

# Supplementary Materials

## Content:

### Table: 7

Table S1. Table S1. PCR specific primer sequence.

Table S2. Table S2. Physiological and biochemical characteristics of strain P1.

Table S3. Genomic characteristics of *Pseudomonas* sp. P1.

Table S4. Description of genes obtained from genome of P1 relevant to BPA degradation.

Table S5. Comparison of BPA degradation rates by various microorganisms

Table S6. Information about functional genes resistant to BPA toxicity.

Table S7. LC-MS data of BPA degradation intermediates

### Figure: 4

Figure S1. Scanning electron microscope (A) and morphological observation (B) of strain P1.

Figure S2. The complete TCA cycle (A) and Benzoate degradation (B) were present in the genome of strain P1. The data are based on RAST analysis. Enzyme committee numbers were obtained from the KEGG database.

Figure S3. (A) PCR results of BPA degradation-related genes. (B) RT-PCR agarose gel electrophoresis of BPA degradation-related genes under different conditions.

Figure S4. Degradation of BPA by strain P1 (A) different temperature, (B) different pH, (C) different inoculum size, (D) different initial concentration.

# 1. Supplementary Tables

Table S1. PCR specific primer sequence

Gene Name	Primer name	Sequence (5' to 3')	Primer locus
GE002964	RT1324-1-P1F	TACAACGCCGTGTCGGAAAT	40
	RT1324-1-P1R	GATCACTGGCAACCTGGATACG	1269
GE002994	RT1324-2-P1F	ACACAACGAGCTGACTAAGGCAT	15
	RT1324-2-P1R	TGGGGTCAAGGCGGATGT	1207
GE001899	RT1324-3-P1F	ATGCCGCTGGTGACATTCCT	1
	RT1324-3-P1R	CGTGGTTGAGCGAATACTTGG	322
GE002971	RT1324-4-P1F	ATGCCCACACTGACCTTTATCG	1
	RT1324-4-P1R	GCCTTCCATGTCTTCACTGATAATC	288
GE002989	RT1324-6-P1F	CACCCCATCCGGGCTACTAC	26
	RT1324-6-P1R	ACCTACCTTGCCTATCTTGGACG	1059
GE003785	RT1324-7-P1F	CTGCAGGTTTCCGCCCTTAC	31
	RT1324-7-P1R	CACGGTAATTCTGCCGCTAAC	1005
GE000741	RT1324-9-P1F	AACCTGGCGATCATCGGTG	13
	RT1324-9-P1R	GGTGGCAGCAGGTCGAGC	1130
GE003776	RT1324-11-P1F	ACCGTCGCTACGCTGATGC	52
	RT1324-11-P3R	CGATTTACGGTCACGGTC	3351
GE000932	RT1324-12-P1F	GCCGGTCTGGGCTGTGAC	12
	RT1324-12-P2R	GGAACAGTAGGTGGCAGTGGTAG	1774
GE001625	RT1324-13-P1F	CGCCTGACTCAGTCGCTGCT	8
	RT1324-13-P1R	CACACAAGGGAAGCAAAACG	725

Table S2. Physiological and biochemical characteristics of strain P1

Test item	Positive(+) / negative(-)	Test item	Positive(+) / negative(-)
O-Nitrobenzene-galactoside	-	Glucose	-
Arginine	+	Mannitol	-
Lysine	-	Inositol	-
Ornisanine	-	Sorbitol	-
Sodium citrate	+	Rhamnose	-
Na <sub>2</sub> S <sub>2</sub> O <sub>3</sub>	-	Sucrose	-
Urea	-	Dense disaccharide	+
Tryptophan	-	Amygdalin	-
Pyruvate	-	Arabinose	-
Kohn gelatin	-	Cytochrome oxidase	+

Table S3. Genomic characteristics of strain P1

features	genome	Database	Number
Genome size (bp)	6,172,654	eggNOG	4,767
GC content (%)	62.43%	GO	4,310
Genes (coding)	87.98%	Kegg	2,990
Genes	5636	Nr	5,602
Gene Island	18	Pfam	4,866
tRNA	74	SwissProt	3,451
rRNA	22	TrEMBL	3,451
5S rRNA	8	CAZy	120
16S rRNA	7	TCDB	1,610
23S rRNA	7		

Table S4. Description of genes obtained from genome of P1 relevant to BPA degradation

Gene ID	KO	Gene Description	E-value
GE000135	K00528	ferredoxin/flavodoxin---NADP+ reductase	2.20e-145
GE000144	K00448	protocatechuate 3,4-dioxygenase, alpha subunit	1.40e-115
GE000145	K00449	protocatechuate 3,4-dioxygenase, beta subunit	8.70e-144
GE000372	K11959	urea transport system substrate-binding protein	1.20e-244
GE000739	K18800	2-polyprenylphenol 6-hydroxylase	4.50e-233
GE000741	K03185	2-octaprenyl-6-methoxyphenol hydroxylase	1.10e-231
GE001421	K06134	3-demethoxyubiquinol 3-hydroxylase	3.70e-117
GE001625	K05810	polyphenol oxidase	5.50e-141
GE001899	K04755	ferredoxin, 2Fe-2S	2.60e-61
GE001914	K07336	PKHD-type hydroxylase	3.00e-130
GE002190	K05524	ferredoxin	1.00e-59
GE002202	K00528	ferredoxin/flavodoxin---NADP+ reductase	6.10e-151
GE002435	K15777	4,5-DOPA dioxygenase extradiol	3.10e-147
GE002948	K04090	indolepyruvate ferredoxin oxidoreductase	0.00e+00
GE002971	K04755	ferredoxin, 2Fe-2S	8.00e-57
GE002973	K05337	ferredoxin	5.50e-39
GE002992	K00632	acetyl-CoA acyltransferase	1.30e-213
GE003196	K00114	alcohol dehydrogenase (cytochrome c)	0.00e+00
GE003201	K00114	alcohol dehydrogenase (cytochrome c)	0.00e+00
GE003202	K00138	aldehyde dehydrogenase	1.10e-294
GE003214	K00005	glycerol dehydrogenase	3.00e-204
GE003216	K00014	shikimate dehydrogenase	1.70e-148
GE003217	K00005	glycerol dehydrogenase	4.10e-223
GE003363	K00019	3-hydroxybutyrate dehydrogenase	8.40e-137
GE003765	K15746	beta-carotene 3-hydroxylase	4.90e-87
GE003794	K03381	catechol 1,2-dioxygenase	7.60e-177
GE003798	K05550	benzoate/toluate 1,2-dioxygenase subunit beta	3.40e-91
GE003799	K05549	benzoate/toluate 1,2-dioxygenase subunit alpha	7.60e-274

GE003811	K08324	succinate-semialdehyde dehydrogenase	3.40e-261
GE004035	K15737	glutarate dioxygenase	1.10e-189
GE004064	K00481	p-hydroxybenzoate 3-monooxygenase	3.70e-232
GE004076	K03615	Na <sup>+</sup> -translocating ferredoxin:NAD <sup>+</sup> oxidoreductase subunit C	1.10e-254
GE004077	K03614	Na <sup>+</sup> -translocating ferredoxin:NAD <sup>+</sup> oxidoreductase subunit D	2.00e-172
GE004215	K03381	catechol 1,2-dioxygenase	8.90e-181
GE004453	K12979	beta-hydroxylase	2.00e-175
GE005094	K00500	phenylalanine-4-hydroxylase	3.50e-154
GE005202	K12979	beta-hydroxylase	1.50e-180
GE005451	K03617	Na <sup>+</sup> -translocating ferredoxin:NAD <sup>+</sup> oxidoreductase subunit A	1.10e-95
GE005452	K03614	Na <sup>+</sup> -translocating ferredoxin:NAD <sup>+</sup> oxidoreductase subunit D	1.40e-181
GE005453	K03612	Na <sup>+</sup> -translocating ferredoxin:NAD <sup>+</sup> oxidoreductase subunit G	2.50e-104
GE005454	K03613	Na <sup>+</sup> -translocating ferredoxin:NAD <sup>+</sup> oxidoreductase subunit E	1.80e-77
GE005464	K02192	bacterioferritin-associated ferredoxin	1.90e-33
GE005589	K01676	fumarate hydratase, class I	1.60e-291
GE001749	K00121	S-(hydroxymethyl)glutathione dehydrogenase / alcohol dehydrogenase	6.3e-218
GE001942	K01607	4-carboxymuconolactone decarboxylase	1.4e-65
GE002182	K00121	S-(hydroxymethyl)glutathione dehydrogenase / alcohol dehydrogenase	5.8e-211
GE002684	K01053	gluconolactonase	6.7e-181
GE003109	K13877	2,5-dioxopentanoate dehydrogenase	1.2e-294
GE003381	K10617	p-cumic alcohol dehydrogenase	1.2e-132
GE003382	K10618	p-cumic aldehyde dehydrogenase	2.5e-286
GE003383	K10616	p-cymene methyl-monooxygenase	6.0e-224
GE003384	K18293	p-cymene methyl-monooxygenase electron transfer component	5.4e-203
GE003387	K18227	p-cumate 2,3-dioxygenase ferredoxin reductase component	6.9e-226
GE003388	K10619	p-cumate 2,3-dioxygenase subunit alpha	3.6e-265
GE003389	K16303	p-cumate 2,3-dioxygenase subunit beta	3.7e-94
GE003390	K10621	2,3-dihydroxy-p-cumate/2,3-dihydroxybenzoate 3,4-dioxygenase	2.1e-185
GE003391	K10620	2,3-dihydroxy-2,3-dihydro-p-cumate dehydrogenase	1.8e-142
GE003392	K16304	p-cumate 2,3-dioxygenase ferredoxin component	6.2e-66
GE003393	K10622	HCOMODA/2-hydroxy-3-carboxy-muconic semialdehyde decarboxylase	1.9e-138
GE003395	K10623	HOMODA hydrolase	6.1e-168

GE003396	K02554	2-keto-4-pentenoate hydratase	2.0e-141
GE003397	K04073	acetaldehyde dehydrogenase	5.3e-173
GE003398	K01666	4-hydroxy 2-oxovalerate aldolase	3.4e-197
GE003404	K10702	2-hydroxy-6-oxohepta-2,4-dienoate hydrolase	2.6e-160
GE003405	K03268	benzene/toluene/chlorobenzene dioxygenase subunit alpha	7.3e-277
GE003406	K16268	benzene/toluene/chlorobenzene dioxygenase subunit beta	2.5e-101
GE003407	K18089	benzene/toluene/chlorobenzene dioxygenase ferredoxin component	2.4e-61
GE003408	K18090	benzene/toluene/chlorobenzene dioxygenase ferredoxin reductase component	1.0e-224
GE003409	K16269	cis-1,2-dihydrobenzene-1,2-diol/chlorobenzene dihydrodiol dehydrogenase	4.5e-152
GE003410	K16270	3-methylcatechol 2,3-dioxygenase	1.5e-169
GE003411	K02554	2-keto-4-pentenoate hydratase	1.8e-142
GE003412	K04073	acetaldehyde dehydrogenase	9.1e-173
GE003413	K01666	4-hydroxy 2-oxovalerate aldolase	4.1e-198
GE003796	K05783	dihydroxycyclohexadiene carboxylate dehydrogenase	2.5e-141
GE003797	K05784	benzoate/toluate 1,2-dioxygenase reductase component	3.5e-191
GE004132	K13877	2,5-dioxopentanoate dehydrogenase	7.3e-260
GE004160	K01821	4-oxalocrotonate tautomerase	4.8e-31
GE004181	K01607	4-carboxymuconolactone decarboxylase	2.1e-67
GE004216	K03464	muconolactone D-isomerase	2.9e-50
GE004217	K01856	muconate cycloisomerase	2.4e-204
GE004358	K00121	S-(hydroxymethyl)glutathione dehydrogenase / alcohol dehydrogenase	7.0e-217
GE004480	K13953	alcohol dehydrogenase, propanol-preferring	4.8e-188
GE005231	K01826	5-carboxymethyl-2-hydroxymuconate isomerase	1.2e-61
GE005244	K13877	2,5-dioxopentanoate dehydrogenase	2.9e-285
GE005565	K01607	4-carboxymuconolactone decarboxylase	3.5e-70
GE005566	K01055	3-oxoadipate enol-lactonase	2.4e-150
GE005567	K01857	3-carboxy-cis,cis-muconate cycloisomerase	8.5e-249
<b>Citrate cycle</b>			
GE000904	K01960	pyruvate carboxylase subunit B	0.0e+00
GE000905	K01959	pyruvate carboxylase subunit A	1.1e-270
GE000926	K00382	dihydrolipoamide dehydrogenase	2.1e-266
GE001129	K18118	succinyl-CoA:acetate CoA-transferase	3.8e-282
GE001245	K01610	phosphoenolpyruvate carboxykinase (ATP) pyruvate dehydrogenase E2 component	3.3e-305
GE001333	K00627	(dihydrolipoamide acetyltransferase)	7.0e-205
GE001334	K00163	pyruvate dehydrogenase E1 component	0.0e+00
GE001550	K00627	pyruvate dehydrogenase E2 component	4.4e-203

		(dihydrolipoamide acetyltransferase)	
GE001551	K00162	pyruvate dehydrogenase E1 component beta subunit	5.5e-192
GE001552	K00161	pyruvate dehydrogenase E1 component alpha subunit	3.8e-182
GE001649	K00024	malate dehydrogenase	1.9e-167
GE001790	K00116	malate dehydrogenase (quinone)	3.0e-287
GE001959	K01679	fumarate hydratase, class II	5.6e-248
GE002318	K01679	fumarate hydratase, class II	8.1e-263
GE002617	K01681	aconitate hydratase	0.0e+00
GE002624	K00116	malate dehydrogenase (quinone)	1.7e-304
GE002813	K01682	aconitate hydratase 2 / 2-methylisocitrate dehydratase	0.0e+00
GE004024	K00116	malate dehydrogenase (quinone)	1.6e-307
GE004666	K00031	isocitrate dehydrogenase	2.2e-243
GE004667	K00031	isocitrate dehydrogenase	0.0e+00
GE004831	K01902	succinyl-CoA synthetase alpha subunit	5.0e-165
GE004832	K01903	succinyl-CoA synthetase beta subunit	8.1e-216
GE004833	K00382	dihydrolipoamide dehydrogenase	1.1e-265
		2-oxoglutarate dehydrogenase E2 component	
GE004834	K00658	(dihydrolipoamide succinyltransferase)	5.4e-170
GE004835	K00164	2-oxoglutarate dehydrogenase E1 component	0.0e+00
		succinate dehydrogenase / fumarate reductase,	
GE004836	K00240	iron-sulfur subunit	1.7e-136
		succinate dehydrogenase / fumarate reductase,	
GE004837	K00239	flavoprotein subunit	0.0e+00
		succinate dehydrogenase / fumarate reductase,	
GE004838	K00242	membrane anchor subunit	1.7e-63
		succinate dehydrogenase / fumarate reductase,	
GE004839	K00241	cytochrome b subunit	2.2e-61
GE004840	K01647	citrate synthase	2.5e-250
GE005066	K00382	dihydrolipoamide dehydrogenase	4.9e-260
GE005250	K00116	malate dehydrogenase (quinone)	0.0e+00

E-value: The expected value of the function annotation result, the smaller the more credible;

Table S5. Comparison of BPA degradation rates by various microorganisms

Microorganism	BPA concentration (mg/L)	Degradation Efficiency(%)	Time(h)	Reference
<i>Lactobacillus reuteri</i>	1	69.83	48	[1]
<i>Streptomyces sp.</i>	1	91	240	[2]
<i>Sphingobium sp.</i> BID32	1	100	4.2	[3]
<i>Streptomyces sp</i>	1	90	96	[2]
<i>Ralstonia eutropha</i>	1-20	15-56	240	[4]
<i>Achromobacter xylosoxidans</i> B-16	3	100	108	[5]
<i>Bacillus sp.</i> GZB	5	92.9	96	[6]

<i>Ochrobactrum</i> sp.	10	52.1	70 days	[7]
<i>P. chrysosporium</i>	20	59	96	[8]
<i>Pseudomonas</i> sp. P1	15-30	71.79-96.89	120	This study
<i>Cupriavidus basilensis</i> JF1	34.2	50	144 days	[9]
<i>Sphingobium</i> sp. YC-JY1	100	100	12	

Table S6. Information about functional genes resistant to BPA toxicity

Gene_ID	KO	KO_function	E-value
<b>Bacterial</b>			
<b>secretion system</b>			
GE000007	K03070	preprotein translocase subunit SecA	0.0e+00
GE000417	K11903	type VI secretion system secreted protein Hcp	1.1e-84
GE000453	K12340	outer membrane protein	7.1e-262
GE000545	K03116	sec-independent protein translocase protein TatA	6.6e-36
GE000546	K03117	sec-independent protein translocase protein TatB	4.1e-52
GE000547	K03118	sec-independent protein translocase protein TatC	1.1e-139
GE000585	K03071	preprotein translocase subunit SecB	8.1e-85
GE000645	K03110	fused signal recognition particle receptor	2.5e-188
GE000732	K02454	general secretion pathway protein E	0.0e+00
GE000972	K03217	YidC/Oxa1 family membrane protein insertase	0.0e+00
GE001435	K03073	preprotein translocase subunit SecE	3.1e-52
GE001468	K03076	preprotein translocase subunit SecY	5.8e-242
GE001885	K03210	preprotein translocase subunit YajC	1.7e-54
GE001886	K03072	preprotein translocase subunit SecD	0.0e+00
GE001887	K03074	preprotein translocase subunit SecF	6.4e-160
GE002053	K03118	sec-independent protein translocase protein TatC	7.8e-135
GE002054	K03117	sec-independent protein translocase protein TatB	6.1e-46
GE002055	K03116	sec-independent protein translocase protein TatA	6.3e-35
GE002056	K02460	general secretion pathway protein K	1.5e-178
GE002060	K02452	general secretion pathway protein C	5.6e-74
GE002061	K02453	general secretion pathway protein D	0.0e+00
GE002062	K02454	general secretion pathway protein E	1.1e-267
GE002063	K02455	general secretion pathway protein F	2.6e-209
GE002064	K02456	general secretion pathway protein G	9.5e-77
GE002065	K02457	general secretion pathway protein H	2.0e-79
GE002066	K02458	general secretion pathway protein I	1.6e-61
GE002067	K02459	general secretion pathway protein J	4.2e-124
GE002068	K02461	general secretion pathway protein L	1.7e-212
GE002071	K11016	hemolysin	0.0e+00
GE002072	K11016	hemolysin	0.0e+00
GE002073	K11017	hemolysin activation/secretion protein	0.0e+00
GE002084	K03106	signal recognition particle subunit SRP54	4.0e-222
GE002361	K12340	outer membrane protein	1.1e-238

GE003138	K11892	type VI secretion system protein ImpK	2.3e-170
GE003139	K11904	type VI secretion system secreted protein VgrG	0.0e+00
GE003865	K11904	type VI secretion system secreted protein VgrG	0.0e+00
GE003881	K11907	type VI secretion system protein VasG	0.0e+00
GE003882	K11906	type VI secretion system protein VasD	4.2e-114
GE003884	K11892	type VI secretion system protein ImpK	3.5e-129
GE003885	K11891	type VI secretion system protein ImpL	0.0e+00
GE003887	K11891	type VI secretion system protein ImpL	0.0e+00
GE003888	K11903	type VI secretion system secreted protein Hcp	3.3e-92
GE003933	K02456	general secretion pathway protein G	6.6e-75
GE003934	K02455	general secretion pathway protein F	5.6e-212
GE003983	K02456	general secretion pathway protein G	5.1e-63
GE003984	K02456	general secretion pathway protein G	3.6e-85
GE003985	K02453	general secretion pathway protein D	0.0e+00
GE003990	K02454	general secretion pathway protein E	0.0e+00
GE004239	K11906	type VI secretion system protein VasD	1.3e-48
GE004240	K11891	type VI secretion system protein ImpL	1.1e-130
GE004701	K11904	type VI secretion system secreted protein VgrG	0.0e+00
<b>Mismatch repair</b>			
GE000294	K02342	DNA polymerase III subunit epsilon	4.5e-109
GE000325	K02340	DNA polymerase III subunit delta	1.2e-191
GE000426	K03572	DNA mismatch repair protein MutL	0.0e+00
GE000497	K01972	DNA ligase (NAD <sup>+</sup> )	0.0e+00
		DNA helicase II / ATP-dependent DNA helicase	
GE000911	K03657	PcrA	0.0e+00
GE000976	K02338	DNA polymerase III subunit beta	2.0e-200
GE001349	K02342	DNA polymerase III subunit epsilon	4.9e-131
GE001479	K03111	single-strand DNA-binding protein	1.3e-70
GE001523	K03602	exodeoxyribonuclease VII small subunit	4.2e-34
GE001992	K02339	DNA polymerase III subunit chi	2.5e-77
GE002039	K03601	exodeoxyribonuclease VII large subunit	8.3e-199
GE002099	K07462	single-stranded-DNA-specific exonuclease	0.0e+00
GE002173	K02337	DNA polymerase III subunit alpha	0.0e+00
GE002191	K03555	DNA mismatch repair protein MutS	0.0e+00
GE002483	K02341	DNA polymerase III subunit delta'	5.5e-181
GE004784	K02342	DNA polymerase III subunit epsilon	1.4e-139
GE004906	K02343	DNA polymerase III subunit gamma/tau	0.0e+00
GE004916	K01972	DNA ligase (NAD <sup>+</sup> )	0.0e+00
GE005442	K10747	DNA ligase 1	0.0e+00
GE005584	K01141	exodeoxyribonuclease I	3.2e-286

E-value: The expected value of the functional annotation results, the smaller the more plausible.



Table S7 LC-MS data of BPA degradation intermediates

Products	MW	M (m/z)	Molecular Formula
1,2-Bis(4-hydroxyphenyl)-2-propanol	244.49	243.2	C <sub>15</sub> H <sub>16</sub> O <sub>3</sub>
4,4'-Dihydroxy- $\alpha$ -methylstilbene	226.27	225	C <sub>15</sub> H <sub>14</sub> O <sub>2</sub>
4-Vinylphenol	120.15	119.1	C <sub>8</sub> H <sub>8</sub> O
4-hydroxybenzoate	138.13	137.1	C <sub>7</sub> H <sub>6</sub> O <sub>3</sub>
phenol	94.11	93	C <sub>6</sub> H <sub>6</sub> O
4-isopropenyl phenol	134.18	133.1	C <sub>9</sub> H <sub>10</sub> O

## 2. Supplementary Figures

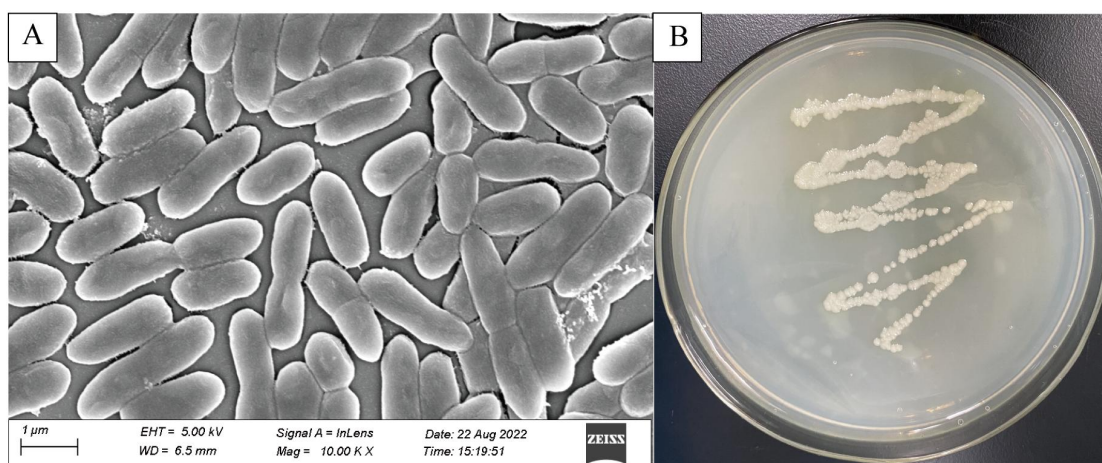


Figure S1. Scanning electron microscope (A) and morphological observation (B) of strain P1

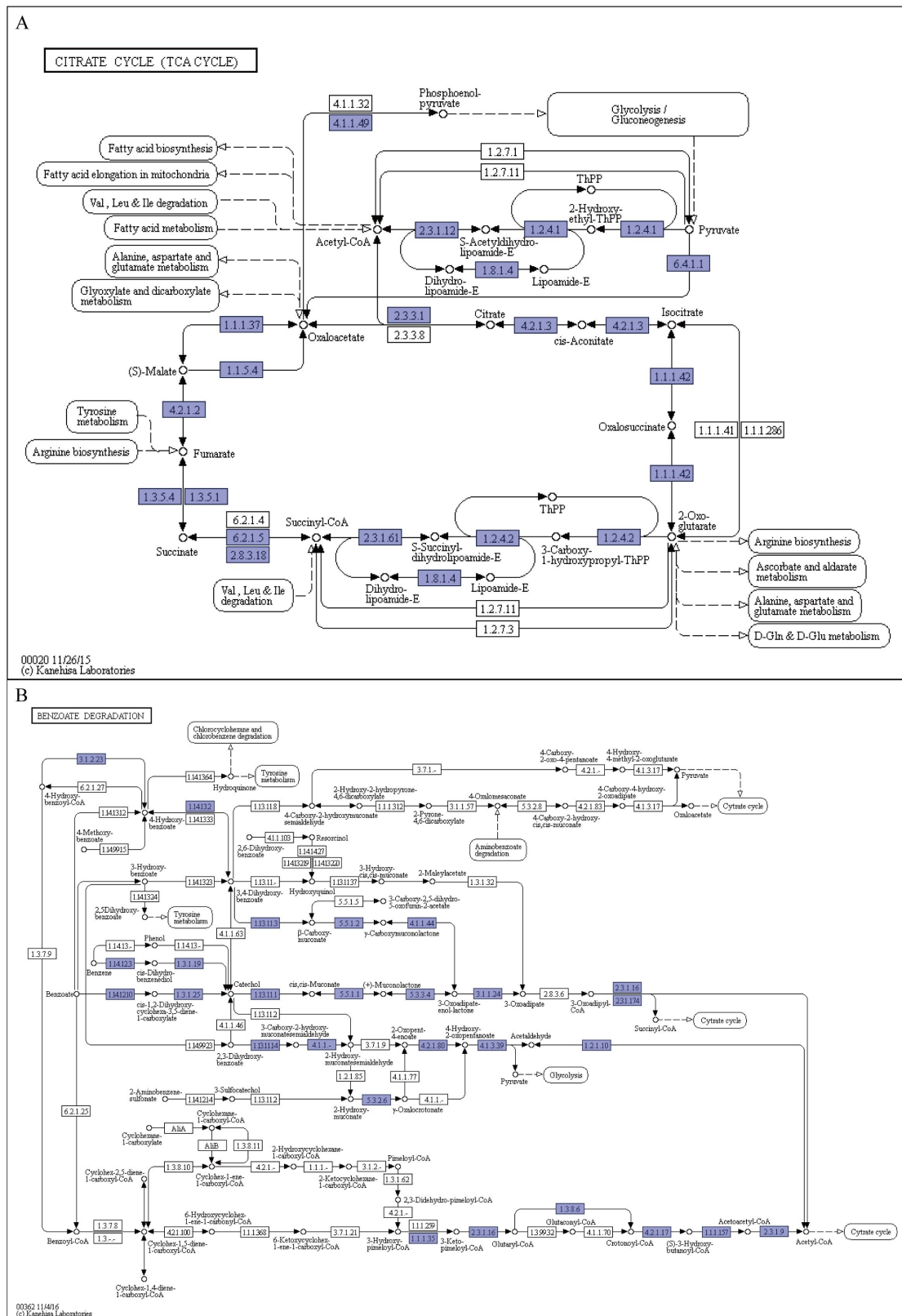


Figure S2. The complete TCA cycle (A) and Benzoate degradation (B) were present in the genome of strain P1. The data are based on RAST analysis. Enzyme committee numbers were obtained from the KEGG database.

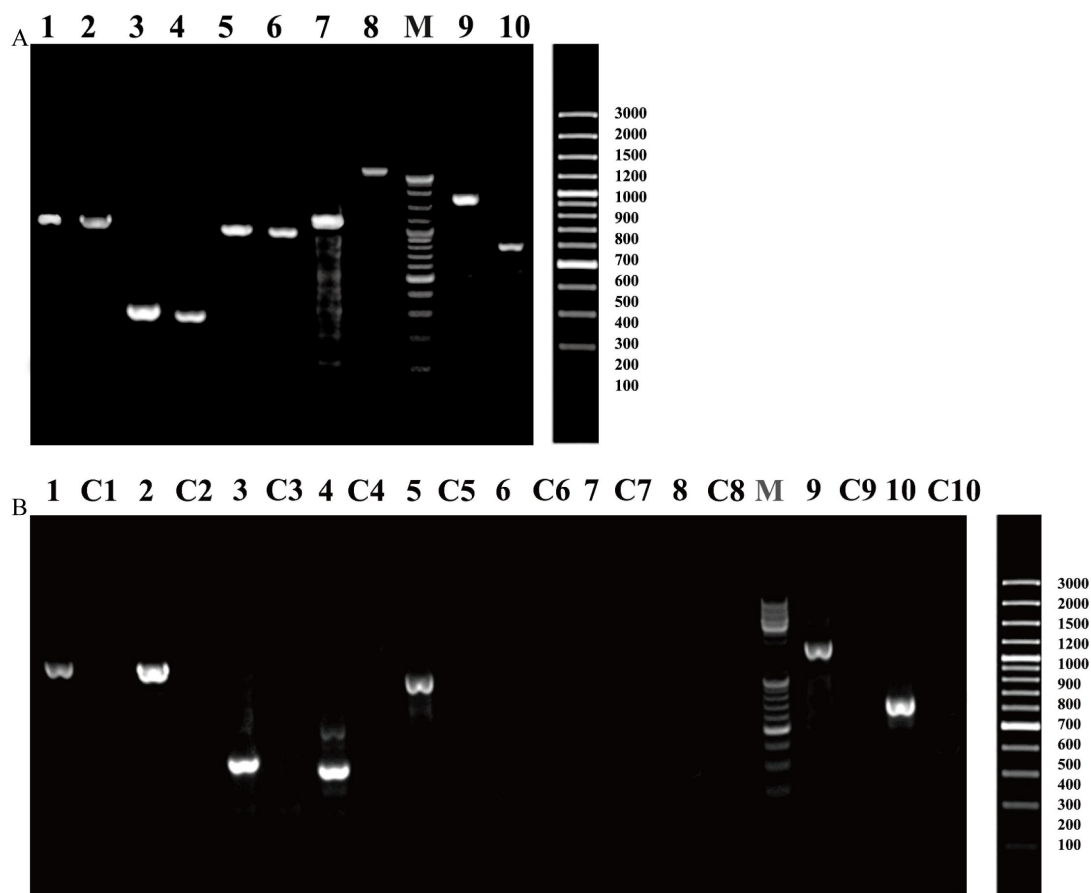


Figure S3. (A) PCR results of BPA degradation-related genes. (B) RT-PCR agarose gel electrophoresis of BPA degradation-related genes under different conditions. The bands of each lane are shown below: M: DNA Marker DL3000; 1. Cytochrome P450; 2. Cytochrome P450; 3. Ferredoxin; 4. Ferredoxin; 5. Aldo/keto reductase; 6. Hydrolase; 7. 2-octaprenyl-6-methoxyphenol hydroxylase; 8. Copper oxidase; 9. Copper oxidase; 10. Laccase.

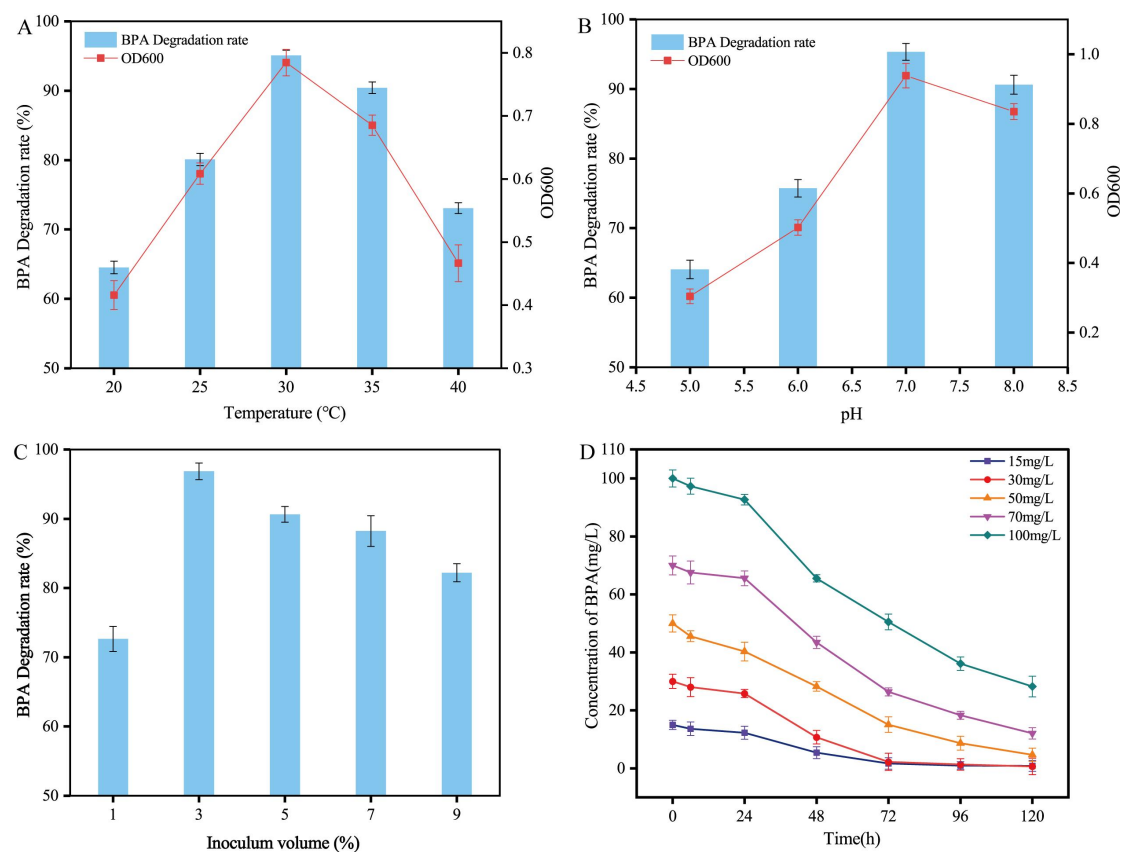


Figure S4. Degradation of BPA by strain P1 (A) different temperature, (B) different pH, (C) different inoculum size, (D) different initial concentration

- Ju, J.; Shen, L.; Xie, Y.F.; Yu, H.; Guo, Y.H.; Cheng, Y.L.; Qian, H.; Yao, W. Degradation potential of bisphenol A by *Lactobacillus reuteri*. *Lwt-Food. Sci. Technol.* 2019, 106, 7-14, <https://doi.org/10.1016/j.lwt.2019.02.022>.
- Kang, J.H.; Ri, N.; Kondo, F. *Streptomyces* sp. strain isolated from river water has high bisphenol A degradability. *Lett. Appl. Microbiol.* 2004, 39, 178-180, <https://doi.org/10.1111/j.1472-765X.2004.01562.x>.
- Zhou, N.A.; Lutovsky, A.C.; Andaker, G.L.; Gough, H.L.; Ferguson, J.F. Cultivation and characterization of bacterial isolates capable of degrading pharmaceutical and personal care products for improved removal in activated sludge wastewater treatment. *Biodegradation.* 2013, 24, 813-827, <https://doi.org/10.1007/s10532-013-9630-9>.
- Heidari, H.; Sedighi, M.; Zamir, S.M.; Shojaosadati, S.A. Bisphenol A degradation by *Ralstonia eutropha* in the absence and presence of phenol. *Int. Bio. Biodegr.* 2017, 119, 37-42, <https://doi.org/10.1016/j.ibiod.2016.10.052>.

5. Zhang, C.; Zeng, G.; Yuan, L.; Yu, J.; Li, J.; Huang, G.; Xi, B.; Liu, H. Aerobic degradation of bisphenol A by *Achromobacter xylosoxidans* strain B-16 isolated from compost leachate of municipal solid waste. *Chemosphere*. 2007, 68, 181-190, <https://doi.org/10.1016/j.chemosphere.2006.12.012>.
6. Li, G.; Zu, L.; Wong, P.-K.; Hui, X.; Lu, Y.; Xiong, J.; An, T. Biodegradation and detoxification of bisphenol A with one newly-isolated strain *Bacillus* sp GZB: Kinetics, mechanism and estrogenic transition. *Bioresource. Technol.* 2012, 114, 224-230, <https://doi.org/10.1016/j.biortech.2012.03.067>.
7. Li, G.; Xiong, J.; Wong, P.K.; An, T. Enhancing tetrabromobisphenol A biodegradation in river sediment microcosms and understanding the corresponding microbial community. *Environ. Pollut.* 2016, 208, 796-802, <https://doi.org/10.1016/j.envpol.2015.11.001>.
8. Wang, J.; Xie, Y.; Hou, J.; Zhou, X.; Chen, J.; Yao, C.; Zhang, Y.; Li, Y. Biodegradation of bisphenol A by alginate immobilized *Phanerochaete chrysosporium* beads: Continuous cyclic treatment and degradation pathway analysis. *Biochem. Eng. J.* 2022, 177, <https://doi.org/10.1016/j.bej.2021.108212>.
9. Jia, Y.; Eltoukhy, A.; Wang, J.; Li, X.; Hlaing, T.S.; Aung, M.M.; Nwe, M.T.; Lamraoui, I.; Yan, Y. Biodegradation of Bisphenol A by *Sphingobium* sp. YC-JY1 and the Essential Role of Cytochrome P450 Monooxygenase. *Int. J. Mol. Sci.* 2020, 21, <https://doi.org/10.3390/ijms21103588>.