1 Supplemental tables

2 **Table S1**. PCR primers used for molecular analyses of DF-degrading bacteria

PCR strategy and target regions	Primer name	Direction	Sequence (5' - 3')
Standard PCR			
AhDOa	PAH2f	Forward	TCVBSTGCMVYTAYCAYGGYTGG
	PAH3r1	Reverse	TCAYCYGKTCCYYTMGGRTGCCA
	PAH3r2	Reverse	TYATBSGGMCCVMKCGGVTGCCA
	PAH4r	Reverse	CSATSRMATASKTCCAVACYTCG
	PAH5r	Reverse	CCRTCRTCSKGBKCRAAHAMACC
Paenibacillus DbfA1	YDA1f	Forward	GGAGCAGCATGTAGTCAGAG
	YDA1r	Reverse	GATCCAGCAAGTGAGCTTCG
Inverse PCR for *Paenibacillus* sp. TSY30			
1, 2, 3*	EHNf	Forward	AGTCCCAAGTCCAAAGCCAGAC
1, 2, 3, 5	EHNPr	Reverse	CTTCCAGTTCGCATGAACGACC
4, 8	NN-2f	Forward	ATGATCCGGTACTGTTGGTGCG
4	NS-1r	Reverse	TCCTGCTGGTAGGCCATAAACG
5	Pst-1f	Forward	TCTGATCATTGCGGTGTCGCTG
6	SacI-1f	Forward	AGCCTTGATGGAGGACTACGAG
6, 8	SN-5r	Reverse	GCAGCAATCCCAGATGATCTCG
7	Not-1f	Forward	GTTCAAGGATACGGATCTGGCC
7	Not-2r	Reverse	GTGACTGCGAACGCTTAGTTCC
Inverse PCR for *Rhizobium* sp. TSY03b			

10, 12, 15*	HNX1f	Forward	ATGATGATCTACCGCACGCGGC
10, 11	HN-1r	Reverse	ACCATAGGTGTACGCGAAGC
11	Nco-1f	Forward	GACTGACAACGAAACCTTCGCC
12	Nde-1r	Reverse	TTGGCAATCTGCGACTCATGGC
13	Sal-1f	Forward	GAATCTGTCGTTCCTGGCAG
13, 15	SX-1r	Reverse	GATGACCCACTTCTGGATGC
14	Sal-2f	Forward	GATACGTGGAAGAGGGTGCAC
14	Sal-2r	Reverse	CAGCTTGCAGATCAGGATCGG
Real-time qPCR for AhDOa from:			
Paenibacillus sp. (NidA1)	TSY30n-2f	Forward	TGGGTCGTTCATGCGAACTG
	TSY30n-2r	Reverse	CCACATTTCTTGCGGCAACC
Paenibacillus sp. (DbfA1)	TSY30d-1f	Forward	TTGAAGTGGCAGGTCCCATC
	TSY30d-1r	Reverse	CGATCCAATTCCAGACCCAC
Rhizobium sp. TSY03b	TSY03b-1f	Forward	GCACGACCTCACATCTGTCCGGCATC
	TSY03b-1r	Reverse	GACACAAGTGTACATCGGTCCGCGAC
N. naphthalenivorans DF261	DF261-1f	Forward	GGAGCCCATCTTCAAGCACTCA
	DF261-1r	Reverse	CCGGAATAAGCGTCCCACAACA

* Figures correspond to the DNA fragment regions shown in Fig. 1b and 1d.

Table S2. Deduced ORFs found in the 7.3 kb nucleotide stretch of cloned DNA from *Paenibacillus* sp. strain TSY30

ORF	Position in accession no.	Calculated molecular mass (Da)	BLAST homology search for protein			
			% Identity	Protein/function	Closest relative as host organism	Accession number
1	56–925	32,812	65	5-Carboxymethyl-2-hydroxymuconate delta-isomerase	*Bacillus tusciae* DSM 2912	YP_003590136
2	944–2137	44,718	55	Monooxygenase FAD-binding protein	*Geobacillus* sp. Y412MC61	ZP_04392202
3	2205–3533	50,860	63	Aromatic-ring-hydroxylating dioxygenase, alpha subunit	*Geobacillus* sp. Y4.1MC1	ZP_05373195
4	3552–4049	19,431	59	Aromatic-ring-hydroxylating dioxygenase, beta subunit	*Geobacillus* sp. Y4.1MC1	ZP_05373196
5	4106–4987	31,337	40	Inner-membrane translocator	*Geobacter lovleyi* SZ	YP_001952098
6	5027–6022	35,919	41	Inner-membrane translocator	*Geobacter uraniumreducens* Rf4	ZP_01141122
7	6019–6810	28,905	50	ABC transporter-related ATP-binding protein	*Acidiphilium cryptum* JF-5	YP_001233501
8	6798-7348*	–	56	ABC transporter	*Paenibacillus* sp. D14	ZP_04853801

* Incomplete sequence in the 3' region.

Table S3. Deduced ORFs found in the 5.9 kb nucleotide stretch of cloned DNA from *Rhizobium* sp. strain TSY03b

ORF	Position in accession no.	Calculated molecular mass (Da)	BLAST homology search for protein			
			% Identity	Protein/function	Closest relative as host organism	Accession number
1	898–1*	–	89	TRAP transporter solute receptor, TAXI family	*Polymorphum gilvum* SL003B-26A1	YP_004305816
2	1106–2466	50,644	94	IPB-dioxygenase, ISP large subunit	*Polymorphum gilvum* SL003B-26A1	YP_004305818
3	2536–3111	22,832	91	Biphenyl 2,3-dioxygenase beta subunit	*Polymorphum gilvum* SL003B-26A1	YP_004305819
4	3122–3427	11,007	71	Ferredoxin	*Xanthobacter polyaromaticivorans*	BAC98958
5	3461–4294	29,127	89	Short-chain dehydrogenase/reductase (dihydrodiol dehydrogenase)	*Polymorphum gilvum* SL003B-26A1	YP_004305821
6	4450–5901	51,690	90	Dehydrogenase PhnF	*Polymorphum gilvum* SL003B-26A1	YP_004305822

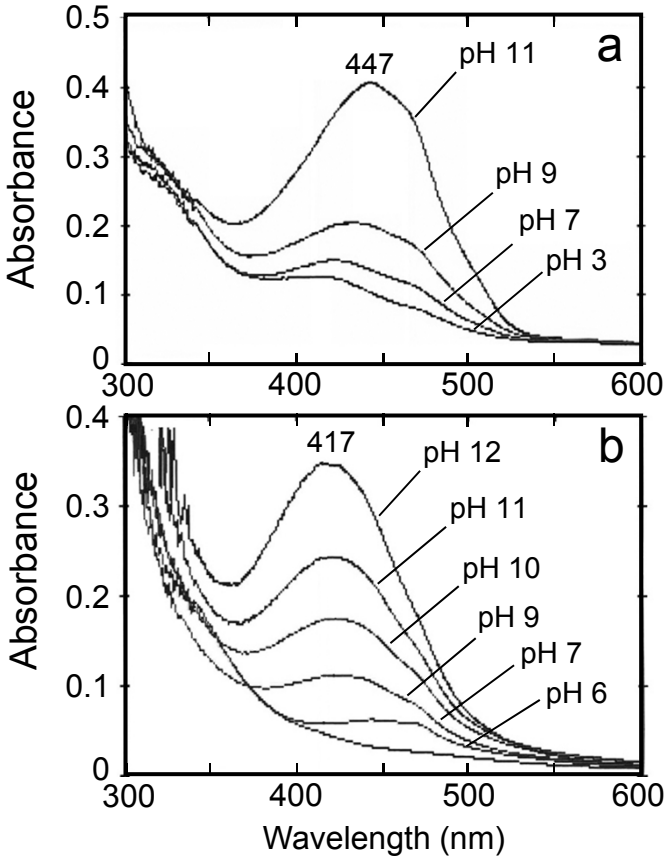
*Incomplete sequence in the complementary 3' region.

Supplemental figures

Fig. S1. Absorption spectra of the yellow-pigmented DF-degrading cultures of *Paenibacillus* sp. strain TSY30 (a) and *Rhizobium* sp. strain TSY03b (b). DF in the culture of *Rhizobium* sp. strain TSY03b was degraded co-metabolically in the presence of naphthalene. Spectral patterns of the pigmented supernatant in response to changes in pH are shown.

Fig. S2. Southern hybridization of digested genomic DNA of *Paenibacillus* sp. strain TSY30 (a, b) and *Rhizobium* sp. strain TSY03b (c, d) with a labeled PCR clone as the probe. The probes used were the PCR clone with primers PAH2f/PHA3r2 (*nidA1*) for *Paenibacillus* sp. strain TSY30 and that with primers PAH2f/PHA5r (*nidA1*) for *Rhizobium* sp. strain TSY03b. (a, c), Agarose electrophoresis with ethidium bromide staining of genomic DNA digested with restriction enzymes, *Eco*RI, *Not*I, *Sal*I, *Pst*I, and *Sac*I; (b, d), hybridization signals on the nylon membrane to which the digested DNAs were transferred. Positive controls are indicated in lane P.

Kaiya et al. Fig. S1



Kaiya et al. Fig. S2