrogen atom from its substrate, often from unreactive positions (Hioe and Zipse, 2012). Of the thousands of predicted radical SAM enzymes only a small number have been biochemically characterized (Sofia et al., 2001; Frey et al., 2008). However, a recent study provided mechanistic details for ring contraction by QueE, the radical SAM enzyme of *Bacillus subtilis* (McCarty et al., 2013). QueE utilizes SAM to abstract a hydrogen atom from 6-carboxy-5,6,7,8-tetrahydropterin (CPH\(_4\)) and perform a ring contraction similar to that observed in the conversion of BHT glucosamine to BHT cyclitol ether (McCarty et al., 2013). Therefore, it is possible that the ring contraction that converts the BHT glucosamine to the cyclitol ether also occurs through a radical SAM mechanism.
Phylogenetic analysis of HpnI and HpnJ homologs

The production of BHT glucosamine has been documented in several species, including Z. mobilis, Geobacter sulfurreducens, G. metallireducens and B. cepacia (Flesch and Rohmer, 1989; Talbot et al., 2007b; Eickhoff et al., 2013). Since the enzyme responsible for the synthesis of this hopanoid has been identified, bioinformatics analysis can be used to predict which bacteria could produce BHT glucosamine. An unrooted maximum likelihood tree was created using the top 250 sequences retrieved via a protein BLAST search of the B. cenocepacia HpnI sequence against the KEGG and NCBI databases (Figure 4). All bacteria contained within this tree encode at least one copy of the squalene-hopene cyclase HpnF, indicating that all of these strains have the capacity to produce hopanoids. The ability to produce BHT glucosamine appears to be widespread among hopanoid producers, with the gene encoding HpnI being present in α-, β-, δ-, and γ-proteobacterial species, as well as in various cyanobacteria and the poorly characterized phylum of acidobacteria. The bacterial taxa in this tree reside in a wide range of water and soil associated environments and must endure variations in temperature, pH and exposure to a variety of chemical and metal stresses (Diels et al., 2009; Loutet and Valvano, 2010; Roger et al., 2012; Mamlouk and Gullo, 2013). It is possible that complex extended hopanoids, like BHT glucosamine are important in maintaining bacterial membrane stability in these constantly changing environments. Most Burkholderia species, including B. cenocepacia, contain only one copy of hpnI, found within the beta proteobacteria clade with the closely related Ralstonia and Cupriavidus spp. However, several Burkholderia species, including B. pseudomallei and B. thailandensis, contain 2 copies of hpnI. This second copy of the gene lies within an alpha proteobacterial clade and may have been acquired through horizontal gene transfer. Hyphomicrobium spp. and Phaeospiroplum molischianum also contain 2 copies of hpnI which are found within clades belonging to 2 different phyla, indicating that they too have likely acquired an extra copy of the gene via horizontal gene transfer.

Many bacterial taxa, including M. fujisawaense (Talbot et al., 2007b), M. extoquorens (Bradley et al., 2010), G. sulfurreducens, G. metallireducens (Eickhoff et al., 2013), B. pseudomallei, B. gladioli, B. cepacia (Cvejic et al., 2000; Talbot et al., 2007b) and Candidatus Chloracidobacterium thermophilum (Costas et al., 2012) produce BHT cyclitol ether. We created a maximum likelihood
tree of the top 250 sequences retrieved via a protein BLAST search of the *B. cenocepacia* HpnJ sequence against the KEGG and NCBI databases (Figure 5). As mentioned previously, HpnJ is a radical SAM protein and BLAST searches of radical SAM hopanoid biosynthesis proteins generally pick up other radical SAM proteins that are not associated with hopanoid biosynthesis. To differentiate between these non-hopanoid biosynthesis radical SAM proteins and true HpnJ homologs the e-value for a bona fide HpnJ was set to e^{-100} or lower, as these was the lowest e-value for which a homolog of known but different function could be identified. The majority of HpnJ homologs were found in species that also contained an HpnI homolog, thereby suggesting that the production of BHT cyclitol ether depends on the production of a BHT glucosamine precursor, as we have observed in *B. cenocepacia*. As *B. cenocepacia* appears to produce much more BHT cyclitol ether than BHT glucosamine (Figure 3a), we speculate that the former plays the dominant role in maintaining membrane stability in response to environmental stresses.

*Extended hopanoids are important in protecting *B. cenocepacia* from environmental stresses*

Our previous work (Schmerk et al., 2011) demonstrated that hopanoid production plays an important role in the ability of *B. cenocepacia* to grow under diverse stress conditions, including low pH, the detergent sodium dodecyl sulfate (SDS), and the antimicrobial lipopeptide polymyxin B. This is likely due to the capacity of hopanoids to maintain membrane stability, a notion that was consistent with the observed retraction of the inner membrane from the outer membrane in the Δshc strain, and the mutant’s inability to produce flagella (Schmerk et al., 2011). To determine whether extended hopanoids play any role in the ability of *B. cenocepacia* to resist stress conditions we monitored the growth of all mutants over a period of 24 h in LB buffered to pH 7.0 or pH 4.0, as well as LB supplemented with 0.03% SDS or 1 mg ml^{-1} polymyxin B. ΔhpnH, which only produces the C_{30} hopanoid diploptene, behaved like Δshc, as it was unable to grow in all conditions tested, except in the pH 7.0 control medium (Figure 6). Therefore, we conclude that the production of diploptene alone is not sufficient for *B. cenocepacia* to fully adapt to the stress conditions tested. The susceptibility of ΔhpnH to both SDS and polymyxin B indicates that this strain likely suffers from increased membrane permeability, as increased sensitivity to detergents and antibiotics are indicators of
membrane damage in Gram-negative bacteria (Begley et al., 2005; Ruiz et al., 2005; Welander et al., 2009; Loutet and Valvano, 2011). We were unable to determine if this membrane damage results in decreased motility, as the construction of the \textit{hpnH} strain required the presence of a complementing plasmid expressing \textit{hpnF2} (pBCAM2831). The pSCRhaB2 vector used for this complementation severely alters motility patterns observed in swarming and swimming assays. There was no significant motility defect observed for any of the other nine mutants tested indicating that diploptene and/or adenosyl hopane, which is produced by \textit{ΔhpnG}, alone can confer sufficient membrane integrity or stability to properly assemble the flagellar apparatus.

The remaining mutants with defects in hopanoid side chain assembly demonstrated a range of phenotypes under stress (Figure 7). \textit{ΔhpnG}, which only produces adenosylhopane, had a phenotype similar to \textit{ΔhpnH} and was unable to grow in all conditions tested aside from the pH 7.0 control. The minimum inhibitory concentration (MIC) of polymyxin B for \textit{ΔhpnG} was 64 µg ml\(^{-1}\) (data not shown), a significantly lower value than that of the wild type (>1024 µg ml\(^{-1}\)), and comparable to that of \textit{Δshc} (128 µg ml\(^{-1}\)). Therefore, lack of hopanoids (\textit{Δshc}) and production of adenosyl hopane (\textit{ΔhpnG}) are detrimental to the bacterium. Introducing a functional \textit{hpnG} gene by complementation with pHpnG restored growth to near wild type levels in the presence of 0.03% SDS, and partially restored growth in pH 4.0 and in the presence of polymyxin B (Figure S5). Since the hopanoid intermediate produced by \textit{ΔhpnG} does not accumulate in the wild type, it is difficult to determine whether the phenotypes observed in the mutant are due to the lack of C\textsubscript{35} extended hopanoids or to the build-up of adenosylhopane itself. It is also possible that adenosylhopane intermediate may be somehow mislocalized within the bacterial cell.

The \textit{ΔhpnI}, \textit{ΔhpnJ}, and \textit{ΔhpnK} mutants could grow similarly to wild type in 0.03% SDS (Figure 7), indicating that the presence of the C\textsubscript{35} extended hopanoid BHT is sufficient to confer a higher degree of membrane integrity than the C\textsubscript{30} hopanoid diploptene. \textit{ΔhpnI} and \textit{ΔhpnJ} were partially resistant to low pH and polymyxin B, and grew slower than wild type (Figure 7). Comparatively, \textit{ΔhpnJ} displayed a less severe phenotype than \textit{ΔhpnI}, demonstrating that the three C\textsubscript{35} extended hopanoids are likely to play unique roles in enhancing the membrane integrity of \textit{B. cenocepacia}. 

\[\text{\textit{hpn}}]
Complementation of the ΔhpnI and ΔhpnJ mutants with pHpnI and pHpnJ, respectively, restored growth at pH 4.0 and in the presence of polymyxin B to wild type levels (Figure S5).

ΔhpnK, which is thought to produce only acetylated BHT glucosamine, grew more poorly than ΔhpnI and ΔhpnJ at pH 4.0 and could not in 1 mg ml⁻¹ polymyxin B (Figure 7). The MIC value of polymyxin B for ΔhpnI, ΔhpnJ, and ΔhpnK was 256 µg ml⁻¹ (data not shown). The acetylated BHT glucosamine detected in this mutant is a hopanoid intermediate that would not normally be produced in the wild type strain. As proposed for the hpnG mutant, it is possible that this intermediate interferes with proper transport or membrane localization causing an increase in membrane permeability when compared to ΔhpnI and ΔhpnJ mutants. Complementation of ΔhpnK via pHpnK was able to partially restore growth at pH 4.0 and restored growth to a level similar to wild type in the presence of polymyxin B (Figure S5).

The remaining mutants tested displayed high variations in their degree of sensitivity to the tested stress conditions (Figure S6 and Table 3). We speculate that since these genes do not play a detectable role in hopanoid side chain biosynthesis they may be involved in the regulation and/or membrane transport of hopanoid molecules. The BCAM2736 and hpnB (BCAM2737) genes are highly conserved among Burkholderia species and other hopanoid producing bacteria; however, the deletion of these genes did not result in any defect in hopanoid biosynthesis or the ability of these mutants to tolerate membrane stress. Burkholderia species are highly adaptive to a wide range of ecological niches (Coenye and Vandamme, 2003), including the ability to colonize various hosts (Loutet and Valvano, 2010). Therefore, the conditions used in our experiments most likely underestimate the full spectrum of situations for which hopanoid production by B. cenocepacia could be required, and it is possible that these genes may be required in situations not modeled by our experiments. There is little information concerning the possible function of HpnL (BCAL1053). The loss of this protein resulted in an intermediate phenotype, being able to grow as well as MH1K in the pH 7.0 buffered control and in 0.03% SDS, but exhibiting delayed growth in both low pH medium and medium containing polymyxin B (Figure S6).

ΔhpnM (BCAM2827) grew slower than MH1K at pH 4.0, and was unable to grow in the presence of both detergent and polymyxin B (Figure S6). HpnM proteins are members of the toluene
tolerance protein Ttg2D family, a group of ABC-like transporters. Ttg2 plays a role in toluene tolerance in *Pseudomonas putida* (Kim et al., 1998), a process that involves increasing the cell membrane rigidity by changing the fatty acid and phospholipid compositions of the outer membrane (Ramos et al., 1997). MlaC is also a member of this protein family and is involved in maintaining lipid asymmetry via the retrograde trafficking of phospholipids from the outer to inner membrane in *E. coli* (Malinverni and Silhavy, 2009). It is likely that HpnM is also involved in the trafficking of lipids, specifically the glucosamine or cyclitol ether hopanoids, in response to environmental cues. HpnN is an RND-family transporter protein shown to be essential in the transport of hopanoids from the inner to outer membrane of *R. palustris* (Doughty et al., 2011). In our previous work, deletion of the *hpnN* gene in *B. cenocepacia* did not result in increased sensitivity to growth in low pH, SDS or polymyxin B but did result in increased sensitivity to other antibiotics (Schmerk et al., 2011).

Together these results suggest that multiple transporter proteins may be involved in coordinating the trafficking of different hopanoids within the membrane of *B. cenocepacia* and likely other hopanoid producing bacteria.

**Conclusions**

In this study, we have defined the majority of the genes involved in the hopanoid biosynthetic pathway of *B. cenocepacia*. This information will illuminate future identification of the unique and specific functions that C\textsubscript{35} extended hopanoids, such as BHT cyclitol ether, play in bacterial membrane physiology. Given that BHT provides a much higher degree of membrane integrity than diploptene, it is clear that C\textsubscript{35} extended hopanoids, even in their most basic form, play a vital role in the function of the *B. cenocepacia* membrane. Identifying the genes responsible for the modification of extended hopanoids has also provided the tools needed to predict their structures based on genomic and metagenomic sequence information, and will help with the interpretation of geomicrobiological data. This work will also lead the way for future studies of functionalized hopanoids, providing insight into their specific biological functions while also allowing for a more informed interpretation of the hopanoid fossil record. Furthermore, the study of hopanoids in *B. cenocepacia* provides an opportunity to explore novel treatment options for cystic fibrosis patients infected with Bcc species.
As these species are intrinsically resistant to most clinically relevant antibiotics, the increased antibiotic sensitivity of the various hopanoid mutants raises the possibility of utilizing unique inhibitors, in combination with current antibiotic treatments, to better control infection in these patients.

**Experimental procedures**

*Bacterial strains, plasmids and growth conditions*

Bacterial strains and plasmids used in this study are listed in supplemental Table S1. Bacteria grew on LB agar plates or in LB broth with shaking at 37°C. When necessary, *Escherichia coli* cultures were supplemented with 40 µg ml⁻¹ kanamycin, and 30 µg ml⁻¹ tetracycline. *B. cenocepacia* cultures were supplemented, as needed, with 100 µg ml⁻¹ trimethoprim, and 150 µg ml⁻¹ tetracycline.

*Construction of deletion strains and complementing plasmids*

The construction of unmarked, nonpolar mutant strains was performed as previously described by Flannagan *et al.* (Flannagan et al., 2008). The deletion mutagenesis plasmids were created by cloning ~600-800-bp DNA amplicons flanking each of the putative hopanoid biosynthesis associated genes. Amplified fragments were ligated into pGPI-SceI to create the desired deletion plasmids. The mutagenic plasmids were mobilized into *B. cenocepacia* MH1K by triparental mating and cointegrants selected using 100 µg ml⁻¹ trimethoprim. Selection against *E. coli* donor and helper strains after the triparental mating was accomplished using 200 µg ml⁻¹ ampicillin in combination with 25 µg ml⁻¹ polymyxin B. The pDAI-SceI-SacB vector was used in the final stage of mutagenesis to induce the second recombination event, leading to an unmarked gene deletion. This vector was mobilized into *B. cenocepacia* MH1K cointegrants, and exconjugants were selected with 150 µg ml⁻¹ tetracycline. Colonies were screened by PCR to confirm the presence of the appropriate gene deletions.

Complementing plasmids were constructed by amplifying *hpnG* (BCAM2830), *hpnI* (BCAL1050) and *hpnJ* (BCAL1051), and *hpnK* (BCAL1052) with the appropriate primer pairs. PCR products were
cloned into pSCrhaB2, resulting in the creation of pHpnG, pHpnI, pHpnJ, and pHpnK. Complementing plasmids were introduced into the desired mutant strains by triparental mating as described above. For unknown reasons, deletion of hpnH (BCAM2739) was not possible using the method described above. To delete this gene the plasmid pDelBCAM2739 was mobilized into the non-hopanoid-producing strain MH1KΔshc (Schmerk et al., 2011), and the ΔhpnH mutant strain was then created as outlined above. To restore hopanoid production following hpnH deletion, the hpnF2 gene (BCAM2831) was introduced via the complementing plasmid pBCAM2831 (Schmerk et al., 2011).

**Analysis of hopanoids**

Lipid extracts from the wild type (MH1K) and mutant strains were prepared using the method of Welander et al. (Welander et al., 2012b). Briefly, 200 ml of stationary phase culture were harvested by centrifugation at 5000g for 10 min at 4°C. Cells were disrupted by sonication in 10 ml of 10:5:4 (v:v:v) methanol (MeOH):dichloromethane (DCM):water for 15 min. Samples were centrifuged at 3000g for 10 min, the supernatant was transferred to a new tube and the pellet was treated once more. Combined supernatants were separated into two phases via the addition of 10 ml DCM and 5 ml water followed by centrifugation at 3000g for 10 min. The organic phase was placed in a new tube and the residual aqueous phase was treated once more with 10 ml DCM and 5 ml water. Following centrifugation, the organic phases were combined and evaporated under a stream of N₂ gas and the total lipid extracts (TLE) were then dissolved in 2 ml DCM. To identify the production of the C₃₀ hopene, acetylated TLEs from each strain were analyzed by high temperature gas chromatography-mass spectrometry (GC-MS) as previously described (Welander et al., 2009). Acetylated TLEs were also analyzed by liquid chromatography-mass spectrometry (LC-MS) to identify any functionalized hopanoids (Welander et al., 2012a). Details of the chromatographic analysis can be found in the supplementary information.

**Phylogenetic analysis**
Homologs of *B. cenocepacia* HpnI and HpnJ were identified in the Kyoto Encyclopedia of Genes and Genomes (KEGG) and National Center for Biotechnology Information (NCBI) databases via TBLASTN (Altschul et al., 1997) and the top 250 sequences were aligned via clustalW2 using the Geneious R6 software version 6.1.2 (Biomatters Ltd., Auckland, New Zealand, http://www.geneious.com/). Maximum likelihood trees were constructed by PhyML (http://www.atgc-montpellier.fr/phyml/) (Guindon et al., 2010) using the LG+gamma model, six gamma rate categories, ten random starting trees, SPR+NNI branch swapping, and substitution parameters estimated from the data. The finalized trees were generated by importing the resulting PhyML tree into iTOL for editing (http://itol.embl.de/) (Letunic and Bork, 2011).

*Environmental stress tests*

Strains grew overnight with shaking in unbuffered LB medium at 37°C. Cultures were adjusted to an OD$_{600}$ 0.005 in the appropriate medium. Buffered LB medium was prepared by adding 100mM (final concentration) MES (4-morpholineethanosulfonic acid) for pH 4.0 or 100mM MOPS (4-morpholione propanesulfonic acid) for pH 7.0. Where appropriate, the pH 7.0 buffered LB medium was supplemented with 0.03% SDS (w/v) or 1 mg ml$^{-1}$ polymyxin B. Growth was determined in a 100-well disposable plate using a Bioscreen C automated microbiology growth curve analysis system (MTX Lab Systems). Growth was monitored over 24 h at 37°C.

*Acknowledgements*

We thank Florence Schubotz and Emily Matys for running the lipid samples for GC-MS and LC-MS analysis. This work was supported by grants from Cystic Fibrosis Canada (to M.A.V.) and from the Natural Sciences and Engineering Research Council of Canada (to M.A.B.). C.L.S. was supported by a postdoctoral fellowship from Cystic Fibrosis Canada. Work at MIT and Stanford was conducted with the support of awards from NSF (EAR-1147755) and the NASA Astrobiology Institute (NASA-NNA13AA90A).
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573 bacterial hopanoids by atmospheric pressure chemical ionisation liquid chromatography/ion trap mass

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593 Identification and characterization of Rhodopseudomonas palustris TIE-1 hopanoid biosynthesis

596 Hopanoids play a role in membrane integrity and pH homeostasis in Rhodopseudomonas palustris

### Table 1 Hopanoid biosynthesis genes deleted in *B. cenocepacia*

<table>
<thead>
<tr>
<th>Gene name</th>
<th>Locus Tag</th>
<th>Annotation</th>
<th>Function</th>
<th>Reference</th>
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<tr>
<td><em>hpnI</em></td>
<td>BCAL1050</td>
<td>Hopanoid-associated glycosyl transferase</td>
<td>Transfer of acetylglucosamine from UDP-acetylglucosamine to BHT</td>
<td>This study</td>
</tr>
<tr>
<td><em>hpnJ</em></td>
<td>BCAL1051</td>
<td>Hopanoid-associated radical SAM superfamily protein</td>
<td>Catalyzes ring contraction to generate BHT cyclitol ether</td>
<td>This study</td>
</tr>
<tr>
<td><em>hpnK</em></td>
<td>BCAL1052</td>
<td>Hopanoid biosynthesis associated protein (ydjC)</td>
<td>Deacetylation of BHT acetylglucosamine</td>
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<td><em>hpnL</em></td>
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<td>Conserved hypothetical protein</td>
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<td>Unassigned</td>
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<td>4-hydroxy-3-methylbut-2-enyl diphosphate reductase</td>
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<td>Hopanoid-associated radical SAM superfamily protein</td>
<td>Addition of adenosine to hopane skeleton</td>
<td>Bradley <em>et al.</em> 2010, Welander <em>et al.</em> 2012b, this study</td>
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<td>Hopanoid-associated nucleosidase</td>
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<td>Bradley <em>et al.</em> 2010, Welander <em>et al.</em> 2012b, this study</td>
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<td><em>hpnF2</em></td>
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<td>Squalene hopene cyclase</td>
<td>Cyclization of squalene</td>
<td>Reipen <em>et al.</em> 1995</td>
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<td>Cyclization of squalene</td>
<td>Reipen <em>et al.</em> 1995</td>
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<td><em>hpnE</em></td>
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<td>Putative dehydrosqualene reductase</td>
<td>Production of squalene</td>
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<td>Squalene/phytoene synthase</td>
<td>Production of squalene</td>
<td>Perzl <em>et al.</em> 1998</td>
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Genes shown in bold were deleted in this study. *Unable to construct this deletion*
Table 2. Hopanoids identified in *B. cenocepacia* K56-2 mutants

<table>
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<tr>
<th>Hopanoids</th>
<th>Bacteriohopanetetrol (BHT)</th>
<th>BHT cyclitol ether</th>
<th>Monounsaturated BHT cyclitol ether or glucosamine</th>
<th>BHT glucosamine</th>
<th>Adenosyl hopane</th>
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<td>1000</td>
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<td><strong>Base Peak</strong>:</td>
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Identification of these hopanoids in the following strains:

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<th>ΔhpnF2 (BCAM2831)</th>
<th>ΔhpnF3 (BCAS0167)</th>
<th>ΔhpnG (BACM2739)</th>
<th>ΔhpnH (BCAM2739)</th>
<th>ΔhpnI (BCAL1050)</th>
<th>ΔhpnJ (BCAL1051)</th>
<th>ΔhpnK (BCAL1052)</th>
<th>ΔhpnL (BCAL1053)</th>
<th>ΔBCAM2736 (BCAM2831)</th>
<th>ΔhpnM (BCAM2827)</th>
<th>ΔhpnN (BCAM2828)</th>
<th>ΔhpnO (smpA/omlA)</th>
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Table 3 Summary of resistance of hopanoid mutants to various environmental stresses

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<tr>
<th>Hopanoid side chain biosynthesis</th>
<th>Resistance to low pH stress</th>
<th>Resistance to SDS</th>
<th>Resistance to polymyxin B</th>
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<tr>
<td>ΔhpnH (BCAM2739)</td>
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<td>ΔhpnI (BCAL1050 )</td>
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Figures Legends

**Figure 1** (a) Hopanoid compounds detected in *B. cenocepacia* K56-2 lipid extracts at stationary phase. The dotted rectangle contains the structures for C-6 and C-11 monounsaturated BHT cyclitol ethers; however, the mass spectra could not distinguish whether the BHT cyclitol ether or the BHT glucosamine is unsaturated and whether the unsaturation occurs at C-6 or C-11 ring positions. (b) The *B. cenocepacia* hopanoid biosynthetic gene clusters are present on chromosome 1, chromosome 2, and chromosome 3. Black arrows indicate genes that have been deleted in this study, white arrows indicate genes that were not deleted, and gray arrows indicate genes that were deleted in a previous study (Schmerk et al. 2011).

**Figure 2** Proposed *B. cenocepacia* hopanoid biosynthesis pathway. Dotted arrows in step 8 represent a proposed desaturation reaction.

**Figure 3** LC-MS extracted ion chromatograms of acetylated total lipid extracts from (a) wild type *B. cenocepacia*, (b) ΔhpnI, (c) ΔhpnK, and (d) ΔhpnJ. The chromatograms are a combination of ions m/z 1002 (I, BHT cyclitol ether and II, BHT glucosamine), 655 (III, bacteriohopanetetrol), and 1000 (IV, monounsaturated BHT cyclitol ether or glucosamine). Hopanoids were identified by comparison of their mass spectra to previously published samples (Talbot et al., 2007a; Talbot et al., 2007b; Talbot et al., 2003a; Talbot et al., 2003b).

**Figure 4** Maximum likelihood phylogenetic tree of hopanoid associated glycosyl transferase, HpnI, among sequenced genomes. The *Methylobacterium* spp. and *Burkholderia* spp. (highlighted in red) clades have been collapsed due to the high number of strains present. Some *Burkholderia* species possess 2 copies of HpnI however *B. cenocepacia* strains contain only 1 copy (found in the blue highlighted clade). All organisms present contain at least one copy of shc in their genome.

**Figure 5** Maximum likelihood phylogenetic tree of hopanoid biosynthesis associated radical SAM protein, HpnJ. The *Methylobacterium* spp., *Cupriavidus* spp., and *Burkholderia* spp. (highlighted in red) clades have been collapsed due to the high number of strains present. With the exception of the collapsed outgroup clades, all organisms contain one or more copies of squalene hopene cyclase in their genome.

**Figure 6** A *B. cenocepacia* ΔhpnH mutant exhibits sensitivity to environmental stresses. Representative growth curves of the wild type (MH1K) and mutant strain in LB buffered to pH 7.0 or pH 4, LB buffered to pH 7.0 supplemented with 0.03% SDS, and LB supplemented with 1 mg ml⁻¹ polymyxin B. Δshc is included as a control that cannot produce any hopanoids. All control strains contain the empty complementing vector pSCRhaB2. The ΔhpnH mutant had to be created in a Δshc mutant background and contains pBCAM2831 to restore hopanoid biosynthesis. Each time point represents the average of three replicate cultures (the error bars represent standard deviations). Each growth curve was repeated at least three times.

**Figure 7** Mutants involved in the biosynthesis of C₃₅ extended hopanoid side chains display a range of sensitivity to environmental stresses. Representative growth curves of the wild type and mutant strains in LB buffered to pH 7.0, LB buffered to pH 4, LB buffered to pH 7.0 and supplemented with 0.03% SDS, and LB with 1 mg ml⁻¹ polymyxin B. Each time point represents the average of three replicate cultures (the error bars represent standard deviations). Each growth curve was repeated at least three times.

Supporting information

**Supporting Information A. Hopanoids analyses**

**Table S1.** Bacterial strain sand plasmids used in this study.
Table S2. Primers used in this study.

Figure S1 Identification of squalene build-up in squalene-hopene cyclase gene deletion mutants.
Non-saponifiable lipids were extracted from the B. cenocepacia ΔhpnF2 strain and separated by GC.
(a) Total ion chromatogram was compared to that of a squalene standard. (b) Full mass spectrum of
the co-eluting peaks from panel (a). The Δshc mutant (lacking both the hpnF2 and hpnF3 genes)
accumulated an identical peak as in (a) (data not shown).

Figure S2. Mass spectra of functionalized hopanoids produced by wild type B. cenocepacia and
hopanoid mutants. The top row contains the mass spectra of the hopanoid illustrated above. The
bottom row shows the MS-MS spectra of the indicated ion. The unsaturated hopanoid could be either
the cyclitol ether or glucosamine hopanoid; it is unclear from the mass spectra which functionalized
hopanoid is unsaturated and where the unsaturation occurs (C-6 or C-11).

Figure S3. LC-MS and GC-MS analysis of B. cenocepacia ΔhpnH acetylated total lipid extract.
(a) LC-MS combined extracted ion chromatogram (m/z 611, 655, 1000, 1002) demonstrating the lack
of functionalized hopanoid production. (b) GC-MS extracted ion chromatogram (m/z 191)
demonstrating the production of diploptene.

Figure S4. LC-MS analysis of B. cenocepacia ΔhpnG acetyalted total lipid extract. (a) Combined
extracted ion chromatogram (m/z 611, 655, 1000, 1002) demonstrating the single adenosyl hopane
peak at 29 minutes. (b) Mass spectra of the adenosyl hopane peak showing the 788 ion representing
intact adenosyl hopane and the 611 ion representing the loss of an adenine molecule.

Figure S5. Complementation of the hopanoid side chain biosynthesis growth defects.
Representative growth curves of the wild type (MH1K), mutant, and complement strains in LB
buffered to pH 7.0, LB buffered to pH 4.0, LB buffered to pH 7.0 and supplemented with 0.03% SDS,
and LB with 1 mg ml⁻¹ polymyxin B. Δshc is included as a control that cannot produce any hopanoids.
All control and mutant strains contain the empty complementing vector pSCRhaB2. Each time point
represents the average of three replicate cultures (the error bars represent standard deviations). Each
growth curve was repeated at least three times.

Figure S6. Mutants that are not directly involved in the biosynthesis of hopanoid side chains display
an array of sensitivity to different environmental stresses. Representative growth curves of the wild
type and mutant strains in LB buffered to pH 7.0, LB buffered to pH 4.0, LB buffered to pH 7.0 and
supplemented with 0.03% SDS, and LB with 1 mg ml⁻¹ polymyxin B. Each time point represents the
average of three replicate cultures (the error bars represent standard deviations). Each growth curve
was repeated at least three times.