

**Table S1.** COG comparison between S72 and other PAH degrading bacteria retrieved from the IMG database.

COG list	Gene abundance			StdErr other	FishersTest Pval	FishersTest adjPval
	S72 (%)	Mean other_PAH_degrading n =17_ (%)	Differences			
Mobilome: prophages, transposons (X)	2.03	0.99	1.05	0.14	0.00	0.00
Amino acid transport and metabolism (E)	6.61	8.87	-2.26	0.38	0.00	0.00
Secondary metabolites biosynthesis, transport and catabolism (Q)	4.52	3.20	1.33	0.28	0.00	0.00
Cell motility (N)	1.50	2.32	-0.83	0.23	0.00	0.01
Translation, ribosomal structure and biogenesis (J)	4.73	6.29	-1.56	0.40	0.01	0.03
Carbohydrate transport and metabolism (G)	6.20	5.06	1.14	0.46	0.01	0.03
Lipid transport and metabolism (I)	6.99	5.85	1.14	0.44	0.01	0.03
Cell wall/membrane/envelope biogenesis (M)	6.58	5.76	0.82	0.26	0.01	0.03
Nucleotide transport and metabolism (F)	1.73	2.43	-0.70	0.12	0.02	0.04
Function unknown (S)	6.35	5.54	0.81	0.25	0.02	0.06
Signal transduction mechanisms (T)	4.65	5.48	-0.83	0.33	0.03	0.06
Extracellular structures (W)	0.51	0.84	-0.33	0.11	0.07	0.13
Replication, recombination and repair (L)	3.33	3.07	0.25	0.18	0.10	0.18
Inorganic ion transport and metabolism (P)	6.22	5.66	0.57	0.17	0.14	0.22
Transcription (K)	7.80	7.79	0.01	0.46	0.21	0.29
Posttranslational modification, protein turnover, chaperones (O)	4.27	4.04	0.23	0.17	0.21	0.29
Intracellular trafficking, secretion, and vesicular transport (U)	1.65	1.97	-0.32	0.16	0.21	0.29
Cell cycle control, cell division, chromosome partitioning (D)	0.79	1.04	-0.25	0.08	0.33	0.42
Coenzyme transport and metabolism (H)	4.95	5.39	-0.44	0.14	0.35	0.42
General function prediction only (R)	9.93	9.37	0.57	0.32	0.47	0.54

Energy production and conversion (C)	6.35	6.60	-0.25	0.23	0.60	0.63
Cytoskeleton (Z)	0.03	0.03	0.00	0.01	0.61	0.63
Defense mechanisms (V)	2.26	2.34	-0.08	0.12	0.90	0.90
RNA processing and modification (A)	0.00	0.02	-0.02	0.00	1.00	1.00
Chromatin structure and dynamics (B)	0.03	0.05	-0.02	0.01	1.00	1.00

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**Table S2.** List of genes in *Spingobium yanoikuyae* S72 which is associated with the degradation of S72.

Locus_tag (GB)	Protein name (GB)	EC NUMBER	Product (Name en PATRIC)	Pathway Name
A6768_06750	acylphosphatase	3.6.1.7	Acylphosphate phosphohydrolase, putative	1,4-Dichlorobenzene degradation
A6768_00755	PQQ-dependent dehydrogenase, methanol/ethanol family	1.1.2.8	Quino(hemo)protein alcohol dehydrogenase, PQQ-dependent	Tetrachloroethene degradation
A6768_08020	2-polyprenyl-6-methoxyphenol hydroxylase	1.14.13.1	Salicylate hydroxylase	Biphenyl degradation
A6768_08130	alkylhydroperoxidase	4.1.1.44	Possible carboxymuconolactone decarboxylase family protein	Benzoate degradation via hydroxylation
A6768_08245	NADPH:quinone reductase	1.1.1.-	Bifunctional protein: zinc-containing alcohol dehydrogenase	Benzoate degradation via hydroxylation
A6768_08265	aldehyde dehydrogenase	1.2.1.3	Aldehyde dehydrogenase	Tetrachloroethene degradation
A6768_08275	aldehyde dehydrogenase	1.2.1.3	Aldehyde dehydrogenase	Tetrachloroethene degradation
A6768_08290	alcohol dehydrogenase	1.1.1.1	Alcohol dehydrogenase	Metabolism of xenobiotics by cytochrome P450
A6768_08315	alkylhydroperoxidase	4.1.1.44	Possible carboxymuconolactone decarboxylase family protein	Benzoate degradation via hydroxylation
A6768_01095	glutathione S-transferase	3.3.2.9	Epoxide hydrolase	Metabolism of xenobiotics by cytochrome P450
A6768_11325	alpha/beta hydrolase	1.2.1.3	Aldehyde dehydrogenase	Tetrachloroethene degradation
A6768_11835	betaine-aldehyde dehydrogenase	4.2.1.17	Enoyl-CoA hydratase	Geraniol degradation
A6768_11870	enoyl-CoA hydratase	2.3.1.16;2.3.1.9	3-ketoacyl-CoA thiolase, Acetyl-CoA acetyltransferase	Geraniol degradation
A6768_11875	acetyl-CoA C-acyltransferase	4.2.1.17	Enoyl-CoA hydratase	Geraniol degradation
A6768_11885	enoyl-CoA hydratase	4.1.1.44	4-carboxymuconolactone decarboxylase	Benzoate degradation via hydroxylation
A6768_12085	carboxymuconolactone decarboxylase	2.3.1.16;2.3.1.9	3-ketoacyl-CoA thiolase , Acetyl-CoA acetyltransferase	Geraniol degradation
A6768_12155	acetyl-CoA C-acyltransferase	3.1.2.-	Acyl-CoA thioesterase II	Benzoate degradation via hydroxylation
A6768_12180	acyl-CoA thioesterase II	4.2.1.17	Enoyl-CoA hydratase	Geraniol degradation
A6768_12205	enoyl-CoA hydratase	3.3.2.9	Epoxide hydrolase,	Metabolism of xenobiotics by cytochrome P450

A6768_12210	enterotoxin	4.2.1.17;1.1.1.35; 5.1.2.3	Enoyl-CoA hydratase, 3-hydroxyacyl-CoA dehydrogenase, 3-hydroxybutyryl-CoA epimerase	Geraniol degradation
A6768_12355	3-hydroxyacyl-CoA dehydrogenase	4.2.1.17	Enoyl-CoA hydratase	Geraniol degradation
A6768_12425	enoyl-CoA hydratase	2.5.1.18	Glutathione S-transferase	Metabolism of xenobiotics by cytochrome P450
A6768_12460	hypothetical protein	4.2.1.17	Enoyl-CoA hydratase	Geraniol degradation
A6768_12490	enoyl-CoA hydratase	2.3.1.16;2.3.1.9	3-ketoacyl-CoA thiolase, Acetyl-CoA acetyltransferase	Geraniol degradation
A6768_12495	acetyl-CoA C-acyltransferase	2.3.1.16	3-ketoacyl-CoA thiolase	Geraniol degradation
A6768_12520	thiolase	1.1.1.-	Bifunctional protein: zinc-containing alcohol dehydrogenase	Benzoate degradation via hydroxylation
A6768_12565	alcohol dehydrogenase	4.2.1.17	Enoyl-CoA hydratase	Geraniol degradation
A6768_12625	enoyl-CoA hydratase	1.14.13.2	P-hydroxybenzoate hydroxylase	Benzoate degradation via hydroxylation
A6768_12975	4-hydroxybenzoate 3-monooxygenase	4.1.1.44	Carboxymuconolactone decarboxylase	Benzoate degradation via hydroxylation
A6768_13690	glutathione S-transferase	3.1.3.1	Alkaline phosphatase	1,4-Dichlorobenzene degradation
A6768_19285	alkylhydroperoxidase	2.5.1.18	Glutathione S-transferase	Metabolism of xenobiotics by cytochrome P450
A6768_04870	LLM class flavin-dependent oxidoreductase	1.14.13.-	Nitrilotriacetate monooxygenase component A	gamma-Hexachlorocyclohexane degradation
A6768_04895	nitrilotriacetate monooxygenase	1.14.13.-	Nitrilotriacetate monooxygenase component A	gamma-Hexachlorocyclohexane degradation

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