

Supplementary material

Genomic analysis of dibenzofuran-degrading *Pseudomonas veronii* Pvy reveals its biodegradative versatility

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Table S1: The loci in the genome of the Pvy strain putatively involved in the metabolism of aromatic compounds including aromatic pollutants. Function of predicted proteins was assessed through BLAST search against UniProtKB/Swiss-Prot and Reference Protein (RefSeq) databases, comparison with literature, and the KEGG database of reference pathways of aromatics degradation.

Chromosome (Genbank accession no. CP039631.3)			
Locus tag	Coding sequence length [bp]	Closest hit (similarity score)	Gene and function assignment
pca region I (positions 155,060– 165,752 in the annotated chromosome sequence) protocatechuate (3,4-dihydroxy benzoate) utilization: from protocatechuate to succinyl-CoA and acetyl-CoA through β -carboxymuconate (protocatechuate intradiol cleavage)			
E4167_00830	393	4-carboxymuconolactone decarboxylase [<i>Acinetobacter baylyi</i> ADP1] (81%)	<i>pcaC</i> , 4-carboxymuconolactone decarboxylase
E4167_00835	792	3-oxoadipate enol-lactonase 1 [<i>Acinetobacter baylyi</i> ADP1] (61%)	<i>pcaD</i> , 3-oxoadipate enol-lactonase
E4167_00840	1,368	3-carboxy-cis,cis-muconate cycloisomerase [<i>Pseudomonas putida</i>] (85%)	<i>pcaB</i> , 3-carboxy-cis,cis-muconate cycloisomerase
E4167_00845	1,296	α -ketoglutarate permease [<i>Escherichia coli</i> K-12] (82%)	<i>pcaT</i> , MFS transporter
E4167_00850	567	Protocatechuate 3,4-dioxygenase α -chain [<i>Acinetobacter baylyi</i> ADP1] (59%)	<i>pcaG</i> , protocatechuate 3,4-dioxygenase α -chain
E4167_00855	705	Protocatechuate 3,4-dioxygenase β -chain [<i>Burkholderia cepacia</i>] (73%)	<i>pcaH</i> , protocatechuate 3,4-dioxygenase β -chain
E4167_00860	1,203	β -keto adipyl-CoA thiolase [<i>Pseudomonas putida</i>] (95%)	<i>pcaF</i> , β -keto adipyl-CoA thiolase
E4167_00865	780	β -keto adipate:succinyl-CoA transferase subunit B [<i>Pseudomonas knackmussii</i> B13] (92%)	<i>pcaJ</i> , β -keto adipate:succinyl-CoA transferase subunit B
E4167_00870	858	β -keto adipate:succinyl-CoA transferase subunit A [<i>Pseudomonas knackmussii</i> B13] (93%)	<i>pcaI</i> , β -keto adipate:succinyl-CoA transferase subunit A
E4167_00880	1,344	4-hydroxybenzoate transporter PcaK [<i>Pseudomonas putida</i>] (94%)	<i>pcaK</i> , secondary metabolite transporter protein
E4167_00885	843	Pca regulon regulatory protein [<i>Pseudomonas putida</i>] (93%)	<i>pcaR</i> , transcription regulatory protein
hmg region (positions 516,382 – 520,500 in the annotated chromosome sequence) degradation of homogentisate: from homogentisate to acetoacetate and fumarate			
E4167_02490	636	Maleylacetoacetate isomerase [<i>Pseudomonas aeruginosa</i> PAO1] (82%)	<i>hmgC</i> , maleylacetoacetate isomerase
E4167_02495	1,287	Fumarylacetoacetase [<i>Pseudomonas putida</i>] (84%)	<i>hmgB</i> , fumarylacetoacetase
E4167_02500	1,284	Homogentisate 1,2-dioxygenase [<i>Pseudomonas fluorescens</i> Pf0-1] (95%)	<i>hmgA</i> , Homogentisate 1,2-dioxygenase

E4167_02505	780	HmgR transcriptional repressor [<i>Pseudomonas putida</i>] (90%)	<i>hmgR</i> , HmgR transcriptional repressor
<i>kyn/ant/cat</i> region (positions 2,778,875 – 2,791,862 in the annotated chromosome sequence) Degradation of tryptophan to catechol through L-formylkynurenine and anthranilate; catechol degradation 3-oxoadipate-enol-lactone (<i>ortho</i> -cleavage pathway)			
E4167_13120	651	kynurenine formamidase [<i>Pseudomonas protegens</i> Pf-5] (92%)	<i>kynB</i> , kynurenine formamidase
E4167_13125	858	Tryptophan 2,3-dioxygenase [<i>Pseudomonas protegens</i> Pf-5] (92%)	<i>kynA</i> , tryptophan 2,3-dioxygenase
E4167_13130	1,401	Aromatic amino acid transport protein AroP [<i>Escherichia coli</i> CFT073] (80%)	<i>aroP</i> , tryptophan permease
E4167_13135	1,008	Anthranilate 1,2-dioxygenase electron transfer component [<i>Acinetobacter baylyi</i> ADP1] (72%)	<i>antC</i> , anthranilate 1,2-dioxygenase electron transfer component
E4167_13140	492	Anthranilate 1,2-dioxygenase small subunit [<i>Acinetobacter baylyi</i> ADP1] (72%)	<i>antB</i> , anthranilate 1,2-dioxygenase small subunit
E4167_13145	1,392	Anthranilate 1,2-dioxygenase large subunit [<i>Acinetobacter baylyi</i> ADP1] (87%)	<i>antA</i> , anthranilate 1,2-dioxygenase large subunit
E4167_13155	993	HTH-type anthranilate 1,2-dioxygenase regulatory protein AndR [<i>Burkholderia cepacia</i>] (46%)	<i>andR</i> , HTH-type transcriptional regulator
E4167_13160	876	HTH-type transcriptional regulator CatR [<i>Pseudomonas putida</i>] (80%)	<i>catR</i> , HTH-type transcriptional regulator
E4167_13165	1,127	Muconate cycloisomerase [<i>Pseudomonas putida</i>] (84%)	<i>catB</i> , muconate cycloisomerase
E4167_13170	291	Muconolactone δ -isomerase [<i>Pseudomonas putida</i>] (86%)	<i>catC</i> , muconolactone δ -isomerase
E4167_13175	930	Catechol 1,2-dioxygenase 2 [<i>Acinetobacter lwoffii</i>] (72%)	<i>catA</i> , catechol 1,2-dioxygenase
E4167_13180	474	branched-chain keto acid dehydrogenase multienzyme complex (Bkd) operon transcriptional regulator [<i>Pseudomonas putida</i>] (61%)	Lrp family transcriptional regulator
E4167_13185	1,251	Kynureninase [<i>Pseudomonas fluorescens</i>] (92%)	<i>kynU</i> , kynureninase; L-kynurenine hydrolase]
<i>dmp/cat</i> region (positions 5,331,963 – 5,346,808 in the annotated chromosome sequence) Utilization of phenol through catechol (<i>meta</i> -cleavage pathway)			
E4167_25315	309	Ferredoxin, plant-type [<i>Pseudomonas putida</i>] (68%)	Ferredoxin
4167_25320	429	No significant hit in UniProtKB/SwissProt databases, RefSeq database: 4-oxalocrotonate tautomerase [<i>Pseudomonas extremaustralis</i>] (89%)	<i>dmpI</i> , 4-oxalocrotonate tautomerase
E4167_25325	756	No significant hit in UniProtKB/SwissProt databases	short-chain alcohol dehydrogenase family protein
E4167_25330	1,059	4-hydroxy-2-oxovalerate aldolase 1 [<i>Azoarcus</i> sp. BH72] (95%)	<i>dmpG</i> , 4-hydroxy-2-oxovalerate aldolase
E4167_25335	915	Acetaldehyde dehydrogenase [acetylating] 1 [<i>Azoarcus</i> sp. BH72] (92%)	<i>dmpF</i> , acetaldehyde dehydrogenase [acetylating]
E4167_25340	213	4-oxalocrotonate tautomerase [<i>Pseudomonas</i> sp. CF600] (65%)	<i>dmpI</i> , 4-oxalocrotonate tautomerase
E4167_25345	804	4-oxalocrotonate decarboxylase [<i>Pseudomonas</i> sp. CF600] (73%)	<i>dmpH</i> , 4-oxalocrotonate decarboxylase
E4167_25350	801	2-hydroxypent-2,4-dienoate hydratase [<i>Pseudomonas putida</i>] (75%)	<i>dmpE</i> , 2-hydroxypent-2,4-dienoate hydratase
E4167_25355	1,461	2-hydroxymuconic semialdehyde dehydrogenase [<i>Pseudomonas</i> sp. CF600] (81%)	<i>dmpC</i> , 2-hydroxymuconic semialdehyde dehydrogenase
E4167_25360	1,062	Phenol 2-monooxygenase P5 component [<i>Pseudomonas</i> sp. CF600] (74%)	<i>dmpP</i> , phenol 2-monooxygenase P5 component
E4167_25365	357	Phenol 2-monooxygenase P4 component [<i>Pseudomonas</i> sp. CF600] (57%)	<i>dmpQ</i> , phenol 2-monooxygenase P4 component

E4167_25370	1,521	Phenol 2-monooxygenase P3 component [<i>Pseudomonas sp. CF600</i>] (76%)	<i>dmpN</i> , phenol 2-monooxygenase P3 component
E4167_25375	270	Phenol 2-monooxygenase P2 component [<i>Pseudomonas sp. CF600</i>] (71%)	<i>dmpN</i> , phenol 2-monooxygenase P2 component
E4167_25380	993	Phenol 2-monooxygenase P1 component [<i>Pseudomonas sp. CF600</i>] (65%)	<i>dmpL</i> , phenol 2-monooxygenase P1 component
E4167_25385	297	Phenol 2-monooxygenase P0 component [<i>Pseudomonas sp. CF600</i>] (58%)	<i>dmpK</i> , phenol 2-monooxygenase P0 component
E4167_25390	930	Catechol 2,3-dioxygenase [<i>Pseudomonas putida</i>] (68%)	<i>catA</i> , catechol 2,3-dioxygenase
E4167_25395	1,695	Phenol regulator MopR [<i>Acinetobacter guillouiae</i>] (61%)	<i>mopR</i> , transcriptional regulator
<i>dmp/ardI</i> region (positions 5,426,546 – 5,437,395 in the annotated chromosome sequence) unknown function – putative aromatic secondary metabolite degradation pathway, nitronate resistance			
E4167_25680	1,029	4-hydroxy-2-oxovalerate aldolase [<i>Pseudomonas putida</i>] (96%)	<i>dmpG</i> , 4-hydroxy-2-oxovalerate aldolase
E4167_25685	942	Acetaldehyde dehydrogenase (acetylating) [<i>Pseudomonas putida</i>] (92%)	<i>dmpF</i> , acetaldehyde dehydrogenase (acetylating)
E4167_25690	1,860	Feruloyl-CoA synthase FadD [<i>Pseudomonas sp. StFLB209</i>] (56%)	Putative acyl-CoA synthase
E4167_25695	783	2-keto-4-pentenoate hydratase 1 [<i>Dechloromonas aromatica</i> RCB] (70%)	<i>dmpE</i> , 2-keto-4-pentenoate hydratase
E4167_25700	972	Propionate 3-nitronate monooxygenase [<i>Paraburkholderia phytofirmans</i> PsJN] (42%)	Putative propionate 3-nitronate monooxygenase
E4167_25705	813	Biphenyl-cis-diol dehydrogenase [<i>Rhodococcus globerulus</i>] (64%)	Aromatic compound-cis-diol dehydrogenase
E4167_25710	531	Biphenyl 2,3-dioxygenase β -subunit [<i>Rhodococcus jostii</i> RHA1] (52%)	ARHD β -subunit, unknown function
E4167_25715	1,350	Biphenyl 2,3-dioxygenase α -subunit [<i>Rhodococcus jostii</i> RHA1] (56%)	ARHD α -subunit, unknown function
E4167_25720	327	Carbazole 1,9a-dioxygenase, ferredoxin component CarAc [<i>Pseudomonas resinovorans</i>] (58%)	ARHD ferredoxin component
E4167_25725	849	Protocatechuate 4,5-dioxygenase β - chain [<i>Sphingobium sp. SYK-6</i>] (44%)	aromatic ring opening dioxygenase, unknown specificity
E4167_25730	339	No significant hit in UniProtKB/SwissProt databases	
E4167_25735	816	2-hydroxymuconate semialdehyde hydrolase [<i>Pseudomonas sp. CF600</i>] (64%)	<i>dmpD</i> , 2-hydroxymuconate semialdehyde hydrolase
<i>iaa</i> region (positions 6,196,771 – 6,204,137 in the annotated chromosome sequence) Indole-3-acetic acid (auxin phytohormone, IAA) degradation pathway			
E4167_29060	501	NADH:flavin oxidoreductase IacG [<i>Pseudomonas putida</i> 1290] (87%)	<i>iacG</i> , NADH:flavin oxidoreductase
E4167_29065	960	Reductase component of an IacF [<i>Pseudomonas putida</i> 1290] (86%)	<i>iacF</i> , reductase component of an ARD
E4167_29070	741	IacE [<i>Pseudomonas putida</i> 1290] (84%)	<i>iacE</i> , product involved in IAA degradation
E4167_29075	480	ARHD small subunit IacD [<i>Pseudomonas putida</i> 1290] (86%)	<i>iacD</i> , ARHD small subunit
E4167_29080	1,266	ARHD large subunit IacC [<i>Pseudomonas putida</i> 1290] (94%)	<i>iacC</i> , ARHD large subunit
E4167_29085	534	Protein of unknown function IacI [<i>Pseudomonas putida</i> 1290] (84%)	<i>iacI</i> , unknown function in IAA degradation
E4167_29090	363	IacB [<i>Pseudomonas putida</i> 1290] (93%)	<i>iacB</i> , auxiliary or accessory protein of the IacE protein
E4167_29095	1,176	indole-3-acetate monooxygenase IacA [<i>Pseudomonas putida</i> 1290] (87%)	<i>iacA</i> , indole-3-acetate monooxygenase
E4167_29100	1,122	Putative amidase IacH [<i>Pseudomonas putida</i> 1290] (77%)	<i>iacH</i> , putative amidase
<i>pca</i> region II (positions 6,222,114 – 6,224,507 in the annotated chromosome sequence) protocatechuate 3,4-dioxygenase			
E4167_29190	603	Protocatechuate 3,4-dioxygenase α -chain [<i>Pseudomonas putida</i>] (87%)	<i>pcaG</i> , Protocatechuate 3,4-dioxygenase α -subunit

E4167_29195	720	Protocatechuate 3,4-dioxygenase β - chain [<i>Pseudomonas putida</i>] (92%)	<i>pcaH</i> , Protocatechuate 3,4-dioxygenase β -subunit
E4167_29200	930	HTH-type transcriptional regulator PcaQ [<i>Agrobacterium fabrum</i> C58] (56%)	<i>pcaQ</i> , transcriptional
<i>mhp/vanAB/vdh</i> region (positions 5,861,936 – 5,889,165 in the annotated chromosome sequence)			
phenylpropanoid metabolism and degradation			
E4167_27540	786	<i>mhp</i> operon transcriptional activator [<i>Escherichia coli</i> K-12] (81%)	<i>hmpR</i> , transcriptional regulator
E4167_27545	1,656	3-(3-hydroxy-phenyl)propionate/3-hydroxycinnamic acid hydroxylase [<i>Klebsiella pneumoniae</i> ssp. <i>pneumoniae</i> MGH 78578] 83%	<i>mhpA</i> , 3-(3-hydroxy-phenyl)propionate/3-hydroxycinnamic acid hydroxylase
E4167_27550	954	3-carboxyethylcatechol 2,3-dioxygenase 1 [<i>Pseudomonas putida</i>] (85%)	<i>mhpB</i> , 3-carboxyethylcatechol 2,3-dioxygenase
E4167_27555	867	2-hydroxy-6-oxonadienedioate/2-hydroxy-6-oxonatrienedioate hydrolase 2 [<i>Pseudomonas putida</i>] (87%)	<i>mhpC</i> , 2-hydroxy-6-oxonadienedioate/2-hydroxy-6-oxonatrienedioate hydrolase
E4167_27560	807	2-hydroxypentadienoic acid hydratase 2 [<i>Pseudomonas putida</i>] (87%)	<i>mhpD</i> , 2-hydroxypentadienoic acid hydratase
E4167_27565	936	Acetaldehyde dehydrogenase [acetylating] [<i>Pseudomonas putida</i>] (92%)	<i>mhpF</i> , acetaldehyde dehydrogenase [acetylating]
E4167_27570	1,011	4-hydroxy-2-oxovalerate aldolase [<i>Pseudomonas putida</i>] (96%)	<i>mhpE</i> , 4-hydroxy-2-oxovalerate aldolase
E4167_27575	1,173	3-(3-hydroxy-phenyl)propionate transporter [<i>Escherichia coli</i> K-12] (80%)	<i>mhpT1</i> , 3-(3-hydroxy-phenyl)propionate:H(+) symporter
E4167_27580	1,272	Porin-like gallate degradation protein [<i>Pseudomonas putida</i> KT2440] (54%)	OprD family outer membrane porin
E4167_27585	1,062	Vanillate O-demethylase oxygenase subunit [<i>Pseudomonas</i> sp. HR199] (89%)	<i>vanA</i> , vanillate O-demethylase oxygenase subunit
E4167_27590	951	Vanillate O-demethylase oxidoreductase [<i>Pseudomonas putida</i>] (88%)	<i>vanB</i> , vanillate O-demethylase oxidoreductase ferredoxin-like protein
E4167_27595	714	Uncharacterized HTH-type transcriptional regulator YdhC [<i>Bacillus subtilis</i> ssp. <i>subtilis</i> str. 168] (51%)	HTH-type transcriptional regulator
E4167_27600	1,755	3-methylmercaptopyropionyl-CoA dehydrogenase [<i>Ruegeria pomeroyi</i> DSS-3] (59%)	acyl-CoA dehydrogenase, unknown function
E4167_27605	1,242	3-oxoadipyl-CoA thiolase [<i>Pseudomonas aeruginosa</i> PAO1] (54%)	acyl-CoA acetyltransferase
E4167_27610	1,875	feruloyl-CoA synthase from multiple pseudomonads e.g. FadD [<i>Pseudomonas</i> sp. StFLB209/BAP42263] (90%)	<i>fadD</i> , feruloyl-CoA synthase
E4167_27615	1,449	Vanillin dehydrogenase [<i>Pseudomonas fluorescens</i>] (96%)	<i>vdh1</i> , vanillin dehydrogenase
E4167_27620	831	<i>trans</i> -feruloyl-CoA hydratase/vanillin synthase [<i>Pseudomonas fluorescens</i>] (98%)	<i>fadB</i> , <i>trans</i> -feruloyl-CoA hydratase/vanillin synthase
E4167_27625	489	No significant hit in UniProtKB/SwissProt databases	HTH-family transcriptional regulator
E4167_27630	1,329	Porin-like protein GalP [<i>Pseudomonas putida</i> KT2440] (57%)	OprD family outer membrane porin
E4167_27635	1,230	3-(3-hydroxy-phenyl)propionate transporter [<i>Escherichia coli</i> K-12] (68%)	<i>mhpT2</i> , MFS family secondary metabolite uptake protein
E4167_27640	948	No significant hit in UniProtKB/SwissProt databases	Putative phenol degradation protein
E4167_27645	768	Coniferyl-alcohol dehydrogenase [<i>Pseudomonas</i> sp. HR199] (79%)	<i>calA</i> , coniferyl-alcohol dehydrogenase
E4167_27650	1,476	Benzaldehyde dehydrogenase [NAD(+)] [<i>Pseudomonas putida</i>] (66%) vanillin dehydrogenase [<i>Pseudomonas fluorescens</i>] (57%)	<i>vdh2</i> , benzaldehyde/vanillin dehydrogenase
<i>ard2</i> region (positions 6,302,574 – 6,319,553 in the annotated chromosome sequence)			
unknown function – resemblance to aerobic phenylpropanoid degradation pathway through CoA thioesters intermediates (Teufel et al. 2010)			
E4167_29580	801	3-oxoacyl-[acyl-carrier-protein] reductase FabG [<i>Bacillus subtilis</i> ssp. <i>subtilis</i> str. 168] 56%	NAD(P)-dependent short-chain dehydrogenases/reductases family protein
E4167_29585	750	No significant hit in UniProtKB/SwissProt databases	hypothetical protein

E4167_29590	576	Biphenyl 2,3-dioxygenase subunit β [<i>Rhodococcus jostii</i> RHA1] (60%)	ARHD subunit β , unknown function
E4167_29595	1,398	Biphenyl 2,3-dioxygenase subunit α [<i>Rhodococcus jostii</i>] (50%)	ARHD subunit α , unknown function
E4167_29600	1,002	4-hydroxyphenylacetate degradation bifunctional isomerase/decarboxylase [<i>Salmonella enterica</i> ssp. <i>enterica</i> serovar Dublin] (50%)	fumarylacetoacetate hydrolase family protein
E4167_29605	702	NAD-dependent glycerol dehydrogenase [<i>Listeria innocua</i> Clip11262] (53%)	NAD(P)-dependent short-chain dehydrogenases/reductases family protein
E4167_29610	399	No significant hit in UniProtKB/SwissProt databases	Zn-ribbon domain-containing acyl-CoA-associated protein
E4167_29615	1,191	3-oxoacyl-[acyl-carrier-protein] synthase 3 [<i>Synechococcus elongatus</i> PCC 7942] (42%)	acyl-CoA acyltransferase
E4167_29620	792	Pca regulon regulatory protein [<i>Pseudomonas putida</i>] (42%)	HTH-family transcription regulator
E4167_29625	1,584	MFS transporter [<i>Pseudomonas stutzeri</i>] (83%)	Major Facilitator Superfamily-transporter
E4167_29630	930	No significant hit in UniProtKB/SwissProt databases	Fumarylacetoacetate (FAA) hydrolase family protein
E4167_29635	942	Iron-dependent extradiol dioxygenase [<i>Rhodococcus jostii</i> RHA1] (47%)	extradiol dioxygenase
E4167_29640	762	No significant hit in UniProtKB/SwissProt databases	3-ketoacyl-ACP reductase
E4167_29645	252	Ferredoxin [<i>Thermococcus litoralis</i>] (58%)	ferredoxin
E4167_29650	1,275	MFS transporter [<i>Pseudomonas stutzeri</i>] (83%)	Major Facilitator Superfamily-transporter
E4167_29655	1,233	Rhodocoxin reductase [<i>Rhodococcus erythropolis</i>] (63%)	ARHD ferredoxin-reductase subunit
E4167_29660	834	Uncharacterized oxidoreductase YusZ [<i>Bacillus subtilis</i> ssp. <i>subtilis</i> 168] (51%)	NAD(P)-dependent short-chain dehydrogenases/reductases family protein
ard3 region (positions 6,353,153 – 6,368,355 in the annotated chromosome sequence) unknown function – resemblance to aerobic phenylpropanoid degradation pathway through CoA thioesters intermediates (Teufel et al. 2010)			
E4167_29795	771	3-oxoacyl-[acyl-carrier-protein] reductase FabG [<i>Thermotoga maritima</i> MSB8] (56%)	NAD(P)-dependent short-chain dehydrogenases/reductases family protein
E4167_29800	1,059	Acyl-CoA dehydrogenase family member 10 [<i>Homo sapiens</i>] (50%)	acyl-CoA dehydrogenase
E4167_29805	1,305	Acyl-CoA dehydrogenase family member 11 [<i>Rattus norvegicus</i>] (58%)	acyl-CoA dehydrogenase
E4167_29810	738	3-oxoacyl-[acyl-carrier-protein] reductase FabG [<i>Chlamydia pneumoniae</i>] (56%)	NAD(P)-dependent short-chain dehydrogenases/reductases family protein
E4167_29815	2,223	Succinyl-CoA-D-citramalate CoA-transferase [<i>Chloroflexus aurantiacus</i> J-10-fl] (36%)	CoA-transferase
E4167_29820	2,031	Methyl-accepting chemotaxis protein McpQ [<i>Pseudomonas putida</i> KT2440] (60%)	Transporter protein
E4167_29825	1,398	Biphenyl 2,3-dioxygenase subunit α [<i>Rhodococcus jostii</i> RHA1] (48%)	ARHD subunit α , unknown function
E4167_29830	576	Biphenyl 2,3-dioxygenase subunit β [<i>Rhodococcus jostii</i> RHA1] (58%)	ARHD subunit β unknown function
E4167_29835	1,308	2-amino-3-carboxymuconate-6-semialdehyde decarboxylase [<i>Dictyostelium discoideum</i>] (38%)	metallo-dependent hydrolase,
E4167_29840	921	Biphenyl-2,3-diol 1,2-dioxygenase [<i>Paraburkholderia xenovorans</i> LB400] (48%)	extradiol ring-opening dioxygenase
E4167_29845	1,583	Phytoene desaturase [<i>Mycococcus xanthus</i>] (37%)	phytoene desaturase

Plasmid pND (Genbank accession no. CP039632.2)			
Locus tag	Coding sequence length [bp]	Significant hit (similarity score)	Gene designation and corresponding putative protein function assignment
ndo/nah region (positions 49,120 – 58,665 in the annotated plasmid sequence) naphthalene degradation and utilization: complete pathway from naphthalene to salicylate			
E4167_33915	987	Naphthalene 1,2-dioxygenase system ferredoxin--NAD(P)(+), reductase component [<i>Pseudomonas putida</i>] (93%)	<i>ndoR</i> , naphthalene 1,2-dioxygenase system ferredoxin--NAD(P)(+), reductase component
E4167_33920	315	Naphthalene 1,2-dioxygenase system, ferredoxin component [<i>Pseudomonas aeruginosa</i>] (100%)	<i>ndoA</i> , naphthalene 1,2-dioxygenase system, ferredoxin component
E4167_35395	1,353	Naphthalene 1,2-dioxygenase α -subunit [<i>Pseudomonas aeruginosa</i>] (98%)	<i>ndoB</i> , naphthalene 1,2-dioxygenase α -subunit
E4167_33935	582	Naphthalene 1,2-dioxygenase β - subunit [<i>Pseudomonas aeruginosa</i>] (99%)	<i>ndoC</i> , Naphthalene 1,2-dioxygenase β -subunit
E4167_33940	780	1,2-dihydroxy-1,2-dihydronaphthalene dehydrogenase [<i>Pseudomonas</i> sp. C18] (94%)	<i>nahB</i> , 1,2-dihydroxy-1,2-dihydronaphthalene dehydrogenase
E4167_33945	1,452	Salicylaldehyde dehydrogenase [<i>Pseudomonas</i> sp. C18] (96%)	<i>nahF</i> , salicylaldehyde dehydrogenase
E4167_33950	909	1,2-dihydroxynaphthalene dioxygenase [<i>Pseudomonas aeruginosa</i>] (99%)	<i>nahC</i> , 1,2-dihydroxynaphthalene dioxygenase
E4167_33955	636	Dibenzothiophene metabolism operon protein PahQ [<i>Pseudomonas aeruginosa</i>] (100%)	<i>pahQ</i> , outer membrane porin
E4167_33960	1,005	2'-hydroxybenzalpyruvate aldolase [<i>Pseudomonas aeruginosa</i>] (100%)	<i>nahE</i> , 2'-hydroxybenzalpyruvate aldolase
E4167_33965	600	2-hydroxychromene-2-carboxylate isomerase [<i>Pseudomonas</i> sp. C18] (100%)	<i>nahD</i> , 2-hydroxychromene-2-carboxylate isomerase
salA/dmp region (positions 83,570 – 94,286 in the annotated plasmid sequence) complete salicylate utilization pathway from salicylate to pyruvate and acetylCoA (<i>meta</i> -cleavage pathway)			
E4167_34150	903	HTH-type transcriptional activator NahR [<i>Pseudomonas putida</i>] (89%)	<i>nahR</i> , transcription regulatory protein
E4167_34155	1,314	salicylate 1-monooxygenase [<i>Pseudomonas putida</i>] (98%)	<i>salA</i> , salicylate 1-monooxygenase
E4167_34160	339	Ferredoxin, plant-type [<i>Pseudomonas putida</i>] (87%)	<i>nahT</i> , ferredoxin
E4167_34165	924	Catechol 2,3-dioxygenase [<i>Pseudomonas aeruginosa</i>] (99%)	<i>dmpB</i> , catechol 2,3-dioxygenase
E4167_34170	1,461	2-hydroxymuconic semialdehyde dehydrogenase [<i>Pseudomonas</i> sp. CF600] (94%)	<i>dmpC</i> , 2-hydroxymuconic semialdehyde dehydrogenase
E4167_34175	864	2-hydroxymuconate semialdehyde hydrolase [<i>Pseudomonas putida</i>] (91%)	<i>dmpD</i> , 2-hydroxymuconate semialdehyde hydrolase
E4167_34180	786	2-oxopent-4-enoate hydratase [<i>Pseudomonas putida</i>] (98%)	<i>dmpE</i> , 2-oxopent-4-enoate hydratase
E4167_34185	924	Acetaldehyde dehydrogenase [acetylating] [<i>Pseudomonas stutzeri</i>] (99%)	<i>dmpF</i> , acetaldehyde dehydrogenase [acetylating]
E4167_34190	1,041	4-hydroxy-2-oxovalerate aldolase [<i>Pseudomonas stutzeri</i>] (100%)	<i>dmpG</i> , 4-hydroxy-2-oxovalerate aldolase
E4167_34195	795	4-oxalocrotonate decarboxylase [<i>Pseudomonas putida</i>] (98%)	<i>dmpH</i> , 4-oxalocrotonate decarboxylase
E4167_34200	192	4-oxalocrotonate tautomerase; Short=4-OT [<i>Pseudomonas stutzeri</i>] (98%)	<i>dmpI</i> , 4-oxalocrotonate tautomerase

Table S2: Utilization of aromatic substrates by Pvy strain. The OD_{600nm} of Pvy cultures after 2 and 6 days of incubation are shown, reduced by the value of a parallel abiotic control (MSM medium with Pvy inoculum without added substrate). The numbers given are mean values obtained from two independent experiments, their variation between the experiments was lower than 20%.

Growth substrate/ concentration	2 days of cultivation			6 days of cultivation		
	5mM	10mM	15mM	5mM	10mM	15mM
dibenzofuran	0	0	0	0	0	0
naphthalene	0.20	0.70	1.04	0.17	0.51	0.83
carbazole	0	0	0	0	0	0
biphenyl	0	0	0	0	0	0
salicylic a.	0.38	0	0	0.37	0.73	0
protocatechuic a.	0.53	1.18	1.51	0.50	1.08	1.37
<i>p</i> -hydroxybenzoic a.	0.58	0.69	0.10	0.48	0.57	0.84
vanillic a.	0.40	0.69	0.52	0.35	0.56	0.61
vanillin	0.17	0.09	0	0.13	0.32	0.46
ferulic a.	0	0	0	0	0	0
<i>t</i> -cinnamic acid	0	0	0	0	0	1.38
caffeic a.	0	0	0	0	0	0
indoleacetic a.	0	0	0	0.32	0.70	1.03

Supplementary text:

Implications from genome analysis II: Heavy metal tolerance

The Pvy genome was found to contain at least 4 regions related to copper tolerance and multiple scattered ORFs encoding for putative copper oxidase/binding proteins. The first region harbors ORFs encoding for a copper chaperone and a TonB-dependent copper receptor (locus tags E4167_04890 and E4167_04900, respectively). The second region (locus tags E4167_19455 - E4167_19460) encodes for copper resistance proteins CopD and CopC. The third region consists of a cluster of ORFs *copABCD* encoding for a copper resistance system composed of the proteins CopA, CopB, CopC and CopD (locus tags E4167_RS24400, E4167_RS24405, E4167_RS24410, E4167_RS24415, respectively) (Cha and Cooksey 1991). Constituents of the *copABCD* operon were also found in *P. veronii* R4 (Montes et al. 2016) and *P. veronii* 1YdBTEX2 (de Lima-Morales et al. 2013). The fourth region in the Pvy chromosome encodes for a copper-efflux P-type ATPase (Takeuchi et al. 2005) and corresponding regulator (locus tags E4167_04660-E4167_04665) (Reeve et al. 2002). The other scattered ORFs encode for a putative multicopper oxidase (E4167_02330) (Lee et al. 2005), and the putative three-component heavy metal-efflux RND transporter CusCBA (locus tag E4167_04440, E4167_04445, E4167_044450).

Two regions putatively determining the arsenate resistance of the Pvy strain were found in the genome. The first region harbors ORFs encoding an arsenic resistance transcriptional regulator ArsR1, arsenical pump membrane protein, arsenate reductase, arsenical resistance operon protein (ArsH), arsenical pump modifier and a ferredoxin-NADP reductase (locus tags E4167_34840, E4167_00570 to E4167_00590) (Nelson et al. 2002). The second region consists of a cluster of ORFs (locus tags E4167_35555, E4167_23900 and E4167_23905) encoding for an arsenic resistance system represented by an arsenical resistance protein (ArsH), arsenical pump membrane protein and arsenic resistance transcriptional regulator (ArsR) (Mo et al. 2011).

Other heavy metal resistance genes were also identified in the Pvy genome, including two adjacent ORFs encoding for a putative Cd²⁺/Pb²⁺-responsive transcriptional regulator CadR and cadmium-efflux exporting P-ATPase (locus tags E4167_09925 and E4167_09930), and two other copies of heavy-metal-efflux P-ATPases (E4167_08470 and E4167_16375). Additionally, the following Zn ABC-transporter components were found: ATP-binding protein ZnuC, the high-affinity zinc uptake system membrane protein ZnuB (locus tags E4167_07455 and E4167_07460) and zinc transporter ZntB (locus tag E4167_16045) (Paulsen et al. 2005). Finally, an isolated ORF encoding for a putative chromate transporter was identified (locus tag E4167_18140).

Implications from genome analysis III: Nutrient metabolism

A common feature of *P. veronii* is the capability of denitrification (Ajithkumar et al. 2003; Montes et al. 2016; Elomari et al. 1996; Morales et al. 2016). The genome of *P. veronii* Pvy contains several regions as well as scattered genes putatively encoding for proteins determining its denitrification ability. Within the positions 4,488,959-4,495,704, there are several ORFs encoding for putative respiratory nitrate reductase α , β and γ -subunits together with a nitrate reductase molybdenum cofactor assembly chaperone (locus tags E4167_21465-E4167_21480). In addition to these, a putative nitrous-oxide reductase (locus tag E4167_21415) and three-component putative nitrite reductase (locus tag E4167_22950-E4167_22960) are carried in the *P. veronii* Pvy genome.

Pvy also bears genetic elements associated with soil organic phosphate mineralization, as was reported for *P. veronii* R4 (Montes et al. 2016). At least 7 ORFs were identified in the Pvy genome encoding for putative alkaline phosphatases. Furthermore, two ORFs encoding for putative paralogous ammonia monooxygenases involved in ammonia-to-nitrite transformation were identified (Daum et al. 1998). Similar monooxygenases were also found in *P. veronii* R4 (Montes et al. 2016). The Pvy genome also contains elements for the synthesis of polyphosphate and recessive phosphate mobilization, which are represented by ORFs encoding for polyphosphate kinase PPK1 (E4167_09455) (Buell et al. 2003), polyphosphate kinase 2 (locus tag E4167_24415) (Larimer et al. 2004) and an exopolyphosphatase (E4167_09460) (Zago et al. 1999).

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