

Table S1. Composition of media used for characteristics of bioaugmentation candidates (section Materials and Methods).

Medium	Composition	Concentration, g/L	Purpose
Mineral Salts Medium (MSM), pH=7.2	Na ₂ HPO ₄ ·12H ₂ O	3.78	Isolating the bacteria from the AS and soil
	KH ₂ PO ₄	0.5	
	NH ₄ Cl	5.0	
	MgSO ₄ ·7H ₂ O	0.2	
	yeast extract	0.01	
Phosphate buffered saline (PBS), pH=7.3	NaCl	0.8	Aggregation/coaggregation assays
	KCl	0.2	
	KH ₂ PO ₄	0.24	
	Na ₂ HPO ₄	1.44	
	KH ₂ PO ₄	0.7	
	Na ₂ HPO ₄	0.9	
	NaNO ₃	0.2	
Modified Mineral Salts Agar (MMSA)	MgSO ₄ ·7H ₂ O	0.4	Screening the biosurfactant production
	CaCl ₂ ·2H ₂ O	0.1	
	agar	20.0	
	FeSO ₄ ·7H ₂ O	0.0040	
	MnSO ₄ ·H ₂ O	0.0030	
	(NH ₄) ₆ Mo ₇ O ₂₄ ·4H ₂ O	0.0012	

Table S2. General characteristics of the genomes of *P. putida* OR45a and *P. putida* KB3.

Characteristics	<i>P. putida</i> OR45a	<i>P. putida</i> KB3
Genome size	5 993 405 bp	5 772 482 bp
DNA G + C content	61.7%	61.3%
Mean coverage	39.69x	55.35x
Number of contigs	165	185
Genes number	5729	5581
tRNA number	72	73
Isolation source	AS	soil
GenBank accession	SPUU00000000.1	SPUT00000000.1

Table S3. A distribution of the genes associated with the clusters of orthologous groups (COG) categories in the genomes of *P. putida* OR45a and *P. putida* KB3.

COG	Description	Genes of <i>P. putida</i> OR45a	%	Genes of <i>P. putida</i> KB3	%
A	RNA processing and modification	1	0.02	1	0.02
B	Chromatin structure and dynamics	3	0.05	2	0.04
C	Energy production and conversion	379	6.65	349	6.56
D	Cell cycle control, cell division, chromosome partitioning	50	0.88	47	0.88
E	Amino acid transport and metabolism	491	8.62	427	8.02
F	Nucleotide transport and metabolism	148	2.60	143	2.69
G	Carbohydrate transport and metabolism	258	4.53	206	3.87
H	Coenzyme transport and metabolism	204	3.58	193	3.63
I	Lipid transport and metabolism	180	3.16	151	2.84
J	Translation, ribosomal structure and biogenesis	227	3.98	216	4.06
K	Transcription	524	9.20	461	8.66
L	Replication, recombination, and repair	200	3.51	237	4.45
M	Cell wall/membrane biogenesis	366	6.42	327	6.14
N	Cell motility	122	2.14	118	2.22
O	Posttranslational modification, protein turnover, chaperones	138	2.42	147	2.76
P	Inorganic ion transport and metabolism	390	6.85	345	6.48
Q	Secondary metabolites biosynthesis, transport and catabolism	166	2.91	127	2.39
S	Function unknown	1031	18.10	1004	18.86
T	Signal transduction mechanisms	315	5.53	289	5.43
U	Intracellular trafficking and secretion	105	1.84	120	2.25
V	Defense mechanisms	54	0.95	51	0.96
Genes not in COGs		345	6.06	362	6.80
Total number of genes		5697	100	5323	100

Table S4. Description of genes responsible for selected features of *P. putida* KB3 and *P. putida* OR45a.

Number	Gene	Protein description	<i>P. putida</i> KB3	<i>P. putida</i> OR45a
Exopolysaccharide production				
1	<i>algD</i>	GDP-mannose 6-dehydrogenase	TFW21123.1	TFW36676.1
2	<i>alg8</i>	Alginate biosynthesis protein Alg8	TFW21122.1	TFW36677.1
3	<i>alg44</i>	Mannuronan synthase	TFW21121.1	TFW36678.1
4	<i>algK</i>	Alginate biosynthesis protein AlgK	TFW21120.1	TFW36679.1
5	<i>algE</i>	Alginate production protein AlgE	TFW21119.1	TFW36680.1
6	<i>algG</i>	Mannuronan C5-epimerase	TFW21118.1	TFW36681.1
7	<i>algX</i>	Alginate biosynthesis protein AlgX	TFW21117.1	TFW36682.1
8	<i>algL</i>	Alginate lyase	TFW21116.1	TFW36683.1
9	<i>algI</i>	Probable alginate O-acetylase AlgI	-	TFW36684.1
10	<i>algJ</i>	Probable alginate O-acetylase AlgJ	TFW21115.1	TFW36685.1
11	<i>algF</i>	Alginate biosynthesis protein AlgF	TFW21114.1	TFW36686.1
12	<i>algA</i>	Alginate biosynthesis protein AlgA	TFW21113.1	TFW36687.1
13	<i>algU</i>	RNA polymerase sigma-H factor	TFW21112.1	TFW36688.1
Biocide and heavy metal resistance				
14	<i>cadR</i>	Transcriptional regulator CadR	TFW18997.1	TFW38200.1
15	<i>mepB</i>	Multidrug/solvent efflux pump membrane transporter MepB; the inner membrane transporter component of an organic solvent and antibiotic efflux pump; confers resistance to toluene, hexane, <i>p</i> -xylene, ampicillin, penicillin G, erythromycin, novobiocin and tetracycline	TFW23930.1	-
16	<i>mepC</i>	Multidrug/solvent efflux pump outer membrane protein MepC; the outer membrane component of an organic solvent and antibiotic efflux pump; confers resistance to toluene, hexane, <i>p</i> -xylene, ampicillin, penicillin G, erythromycin, novobiocin and tetracycline	TFW23931.1	-
17	<i>mexE</i>	Multidrug efflux RND membrane fusion protein MexE; part of mexE-mexF-oprN efflux operon, confers resistance to triclosan, <i>n</i> -hexane and <i>p</i> -xylene	TFW22484.1	TFW37358.1
18	<i>mexF</i>	Multidrug efflux RND transporter, permease protein MexF; part of mexE-mexF-oprN efflux operon, confers resistance to triclosan, <i>n</i> -hexane and <i>p</i> -xylene	TFW22485.1	TFW37357.1
19	<i>ruvB</i>	Oxidoreductase from malic enzyme family	TFW24205.1	TFW35747.1
20	<i>osca</i>	Involved in the sulphur starvation response and in Cr(VI) resistance	TFW19225.1	TFW38233.1
21	<i>srpA</i>	Solvent-resistant efflux pump periplasmic linker SrpA; a component of an organic solvent efflux pump srpABC	TFW17525.1	TFW39932.1, TFW35140.1
22	<i>srpR</i>	Solvent efflux pump srpABC operon corepressor SrpR	TFW17523.1	TFW35142.1
23	<i>srpS</i>	Solvent efflux pump srpABC operon corepressor SrpS; In conjunction with SrpR represses the srpABC operon	-	TFW39933.1
24	<i>ttgA</i>	Toluene efflux pump periplasmic linker protein, involved in export of toluene, styrene, <i>m</i> -xylene, propylbenzene and ethylbenzene	TFW23929.1	TFW35252.1
25	<i>ttgB</i>	The inner membrane transporter component, involved in export of toluene, styrene, <i>m</i> -xylene, propylbenzene and ethylbenzene	-	TFW35253.1
26	<i>ttgC</i>	The outer membrane component, involved in export of toluene, styrene, <i>m</i> -xylene, propylbenzene and ethylbenzene	-	TFW35254.1
27	<i>ttgH</i>	The inner membrane transporter component, involved in export of toluene, styrene, <i>m</i> -xylene, propylbenzene and ethylbenzene	-	TFW39931.1, TFW35139.1
28	<i>ttgI</i>	The outer membrane component, involved in export of toluene, styrene, <i>m</i> -xylene, propylbenzene and ethylbenzene	TFW17357.1	TFW39930.1, TFW35138.1
29	<i>ttgR</i>	Toluene efflux pump ttgABC operon repressor ttgR	TFW23928.1	TFW35251.1
30	<i>ttgV</i>	HTH-type transcriptional regulator TtgV	TFW17524.1	TFW35141.1
31	<i>chrR</i>	A soluble quinone reductase that defends against H ₂ O ₂ , confers	TFW19616.1	TFW39953.1

resistance to pottasium ferricyanide

32	<i>merA</i>	Mercury reductase enzyme	TFW17956.1	-
33	<i>merD</i>	HTH-type transcriptional regulator	TFW17957.1	-
34	<i>merE</i>	Mercuric resistance protein	TFW17958.1	-
35	<i>merP</i>	Part of the first pPB mer operon	TFW17955.1	-
36	<i>merR</i>	Mercuric resistance operon regulatory protein	TFW17953.1	-
37	<i>merT</i>	Part of the second pPB mer operon	TFW17954.1	-
38	<i>sodB</i>	Fe-dependent superoxide dismutase	TFW26874.1	TFW38846.1
Metabolism of aromatic compounds				
39	<i>pcaG</i>	Protocatechuate 3,4-dioxygenase, alpha	TFW21608.1	TFW36756.1
40	<i>pcaH</i>	Protocatechuate 3,4-dioxygenase, beta	TFW21607.1	TFW36757.1
41	<i>pcaB</i>	3-carboxy- <i>cis,cis</i> -muconate cycloisomerase	TFW23936.1	TFW35259.1
42	<i>pcaC</i>	4-carboxymuconolactone decarboxylase	TFW23934.1	TFW35257.1
43	<i>npd</i>	2-nitropropane dioxygenase	TFW26424.1	TFW38619.1
44	<i>catA</i>	Catechol 1,2-dioxygenase	TFW26313.1, TFW23377.1	TFW39591.1, TFW38715.1, TFW34356.1
45	<i>catB</i>	Muconate cycloisomerase	TFW26315.1	TFW38713.1, TFW34354.1
46	<i>catC</i>	Muconolactone D-isomerase	TFW26314.1	TFW38714.1, TFW34355.1
47	<i>pcaD</i>	3-oxoadipate enol-lactonase	TFW23935.1	TFW35258.1
48	<i>pcaI</i>	3-oxoadipate CoA-transferase, alpha	TFW26463.1	TFW40084.1
49	<i>pcaJ</i>	3-oxoadipate CoA-transferase, beta	TFW26464.1	TFW40083.1
50	<i>benR</i>	BenABC operon transcriptional activator BenR	TFW23383.1	TFW39585.1
51	<i>benA</i>	Benzoate 1,2-dioxygenase, alpha	TFW23382.1	TFW39586.1
52	<i>benB</i>	Benzoate 1,2-dioxygenase, beta	TFW23381.1	TFW39587.1
53	<i>benC</i>	Benzoate 1,2-dioxygenase electron transfer component	TFW23380.1	TFW39588.1
54	<i>benD</i>	1,6-dihydroxycyclohexa-2,4-diene-1-carboxylate dehydrogenase	TFW23379.1	TFW39589.1
55	<i>hcaA2</i>	Aromatic-ring-hydroxylating dioxygenase	-	TFW39785.1, TFW34369.1
56	<i>dmpK</i>	Phenol hydroxylase P0 protein	TFW19854.1	TFW33964.1
57	<i>dmpL</i>	Phenol hydroxylase P1 protein	TFW19855.1	TFW33965.1
58	<i>dmpM</i>	Phenol hydroxylase P2 protein	TFW19856.1	TFW33966.1
59	<i>dmpN</i>	Phenol hydroxylase P3 protein	TFW19857.1	TFW33967.1
60	<i>dmpO</i>	Phenol hydroxylase P4 protein	TFW19858.1	TFW33968.1
61	<i>dmpP</i>	Phenol hydroxylase P5 protein	TFW19859.1	TFW33969.1
62	<i>dmpB</i>	Catechol 2,3-dioxygenase	TFW19861.1	TFW33971.1
63	<i>dmpC</i>	2-hydroxymuconic semialdehyde dehydrogenase	TFW19862.1	TFW33972.1
64	<i>dmpD</i>	2-hydroxymuconic semialdehyde hydrolase	TFW19863.1	TFW33973.1
65	<i>dmpE</i>	2-oxopent-4-dienoate hydratase	TFW19864.1	TFW33974.1
66	<i>dmpF</i>	Acetaldehyde dehydrogenase	TFW19865.1	TFW33975.1
67	<i>dmpG</i>	4-hydroxy-2-oxovalerate aldolase	TFW19866.1	TFW33976.1
68	<i>dmpH</i>	4-oxalocrotonate decarboxylase	TFW19867.1	TFW33977.1
69	<i>dmpI</i>	2-hydroxymuconate tautomerase	TFW19868.1	TFW33978.1