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Ring-hydroxylating dioxygenases involved in PAH biodegradation : structure, function, biodiversity

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Abstract

The first step in the biodegradation of PAHs by aerobic bacteria is catalyzed by metalloenzymes known as ring-hydroxylating dioxygenases (RHDs). Because of the hydrophobic nature and chemical resistance of PAHs, their initial attack by RHDs is a difficult reaction, which is critical to the whole degradation process. This chapter gives an overview of the current knowledge on the genetics, structure, catalytic mechanism and diversity of RHDs involved in PAH degradation. In the past decade, the crystal structures of 10 RHDs have been determined, giving insights into the mechanism of substrate recognition and regioselectivity of dioxygenation. The reaction catalyzed by the archetypal naphthalene dioxygenase has been investigated in detail, thus providing a better understanding of the RHD catalytic mechanism. Studies on the catabolic genes responsible for PAH degradation in several bacterial taxa have highlighted the great phylogenetic diversity of RHDs. The implementation of culture-independent methods has afforded means to further explore the environmental diversity of PAH-degrading bacteria and RHDs. Recent advances in this field now allow the *in situ* identification of bacteria responsible for pollutant removal. Further biotechnological developments based on microarrays and functional metagenomics should lead to the conception of molecular tools useful for the bioremediation of PAH-contaminated ecosystems.

Introduction

In the biodegradation of numerous aromatic hydrocarbons including polycyclic aromatic hydrocarbons (PAHs) by aerobic microorganisms, oxygenases play a central role. Most common oxygenases are either heme-containing cytochromes P450 that catalyze single hydroxylations, or dioxygenases that incorporate both oxygen atoms of the O_2 molecule into the substrate. Dioxygenases are metalloenzymes that generally contain non-heme iron at the active site and fall into two categories: ring-hydroxylating dioxygenases (RHDs), which catalyze a double hydroxylation on two adjacent carbons of the substrate, and ring-cleaving dioxygenases, which catalyze the opening of the ring of catecholic substrates (Harayama et al., 1992). RHDs are multicomponent enzymes (E.C.1.14.12.-) consisting of an oxygenase associated with one or two specific electron carriers. They utilize NAD(P)H as a reductant and transfer electrons to the active site for activation of dioxygen, a prerequisite to substrate hydroxylation. In most cases, the oxygenase component is hexameric ($\alpha_3\beta_3$), with each alpha subunit containing a Rieske-type [2Fe-2S] cluster and a mononuclear iron center where the dioxygenation reaction takes place. RHDs are widely distributed in various taxa among Gram positive and Gram negative bacteria. To date, over 1300 RHDs have been identified on the basis of sequence similarities and have been compiled in the NCBI databases. Current knowledge, based on well-studied enzymes such as naphthalene dioxygenase, indicates that RHDs have relatively broad substrate specificities.

This chapter will focus primarily on RHDs involved in PAH degradation with special emphasis on enzyme systems that have been described in the last decade. RHDs from representative PAH-degrading bacteria isolated so far are compared on the basis of their genetic organization, sequence relatedness, and substrate specificity. Aspects related to the structure and catalytic mechanism of RHDs are only briefly discussed, but reviews on these topics have been published recently (Ferraro et al., 2005; Kovaleva and Lipscomb, 2008). A section is devoted to recent studies exploring the biodiversity of PAH-degrading bacteria and associated RHDs in various terrestrial and aquatic environments using culture-independent methods. Finally, we present a brief outlook on the possible strategies to improve PAH bioremediation through bioengineering of RHDs. For general aspects of PAH degradation or RHD biocatalysis that are not covered in this chapter, the reader is referred to recently published reviews (Doyle et al., 2008; Habe and Omori, 2003; Parales and Resnick, 2006; Peng et al., 2008).

General properties and classification

Ring-hydroxylating dioxygenases, also called Rieske non-heme iron oxygenases are multicomponent enzymes generally consisting of a catalytic component with hydroxylase activity, associated with one or two electron carrier proteins. In most cases, the hydroxylase component is itself composed of two subunits, an alpha subunit of about 50 kDa and a beta subunit of around 20 kDa, which assemble in an $\alpha_3\beta_3$ heterohexamer. However, the hydroxylase component of carbazole dioxygenase contains only alpha subunits (Sato et al., 1997). Each alpha subunit consists of two domains, the N-terminal Rieske domain, which contains a [2Fe-2S] cluster, and the C-terminal catalytic domain, which contains a mononuclear ferrous ion close to the substrate-binding site. The catalytic component needs electrons in order to activate oxygen at each cycle of hydroxylation of the substrate. Two auxiliary proteins, a ferredoxin and a flavin-containing oxidoreductase, usually provide the necessary reductant at the expense of NAD(P)H oxidation. Sometimes, the two proteins are fused in a single polypeptide chain, as is the case for benzoate dioxygenase (Karlsson et al., 2002) and anthranilate dioxygenase (Eby et al., 2001).

RHDs share common structural features, including quaternary structure and conserved residues in the Rieske and catalytic domains of the alpha subunit that are involved in binding of the metal centers (see below). However, they differ considerably in terms of amino acid sequence and with respect to the structure of the associated electron carriers. Almost twenty years ago, Batie et al. proposed a classification of dioxygenases based on the number of associated electron carriers and the nature of their redox centers (Batie et al., 1992). Three classes of RHDs were defined, comprising two-component enzyme systems such as the phthalate dioxygenase from *Burkholderia cepacia* (Correll et al., 1992) (class I), three-component enzymes containing an FAD-containing reductase and a [2Fe-2S] ferredoxin, as exemplified by the biphenyl dioxygenase (Furusawa et al., 2004) (class II), and three-component enzymes in which the reductase contains both a FAD and a [2Fe-2S] cluster, as represented by the naphthalene dioxygenase (Kauppi et al., 1998) (class III). Later, new RHDs were identified and characterized, some of which did not fit into this classification system. This was the case for the carbazole dioxygenase from *Pseudomonas* sp. CA10 (Sato et al., 1997) and for three-component enzymes in which the ferredoxin contains a [3Fe-4S] cluster instead of the more common [2Fe-2S] cluster (Martin and Mohn, 1999; Takagi et al., 2005). Nam et al. therefore proposed an alternative classification system based on amino acid sequence similarities between the alpha subunits of hydroxylase components (Nam et al.,

2001). RHDs were then organized into four families of proteins according to phylogenetic criteria, each family corresponding to types of enzyme with similar substrate specificities. For example, type II enzymes are represented by benzoate/toluate dioxygenases, type III enzymes by naphthalene and PAH dioxygenases, and type IV enzymes by biphenyl and toluene dioxygenases. Type I enzymes have in common the presence of a hydroxylase composed of alpha subunits only, and show greater disparity than the other familiies in terms of amino acid sequences and substrate range. An advantage of this classification system lies in the possibility to classify any new oxygenase sequence derived from a nucleotide sequence, even though the associated electron carriers are unknown. Such a situation is encountered in bacterial genomes where catabolic genes are dispersed, and especially when genes encoding hydroxylase component do not lie close to the genes encoding electron carriers. This is frequently the case in PAH-degrading bacteria such as *Mycobacteria* and *Sphingomonadaceae* (see below). Recently, a more sophisticated classification system has been proposed, which takes into account the sequences of associated electron carriers in the phylogenetic analysis of RHDs (Kweon et al., 2008). In addition to the 4 subclasses of RHDs described by Nam et al., a new group was defined comprising enzymes found in Gram-positive PAH-degrading bacteria (Kim et al., 2006; Krivobok et al., 2003; Saito et al., 2000). A distinctive feature of these Type V RHDs is that their associated ferredoxin contains a [3Fe-4S] cluster, in contrast to type III PAH dioxygenases from Gram-negative bacteria, which use [2Fe-2S] ferredoxins. A phylogenetic tree based on alignments of α subunit sequences of representative RHDs is shown in Fig. 1.

Figure 1

Genetics and diversity of RHDs involved in PAH degradation

Genetics and diversity of RHDs in Gram-negative bacteria

Genes responsible for PAH degradation were first studied in *Pseudomonas* strains isolated on naphthalene as carbon source. Naphthalene degradation genes are generally clustered in two closely linked operons carried on a specific plasmid, as initially reported for the NAH7 plasmid of *P. putida* G7 (Yen and Gunsalus, 1982; Yen and Serdar, 1988). The upper operon contains genes coding for the naphthalene dioxygenase (*nahAaAbAcAd*) as well as genes specifying the enzymes catalyzing six additional oxidation steps to produce salicylate (*nahABFCQED*). The lower operon also called the *sal* operon, (*nahGTHINLOMKJ*) encodes

the enzymes required to convert salicylate to Krebs cycle intermediates. Between the two operons and oriented in the opposite direction lies the *nahR* gene encoding a LysR-type transcriptional regulator, which controls the expression of both operons (Schell, 1985; Tropel and van der Meer, 2004). The NahR regulator activates transcription by binding to specific sequences in the promoter regions of the two *nah* operon and within its own promoter (autoregulation), in a manner dependent on the presence of salicylate. The organization of the naphthalene degradation genes and their nucleotide sequence was found to be very similar in other *Pseudomonas* strains, including NCIB 9816-4 (Simon et al., 1993) and *P. stutzeri* (Bosch et al., 1999; Bosch et al., 2000).

In *Comamonas testosteroni* strains isolated on phenanthrene, the genes encoding the initial dioxygenase did not hybridize with the *nahA* probes, indicating that their sequences diverge significantly from that of counterparts found in *Pseudomonas* strains (Goyal and Zylstra, 1996). The organization of the phenanthrene catabolic genes (*phd*) was similar to that observed in *Pseudomonas*, except that a gene encoding a dihydrodiol dehydrogenase (*phdB*) was inserted between the genes encoding phenanthrene dioxygenase (Goyal and Zylstra, 1997) (Fig. 2). A remarkably similar organization was found in the gene cluster responsible for phenanthrene degradation in *Alcaligenes faecalis* AKF2 (Kiyohara et al., 1982). However, the latter strain degrades phenanthrene via the o-phthalic acid pathway found in Gram positive bacteria, whereas *C. testosteroni* strains utilize the salicylate pathway, like Pseudomonads.

Figure 2

A recently isolated phenanthrene degrader identified as an *Acidovorax* strain (NA3) was shown to contain a catabolic cluster highly similar to that found in strain AKF2 (Singleton et al., 2009). The alpha subunit of strain NA3 phenanthrene dioxygenase exhibited the highest amino acid sequence identity with counterparts from AFK2 and *Burkholderia* strains. On the basis of transcriptional analysis by real-time qPCR, the phenanthrene degradation genes were found to be highly expressed in cells exposed to phenanthrene or naphthalene, but were not expressed in the presence of other PAHs.

The phenanthrene degrader *Burkholderia* sp. strain RP007 contains a cluster of genes similar in sequence to those found in strain AKF2 but showing an arrangement different from that described in the two strains above (Laurie and Lloyd-Jones, 1999) (Fig. 2). The catabolic cluster *phnRSFECDAcAdB* contains 9 genes including the *phnAcAd* coding for the hydroxylase component of phenanthrene dioxygenase but lacks the genes specifying

associated electron carriers. Sequence analysis suggested that PhnR and PhnS are transcriptional regulators, the latter being of the LysR-type, similar to NahR.

In *Ralstonia* sp. strain U2, isolated on naphthalene, the catabolic genes also form a tight cluster *nagAaGHAbAcAdBFCQED* in which two genes, *nagGH,* appear to be inserted between the *nagAa-d* genes encoding the naphthalene dioxygenase (Fuenmayor et al., 1998). In contrast to the previously discussed PAH degraders, strain U2 does not convert salicylate into catechol but into gentisate thanks to a salicylate 5-dioxygenase coded by the *nagGH* genes (Zhou et al., 2001). The *nag* genes are positively regulated via NagR, a regulator very similar to NahR, which is also activated by salicylate (Jones et al., 2003).

Another naphthalene degrader, called *Polaromonas naphthalenivorans* CJ2, also exhibited a degradation pathway involving gentisate as an intermediate. The cluster of *nag* genes of CJ2 is very similar in organization and sequences to that found in *Ralstonia* U2 (Jeon et al., 2006). These genes are controlled, at the transcriptional level, by the regulator NagR1, which functions in a salicylate-dependent manner as mentioned above. Contrary to strain U2, strain CJ2 lacks the *nagY, nagM* and *nagN* genes, one of which encodes a chemotaxis protein. Moreover, strain CJ2 contains another set of genes responsible for the complete degradation of gentisate, which is regulated by NagR2 another type of regulator that is not activated by salicylate nor by naphthalene.

Bacteria belonging to the genus *Cycloclasticus* are thought to play a major role in the degradation of PAHs in marine environments (Kasai et al., 2002). In *Cycloclasticus* strain A5, which is able to grow on naphthalene, methylnaphthalenes and phenanthrene, the *phnA1A2* genes encoding the dioxygenase and the *phnA3A4* encoding a ferredoxin and a reductase are part of a 10.5-kb gene cluster (Kasai et al., 2003) (Fig. 2). The dioxygenase of strain A5 showed moderate sequence homology with those from other PAH degraders, the closely related enzymes being dioxygenases from Sphingomonads (60% and 52% identities at best for the α and β subunits of the hydroxylase, respectively).

Sphingomonads

The genus *Sphingomonas* initially designated a group of bacteria known for their ability to degrade a wide range of organic pollutants, including dibenzo-*p*-dioxin and dibenzofuran (Armengaud et al., 1998), pesticides (Kumari et al., 2002) and PAHs (Leys et al., 2004). This taxonomic group has been split into new genera called *Sphingobium, Novosphingobium, Sphingopyxis* in 2001 (Takeuchi et al., 2001). Genetic analyses of PAH-degrading strains showed that catabolic genes had a unique organization where genes involved in polyaromatic

degradation were interspersed with *xyl* genes responsible for monoaromatic degradation (Fig. 3) (Kim and Zylstra, 1999; Pinyakong et al., 2003a; Romine et al., 1999). In *Novosphingobium aromaticivorans* F199, 79 genes thought to associated with the metabolism or transport of aromatic hydrocarbons are carried on a 184-kb plasmid called pNL1 (Romine et al., 1999). As many as six gene pairs possibly encoding the α and β subunits of distinct hydroxylases were identified on pNL1, but their specific function was unknown (Fig. 3). In *Sphingomonas* CHY-1, a strain able to grow on chrysene (Willison, 2004), the pair of genes encoding the initial PAH dioxygenase has been identified and genetic evidence showed that this dioxygenase was the only enzyme required to catalyze the primary oxidation of PAHs (Demaneche et al., 2004). The cluster of catabolic genes in strain F199 and in related strains, contain a single copy each of a gene encoding a ferredoxin and a gene encoding a reductase, located more than 20 kb apart. This observation suggested that the multiple terminal hydroxylases coded by the catabolic cluster shared the same electron carriers. Consistent with this idea, it was found that the initial PAH dioxygenase from strain CHY-1, called PhnI, and another hydroxylase coded by $phnA1_bA2_b$ (PhnII), utilized the same electron carriers (Demaneche et al., 2004; Jouanneau et al., 2007).

Figure 3

The PhnII enzyme, which shares many structural features with classical three-componennt dioxygenases, has been characterized as a salicylate 1-hydroxylase that converts salicylate and several substituted derivates of salicylate to catecholic products (Jouanneau et al., 2007). This enzyme substitutes for the monomeric salicylate hydroxylases found in Pseudomonads although the two types of enzymes are phylogenetically unrelated. The three-component enzyme from *Sphingomonas* CHY-1 also differs from the monomeric type in that it is inactive on 1-hydroxy-2-naphthoate, and therefore does not participate in the degradation pathway of 3-ring PAHs such as phenanthrene or anthracene. In *Sphingobium* P2, it was found that three of the multiple hydroxylases encoded by the catabolic cluster were salicylate hydroxylases analogous to PhnII (Pinyakong et al., 2003b).

Salicylate 5-hydroxylase from *Ralstonia* U2 and anthranilate dioxygenase from *Burkholderia cepacia* DBO1 (Chang et al., 2003) are phylogentically related to three component salicylate hydroxylases with which they form a distinct subgroup among RHDs (Fig. 1).

Sphingomonas macrogolitabida TFA has been studied for its ability to utilize tetralin (1,2,3,4-tetrahydronaphthalene) as a carbon source. The *thn* genes responsible for this degradation are clustered in two separate and divergently transcribed operons (Moreno-Ruiz et al., 2003). The *thnA1A2* genes encoding the catalytic component of the initial dioxygenase are located in the

main operon, whereas the *thnA3A4* genes coding for the associated electron carriers are part of the other operon. The oxygenase component of this enzyme appeared to be distantly related to PAH dioxygenases from Gram-negative bacteria (Fig. 1).

The dioxin dioxygenase from *Sphingomonas* RW1, which catalyzes an angular attack on dibenzo-*p*-dioxin and dibenzofuran, is encoded by genes dispersed in the genome (Armengaud et al., 1998). In the main locus, the *dxnA1A2* genes encoding the hydroxylase component are associated with *dxnB*, which encodes a ring-cleavage dioxygenase that catalyzes the next degradation step. The genes encoding the associated ferredoxin and reductase components are located in two distant and separate loci. The deduced amino acid sequence of the terminal dioxygenase showed weak homology with counterparts from other bacteria, the closest relatives being biphenyl dioxygenases (Armengaud et al., 1998).

Genetics and diversity of RHDs in Gram-positive bacteria

Gram-positive bacteria able to degrade PAHs fall into two categories, those which can attack fluorene, dibenzofuran and similar substrates by angular dioxygenation, including *Terrabacter* and *Rhodococcus* strains, and those which can utilize phenanthrene and 4-ring PAHs, including *Nocardioides* and *Mycobacterium* strains.

In the first category, *Terrabacter* sp. strain DBF63 is one of the best-studied dibenzofuran and fluorene degraders. The initial attack on these compounds is catalyzed by an angular dioxygenase, the catalytic component of which is encoded by *dbfA1A2* (Habe et al., 2004; Habe et al., 2003). These genes are part of a large cluster including the *flnBdbfA1A2flnEflnD1D2flnC* operon and genes involved in phthalate degradation. A gene (*dbfA3*) was later identified downstream from *dbfA1A2*, which encodes a [3Fe-4S] ferredoxin able to serve as electron donor to the hydroxylase component of the dioxygenase (Takagi et al., 2005). The initial dioxygenase catalyzes two types of reaction on fluorene, first a single hydroxylation on the carbon in C9 position to yield 9-fluorenol, then an angular dihydroxylation to give 1,1a-dihydroxy-1-hydro-9-fluorenone. This compound is then converted by FlnB to 2'-carboxy-2,3-dihydroxybiphenyl, which is further transformed to phthalate in two steps catalyzed by FlnD1D2 and FlnC. Genes homologous to *dbfA1A2* were identified in other Gram-positive dibenzofuran degraders, including *Terrabacter* sp. strain YK3 (Iida et al., 2002), various *Rhodococcus* strains (Aly et al., 2008), but also in two *Sphingomonas* strains able to metabolize carbazole (Shintani et al., 2007) and fluorene (Schuler et al., 2008). In *Terrabacter* YK3 and *Rhodococcus* YK2, the genes responsible for dibenzofuran degradation, including the *dfdA1A2A3A4* coding for the angular dioxygenase,

are carried on a plasmid (Iida et al., 2002). Recently, the *dfd* genes were found to be regulated by a new type of regulator (DfdR) that activates transcription in response to the presence of dibenzofuran or a few other hydrophobic hydrocarbons (Iida et al., 2009b). In *Rhodococcus* HA01, two inducible angular dioxygenases encoded by *DfdA1A2A3A4* and *DbfA1A2*, have been described (Aly et al., 2008). The first set of genes was highly similar to that found in *Terrabacter* YK3, whereas the second set was closely related to that coding for dibenzofuran dioxygenase from strain DBF63. The two enzymes, which appeared to be simultaneously expressed in strain HA01, exhibited complementary activities towards chlorinated substrates, with DfdA1A2 performing the angular dioxygenation of 3-chlorodibenzofuran and DbfA1A2 transforming 2-chlorodibenzofuran.

Two *Sphingomonas* strains were found to degrade fluorene through a degradation pathway similar to that described in *Terrabacter*, suggesting an initial attack by angular dioxygenation. In *Sphingomonas* sp. LB126, the operon responsible for fluorene degradation exhibited a gene organization similar to that found in strain DBF63, but the gene products were only distantly related, as exemplified by the α and β subunits of the dioxygenase, which showed 63 and 52 % sequence identities with DbfA1 and DbfA2, respectively (Schuler et al., 2008). The oxygenase from strain LB126 converted fluorene to 9-fluorenol and subsequently to the angular dihydrodiol product like the DBF63 enzyme. It also transformed dibenzofuran and attacked other 2- and 3-ring PAHs, fluorene and phenanthrene being the preferred substrates (Schuler et al., 2008).

The marine strain *Nocardioides* sp. KP7 was one of the first PAH-degrading Gram-positive bacterium to be genetically characterized (Saito et al., 1999; Saito et al., 2000). The genes responsible for the oxidative breakdown of phenanthrene to phthalate were found to be different in terms of organization and sequence from what had been previously reported in Gram-negative bacteria (Fig. 2). The main cluster *phdEFABGHCD* contained the genes coding for the α and β subunits of phenanthrene dioxygenase (*phdAB*), preceded by genes encoding a dihydrodiol dehydrogenase (*phdE*) and an extradiol dioxygenase (*phdF*). The four genes located downstream specified an aldolase-hydratase (*phdG*), an aldehyde dehydrogenase (*phdH*), a ferredoxin (*phdC*) and a reductase (*phdD*), the latter two gene products being the electron carriers specifically associated with phenanthrene dioxygenase. Altogether, the enzymes coded by this cluster catalyzed five oxidation steps to convert phenanthrene to 1-hydroxy 2-naphthoate. The latter intermediate was further metabolized to phthalate by three enzymes coded by the *phdIJK* gene cluster located about 6-kb apart (Saito

et al., 2000). The dioxygenase from strain KP7 was the first member of a new subclass of enzymes essentially found in *Mycobacterium* and *Rhodococcus* strains, forming a distinctive phylogenetic group (Fig. 1) and featuring a [3Fe-4S] ferredoxin as typical electron carrier.

Several members of the genus *Mycobacterium* have been studied for their ability to degrade high molecular weight PAHs, including pyrene and fluoranthene (Heitkamp et al., 1988; Khan et al., 2001; Krivobok et al., 2003; Schneider et al., 1996; Sho et al., 2004; Stingley et al., 2004; Vila et al., 2001). The genes encoding what appeared to be the hydroxylase component of a pyrene dioxygenase were first described in *M. vanbaalenii* PYR-1, and designated *nidBA* (*nid* for *n*aphthalene *ind*uced) (Khan et al., 2001). Analysis of protein profiles by 2D gel electrophoresis indicated that six proteins were induced by pyrene and phenanthrene, one of which was the alpha subunit of the dioxygenase (NidA). In another pyrene degrader, called *Mycobacterium* 6PY1, a thorough proteomic analysis of pyrene- and phenanthrene-induced polypeptides identified 23 proteins, four of which were subunits of two dioxygenase terminal components named Pdo1 and Pdo2 (Krivobok et al., 2003). The other induced proteins showed significant similarities with enzymes previously implicated in phenanthrene metabolism in *Nocardioides* KP7. The genes encoding Pdo1 and Pdo2 were located in two separate loci, and no genes encoding possibly associated electron carriers were found in either locus. Nevertheless, the two dioxygenases could be successfully expressed in *E. coli* and their activity was enhanced by co-expressing the PhdC and PhdD electron carriers from strain KP7. Amino acid sequence comparison indicated that Pdo1 was highly similar to the pyrene dioxygenase from strain PYR-1, whereas Pdo2 was related to the phenanthrene dioxygenase from strain KP7 (Krivobok et al., 2003). Other *Mycobacterium* strains able to degrade pyrene or fluoranthene were found to express RHDs homologous to Pdo1 or Pdo2 in a regulated manner (Liang et al., 2006; Pagnout et al., 2007; Sho et al., 2004). More recently, Kim et al. assigned a gene product to nearly all steps of the pyrene degradation pathway in strain PYR-1 based on a detailed analysis involving exhaustive genomic and proteomic data, (Kim et al., 2007). However, some of the proposed gene functions remain hypothetical and need to be assessed experimentally. The PAH catabolic genes are part of a large cluster extending over 150 kb and encoding multiple terminal components of oxygenases (Kim et al., 2008). Although many of these oxygenases have still unknown functions, at least four of them have been assigned a catalytic role, including a phenanthrene dioxygenase homologous to Pdo2 from 6PY1, a phthalate dioxygenase encoded by *phtAaAb,* another PAH dioxygenase encoded by *nidA3B3*, and the pyrene dioxygenase discussed above (*nidBA*). The NidA3B3

terminal oxygenase showed a preference for fluoranthene (Kim et al., 2006) and was expressed to a relatively high level in *M. vanbaalenii* PYR-1 when grown on this PAH as substrate (Kweon et al., 2007). The entire cluster contains only two electron carrier genes closely linked to *phtAaAb*, *phtAc* encoding a [3Fe-4S] ferredoxin and *phtAd* encoding a reductase, suggesting that the multiple hydroxylases specified by the catabolic cluster share the same electron carriers, a situation similar to that encountered in Sphingomonads. Interestingly, the genomes of four other PAH-degrading *Mycobacterium* strains, including *M. gilvum* strain PYR-GCK (NC009338), *Mycobacterium* sp. KMS (NC008705), MCS (NC008146) and JLS (NC009077) appeared to contain a catabolic cluster very similar in gene sequence and organization to that found in strain PYR-1, except that a large portion of the cluster was duplicated on the chromosome (strain PYR-GCK) or on plasmids (strains MCS and KMS).

The naphthalene degrader *Rhodococcus* sp. strain NCIMB12038 contains a RHD whose hydroxylase component showed little sequence similarities with naphthalene dioxygenases from Pseudomonads but significant homology with the Gram-positive RHDs described above (Larkin et al., 1999).

The catalytic mechanism of RHDs : the example of naphthalene dioxygenase from *Pseudomonas* sp. NCBI 9816-4

Chemically speaking, the initial oxygenation of the aromatic ring is the most difficult catalytic step in the aerobic degradation of PAHs. Bacterial RHDs catalyze the incorporation of the two atoms of molecular oxygen into one of the highly stable aromatic ring, thus allowing further breakdown of the substrate molecule by subsequent dehydrogenation and ring cleavage. The mechanism of the reaction catalyzed by RHDs has been studied in detail with the naphthalene dioxygenase from *P. putida* as model enzyme, taking advantage of the crystal structure of the terminal oxygenase component, which was determined in 1998 (Kauppi et al., 1998). The dihydroxylation of naphthalene occurs at the enzyme active site, which is a ferrous ion bound to the alpha subunit through the side chains of two His and one Asp residues. The reaction involves reduction and cleavage of molecular oxygen, and insertion of the oxygen atoms on the C1 and C2 carbon atoms of the substrate to yield *cis-(1R,2S)*-dihydroxy-1,2-dihydronaphthalene. Although the reductase and ferredoxin components are required for continuous catalytic turnover of the enzyme, it has been

demonstrated that the hydroxylase component alone can catalyze the dioxygenation of naphthalene in single turnover experiments (Wolfe et al., 2001). As isolated, the oxygenase component is unreactive with oxygen. However, upon stoichiometric reduction of the Rieske cluster, naphthalene and oxygen react with the hydroxylase to form the dihydrodiol product. Stopped-flow analyses and spectroscopic measurements indicated that product formation was concomitant with the oxidation of the Rieske and mononuclear iron centers. Moreover, it was found that the oxygenase component could convert naphthalene to dihydrodiol in the presence of hydrogen peroxide, a reaction that stopped after one turnover with the product trapped in the active site (Wolfe and Lipscomb, 2003). This reaction, known as the peroxide shunt, suggested that the normal catalytic cycle of the dioxygenase involves a peroxo intermediate, and that the release of the product requires reduction of the mononuclear iron center. Altogether, the results obtained with naphthalene dioxygenase led Wolfe et al. to propose a mechanism for the reaction cycle of RHDs (Wolfe and Lipscomb, 2003). In this scheme, the oxygenase component is reduced first, then binds sequentially the substrate and O_2 to form an Fe(III)-hydroperoxo intermediate. The exact nature of the reactive species generating the dihydrodiol product is still unknown, but it seems likely that the release of the reaction product requires another reduction step to regenerate the ferrous state of the mononuclear center. Using phthalate dioxygenase as a model, other authors found that this scheme did not fit their data because single turnover reactions yielded one half the expected amount of product and ended with the active site in the ferrous state (Tarasev and Ballou, 2005). It has been proposed that the catalytic cycle of phthalate dioxygenase required the participation of the reductase component to deliver one electron equivalent per cycle.

The occurrence of a hydroperoxo intermediate in the reaction cycle has been substantiated by the discovery that oxygen binds side-on at the active site of naphthalene dioxygenase and by the structural description of a ternary complex of the oxygenase component with O_2 and indole (Karlsson et al., 2003). The particular binding mode of oxygen on the active site iron and the rigorous positioning of the substrate would afford a mechanism whereby both atoms of O_2 react in concert with the substrate to form the dihydrodiol. However, it is still uncertain whether it is an Fe(III)-hydroperoxo or an Fe(V)-oxo-hydroxo reactive species that eventually attacks the substrate to yield the dihydrodiol product (Kovaleva and Lipscomb, 2008).

Comparison of available structures of RHD catalytic components

The catalytic component of the naphthalene dioxygenase from *Pseudomonas* sp. strain

NCIB9816-4 (NDO) was the first enzyme to be structurally characterized (Kauppi et al., 1998). Since then, nine crystal structures from other dioxygenase systems have been reported (Ferraro et al., 2005), including three enzymes able to attack PAHs, namely the oxygenases from *Rhodococcus* NCIMB12038 (Gakhar et al., 2005), *Sphingobium yanoikuyae* B1 (Ferraro et al., 2007) and *Sphingomonas* CHY-1 (Jakoncic et al., 2007a; Jakoncic et al., 2007b). All enzymes exhibit an $\alpha_3\beta_3$ quaternary structure, except for the carbazole oxygenase from *P. resinovorans* CA10 (Nojiri et al., 2005)and the oxoquinoline 8-monooxygenase from *P. putida* strain 86 (Martins et al., 2005), which are homotrimers consisting of alpha subunits only. The following discussion will be focused on enzymes implicated in PAH degradation.

All $\alpha_3\beta_3$ oxygenases exhibit a mushroom-like overall structure similar to that reported for NDO, with the trimer of alpha subunits sitting on a base consisting of the beta subunits. The alpha/beta pairs of subunits have almost identical folds and are arranged around a threefold axis of symmetry. The alpha subunits are composed of two domains, the N-terminal Rieske domain that contains the [2Fe-2S] cluster and the catalytic domain containing the substrate binding site and the mononuclear iron center. The fold of the Rieske domain is similar to that found in the cytochrome bc_1 complex of the respiratory chain. The cluster is bound to the protein through four conserved ligand residues, two cysteines and two histidines. In the catalytic domain, the iron atom is coordinated by two histidines and one aspartate (as a bidentate) and one water molecule. The last position of coordination (axial) is occupied by the side chain oxygen atom of a conserved asparagine residue but the O-Fe distance is > 3.75 Å. The distance between the Rieske center and the mononuclear iron is about 44 Å within the same alpha subunit. The Rieske center is however much closer to the iron center of the neighboring subunit (12 Å), indicating that electron transfer occurs via the metal centers of two adjacent alpha subunits. In addition, these two metal centers are connected through a hydrogen bond network involving a conserved aspartate residue (Asp205 in NDO). This residue binds a histidine ligand of the iron center (His208) and a histidine ligand of the Rieske cluster (His104), thus forming a plausible bridge for electron transfer (Kauppi et al., 1998). The essential role of the Asp205 residue was demonstrated in experiments where its replacement through site-directed mutagenesis resulted in a total loss of enzyme activity (Parales et al., 1999). Its role in electron transfer between the metal centers is, however, controversial. A study using anthranilate dioxygenase and variants carrying substitutions of the conserved Asp residue concluded that this residue rather served to maintain the protonation state and reduction potential of the Rieske cluster (Beharry et al., 2003).

The substrate-binding site appears as a hydrophobic pocket open to the solvent on one side and ending at the iron center on the other. Seventeen residues lining and shaping the substrate binding site have been identified in NDO (Carredano et al., 2000), three of which are strictly conserved, including the two histidine ligands of the ferrous iron (His208 and His213 in NDO) and the Asp205 residue discussed above. Other semi-conserved residues include Asn201, which is replaced by a glutamine in the biphenyl dioxygenase from *Rhodococcus* RHA1, and Phe202, Gly251 and Phe358, which are replaced by other residues only in trimeric (α_3) oxygenases. Differences observed in the active site residues among dioxygenases might explain in part differences in substrate specificity (Ferraro et al., 2005). Indeed, interactions between substrates and active site residues are believed to control the orientation of the substrate relative to the ferrous center and eventually the regio- and enantio-selectivity of the catalytic reaction.

Although the nitrobenzene dioxygenase (NBDO) acts chiefly on monoaromatic substrates, its structure is remarkably similar to that of NDO (Friemann et al., 2005). Only five differences were observed in the residues lining the substrate-binding site. The crystal structure of NBDO in complex with nitrobenzene showed that nitrobenzene is maintained in the correct position for catalysis through hydrogen bonding between the nitro group of the substrate and a specific Asn residue (Asn258). Replacement by this residue by a valine (the analogous residue in NDO) changed the regio-selectivity of the reaction with 2-nitrotoluene, yielding 2-nitro benzyl alcohols rather than catechol (Ferraro et al., 2005).

The oxygenase from strain NCIMB12038 is structurally similar to NDO although the two enzymes share only 30 % sequence identity. Moreover, indole was found to bind to the active site of the enzyme in the same position as that described for the NDO-indole complex (Gakhar et al., 2005), although a few differences were observed in the residues lining the active site.

The crystal structure of the broad-substrate-range dioxygenase from *Sphingomonas* CHY-1 (Jakoncic et al., 2007b) and that of the highly similar biphenyl dioxygenase from *Sphingobium yanoikuyae* B1 (Ferraro et al., 2007) were published almost at the same time. The following description concerns the former enzyme.

The RHD from strain CHY-1 is unique in that it can oxidize a very large panel of PAHs ranging from naphthalene to the 5-ring benzo[a]pyrene (Jouanneau et al., 2006). The catalytic component, called PhnI, exhibits a folding pattern very similar to that of NDO, the α carbon chains of the two proteins being superimposable within a 1.2 Å root-mean square deviation. However, PhnI features the largest substrate-binding pocket ever reported for a RHD (Fig. 4).

This 12-Å long hydrophobic cavity extends from the iron center on one side to the solvent on the other. The entrance of the cavity is delimited by two flexible loops, which might control the access of the substrates to the active site. Compared to NDO, two leucine residues on loop L1 (Leu223 and Leu226) are moved towards the solvent, thus elongating the catalytic pocket by at least 2 Å (Jakoncic et al., 2007a). Conserved residues line the part of the cavity proximal to the iron center, whereas Phe350, Leu356 and Phe404 shape the central and distal parts. Molecular modeling indicated that the substrate binding cavity was large enough to accommodate the 5-ring substrate benzo[a]pyrene with minor changes in the positions of lining residues (Fig 4). The predicted position of this substrate suggested a hydroxylation of carbons C9 and C10 (Jakoncic et al., 2007a), which is consistent with the position of the hydroxyls on the experimentally obtained dihydrodiol (Jouanneau et al., 2006). Further modeling experiments gave plausible positions for other substrates, such as phenanthrene end benz(a)anthracene, in the substrate binding pocket, which were also in good agreement with the regioselectivity of the hydroxylation reactions. This suggested that the large size and the particular topology of the substrate-binding site of PhnI were the main determinants of its broad substrate specificity.

Fig. 4

Carbazole dioxygenase is a singular RHD in that it catalyzes angular hydroxylation and because its catalytic component is made up of alpha subunits only. The crystal structure of the trimeric protein exhibits a doughnut-like shape in which interactions between specific loops of adjacent alpha subunits stabilize the trimer (Nojiri et al., 2005). The fold of the alpha subunit is roughly similar to that in the $\alpha_3\beta_3$ NDO structure, although the two proteins share only 17% sequence identity. The substrate-binding site differs from that of other RHDs in that the distal part of the hydrophobic pocket is lined by rather polar residues. Docking simulation of carbazole in the substrate-binding site indicated that, in the predicted position, the carbon C1 and C9a of carbazole were the carbon atoms closest to the iron center, consistent with an angular dioxygenation reaction. Carbazole dioxygenase is the only RHD system for which the structure of a binary complex between the oxygenase and the ferredoxin components has been solved (Ashikawa et al., 2006). In the complex, three ferredoxin molecules were bound at the intersubunit boundary of the trimeric oxygenase, each protein-protein interaction involving a combination of electrostatic, hydrophobic and hydrogen bonds between specific residues of the two partners. Protein interactions and conformational changed brought the Rieske clusters of each partner to a distance of around 12 Å suitable for electron transfer. The ferredoxin binding site has been described as a depression on the surface of the oxygenase trimer at the

interface of adjacent alpha subunits. A similar depression has been observed between the alpha and beta subunits of NDO, suggesting that it might be the binding site for the ferredoxin in this hexameric oxygenase (Ashikawa et al., 2006). Analysis of a ternary complex between the oxygenase and ferredoxin components and carbazole showed that upon binding of the substrate, conformational changes resulted in the closure of a lid over it, as if it were trapped in the substrate binding pocket.

Substrate specificity of RHDs with respect to PAHs

RHDs are generally endowed with relaxed substrate specificity, thus allowing bacteria to initiate the degradation of a wide range of aromatic hydrocarbons. In addition, they are remarkable catalysts in that they can perform several types of oxidation reaction, including *cis*-dihydroxylation, monooxygenation, desaturation and sulfoxidation. The impressive range of oxidative reactions catalyzed by naphthalene dioxygenase has been reviewed by Resnick et alnd Gibson (Resnick and Gibson, 1996). Many of the reactions catalyzed by RHDs, especially the generation of various *cis*-dihydroarenediols, might be exploited in the synthesis of products useful in chemistry and medicine (Hudlicky et al., 1999).

Despite the fact that RHDs can attack a wide range of substrates, most of them are only active on a limited number of the 16 priority PAHs, essentially those comprising 2 or 3 rings. Some RHDs, like carbazole dioxygenase, specialize in the angular *cis*-dihydroxylation of tricyclic substrates containing one heterocycle. At the other extreme, a few RHDs able to oxidize 4- and 5-ring PAHs have been described, mainly in strains belonging to the Sphingomonads or the *Mycobacterium* genus, and quite different substrate specificities have been observed. Here, the discussion has been focused on the catalytic abilities of the latter category of RHDs as well as on angular dioxygenases.

Angular dioxygenases

The carbazole dioxygenase from *Pseudomonas resinovorans* CA10 can perform angular dioxygenation of several carbazole-like compounds, including dibenzofuran, dibenzo-*p*-dioxin, as well as regular *cis*-dihydroxylation on a variety of 2- and 3-ring substrates such as naphthalene and biphenyl. It can also transform dibenzothiophene to the corresponding sulfoxide and fluorene to 9-fluorenol (Nojiri et al., 1999). Studies on variants of the CA10 RHD obtained by site-directed mutagenesis indicated that three residues lining the substrate-

binding pocket were important for controlling angular *cis*-dihydroxylation (Uchimura et al., 2008). The dibenzofuran dioxygenase from *Terrabacter* DBF63 showed similar substrate specificity except that it could not transform carbazole (Kasuga et al., 2001). The RHD from the fluorene degrader *Sphingomonas* LB126 exhibited a broader substrate range since it proved capable of angular dioxygenation on fluorene and on the three tricyclic substrates mentioned above. In addition, the LB126 RHD could transform phenanthrene and anthracene but generated unusual dihydrodiol products, i.e. *cis*-9,10-dihydro-9,10-dihydroxy-phenanthrene for the former and a compound tentatively identified as 2,3-dihydro-2,3-dihydroxyanthracene for the latter (Schuler et al., 2008). These compounds are considered by-products that cannot be further degraded through the main catabolic pathway of PAH degraders. They might arise from incorrect positioning of the substrates in the enzyme active site.

Regular dioxygenases

Naphthalene dioxygenase from *P. putida* sp. strain 9816-4 converts indole to indigo (Ensley et al., 1983) and dihydroxylates biphenyl and PAHs up to three rings with high regio- and enantioselectivity (Parales et al., 2000; Resnick et al., 1996). Studies of variants obtained by site-directed mutagenesis indicated that the enzyme could tolerate single amino acid substitutions near the active site with only minor changes to its specificity (Parales et al., 2000). However, replacement of Phe352 by smaller amino acids resulted in variants with altered regioselectivity. While the wild-type enzyme converted biphenyl to the *cis*-2,3-dihydrodiol with minor amounts of the *cis*-3,4-dihydrodiol, all the variants tested produced a large excess of the 3,4-isomer. Likewise, phenanthrene was mainly hydroxylated in the 3,4 positions by the wild-type enzyme, whereas mutant enzymes produced more of the 1,2-dihydrodiol. The enantioselectivity of the reaction was also altered (Parales et al., 2000). Interestingly, replacement of the phenylalanine residue equivalent to NDO Phe352 by smaller residues in other RHDs, including biphenyl dioxygenase (Suenaga et al., 2002) and tetrachlorobenzene dioxygenase (Pollmann et al., 2003), resulted in significant alterations of oxygenase specificity. The important role of the Phe352 residue in NDO has been studied from a structural point of view by elucidating the 3D structure of a F352V variant, either alone or as a complex with substrates (Ferraro et al., 2006). This variant exhibited a broader substrate-binding pocket, allowing phenanthrene to bind in a different position than in the wild-type enzyme in which the C1 and C2 carbons are close to the mononuclear iron center. These results are consistent with previous enzyme assays showing that this variant mainly

generated *cis*-1,2-dihydroxy-1,2-dihydrophenanthrene rather than the 3,4-dihydrodiol. They also provide a structural basis for the notion that the orientation of the substrate binding at the active site is the primary determinant of the regio- and stereoselectivity of RHD-catalyzed oxygenation reactions.

Besides NDO from strain NCIB 9816-4, only a few RHDs have been studied for their ability to utilize PAHs as substrates. In addition, most published data have been obtained with *E. coli* strains producing recombinant RHDs using various expression systems, thus precluding meaningful comparisons of activities towards PAHs. The RHD from *Sphingomonas* CHY-1 exhibits one of the broadest substrate ranges ever reported, since it is able to attack 9 of the 16 priority PAHs. Also, it is one of the rare cases where the catalytic activity towards each PAH was measured using the purified enzyme, thus allowing the kinetic parameters and the stoichiometry of the dioxygenase reaction to be determined (Jouanneau et al., 2006). The dioxygenase activity was maximal with naphthalene and declined as a function of the substrate ring number, to reach 2% of the maximum with benzo[a]pyrene. With naphthalene as substrate, the CHY-1 dioxygenase exhibited an apparent k_{cat} of 1.82 ± 0.03 s^{-1} and a specificity constant of 2.0 ± 0.3 μM^{-1} s^{-1}. These values are comparable to those reported for biphenyl dioxygenase (k_{cat} = 7.0 ± 0.2 s^{-1}, specificity constant of 1.2 μM^{-1} s^{-1}; (Imbeault et al., 2000)) and 2-nitrotoluene dioxygenase (k_{cat} = 2.4 s^{-1} ; (Parales et al., 2005)) and indicate that RHDs are intrinsically slow enzymes. Most PAHs were converted to a single dihydrodiol, except for fluorene, fluoranthene and benz[a]anthracene, which yielded up to three diols (Jouanneau et al., 2006). The four-ring benz[a]anthracene was transformed to three dihydrodiol isomers bearing hydroxyls in positions 1,2- , 8,9- , and 10,11-. The 1,2- and 10,11-dihydrodiols were found to be substrates of the enzyme and were converted in a subsequent reaction to a *bis*-*cis*-dihydrodiol hydroxylated on carbon positions 1,2,10 and 11. It was observed that the coupling between substrate oxidation and O_2 (and NADH) utilization varied depending on PAHs and decreased with substrate size. Uncoupling was associated with a release of hydrogen peroxide, which might be toxic for the cells if such a side reaction also occurs in vivo. Hence, the unproductive NADH oxidation that was associated mainly to 4- and 5-ring PAH oxidation might in part explain the slow metabolism and poor yields observed during bacterial growth on such PAHs.

The RHD from *Sphingobium yanoikuyae* B1 exhibits 91-93% amino acid sequence identity with its counterpart from strain CHY-1, and yet displays significant differences in substrate specificity (Chadhain et al., 2007). The purified B1 RHD apparently utilizes biphenyl as its preferred substrate and was therefore referred to as a biphenyl dioxygenase (Yu et al., 2007),

although it falls into the subgroup of PAH RHDs (from Gram-negative bacteria) based on phylogenetic analysis (Fig. 1) and on its substrate specificity. Like the CHY-1 RHD, the B1 enzyme was also shown to dihydroxylate naphthalene, phenanthrene and benzo[a]pyrene, the latter two substrates yielding 2 dihydrodiol isomers instead of one (Yu et al., 2007). Previous studies using a mutant strain derived from strain B1 indicated that the same RHD was capable of converting chrysene (Boyd et al., 1997) and benz[a]anthracene (Gibson et al., 1975), the latter substrate giving three dihydrodiols just like the CHY-1 RHD.

The phenanthrene degrader *Sphinogomonas* LH128 produces an RHD exhibiting 78% (α subunit) and 63% (β subunit) identities with the CHY-1 enzyme (Schuler et al., 2009). Its substrate range was found to be similar, with a marked preference for naphthalene. Nevertheless, the LH128 RHD was less competent in the dioxygenation of large PAHs than the CHY-1 enzyme, as it failed to transform benzo[a]pyrene.

The differences in substrate specificity between the three related enzymes above may be tentatively interpreted in structural terms, based on the crystallographic data known for two of them. The substrate-binding pocket is almost identical in all three enzymes as judged from the conservation of the residues lining this cavity. Two conservative changes are however observed in the B1 enzyme (Ile replaces Val202 and Leu replaces Ile260). Much more variation can be noticed in the sequences of the two loops located at the entrance of the active site, which are thought to control substrate access (Jakoncic et al., 2007b). Differences in substrate specificity might also be due to changes of resides more distant from the active site. This notion is supported by studies regarding biphenyl dioxygenases in which three specific regions of the alpha subunit have been shown to determine the selectivity of enzymes towards PCBs (Furukawa et al., 2004).

The RHD from *Cycloclasticus* A5, which is distantly related to the PAH dioxygenases from Sphingomonads, exhibits a markedly different selectivity. Based on biotransformation assays using a recombinant *E. coli* strain overexpressing this RHD, it was found that the enzyme was able to oxidize biphenyl, naphthalene, phenanthrene and methylnaphthalenes, but it failed to transform anthracene and larger PAHs (Kasai et al., 2003).

The RHD from the acenaphthene degrader *Sphingomonas* sp. strain A4 was found to oxidize acenaphthylene, naphthalene, phenanthrene, anthracene and fluoranthene, although strain A4 could not grow on the latter four hydrocarbons (Pinyakong et al., 2004). Unlike RHDs from other Sphingomonadaceae, the A4 enzyme is related, although distantly, to RHDs from betaproteobacteria, the phenanthrene dioxygenase from *Burkholderia* RP007 being the closest homologue (56% identity).

Gram-positive bacteria belonging to the *Mycobacterium* genus were found to degrade a range of PAHs up to 5 rings in a process likely involving multiple RHDs since several such enzymes were expressed in PAH-grown cells (see section 2 above) . In *M. vanbaalenii* PYR-1, two RHDs encoded by *nidBA* and *nidA3B3* have been shown to dihydroxylate the 4-ring PAHs pyrene and fluoranthene, respectively (Khan et al., 2001; Kim et al., 2006). Based on biotransformation assays, NidA3B3 was also found to attack several 2- to 4-ring PAHs including naphthalene, phenanthrene, anthracene and pyrene but preferentially transformed fluoranthene, consistent with the finding that this enzyme was maximally induced in cells grown with that PAH as sole substrate. In *Mycobacterium* 6PY1, two RHDs with markedly different PAH specificities have been studied: the Pdo1enzyme preferentially attacked pyrene but also converted phenanthrene to two dihydrodiols bearing hydroxyls in position 3,4-, and 9,10-, whereas the Pdo2 enzyme only dihydroxylated 2- and 3-ring PAHs, phenanthrene being the best substrate (Krivobok et al., 2003). All data reported so far on the PAH selectivity of *Mycobacterium* RHDs were from biotransformation assays using *E. coli* recombinant systems in which dioxygenases were generally poorly expressed. In addition, the associated electron carriers being unknown, oxygenase components were expressed alone or in combination with heterologous electron carriers, thus resulting in non-optimal and probably underestimated enzyme activities. Recently, the Pdo1 and Pdo2 oxygenase components from strain 6PY1 were obtained in highly active soluble forms in *E. coli* using non-commercial expression systems (Krivobok, Meyer and Jouanneau, unpublished work). Moreover, two genes designated *phtAc* and *phtAd* encoding a [3Fe-4S] ferredoxin and a reductase, respectively, were cloned from the *Mycobacterium* 6PY1 genome and successfully co-expressed with the oxygenase components. The co-expression of these electron carriers resulted in a 8-fold (Pdo1) or 2-fold (Pdo2) enhancement of the enzyme activity in biotransformation assays (unpublished results). Pdo1 appeared as a unique RHD in that it could utilize 3- and some 4-ring PAHs as substrates, including phenanthrene, anthracene, fluoranthene and pyrene but was unable to hydroxylate smaller substrates like naphthalene and biphenyl. Confronted with the problem of poor expression of RHDs from Gram-positive actinomycetes in *E. coli*, Pagnout et al. utilized *Mycobacterium smegmatis* as host for overproducing a RHD from the PAH-degrader *Mycobacterium* SNP11 (Pagnout et al., 2007). In this expression system, the SNP11 RHD, which is very similar to Pdo2 (>98% sequence identity), efficiently oxidized phenanthrene and anthracene but also fluorene and fluoranthene. More recently, an expression system involving a *Rhodococcus* strain as host for

studying recombinant RHDs has been developed. Interestingly, three RHDs expressed in this system exhibited different regio-specificities and relative preference towards dibenzofurans and chlorinated dioxins compared to the enzymes produced in *E. coli* (Iida et al., 2009). Hopefully, convenient expression systems for overproduction of Actinobacterial RHDs in highly active form will emerge, thus allowing purification and further characterization of these enzymes, which show PAH selectivities quite different from those of their Gram-negative counterparts.

Exploring the natural biodiversity of RHD involved in PAH degradation

Early studies on the biodiversity of PAH-degrading bacteria relied on microbial culture and selection on defined growth media as a means to isolate strains with the desired traits. This approach appeared inappropriate when it was realized that a large majority of the bacterial species present in the environment (>90%) were not culturable under standard laboratory growth conditions. Various culture-independent methods were then developed to study microbial diversity, most of which were based on DNA extraction from environmental samples followed by PCR-amplification of selected molecular markers i.e. genes (or gene regions) encoding the 16S ribosomal RNA subunit (see (Kirk et al., 2004) for review). Bacterial species identification and classification based on sequence analysis of 16S rRNA genes recovered from the environment is now the most commonly used method to probe biodiversity, although some pitfalls and biases due to PCR must be taken into consideration (Wintzingerode et al., 1997). In the last decade, studies targeting a specific population of bacteria in complex environment such as soils have emerged, due to the implementation of new techniques involving *in situ* labeling of a population of interest with a naturally rare stable isotope and subsequent isolation and analysis of the labeled DNA. This approach known as stable isotope probing (SIP) has been used recently to identify PAH degraders in soils or sediments (Jeon et al., 2003; Singleton et al., 2005). Besides, the diversity of RHDs in soils has been assessed directly by PCR amplification and sequence analysis of relevant gene portions recovered from environmental samples (Yeates et al., 2000). Here, the contribution of recent studies to our understanding of the biodiversity of PAH-degraders and associated RHDs is discussed.

Relative abundance and diversity of known PAH degraders in the environment

Since Sphingomonadaceae are very often found on PAH-polluted sites, their diversity has been investigated by PCR-based analysis of 16S rRNA genes using family-specific primers (Leys et al., 2004). Sequence analysis revealed that most 16S rRNA genes were significantly different from those of known isolates, suggesting that species different from those studied so far are present in PAH-contaminated soils. A similar study was conducted to examine the community composition of fast-growing *Mycobacterium* in various contaminated soils (Leys et al., 2005). Species identified included known PAH degraders such as *M. austroafricanum* and *M. frederiksbergense* but also *M. tusciae*, a species not previously reported to degrade PAHs.

In marine environment, classical isolation of PAH-degraders from contaminated sediment in the Gulf of Mexico led to 23 strains which all belonged to the *Cycloclasticus* genus (Geiselbrecht et al., 1998). Several culture-independent studies conducted all around the world showed that bacterial communities involved in PAH degradation in coastal and estuarine sediments were actually dominated by *Cycloclasticus* in all marine environments tested (Kasai et al., 2002; McKew et al., 2007; Niepceron et al., 2010; Zhou et al., 2009). Members belonging to this genus were also found to be most abundant in sediment of the deep ocean (Cui et al., 2008). On the other hand, in a coastal environment heavily impacted by oil spill, members of the classes Alphaproteobacteria (Sphingomonadaceae) and Actinobacteria (*Mycobacterium, Rhodococcus*) were found to prevail (Alonso-Gutierrez et al., 2009).

Direct analysis of the RHD biodiversity through PCR-based approaches

In recent studies, RHD biodiversity in PAH-contaminated marine environments was investigated by PCR-based analysis of a portion of the dioxygenase alpha subunit gene. *Cycloclasticus*-like RHD genes appeared to be well represented in coastal sediments from Patagonia (Lozada et al., 2008), consistent with the dominance of this genus in such habitats. Seven other RHD gene types were detected, five of which were distantly related to RHD sequences from known bacteria and two of them clustered with *nahAc*-like (*Pseudomonas*) and *phnAc*-like (*A. faecalis* AFK2) genes. On this other hand, RHDs similar to those found in Pseudomonads (*nahAc*) and beta proteobacteria (*nagAc, pahAc*) were mostly detected in marine microbial mats subjected to an oil contamination (Bordenave et al., 2008). In mangrove sediments, RHD genes similar to those found in Actinobacteria and in Sphingomonads were detected by PCR in bacterial isolates recovered from these habitats (Zhou et al., 2006).

Differences in the observed biodiversity of RHDs in PAH-polluted sites might reflect the natural variability of microbial communities in geographically distant sites. On the other hand, differences might also be due to the PCR-based methods used for amplification of the RHD genes. The genes encoding the α subunits of RHDs are highly variable in sequence (see Fig. 1) and various sets of degenerate primers have been used to amplify different gene regions (Bordenave et al., 2008; Lozada et al., 2008; Ni Chadhain et al., 2006). None of the proposed primer sets has the potential to amplify all types of RHD genes and biases in the PCR-based approaches are therefore to be expected. Nevertheless, one can use primer sets specific for a defined group of RHDs, for instance those found in Gram-positive PAH degraders. Analysis of subantartic marine sediments using a PCR-based approach with primers targeting Gram-positive RHDs led to the identification of 14 groups of genes, most of which were related to dioxygenases genes found in *Mycobacterium, Rhodococcus*, *Nocardioides* and *Terrabacter* (Marcos et al., 2009). As a means to detect a wide range of RHD genes without compromising specificity, Ni Chadain et al. designed generic primers to amplify a small PCR product encoding a relatively conserved region of the α subunit around the Rieske-cluster binding site (Ni Chadhain et al., 2006). Although the primers were successfully tested against DNA from various isolated bacteria, PCR products obtained from environmental samples were essentially related to RHDs from Gram-negative bacteria. No product could be attributed to Actinobacteria RHD while this bacterial group represented a significant part of the microbial diversity as determined from 16S rRNA genotyping. Another drawback of this approach was the limited information gained from the sequences of the short PCR products representing only about 6% of the α subunit gene length. Yet, this study was one of the first to combine the analysis of rRNA profiles and RHD profiles, providing useful information for assessing the bioremediation potential of a contaminated soil. In another study, a similar PCR-based approach was used to examine the RHD diversity of a coal tar contaminated aquifer in relation with the naphthalene degradation potential (Yagi and Madsen, 2009). Results indicated a broad diversity dominated by *nagAc*-type genes, the relative abundance of which fluctuated substantially over a 9-month as determined by quantitative PCR. Good agreement was observed between in field gene expression as monitored by *nagAc* specific mRNA and the naphthalene degradation potential in the aquifer.

As a means to determine the occurrence or relative abundance of specific RHD genes in a given soil or sediment, methods based on quantitative PCR have been developed using

specific primers (Baldwin et al., 2003; Cebron et al., 2008; DeBruyn et al., 2007; Park and Crowley, 2006). Due to the sequence divergence between RHDs from Gram-positive and Gram-negative bacteria, Cebron et al. designed one set of primers for each RHD category. The primer sets were used for quantification of RHD genes in soil by Real Time qPCR. Data could be normalized relative to the 16S rRNA gene copy number, thus allowing an estimation of the PAH degrader population of up to 1% of the whole bacterial community (Cebron et al., 2008). RHD gene enumeration by qPCR was used as a means to monitor biodegradation activity during treatment of a BTEX contaminated site. Fluctuations in the RHD levels detected were correlated with dynamic changes of the microbial population as a function of oxygen availability (Nebe et al., 2009).

The presence of RHDs genes as revealed by PCR amplification in a given environmental sample does not prove that the corresponding enzymes are expressed *in situ*. In order to identify RHDs that are expressed *in situ*, one approach consists of analyzing specific transcripts by RT-PCR using bulk RNA extracted from environmental samples. For example, transcripts of *nahAc*-like genes corresponding to 28 gene sequences potentially coding for naphthalene dioxygenases were detected in groundwater from a coal tar contaminated site (Wilson et al., 1999). More recently, real-time PCR of RHD transcripts and microarrays were employed to monitor changes in the diversity and degradation potential of high Arctic soil bacteria upon hydrocarbon pollution (Yergeau et al., 2009).

Identification of PAH-degraders in situ *by stable isotope probing*

Even though DNA or RNA-based molecular methods to investigate the microbial biodiversity of polluted sites have made significant progresses especially during the last decade, it is still a challenge to identify those bacterial species that are most active at removing pollutants *in situ*. In order to meet this challenge, one of the best experimental approach employed so far, called stable isotope probing (SIP), was first described 10 years ago (Radajewski et al., 2000). The method involves incorporation of a rare stable isotope, most often ^{13}C or ^{15}N, into the biological material of a subpopulation of microorganisms that can metabolize the organic compounds of interest, here the PAHs. For this purpose, a fully labeled organic compound is incubated with the microbial population of an environmental sample to allow selective incorporation of the isotope in targeted bacteria. Subsequent isolation of bulk DNA or RNA from the environmental sample, followed by separation and recovery of labeled nucleic acids by density centrifugation on cesium salt gradient, allows analysis of labeled biomarkers (i.e. rRNA gene sequences) and identification of relevant target bacteria (Dumont and Murrell,

2005; Kreuzer-Martin and Jarman, 2007; Neufeld et al., 2007). Using a field-based SIP strategy to track naphthalene degraders on a coal tar contaminated site, Jeon et al. found out that bacteria most active on the dicyclic hydrocarbon belonged to the class of beta proteobacteria (Jeon et al., 2003). The dominant naphthalene degrader was isolated and identified as a previously undescribed *Polaromonas* strain, host of a RHD related to that found in *Comamonas* strains. This study brought clear evidence that the bacteria having a major role in pollutant removal *in situ* had nothing to do with the great majority of naphthalene degraders studied so far, mainly Pseudomonads derived from classical microbiological selection and cultivation methods.

In a SIP study targeting naphthalene- and phenanthrene-degrading bacteria in a bioreactor treating PAH-contaminated soil, Singleton et al. observed that the bacterial groups detected differed depending on the PAH-substrate used as probe (Singleton et al., 2005). Bacteria selected on naphthalene primarily belonged to the *Pseudomonas* and *Ralstonia* genera, whereas those selected on phenanthrene were dominated by *Acidovorax*. The same authors examined the diversity of pyrene-degrading bacteria from the microbial community of a similar bioreactor (Singleton et al., 2006). The primary species identified based on 16S rRNA genotyping were uncultivated members of the beta and gamma classes of proteobacteria. In a later study also using ^{13}C-pyrene as a probe, relevant degraders were tracked in creosote-polluted soil under static conditions or under agitation (Jones et al., 2008). Although pyrene mineralization was stimulated by agitation, the dominant bacterial degraders identified based on 16S rRNA sequences under either conditions were very similar. The rRNA gene sequences obtained were closely related to those of uncultured gamma proteobacteria, and were also remarkably similar to those previously found as dominant in a slurry bioreactor (Singleton et al., 2006). None of the sequences matched that of Actinobacteria rRNA, although members of this class, especially fast-growing *Mycobacteria*, are the most studied, cultivated group of pyrene-degrading bacteria.

SIP techniques eliminate the need for growth outside the natural microenvironment, thereby reducing bias associated with growth in artificial media and permitting the exploration of the vast majority of uncultured bacteria present in natural or contaminated environments. It is also a suitable approach for studying changes in the composition of the subpopulation of degraders as a function of contaminant concentration or availability, although such investigations are still rare. In this respect, we have recently initiated an analysis of the biodiversity of PAH degraders in the soil of a wetland station collecting road runoff. Using ^{13}C-phenanthrene as a probe, we observed that the population of PAH degraders changed

dramatically as a function of phenanthrene availability (F. Martin and Y. Jouanneau, unpublished). Possible limitations to the SIP approach are the uncertainties linked to carbon cross-feeding; that is the incorporation of stable isotope into the biomass of trophically related bacteria, through uptake of labeled metabolites or scavenging of labeled biomass. DeRito et al. showed that ^{13}C-labeled biomass from primary phenol-degraders could be used by other soil bacteria (DeRito et al., 2005). However, cross-feeding can be avoided by reducing the incubation of microbial populations with the labeled substrate to a time shorter than that required for its complete mineralization, which can be monitored by $^{13}CO_2$ respirometry (Padmanabhan et al., 2003).

Beyond the advantage of straightforward rRNA-based identification of bacteria responsible for pollutant degradation, the selective labeling of DNA *in situ* offers the possibility of PCR based analysis of any functional gene involved in the degradation. In this respect, the diversity of RHDs involved in PAH degradation might be explored by PCR amplification of relevant portion of the genes.

Strategies for improving PAH bioremediation based on current knowledge on RHDs

From the current knowledge of their catalytic properties, RHDs appear as rather slow enzymes with limited activity towards large polycyclic hydrocarbons. Most studied enzymes cannot oxidize PAHs composed of more than three aromatic rings, and even RHDs displaying a broader substrate specificity, such as the *Sphingomonas* CHY-1 RHD, are poorly efficient in the oxidation of 4- and 5-ring substrates (Jouanneau et al., 2006). Given that RHDs catalyze a critical step in PAH degradation, which can limit substrate processing through the downstream catabolic pathway, strategies based on genetic engineering to improve enzyme activity or expand substrate specificity might be implemented to enhance bioremediation, especially with respect to recalcitrant 4- and 5-ring PAHs. So far, bioengineering studies were essentially focused on biphenyl dioxygenases in attempts to improve the biodegradation of polychlorobiphenyls (PCb) (Barriault et al., 2002; Furukawa, 2000; Furukawa et al., 2004). Such studies aimed at improving the substrate specificity and catalytic efficiency of biphenyl dioxygenases towards PCB are reviewed in detail in another chapter of this book. Generally, the most successful approach employed to improve the catalytic activity of dioxygenases relied on directed molecular evolution involving DNA shuffling of the gene of interest according to Stemmer (Stemmer, 1994). In the case of RHDs, only the gene encoding the α subunit of the catalytic component has been the target of DNA shuffling, since this subunit

contains the active site and the substrate-binding pocket, which determines specificity. In an interesting development of this technique, Vezina et al. amplified partial sequences of the *bphA* gene encoding the dioxygenase alpha subunit from soil DNA and used them in shuffling experiments to improve the activity of biphenyl dioxygenase toward 2,2'-substituted PCB, thus taking advantage of the catalytic biodiversity available in soil for engineering new enzymes (Vezina et al., 2007).

The naphthalene dioxygenase from *Ralstonia* strain U2 was engineered to oxidize nitroaromatic compounds (Keenan et al., 2005). Saturation mutagenesis of the residue F350 in the alpha subunit of the enzyme led to the isolation of a variant with acquired dioxygenase activity towards dinitrotoluenes. Additional mutagenesis through DNA shuffling identified two other residues that influenced the regiospecificity of the enzyme and allowed the generation of variant with three substitutions, which exhibited enhanced activity towards dinitrotoluenes. As another option to expand the range of substrates oxidized by a given bacterium, it has been proposed to co-express in a single cell catalytic components of dioxygenases sharing the same electron carriers. An *E. coli* strain carrying two such recombinant oxygenases could simultaneously oxidize naphthalene and dinitrotoluene (Keenan and Wood, 2006).

In techniques such as DNA shuffling, large mutant libraries are generated, and the selection of enzymes with the desired activity requires the implementation of efficient screening strategies (Tee and Schwaneberg, 2007). For biphenyl dioxygenases, screening is based on the detection of a yellow product generated from biphenyl or PCBs by two enzymes that are co-expressed with the RHD in recombinant cells, which convert the biphenyl dihydrodiol to a colored cleavage product. A similar strategy might not be applicable for PAH dioxygenases, because the cleavage product obtained from the first ring cleavage of PAHs is not easy to detect. Hence, the selection of RHDs with higher activity towards PAHs, especially 4- and 5-ring hydrocarbons, through DNA shuffling would require another high throughput assay for measuring the activity of recombinant RHDs. In this respect, Joern et al. have developed a solid-phase screen for the detection of dioxygenase activity in recombinant clones (Joern et al., 2001). In the assay, the dihydrodiol produced by the dioxygenase reaction is indirectly measured after chemical or enzymatic conversion to an oxidation product that reacts with Gibbs reagent to form a blue complex. After screening 9000 clones using this procedure, a variant of toluene dioxygenase was selected with an activity twice as high as that of the wild-type enzyme (Joern et al., 2001). In practice, we found that the method is laborious, not very sensitive and inadequate for the detection of highly unstable dihydroxylated PAH such as 1,2-

dihydroxyanthracene. As an alternative, we recently developed an assay based on the direct fluorescence detection of the dihydrodiols formed, which has been adapted to the microplate format. Although the assay is limited to PAH yielding dihydrodiols with high enough intrinsic fluorescence (anthracene, chrysene, pyrene, benzo[a]pyrene), preliminary results suggest that it is suitable for the screening of RHDs with activity towards 4- and 5-ring PAHs (Jouanneau, unpublished).

Conclusions and perspectives

Over the last decade, considerable progress in our understanding of RHD catalytic function has been achieved thanks to detailed structural analyses of representative oxygenase components through X-ray crystallography. The regio- and stereo-selectivity of RHDs can be easily explained from studies on enzyme-substrate complexes showing the critical role of the substrate-binding pocket in the positioning of the substrate relative to the active-site iron atom. The size and topology of the substrate-binding site are certainly important factors in controlling enzyme specificity, but the structural determinants responsible for substrate recognition are still largely unknown. This is an important issue in the context of PAH biodegradation, because the most genotoxic 4- and 5-ring hydrocarbons are poor substrates for most RHDs. Taking advantage of the accumulated structural information on RHDs, one can try to improve RHD catalytic efficiency or enlarge substrate range toward recalcitrant PAHs by employing bioengineering strategies based on rational design or directed molecular evolution. Such strategies, especially those involving DNA shuffling, have been successfully implemented to improve the substrate range of biphenyl dioxygenases towards PCBs (Furukawa, 2000; Furukawa et al., 2004). Hence, provided that efficient screening systems are developed to select for enzymes with desired characters, significant improvements in the performances of PAH oxidizing RHDs may be expected from future bioengineering studies, especially those based on molecular directed evolution.

In recent years, new tools have emerged to explore the biodiversity of highly complex microbial populations in their environmental habitats. In particular, it becomes possible to identify bacteria that are most active in the degradation of pollutants *in situ* without the need to cultivate and isolate them. In the case of PAH polluted sites, the use of approaches such as stable isotope probing led to the discovery that the dominant PAH degraders were different from the bacterial species that had previously been isolated and studied under standard laboratory conditions. This observation is consistent with the general assumption that >90%

of bacterial species present in the environment are unknown, uncultured microorganisms. Consequently, knowledge derived from PAH degraders studied so far need to be revisited by focusing on species that play a major role in pollutant removal *in situ*. In this respect, it will be necessary to develop novel cultivation conditions and isolation procedures in order to study these bacterial species and eventually to identify their PAH catabolic enzymes. Further developments of culture-independent methods might combine stable isotope labeling with *in situ* hybridization for the analysis of single cells (Huang et al., 2009), or with metagenomics to couple sequence information from a specific subpopulation with metabolic function (Kalyuzhnaya et al., 2008; Leigh et al., 2007).

PCR-based methods were also developed to analyze directly the biodiversity of RHDs in environmental samples. Since the genes encoding RHDs display great sequence variability, and no region is sufficiently conserved to design universal primers, many studies relying on a single set of degenerate primers introduce biases resulting in a limited sequence sampling of the biodiversity. This problem can be overcome by using multiple sets of primers to amplify different families of RHDs. For instance, two sets of primers were designed to amplify separately RHDs from Gram-positive and Gram-negative PAH degraders (Cebron et al., 2008). Yet, these PCR-based methods do not provide unambiguous evidence that the detected RHD genes are all related to the metabolic function of interest and expressed under the studied conditions. Again, labeling methods such DNA-based or RNA-based stable isotope-probing have the potential to specifically target pollutant degraders and their associated RHDs. For example, bacteria and functional genes associated with biphenyl degradation were identified in a PCB-polluted site using DNA-SIP coupled to analyses including gene detection by DNA microarray and RHD-specific PCR amplification (Leigh et al., 2007). Similar approaches might be used to target RHDs and other functional genes involved in PAH degradation in polluted sites. The resulting genetic information might be useful for the development of quantitative analysis of specific catabolic genes such as real time qPCR, and for the conception of specific microarrays designed to detect relevant genes and their transcripts in situ. The development of such molecular tools to detect, quantify and monitor bacterial populations involved in PAH degradation, as well as their specific catabolic enzymes, is likely to be of benefit to bioremediation technologies in the near future.

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Legends to figures

Figure 1 : Phylogenetic tree of alpha subunits of selected RHDs. Sequence alignment and the generation of a tree by neighbour-joining analysis were performed using Clustal X software. The scale bar represents substitutions per amino acid. Sequences were grouped by subfamilies according to substrate specificity. Alpha subunits were from the following dioxygenase/organism systems : PhnAc_AFK2, *Alcalingenes faecalis* AFK2 (AB024945); ArhA1_A4, *Sphingomonas* sp. strain A4 (BAD34447); PhnAc_RP007, *Burkholderia* sp. RP007 (AF061751); PahA3_PaK1, *Pseudomonas aeruginosa* PaK1 (D84146); NagAc_U2, *Ralstonia* sp. U2 (AF036940); NahAc_G7, *Pseudomonas putida* G7 (YP_534822); NdoB_NCIB9816, *Pseudomonas putida* NCIB9816 (M23914); NahAc_NCIB9816-4, *Pseudomonas putida* NCIB9816-4 (NP_863072); NtdAc_JS42, *Pseudomonas* sp. JS42 (U49504); DntAc_DNT, *Burkholderia* sp. DNT (U62430); PhnA1_A5, *Cycloclasticus* sp. strain A5 (AB102786); BphA1f_F199, *Sphingomonas aromaticivorans* F119 (AF079317); PhnA1f_LH128, *Sphingomonas* sp. strain LH128 (EU024112); BphA1f_B1, *Sphingomonas yanoikuyae* B1 (ABM91740); PhnA1a_CHY1, *Sphingomonas* sp. strain CHY-1 (AJ633551); PhtAa_12B, *Arthrobacter keyseri* 12B (AF331043); NidA_I24, *Rhodococcus* sp. I24 (AF121905); NarAa_NCIMB12038, *Rodococcus* sp. NCIMB12038 (AF082663); NidA3_PYR-1, *Mycobacterium vanbaalenii* PYR-1 (AAY85176); PhdA_KP7, *Nocardioides* sp. KP7 (AB017794); PdoA2_6PY1, *Mycobacterium* sp. strain 6PY1 (CAD38643); NidA_PYR-1, *Mycobacterium vanbaaleni* PYR-1 (AF249301); NidA_S65, *Mycobacterium* sp. S65 (AF 546904); PdoA1_6PY1, *Mycobacterium* sp. strain 6PY1 (CAD38647); DitA1_BKME-9, *Pseudomonas abietaniphila* BKME-9 (AF119621); AntA_ADP1, *Acinetobacter calcoaceticus* ADP1 (AF071556); CbdA_2CBS, *Burkholderia cepacia* 2CBS (X79076); XylX_mt2, *Pseudomonas putida* mt2 (M64747); BenA_ADP1, *Acinetobacter calcoaceticus* ADP1 (AF009224) ; OphA2_DBO1, *Burkholderia cepacia* DBO1 (AF095748); IphA2_YZW-D, *Comamonas testosteroni* YZW-D (AY923836); CarAa_CA10, *Pseudomonas resinovorans* CA10 (AB088420); OxoO_86, *Pseudomonas putidas* 86 (Y12655); DbfA1_KA1, *Sphingomonas* sp. KA1 (BAF03470); DbfA1_YK5, *Paenibacillus* sp. strain YK5 (BAF 53401); FlnA1_LB126, *Sphingomonas* sp. strain LB126 (EU024110); DbfA1_DBF63, *Terrabacter* sp. strain DBF63 (BAC75993); DbfA1_YK2, *Rhodococcus* sp. strain YK2 (BAC00802) ; DbfA1_YK3, *Terrabacter* sp. strain YK3 (BAC06602); CarAa_CB3, *Sphingomonas* CB3 (AF 060489); DxnA1_RW1, *Sphingomonas* sp. RW1 (X72850); XylC1_RB1, *Cycloclasticus oliotropus* RB1 (U51165); BphA1_P6, *Rhodococcus*

globerulus P6 (X80041); TcbAa_P51, *Pseudomonas* sp. P51 (U15298); TodC1_F1, *Pseudomonas putida* F1 (J04996); BphA_B-356, -356, *Comamonas testosteroni* B-356 (U47637); BphA_LB400, *Burkholderia xenovorans* LB400 (M86348); ThnA1_TFA, *Sphingopyxis macrogoltabida* TFA (AF157565);

Figure 2 : Genetic organization of PAH catabolic genes in representative Proteobacteria. The relevant gene cluster from the phenanthrene-degrading Gram-positive bacterium *Nocardioides* sp. KP7 is also shown for comparison. The figure was adapted from Schuler (Schuler, 2008) with permission.

Figure 3 : Genetic organization of PAH, biphenyl and xylene catabolic genes in Sphingomonads. Gene clusters are from *Novosphingobium aromaticivorans* F199, *Sphingobium yanoikuyae* B1, *Sphingobium* sp. P2, *Sphingomonas* sp. LH128, *Sphingomonas* sp. CHY-1, *Sphingobium agrestis* HV3, and *Sphingomonas chungbukensis* DJ77. The figure was adapted from Schuler (Schuler, 2008) with permission.

Figure 4 : Representation of the substrate-binding pocket of the RHD from *Sphingomonas* CHY-1 and modeling of a benzo[a]pyrene molecule bound at the active site. The entrance into the pocket is sindicated by the broad arrow. Residues that are thought to be important for regioselectivity (Phe 350) or substrate specificity (Leu 223 and Ile 260) are highlighted. The figure was reproduced from Jakoncic et al. (Jakoncic et al., 2007a) with permission.

References

Alonso-Gutierrez, J., Figueras, A., Albaiges, J., Jimenez, N., Vinas, M., Solanas, A.M., and Novoa, B. (2009). Bacterial communities from shoreline environments (Costa da Morte, Northwestern Spain) affected by the Prestige oil spill. Appl. Environ. Microbiol. *75*, 3407-3418.

Aly, H.A.H., Huu, N.B., Wray, V., Junca, H., and Pieper, D.H. (2008). Two angular dioxygenases contribute to the metabolic versatility of dibenzofuran-degrading *Rhodococcus* sp. strain HA01. Appl. Environ. Microbiol. *74*, 3812-3822.

Armengaud, J., Happe, B., and Timmis, K.N. (1998). Genetic analysis of dioxin dioxygenase of *Sphingomonas* sp. Strain RW1: catabolic genes dispersed on the genome. J. Bacteriol. *180*, 3954-3966.

Ashikawa, Y., Fujimoto, Z., Noguchi, H., Habe, H., Omori, T., Yamane, H., and Nojiri, H. (2006). Electron transfer complex formation between oxygenase and ferredoxin components in Rieske nonheme iron oxygenase system. Structure *14*, 1779-1789.

Baldwin, B.R., Nakatsu, C.H., and Nies, L. (2003). Detection and enumeration of aromatic oxygenase genes by multiplex and real-time PCR. Appl. Environ. Microbiol. *69*, 3350-3358.

Barriault, D., Plante, M.M., and Sylvestre, M. (2002). Family shuffling of a targeted *bphA* region to engineer biphenyl dioxygenase. J. Bacteriol. *184*, 3794-3800.

Batie, C.J., Ballou, D.P., and Correll, C.C. (1992). Phthalate dioxygenase reductase and related flavin-iron-sulfur containing electron transferases, In Chemistry and Biochemistry of Flavoenzymes, F. Müller, ed. (Boca Raton, Fla: CRC Press), pp. 543-556.

Beharry, Z.M., Eby, D.M., Coulter, E.D., Viswanathan, R., Neidle, E.L., Phillips, R.S., and Kurtz, D.M. (2003). Histidine ligand protonation and redox potential in the Rieske dioxygenases: Role of a conserved aspartate in anthranilate 1,2-dioxygenase. Biochemistry *42*, 13625-13636.

Bordenave, S., Goni-urriza, M., Vilette, C., Blanchard, S., Caumette, P., and Duran, R. (2008). Diversity of ring-hydroxylating dioxygenases in pristine and oil contaminated microbial mats at genomic and transcriptomic levels. Environ. Microbiol. *10*, 3201-3211.

Bosch, R., Garcia-Valdes, E., and Moore, E.R. (1999). Genetic characterization and evolutionary implications of a chromosomally encoded naphthalene-degradation upper pathway from *Pseudomonas stutzeri* AN10. Gene *236*, 149-157.

Bosch, R., Garcia-Valdes, E., and Moore, E.R. (2000). Complete nucleotide sequence and evolutionary significance of a chromosomally encoded naphthalene-degradation lower pathway from *Pseudomonas stutzeri A*N10. Gene *245*, 65-74.

Boyd, D.R., Sharma, N.D., Agarwal, R., Resnick, S.M., Schocken, M.J., Gibson, D.T., Sayer, J.M., Yagi, H., and Jerina, D.M. (1997). Bacterial dioxygenase-catalysed dihydroxylation and chemical resolution routes to enantiopure *cis*-dihydrodiols of chrysene. J. Chem. Soc. Perkin Trans. 1, 1715-1723.

Carredano, E., Karlsson, A., Kauppi, B., Choudhury, D., Parales, R.E., Parales, J.V., Lee, K., Gibson, D.T., Eklund, H., and Ramaswamy, S. (2000). Substrate binding site of naphthalene 1,2-dioxygenase: functional implications of indole binding. J. Mol. Biol. *296*, 701-712.

Cebron, A., Norini, M.P., Beguiristain, T., and Leyval, C. (2008). Real-Time PCR quantification of PAH-ring hydroxylating dioxygenase (PAH-RHD alpha) genes from Gram positive and Gram negative bacteria in soil and sediment samples. J. Microbiol. Meth. *73*, 148-159.

Chadhain, S.M.N., Moritz, E.M., Kim, E., and Zylstra, G.J. (2007). Identification, cloning, and characterization of a multicomponent biphenyl dioxygenase from *Sphingobium yanoikuya*e B1. J. Ind. Microbiol. Biotechnol. *34*, 605-613.

Chang, H.-K., Mohseni, P., and Zylstra, G.J. (2003). Characterization and regulation of the genes for a novel anthranilate 1,2-dioxygenase from *Burkholderia cepacia* DBO1. J. Bacteriol. *185*, 5871-5881.

Correll, C.C., Batie, C.J., Ballou, D.P., and Ludwig, M.L. (1992). Phthalate dioxygenase reductase: a modular structure for electron transfer from pyridine nucleotides to [2Fe-2S]. Science *258*, 1604-1610.

Cui, Z.S., Lai, Q.L., Dong, C.M., and Shao, Z.Z. (2008). Biodiversity of polycyclic aromatic hydrocarbon-degrading bacteria from deep sea sediments of the Middle Atlantic Ridge. Environ. Microbiol. *10*, 2138-2149.

DeBruyn, J.M., Chewning, C.S., and Sayler, G.S. (2007). Comparative quantitative prevalence of *Mycobacteria* and functionally abundant *nidA, nahAc,* and *nagAc* dioxygenase genes in coal tar contaminated sediments. Environ. Sci. Technol. *41*, 5426-5432.

Demaneche, S., Meyer, C., Micoud, J., Louwagie, M., Willison, J.C., and Jouanneau, Y. (2004). Identification and functional analysis of two aromatic ring-hydroxylating dioxygenases from a *Sphingomonas* strain degrading various polycyclic aromatic hydrocarbons. Appl. Environ. Microbiol. *70*, 6714-6725.

DeRito, C.M., Pumphrey, G.M., and Madsen, E.L. (2005). Use of field-based stable isotope probing to identify adapted populations and track carbon flow through a phenol-degrading soil microbial community. Appl. Environ. Microbiol. *71*, 7858-7865.

Doyle, E., Muckian, L., Hickey, A.M., and Clipson, N. (2008). Microbial PAH Degradation. Adv. Appl. Microbiol. *65*, 27-66.

Dumont, M.G., and Murrell, J.C. (2005). Stable isotope probing - linking microbial identity to function. Nature Rev. Microbiol. *3*, 499-504.

Eby, D.M., Beharry, Z.M., Coulter, E.D., Kurtz, D.M., Jr., and Neidle, E.L. (2001). Characterization and evolution of anthranilate 1,2-dioxygenase from *Acinetobacter* sp. strain ADP1. J. Bacteriol. *183*, 109-118.

Ensley, B.D., Ratzkin, B.J., Osslund, T.D., Simon, M.J., Wackett, L.P., and Gibson, D.T. (1983). Expression of naphthalene oxidation genes in *Escherichia coli* results in the biosynthesis of indigo. Science *222*, 167-169.

Ferraro, D.J., Brown, E.N., Yu, C.L., Parales, R.E., Gibson, D.T., and Ramaswamy, S. (2007). Structural investigations of the ferredoxin and terminal oxygenase components of the biphenyl 2,3-dioxygenase from *Sphingobium yanoikuyae* BI. BMC Struct. Biol. *7*.

Ferraro, D.J., Gakhar, L., and Ramaswamy, S. (2005). Rieske business: Structure-function of Rieske non-heme oxygenases. Biochem. Biophys. Res. Commun. *338*, 175-190.

Ferraro, D.J., Okerlund, A.L., Mowers, J.C., and Ramaswamy, S. (2006). Structural basis for regioselectivity and stereoselectivity of product formation by naphthalene 1,2-dioxygenase. J. Bacteriol. *188*, 6986-6994.

Friemann, R., Ivkovic-Jensen, M.M., Lessner, D.J., Yu, C.L., Gibson, D.T., Parales, R.E., Eklund, H., and Ramaswamy, S. (2005). Structural insight into the dioxygenation of nitroarene compounds: the crystal structure of nitrobenzene dioxygenase. J. Mol. Biol. *348*, 1139-1151.

Fuenmayor, S.L., Wild, M., Boyes, A.L., and Williams, P.A. (1998). A gene cluster encoding steps in conversion of naphthalene to gentisate in *Pseudomonas* sp. strain U2. J. Bacteriol. *180*, 2522-2530.

Furukawa, K. (2000). Engineering dioxygenases for efficient degradation of environmental pollutants. Cur. Opin. Biotechnol. *11*, 244-249.

Furukawa, K., Suenaga, H., and Goto, M. (2004). Biphenyl dioxygenases: Functional versatilities and directed evolution. J. Bacteriol. *186*, 5189-5196.

Furusawa, Y., Nagarajan, V., Tanokura, M., Masai, E., Fukuda, M., and Senda, T. (2004). Crystal structure of the terminal oxygenase component of biphenyl dioxygenase derived from *Rhodococcus* sp. strain RHA1. J. Mol. Biol. *342*, 1041-1052.

Gakhar, L., Malik, Z.A., Allen, C.C. R., Lipscomb, D.A., Larkin, M.J., and Ramaswamy, S. (2005). Structure and increased thermostability of *Rhodococcus* sp naphthalene 1,2-dioxygenase. J. Bacteriol. *187*, 7222-7231.

Geiselbrecht, A.D., Hedlund, B.P., Tichi, M.A., and Staley, J.T. (1998). Isolation of marine polycyclic aromatic hydrocarbon (PAH)-degrading *Cycloclasticus* strains from the Gulf of Mexico and comparison of their PAH degradation ability with that of Puget Sound *Cycloclasticus* strains. Appl. Environ. Microbiol. *64*, 4703-4710.

Gibson, D.T., Mahadevan, V., Jerina, D.M., Yogi, H., and Yeh, H.J. (1975). Oxidation of the carcinogens benzo[a]pyrene and benzo[a]anthracene to dihydrodiols by a bacterium. Science *189*, 295-297.

Goyal, A.K., and Zylstra, G.J. (1996). Molecular cloning of novel genes for polycyclic aromatic hydrocarbon degradation from *Comamonas testosteroni* GZ39. Appl. Environ. Microbiol. *62*, 230-236.

Goyal, A.K., and Zylstra, G.J. (1997). Genetics of naphthalene and phenanthrene degradation by *Comamonas testosteroni*. J. Ind. Microbiol. Biotechnol. *19*, 401-407.

Habe, H., Chung, J.S., Kato, H., Ayabe, Y., Kasuga, K., Yoshida, T., Nojiri, H., Yamane, H., and Omori, T. (2004). Characterization of the upper pathway genes for fluorene metabolism in *Terrabacter* sp strain DBF63. J. Bacteriol. *186*, 5938-5944.

Habe, H., Miyakoshi, M., Chung, J., Kasuga, K., Yoshida, T., Nojiri, H., and Omori, T. (2003). Phthalate catabolic gene cluster is linked to the angular dioxygenase gene in Terrabacter sp. strain DBF63. Appl. Microbiol. Biotechnol. *61*, 44 - 54.

Habe, H., and Omori, T. (2003). Genetics of polycyclic aromatic hydrocarbon metabolism in diverse aerobic bacteria. Biosci. Biotech. Biochem. *67*, 225-243.

Harayama, S., Kok, M., and Neidle, E.L. (1992). Functional and evolutionary relationships among diverse oxygenases. Annu. Rev. Microbiol. *46*, 565 - 601.

Heitkamp, M.A., Freeman, J.P., Miller, D.W., and Cerniglia, C.E. (1988). Pyrene degradation by a *Mycobacterium* sp.: identification of ring oxidation and ring fission products. Appl. Environ. Microbiol. *54*, 2556-2565.

Huang, W.E., Ferguson, A., Singer, A.C., Lawson, K., Thompson, I.P., Kalin, R.M., Larkin, M.J., Bailey, M.J., and Whiteley, A.S. (2009). Resolving genetic functions within microbial

1 populations: In situ analyses using rRNA and mRNA stable isotope probing coupled with
2 single-cell Raman-fluorescence in situ hybridization. Appl. Environ. Microbiol. *75*, 234-241.
3 Hudlicky, T., Gonzalez, D., and Gibson, D.T. (1999). Enzymatic dihydroxylation of
4 aromatics in enantioselective synthesis: expanfing asymetric methodology. Aldrichimica Acta
5 *32*, 35-62.
6 Iida, T., Moteki, Y., Nakamura, K., Taguchi, K., Otagiri, M., Asanuma, M., Dohmae, N.,
7 Usami, R., and Kudo, T. (2009). Functional expression of three Rieske non-heme iron
8 oxygenases derived from *Actinomycetes* in *Rhodococcus* species for investigation of their
9 degradation capabilities of dibenzofuran and chlorinated dioxins. Biosci. Biotech. Biochem.
10 *73*, 822-827.
11 Iida, T., Mukouzaka, Y., Nakamura, K., and Kudo, T. (2002). Plasmid-borne genes code for
12 an angular dioxygenase involved in dibenzofuran degradation by *Terrabacter* sp. strain YK3.
13 Appl. Environ. Microbiol. *68*, 3716-3723.
14 Iida, T., Waki, T., Nakamura, K., Mukouzaka, Y., and Kudo, T. (2009b). The GAF-like-
15 domain-containing transcriptional regulator DfdR Is a sensor protein for dibenzofuran and
16 several hydrophobic aromatic compounds. J. Bacteriol. *191*, 123-134.
17 Imbeault, N.Y., Powlowski, J.B., Colbert, C.L., Bolin, J.T., and Eltis, L.D. (2000). Steady-
18 state kinetic characterization and crystallization of a polychlorinated biphenyl-transforming
19 dioxygenase. J. Biol. Chem. *275*, 12430-12437.
20 Jakoncic, J., Jouanneau, Y., Meyer, C., and Stojanoff, V. (2007a). The catalytic pocket of the
21 ring-hydroxylating dioxygenase from *Sphingomonas* CHY-1. Biochem. Biophys. Res.
22 Commun. *352*, 861-866.
23 Jakoncic, J., Jouanneau, Y., Meyer, C., and Stojanoff, V. (2007b). The crystal structure of the
24 ring-hydroxylating dioxygenase from *Sphingomonas* CHY-1. Febs J. *274*, 2470-2481.
25 Jeon, C.O., Park, M., Ro, H.S., Park, W., and Madsen, E.L. (2006). The naphthalene catabolic
26 (nag) genes of *Polaromonas naphthalenivorans* CJ2: Evolutionary implications for two gene
27 clusters and novel regulatory control. Appl. Environ. Microbiol.
28 *72*, 1086-1095.
29 Jeon, C.O., Park, W., Padmanabhan, P., DeRito, C., Snape, J.R., and Madsen, E.L. (2003).
30 Discovery of a bacterium, with distinctive dioxygenase, that is responsible for in situ
31 biodegradation in contaminated sediment. Proc. Natl. Acad. Sci. U S A *100*, 13591-13596.
32 Joern, J.M., Sakamoto, T., Arisawa, A.A., and Arnold, F.H. (2001). A versatile high
33 throughput screen for dioxygenase activity using solid-phase digital imaging. J. Biomol. Scr.
34 *6*, 219-223.

Jones, M.D., Singleton, D.R., Carstensen, D.P., Powell, S.N., Swanson, J.S., Pfaender, F.K., and Aitken, M.D. (2008). Effect of incubation conditions on the enrichment of pyrene-degrading bacteria identified by stable-isotope probing in an aged, PAH-contaminated soil. Microbial Ecol. *56*, 341-349.

Jones, R.M., Britt-Compton, B., and Williams, P.A. (2003). The naphthalene catabolic (*nag*) genes of *Ralstonia* sp. strain U2 are an operon that is regulated by NagR, a LysR-type transcriptional regulator. J. Bacteriol. *185*, 5847 - 5853.

Jouanneau, Y., Meyer, C., Jakoncic, J., Stojanoff, V., and Gaillard, J. (2006). Characterization of a naphthalene dioxygenase endowed with an exceptionally broad substrate specificity toward polycyclic aromatic hydrocarbons. Biochemistry *45*, 12380-12391.

Jouanneau, Y., Micoud, J., and Meyer, C. (2007). Purification and characterization of a three-component salicylate 1-hydroxylase from *Sphingomonas* sp. strain CHY-1. Appl. Environ. Microbiol. *73*, 7515-7521.

Kalyuzhnaya, M.G., Lapidus, A., Ivanova, N., Copeland, A.C., McHardy, A.C., Szeto, E., Salamov, A., Grigoriev, I.V., Suciu, D., Levine, S.R.*, et al.* (2008). High-resolution metagenomics targets specific functional types in complex microbial communities. Nature Biotechnol. *26*, 1029-1034.

Karlsson, A., Beharry, Z.M., Eby, D.M., Coulter, E.D., Neidle, E.L., Kurtz, D.M., Eklund, H., and Ramaswamy, S. (2002). X-ray crystal structure of benzoate 1,2-dioxygenase reductase from Acinetobacter sp strain ADP1. J. Mol. Biol. *318*, 261-272.

Karlsson, A., Parales, J.V., Parales, R.E., Gibson, D.T., Eklund, H., and Ramaswamy, S. (2003). Crystal structure of naphthalene dioxygenase: side-on binding of dioxygen to iron. Science *299*, 1039-1042.

Kasai, Y., Kishira, H., and Harayama, S. (2002). Bacteria belonging to the genus *Cycloclasticus* play a primary role in the degradation of aromatic hydrocarbons released in a marine environment. Appl. Environ. Microbiol. *68*, 5625-5633.

Kasai, Y., Shindo, K., Harayama, S., and Misawa, N. (2003). Molecular characterization and substrate preference of a polycyclic aromatic hydrocarbon dioxygenase from *Cycloclasticus* sp strain A5. Appl. Environ. Microbiol. *69*, 6688-6697.

Kasuga, K., Habe, H., Chung, J.S., Yoshida, T., Nojiri, H., Yamane, H., and Omori, T. (2001). Isolation and characterization of the genes encoding a novel oxygenase component of angular dioxygenase from the Gram-positive dibenzofuran-degrader *Terrabacter* sp strain DBF63. Biochem. Biophys. Res. Commun. *283*, 195-204.

Kauppi, B., Lee, K., Carredano, E., Parales, R.E., Gibson, D.T., Eklund, H., and Ramaswamy, S. (1998). Structure of an aromatic-ring-hydroxylating dioxygenase-naphthalene 1,2-dioxygenase. Structure *6*, 571-586.

Keenan, B.G., Leungsakul, T., Smets, B.F., Mori, M.A., Henderson, D.E., and Wood, T.K. (2005). Protein engineering of the archetypal nitroarene dioxygenase of *Ralstonia* sp. strain U2 for activity on aminonitrotoluenes and dinitrotoluenes through alpha-subunit residues leucine 225, phenylalanine 350, and glycine 407. J. Bacteriol. *187*, 3302-3310.

Keenan, B.G., and Wood, T.K. (2006). Orthric Rieske dioxygenases for degrading mixtures of 2,4-dinitrotoluene/naphthalene and 2-amino-4,6-dinitrotoluene/4-amino-2,6-dinitrotoluene. Appl. Microbiol. Biotechnol. *73*, 827-838.

Khan, A.A., Wang, R.F., Cao, W.W., Doerge, D.R., Wennerstrom, D., and Cerniglia, C.E. (2001). Molecular cloning, nucleotide sequence, and expression of genes encoding a polcyclic aromatic ring dioxygenase from *Mycobacterium* sp strain PYR-1. Appl. Environ. Microbiol. *67*, 3577-3585.

Kim, E., and Zylstra, G.J. (1999). Functional analysis of genes involved in biphenyl, naphthalene, phenanthrene, and m-xylene degradation by *Sphingomonas yanoikuyae* B1. J. Ind. Microbiol. Biotechnol. *23*, 294-302.

Kim, S.J., Kweon, O., Jones, R.C., Edmondson, R.D., and Cerniglia, C.E. (2008). Genomic analysis of polycyclic aromatic hydrocarbon degradation in *Mycobacterium vanbaalenii* PYR-1. Biodegradation *19*, 859-881.

Kim, S.J., Kweon, O.G., Freeman, J.P., Jones, R.C., Adjei, M.D., Jhoo, J.W., Edmondson, R.D., and Cerniglia, C.E. (2006). Molecular cloning and expression of genes encoding a novel dioxygenase Involved in low- and high-molecular-weight polycyclic aromatic hydrocarbon degradation in *Mycobacterium vanbaalenii* PYR-1. Appl. Environ. Microbiol. *72*, 1045 - 1054.

Kirk, J.L., Beaudette, L.A., Hart, M., Moutoglis, P., Klironomos, J.N., Lee, H., and Trevors, J.T. (2004). Methods of studying soil microbial diversity. J. Microbiol. Meth. *58*, 169-188.

Kiyohara, H., Nagao, K., Kouno, K., and Yano, K. (1982). Phenanthrene-degrading phenotype of *Alcaligenes faecalis* AFK2. Appl. Environ. Microbiol. *43*, 458 - 461.

Kovaleva, E.G., and Lipscomb, J.D. (2008). Versatility of biological non-heme Fe(II) centers in oxygen activation reactions. Nature Chem. Biol. *4*, 186-193.

Kreuzer-Martin, H.W., and Jarman, K.H. (2007). Stable isotope ratios and forensic analysis of microorganisms. Appl. Environ. Microbiol. *73*, 3896-3908.

Krivobok, S., Kuony, S., Meyer, C., Louwagie, M., Willison, J.C., and Jouanneau, Y. (2003). Identification of pyrene-induced proteins in *Mycobacterium* sp. 6PY1 : Evidence for two ring-hydroxylating dioxygenases. J. Bacteriol. *185*, 3828-3841.

Kumari, R., Subudhi, S., Suar, M., Dhingra, G., Raina, V., Dogra, C., Lal, S., van der Meer, J.R., Holliger, C., and Lal, R. (2002). Cloning and characterization of *lin* genes responsible for the degradation of hexachlorocyclohexane isomers by *Sphingomonas paucimobilis* strain B90. Appl. Environ. Microbiol. *68*, 6021-6028.

Kweon, O., Kim, S.-J., Baek, S., Chae, J.-C., Adjei, M., Baek, D.-H., Kim, Y.-C., and Cerniglia, C.E. (2008). A new classification system for bacterial Rieske non-heme iron aromatic ring-hydroxylating oxygenases. BMC Biochemistry *9*, 11.

Kweon, O., Kim, S.J., Jones, R.C., Freeman, J.P., Adjei, M.D., Edmondson, R.D., and Cerniglia, C.E. (2007). A polyomic approach to elucidate the fluoranthene-degradative pathway in *Mycobacterium vanbaalenii* PYR-1. J. Bacteriol. *189*, 4635-4647.

Larkin, M.J., Allen, C.C., Kulakov, L.A., and Lipscomb, D.A. (1999). Purification and characterization of a novel naphthalene dioxygenase from *Rhodococcus* sp. strain NCIMB12038. J. Bacteriol. *181*, 6200-6204.

Laurie, A.D., and Lloyd-Jones, G. (1999). The *phn* genes of *Burkholderia* sp. strain RP007 constitute a divergent gene cluster for polycyclic aromatic hydrocarbon catabolism. J. Bacteriol. *181*, 531-540.

Leigh, M.B., Pellizari, V.H., Uhlik, O., Sutka, R., Rodrigues, J., Ostrom, N.E., Zhou, J.H., and Tiedje, J.M. (2007). Biphenyl-utilizing bacteria and their functional genes in a pine root zone contaminated with polychlorinated biphenyls (PCBs). Isme J. *1*, 134-148.

Leys, N.M., Ryngaert, A., Bastiaens, L., Wattiau, P., Top, E.M., Verstraete, W., and Springael, D. (2005). Occurrence and community composition of fast-growing *Mycobacterium* in soils contaminated with polycyclic aromatic hydrocarbons. FEMS Microbiol. Ecol. *51*, 375-388.

Leys, N.M., Ryngaert, A., Bastiaens, L., Verstraete, W., Top, E.M., and Springael, D. (2004). Occurrence and phylogenetic diversity of *Sphingomonas* strains in soils contaminated with polycyclic aromatic hydrocarbons. Appl. Environ. Microbiol. *70*, 1944-1955.

Liang, Y., Gardner, D.R., Miller, C.D., Chen, D., Anderson, A.J., Weimer, B.C., and Sims, R.C. (2006). Study of biochemical pathways and enzymes involved in pyrene degradation by *Mycobacterium* sp strain KMS. Appl. Environ. Microbiol. *72*, 7821-7828.

Lozada, M., Mercadal, J.P.R., Guerrero, L.D., Di Marzio, W.D., Ferrero, M.A., and Dionisi, H.M. (2008). Novel aromatic ring-hydroxylating dioxygenase genes from coastal marine sediments of Patagonia. BMC Microbiol. *8*.

Marcos, M.S., Lozada, M., and Dionisi, H.M. (2009). Aromatic hydrocarbon degradation genes from chronically polluted Subantarctic marine sediments. Lett. Appl. Microbiol. *49*, 602-608.

Martin, V.J., and Mohn, W.W. (1999). A novel aromatic-ring-hydroxylating dioxygenase from the diterpenoid-degrading bacterium *Pseudomonas abietaniphila* BKME-9. J. Bacteriol. *181*, 2675-2682.

Martins, B.M., Svetlitchnaia, T., and Dobbek, H. (2005). 2-oxoquinoline 8-monooxygenase oxygenase component: Active site modulation by Rieske-[2Fe-2S] center oxidation/reduction. Structure *13*, 817-824.

McKew, B.A., Coulon, F., Osborn, A.M., Timmis, K.N., and McGenity, T.J. (2007). Determining the identity and roles of oil-metabolizing marine bacteria from the Thames estuary, UK. Environ. Microbiol. *9*, 165-176.

Moreno-Ruiz, E., Hernaez, M.J., Martinez-Perez, O., and Santero, E. (2003). Identification and functional characterization of *Sphingomonas macrogolitabida* strain TFA genes involved in the first two steps of the tetralin catabolic pathway. J. Bacteriol. *185*, 2026-2030.

Nam, J.W., Nojiri, H., Yoshida, T., Habe, H., Yamane, H., and Omori, T. (2001). New classification system for oxygenase components involved in ring- hydroxylating oxygenations. Biosci. Biotechnol. Biochem. *65*, 254-263.

Nebe, J., Baldwin, B.R., Kassab, R.L., Nies, L., and Nakatsu, C.H. (2009). Quantification of aromatic oxygenase genes to evaluate enhanced bioremediation by oxygen releasing materials at a gasoline-contaminated site. Environ. Sci. Technol. *43*, 2029-2034.

Neufeld, J.D., Vohra, J., Dumont, M.G., Lueders, T., Manefield, M., Friedrich, M.W., and Murrell, J.C. (2007). DNA stable-isotope probing. Nature Protocols *2*, 860-866.

Ni Chadhain, S.M., Norman, R.S., Pesce, K.V., Kukor, J.J., and Zystra, G.J. (2006). Microbial dioxygenase gene population shifts during polycyclic aromatic hydrocarbon biodegradation. Appl. Environ. Microbiol. *72*, 4078-4087.

Niepceron, M., Portet-Koltalo, F., Merlin, C., Motelay-Massei, A., Barray, S., and Bodilis, J. (2010). Both *Cycloclasticus* spp. and *Pseudomonas* spp. as PAH-degrading bacteria in the Seine estuary (France). FEMS Microbiol. Ecol. *71*, 137-147.

Nojiri, H., Ashikawa, Y., Noguchi, H., Nam, J.W., Urata, M., Fujimoto, Z., Uchimura, H., Terada, T., Nakamura, S., Shimizu, K.*, et al.* (2005). Structure of the terminal oxygenase component of angular dioxygenase, carbazole 1,9a-dioxygenase. J. Mol. Biol. *351*, 355-370.

Nojiri, H., Nam, J.W., Kosaka, M., Morii, K.I., Takemura, T., Furihata, K., Yamane, H., and Omori, T. (1999). Diverse oxygenations catalyzed by carbazole 1,9a-dioxygenase from *Pseudomonas* sp strain CA10. J. Bacteriol. *181*, 3105-3113.

Padmanabhan, P., Padmanabhan, S., DeRito, C., Gray, A., Gannon, D., Snape, J.R., Tsai, C.S., Park, W., Jeon, C., and Madsen, E.L. (2003). Respiration of 13C-labeled substrates added to soil in the field and subsequent 16S rRNA gene analysis of 13C-labeled soil DNA. Appl. Environ. Microbiol. *69*, 1614-1622.

Pagnout, C., Frache, G., Poupin, P., Maunit, B., Muller, J.F., and Ferard, J.F. (2007). Isolation and characterization of a gene cluster involved in PAH degradation in *Mycobacterium* sp strain SNP11: Expression in *Mycobacterium smegmatis* mc(2)155. Res. Microbiol. *158*, 175-186.

Parales, R.E., Huang, R., Yu, C.L., Parales, J.V., Lee, F.K., Lessner, D.J., Ivkovic-Jensen, M.M., Liu, W., Friemann, R., Ramaswamy, S., and Gibson, D.T. (2005). Purification, characterization, and crystallization of the components of the nitrobenzene and 2-nitrotoluene dioxygenase enzyme systems. Appl. Environ. Microbiol. *71*, 3806-3814.

Parales, R.E., Lee, K., Resnick, S.M., Jiang, H.Y., Lessner, D.J., and Gibson, D.T. (2000). Substrate specificity of naphthalene dioxygenase: Effect of specific amino acids at the active site of the enzyme. J. Bacteriol. *182*, 1641-1649.

Parales, R.E., Parales, J.V., and Gibson, D.T. (1999). Aspartate 205 in the catalytic domain of naphthalene dioxygenase is essential for activity. J. Bacteriol. *181*, 1831-1837.

Parales, R.E., and Resnick, S.M. (2006). Aromatic ring hydroxylating dioxygenases, In Pseudomonas, J.L. Ramos, and R.C. Levesque, eds. (Springer), pp. 287-340.

Park, J.W., and Crowley, D.E. (2006). Dynamic changes in *nahAc* gene copy numbers during degradation of naphthalene in PAH-contaminated soils. Appl. Environ. Microbiol. *72*, 1322-1329.

Peng, R.H., Xiong, A.S., Xue, Y., Fu, X.Y., Gao, F., Zhao, W., Tian, Y.S., and Yao, Q.H. (2008). Microbial biodegradation of polyaromatic hydrocarbons. FEMS Microbiol. Rev. *32*, 927-955.

Pinyakong, O., Habe, H., Kouzuma, A., Nojiri, H., Yamane, H., and Omori, T. (2004). Isolation and characterization of genes encoding polycyclic aromatic hydrocarbon

dioxygenase from acenaphthene and acenaphthylene degrading *Sphingomonas* sp strain A4. Fems Microbiol. Let. *238*, 297-305.

Pinyakong, O., Habe, H., and Omori, T. (2003a). The unique aromatic catabolic genes in sphingomonads degrading polycyclic aromatic hydrocarbons (PAHs). J. Gen. Appl. Microbiol. *49*, 1-19.

Pinyakong, O., Habe, H., Yoshida, T., Nojiri, H., and Omori, T. (2003b). Identification of three novel salicylate 1-hydroxylases involved in the phenanthrene degradation of *Sphingobium s*p. strain P2. Biochem. Biophys. Res. Commun. *301*, 350 - 357.

Pollmann, K., Wray, V., Hecht, H.J., and Pieper, D.H. (2003). Rational engineering of the regioselectivity of TecA tetrachlorobenzene dioxygenase for the transformation of chlorinated toluenes. Microbiology *149*, 903-913.

Radajewski, S., Ineson, P., Parekh, N.R., and Murrell, J.C. (2000). Stable-isotope probing as a tool in microbial ecology. Nature *403*, 646-649.

Resnick, S.M., and Gibson, D.T. (1996). Regio- and stereospecific oxidation of fluorene, dibenzofuran, and dibenzothiophene by naphthalene dioxygenase from *Pseudomonas* sp. strain NCIB 9816-4. Appl. Environ. Microbiol. *62*, 4073-4080.

Resnick, S.M., Lee, K., and Gibson, D.T. (1996). Diverse reactions catalyzed by naphthalene dioxygenase from *Pseudomonas* sp. strain NCIB 9816. J. Ind. Microbiol. Biotechnol. *17*, 438-457.

Romine, M.F., Stillwell, L.C., Wong, K.K., Thurston, S.J., Sisk, E.C., Sensen, C., Gaasterland, T., Fredrickson, J.K., and Saffer, J.D. (1999). Complete sequence of a 184-kilobase catabolic plasmid from *Sphingomonas aromaticivorans* F199. J. Bacteriol. *181*, 1585 - 1602.

Saito, A., Iwabuchi, T., and Harayama, S. (1999). Characterization of genes for enzymes involved in the phenanthrene degradation in *Nocardioides* sp. KP7. Chemosphere *38*, 1331-1337.

Saito, A., Iwabuchi, T., and Harayama, S. (2000). A novel phenanthrene dioxygenase from *Nocardioides* sp strain KP7: Expression in *Escherichia coli*. J. Bacteriol. *182*, 2134-2141.

Sato, S.I., Nam, J.W., Kasuga, K., Nojiri, H., Yamane, H., and Omori, T. (1997). Identification and characterization of genes encoding carbazole 1,9a-dioxygenase in *Pseudomonas* sp. strain CA10. J. Bacteriol. *179*, 4850-4858.

Schell, M.A. (1985). Transcriptional control of the *nah* and *sal* hydrocarbon-degradation operons by the *nahR* gene product. Gene *36*, 301-309.

Schneider, J., Grosser, R., Jayasimhulu, K., Xue, W., and Warshawsky, D. (1996). Degradation of pyrene, benz[a]anthracene, and benzo[a]pyrene by *Mycobacterium* sp. strain RJGII-135, isolated from a former coal gasification site. Appl. Environ. Microbiol. *62*, 13-19.

Schuler, L. (2008) Identification of genes involved in the degradation of polycyclic aromatic hydrocarbons by two *Sphingomonas spp*. PhD thesis, Catholic University of Louvain, Louvain (Belgium).

Schuler, L., Ni Chadhain, S.M., Jouanneau, Y., Meyer, C., Zylstra, G.J., Hols, P., and Agathos, S.N. (2008). Characterization of a novel angular dioxygenase from fluorene-degrading *Spingomonas* sp strain LB126. Appl. Environ. Microbiol. *74*, 1050-1057.

Schuler, L., Jouanneau, Y., Ni Chadhain, S.M., Meyer, C., Pouli, M., Zylstra, G.J., Hols, P., and Agathos, S.N. (2009). Characterization of a ring-hydroxylating dioxygenase from phenanthrene-degrading *Sphingomonas* sp. strain LH128 able to oxidize benz[a]anthracene. Appl. Microbiol. Biotechnol. *83*, 465-475.

Shintani, M., Urata, M., Inoue, K., Eto, K., Habe, H., Omori, T., Yamane, H., and Nojiri, H. (2007). The *Sphingomonas* plasmid pCAR3 is involved in complete mineralization of carbazole. J. Bacteriol. *189*, 2007-2020.

Sho, M., Hamel, C., and Greer, C.W. (2004). Two distinct gene clusters encode pyrene degradation in *Mycobacterium* sp. strain S65. FEMS Microbiol. Ecol. *48*, 209 - 220.

Simon, M.J., Osslund, T.D., Saunders, R., Ensley, B.D., Suggs, S., Harcourt, A., Suen, W.C., Cruden, D.L., Gibson, D.T., and Zylstra, G.J. (1993). Sequences of genes encoding naphthalene dioxygenase in *Pseudomonas putida* strains G7 and NCIB 9816-4. Gene *127*, 31-37.

Singleton, D.R., Powell, S.N., Sangaiah, R., Gold, A., Ball, L.M., and Aitken, M.D. (2005). Stable-isotope probing of bacteria capable of degrading salicylate, naphthalene, or phenanthrene in a Bioreactor treating contaminated soil. Appl. Environ. Microbiol. *71*, 1202-1209.

Singleton, D.R., Ramirez, L.G., and Aitken, M.D. (2009). Characterization of a polycyclic aromatic hydrocarbon degradation gene cluster in a phenanthrene-degrading *Acidovorax* Strain. Appl. Environ. Microbiol. *75*, 2613-2620.

Singleton, D.R., Sangaiah, R., Gold, A., Ball, L.M., and Aitken, M.D. (2006). Identification and quantification of uncultivated Proteobacteria associated with pyrene degradation in a bioreactor treating PAH-contaminated soil. Environ. Microbiol. *8*, 1736-1745.

Stemmer, W.P. (1994). DNA shuffling by random fragmentation and reassembly: in vitro recombination for molecular evolution. Proc. Natl. Acad. Sci. U S A *91*, 10747-10751.

Stingley, R.L., Khan, A.A., and Cerniglia, C.E. (2004). Molecular characterization of a phenanthrene degradation pathway in *Mycobacterium vanbaalen*i PYR-1. Biochem. Biophys. Res. Commun. *322*, 133-146.

Suenaga, H., Watanabe, T., Sato, M., Ngadiman, and Furukawa, K. (2002). Alteration of regiospecificity in biphenyl dioxygenase by active-site engineering. J. Bacteriol. *184*, 3682-3688.

Takagi, T., Habe, H., Yoshida, T., Yamane, H., Omori, T., and Nojiri, H. (2005). Characterization of [3Fe-4S] ferredoxin DbfA3, which functions in the angular dioxygenase system of sp strain DBF63. Appl. Microbiol. Biotechnol. *68*, 336-345.

Takeuchi, M., Hamana, K., and Hiraishi, A. (2001). Proposal of the genus *Sphingomonas* sensu stricto and three new genera, *Sphingobium, Novosphingobium* and *Sphingopyxis*, on the basis of phylogenetic and chemotaxonomic analyses. Int. J. Syst. Evol. Microbiol. *51*, 1405-1417.

Tarasev, M., and Ballou, D.P. (2005). Chemistry of the catalytic conversion of phthalate into its *cis*-dihydrodiol during the reaction of oxygen with the reduced form of phthalate dioxygenase. Biochemistry *44*, 6197-6207.

Tee, K.L., and Schwaneberg, U. (2007). Directed evolution of oxygenases: Screening systems, success stories and challenges. Combin. Chem. High Throughput Scr. *10*, 197-217.

Tropel, D., and van der Meer, J.R. (2004). Bacterial transcriptional regulators for degradation pathways of aromatic compounds. Microbiol. Mol. Biol. Rev. *68*, 474-500.

Uchimura, H., Horisaki, T., Umeda, T., Noguchi, H., Usami, Y., Li, L., Terada, T., Nakamura, S., Shimizu, K., Takemura, T.*, et al.* (2008). Alteration of the substrate specificity of the angular dioxygenase carbazole 1,9a-dioxygenase. Biosci. Biotech. Biochem. *72*, 3237-3248.

Vezina, J., Barriault, D., and Sylvestre, M. (2007). Family shuffling of soil DNA to change the regiospecificity of *Burkholderia xenovorans* LB400 biphenyl dioxygenase. J. Bacteriol. *189*, 779-788.

Vila, J., Lopez, Z., Sabate, J., Minguillon, C., Solanas, A. M., and Grifoll, M. (2001). Identification of a novel metabolite in the degradation of pyrene by *Mycobacterium* sp strain AP1: Actions of the isolate on two- and three-ring polycyclic aromatic hydrocarbons. Appl. Environ. Microbiol. *67*, 5497-5505.

Willison, J.C. (2004). Isolation and characterization of a novel sphingomonad capable of growth with chrysene as sole carbon and energy source. FEMS Microbiol. Lett. *241*, 143-150.

Wilson, M.S., Bakermans, C., and Madsen, E.L. (1999). In situ, real-time catabolic gene expression: Extraction and characterization of naphthalene dioxygenase mRNA transcripts from groundwater. Appl. Environ. Microbiol. *65*, 80-87.

Wintzingerode, F., Göbel, U.B., and Stackebrandt, E. (1997). Determinatiion of microbial diversity in environmental samples: pitfalls of PCR-based rRNA analysis. FEMS Microbiol. Rev. *21*, 213-229.

Wolfe, M.D., and Lipscomb, J.D. (2003). Hydrogen peroxide-coupled *cis*-diol formation catalyzed by naphthalene 1,2-dioxygenase. J. Biol. Chem. *278*, 829-835.

Wolfe, M.D., Parales, J.V., Gibson, D.T., and Lipscomb, J.D. (2001). Single turnover chemistry and regulation of O-2 activation by the oxygenase component of naphthalene 1,2-dioxygenase. J. Biol. Chem. *276*, 1945-1953.

Yagi, J.M., and Madsen, E.L. (2009). Diversity, abundance, and consistency of microbial oxygenase expression and biodegradation in a shallow contaminated aquifer. Appl. Environ. Microbiol. *75*, 6478-6487.

Yeates, C., Holmes, A.J., and Gillings, M.R. (2000). Novel forms of ring-hydroxylating dioxygenases are widespread in pristine and contaminated sails. Environ. Microbiol. *2*, 644-653.

Yen, K.M., and Gunsalus, I.C. (1982). Plasmid gene organization: naphthalene/salicylate oxidation. Proc. Natl. Acad. Sci. U S A *79*, 874-878.

Yen, K.M., and Serdar, C.M. (1988). Genetics of naphthalene catabolism in *Pseudomonads*. CRC Crit. Rev. Microbiol. *15*, 247-268.

Yergeau, E., Arbour, M., Brousseau, R., Juck, D., Lawrence, J.R., Masson, L., Whyte, L.G., and Greer, C.W. (2009). Microarray and Real-Time PCR analyses of the responses of high-arctic soil bacteria to hydrocarbon pollution and bioremediation treatments. Appl. Environ. Microbiol. *75*, 6258-6267.

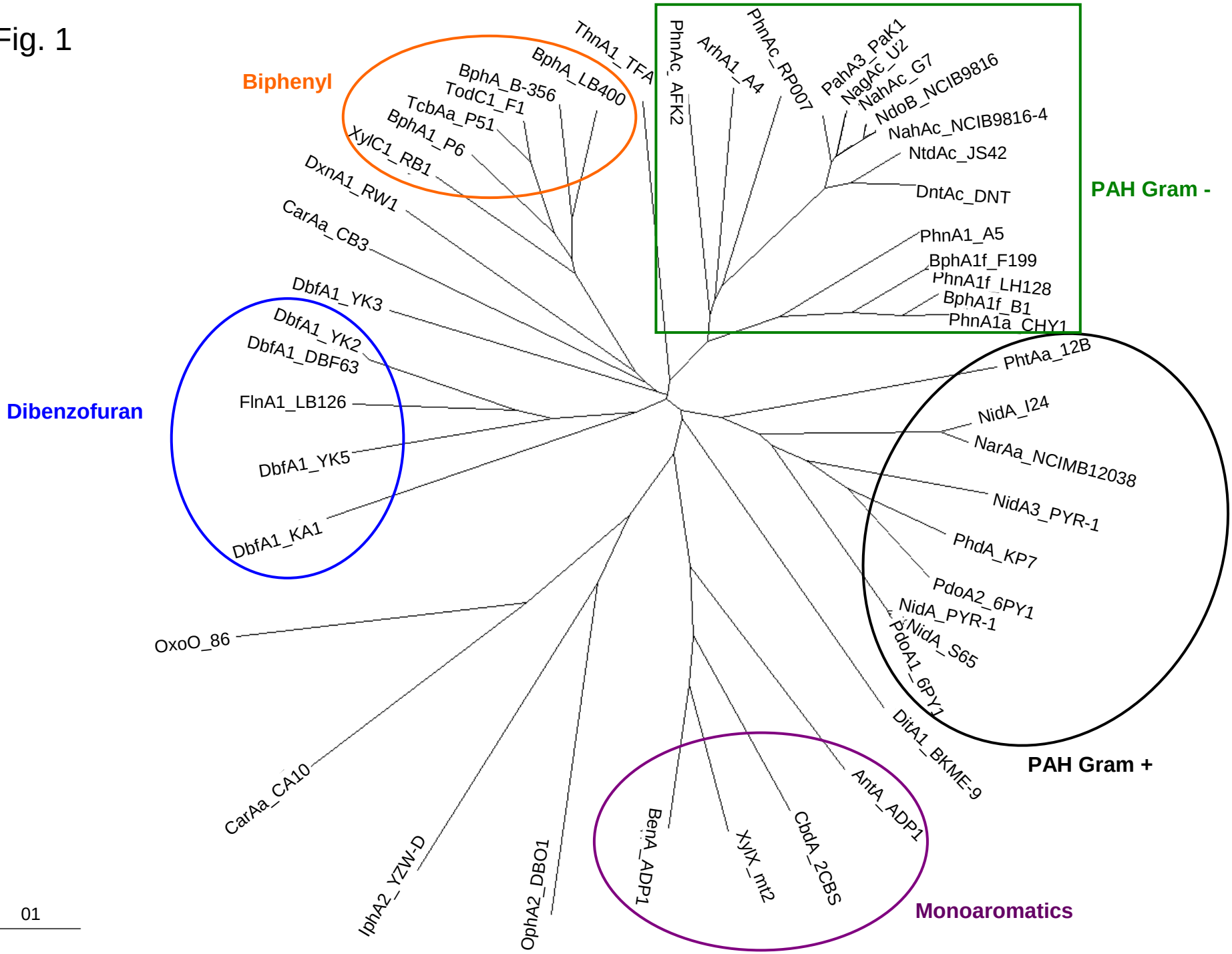
Yu, C.L., Liu, W., Ferraro, D.J., Brown, E.N., Parales, J.V., Ramaswamy, S., Zylstra, G.J., Gibson, D.T., and Parales, R.E. (2007). Purification, characterization, and crystallization of the components of a biphenyl dioxygenase system from *Sphingobium yanoikuyae* B1. J. Ind. Microbiol. Biotechnol. *34*, 311-324.

Zhou, H.W., Guo, C.L., Wong, Y.S., and Tam, N.F.Y. (2006). Genetic diversity of dioxygenase genes in polycyclic aromatic hydrocarbon-degrading bacteria isolated from mangrove sediments. FEMS Microbiol. Lett. *262*, 148-157.

Zhou, H.W., Wong, A.H.Y., Yu, R.M.K., Park, Y.D., Wong, Y.S., and Tam, N.F.Y. (2009). Polycyclic Aromatic Hydrocarbon-Induced Structural Shift of Bacterial Communities in Mangrove Sediment. Microbial Ecol. *58*, 153-160.

Zhou, N.Y., Fuenmayor, S.L., and Williams, P.A. (2001). *nag* genes of *Ralstonia* (formerly *Pseudomonas*) sp. strain U2 encoding enzymes for gentisate catabolism. J. Bacteriol. *183*, 700-708.

Fig. 1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PAH Gram +
OxoO_86
CarAa_CA10
IphA2_YZW-D
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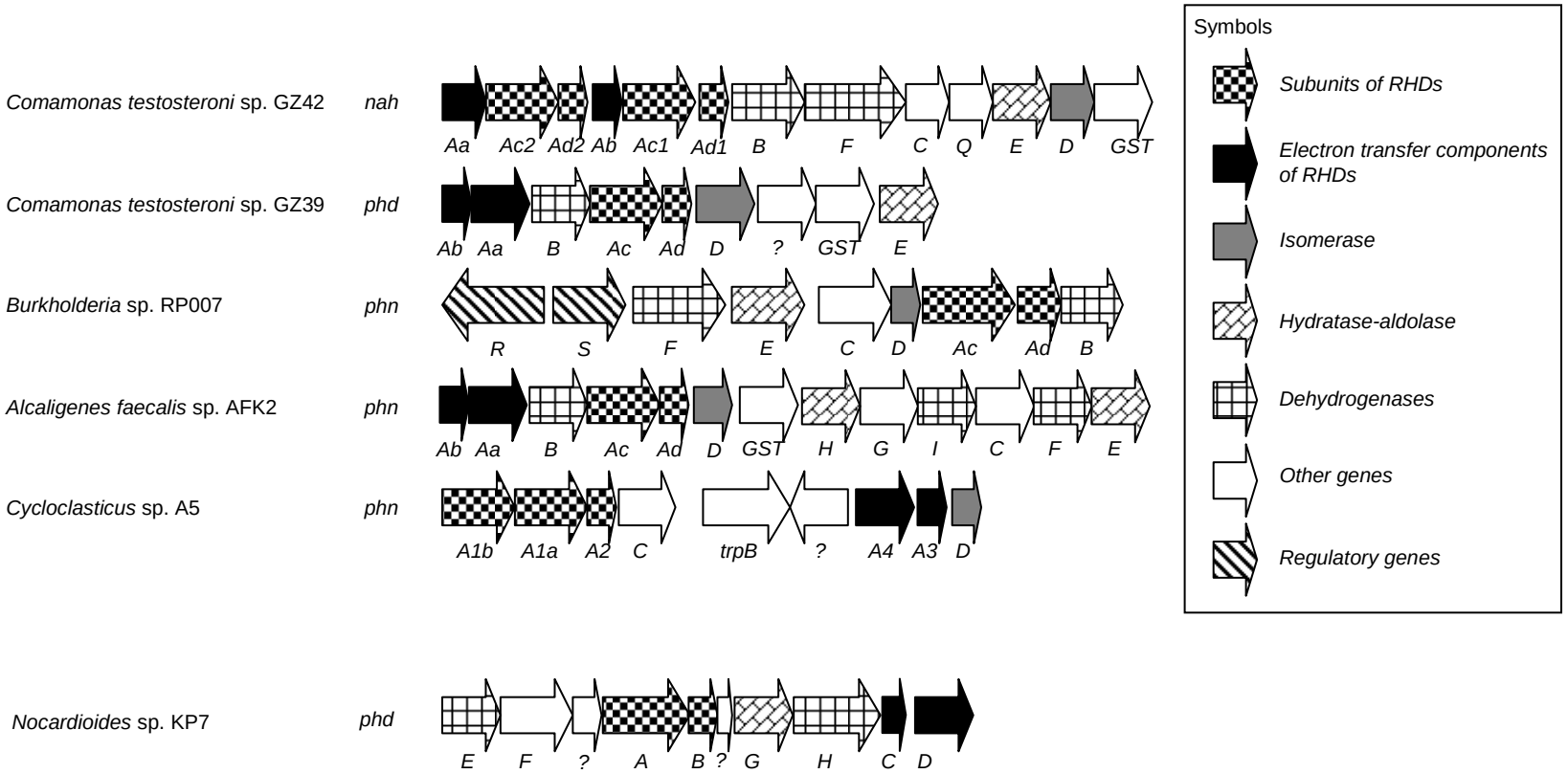
Monoaromatics
01

Fig. 2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phn
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Nocardioides sp. KP7
phd
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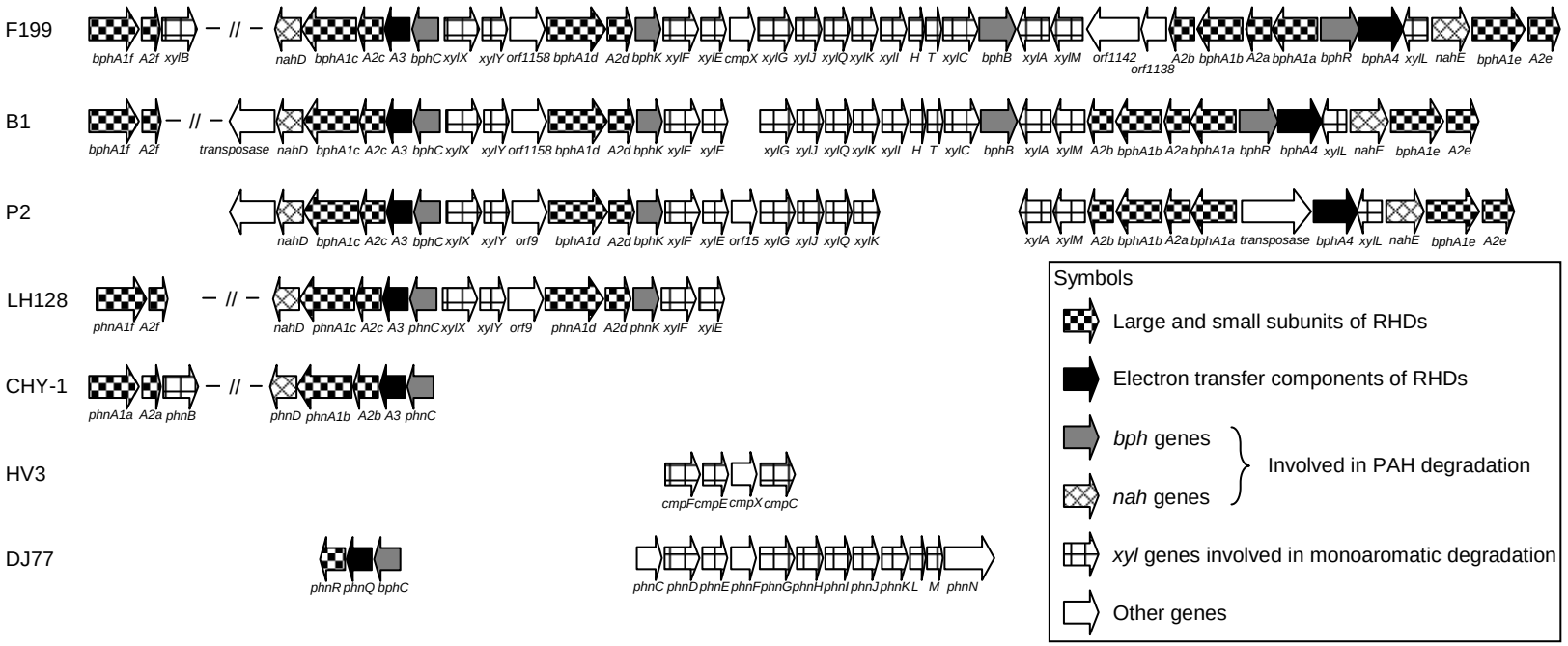
Electron transfer components of RHDs
Isomerase
Hydratase-aldolase
Dehydrogenases
Other genes
Regulatory genes

Fig. 3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phnD phnA1b A2b A3 phnC
HV3
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DJ77
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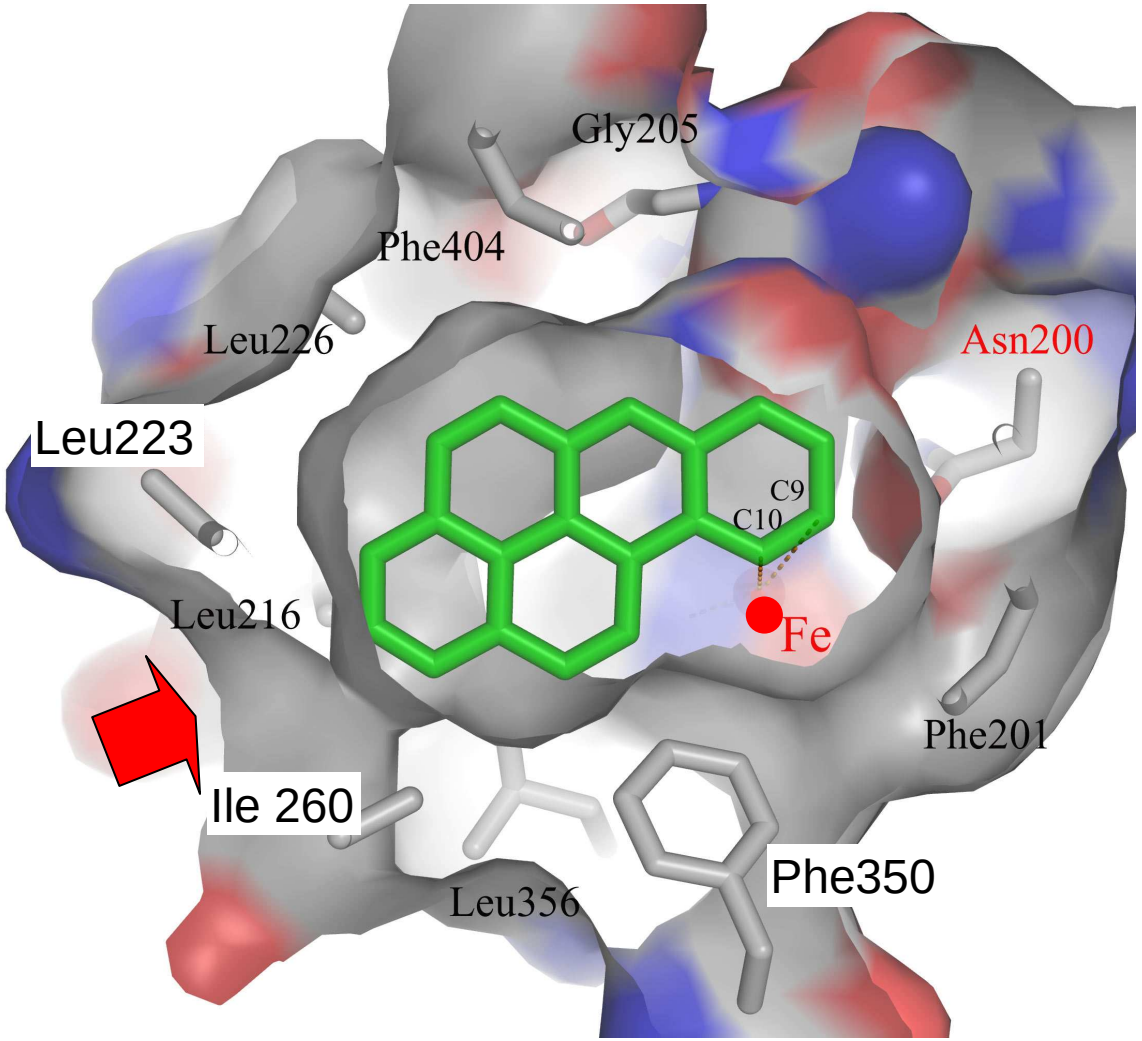
phnC phnD phnE phnF phnG phnH phnI phnJ phnK L M phnN
Symbols
Large and small subunits of RHDs
Electron transfer components of RHDs
bph genes
nah genes
Involved in PAH degradation
xyl genes involved in monoaromatic degradation
Other genes

Fig. 4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