



Supplementary Material

Structure-Based Long-Term Biodegradation of the Azo Dye: Insights from the Bacterial Community Succession and Efficiency Comparison

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Table S1. Chemical characteristics of inspected azo dyes.

Name	Molecular weight	Chemical structure	λ_{max}
Methyl orange	327		484
Methyl red	269		484
Orange I	350		484
Orange G	452		480
Tartrazine	534		424
Alizarin yellow R sodium salt	309		456

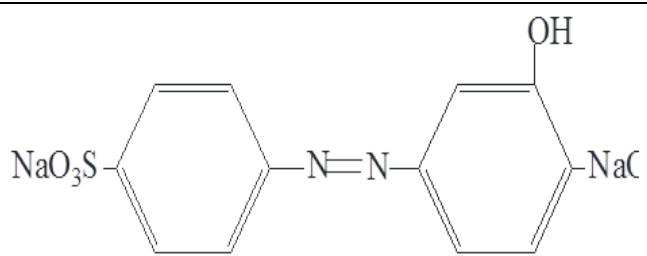


Table S2. Features of isolated strains from acclimated activated sludge.

Colony no.	Strain (access No. in NCBI and % similarity)	Thickness	Size	Density	Surfaces	Edge	Shape	Color difference between up and down side of the colony	Water soluble pigment	Transparency
T-1	<i>Bacillus aerophilus</i> strain KG-J-2(JX027507, 97%)	relatively thick	1~1.8 mm		Rough	Wavy	Curley	Different	Pink	—
T-2	<i>Klebsiella variicola</i> strain RVEV3(KF03618 4, 97%)	Thin	1~1.3 mm		Smooth	Neat	Flat	Different	Red	—
T-3	<i>Exiguobacterium aestuarii</i> strain YS6 (FJ462716, 90)	Thin	1.2~1.5 mm		Smooth	Neat	Flat	Different	White	—
T-4	<i>Paracoccus verus</i> strain NMD4 (KF715850, 99)	relatively thick	0.8~1.2 mm		Smooth	Neat	Low convex	Same	Colorless	Slightly transparent
T-5	<i>Bacillus anthracis</i> strain WY2 (KF641920, 97%)	relatively thick	1.2~2 mm	Loose	Rough	Round teeth	Low convex	Same	Colorless	—
T-6	<i>Pseudomonas geniculata</i> strain Ka38 (JF460769, 96%)	relatively thick	0.8~1.5 mm		Smooth	Neat	Papillary	Different	Yellow	—
T-7	<i>Bacillus cereus</i> strain BVC79 (JQ660662, 99%)	relatively thick	0.8~1.2 mm		Smooth	Teeth	Predentary	Same	Colorless	Slightly transparent
T-8	<i>Stenotrophomonas maltophilia</i> strain T11 (JX130396, 99%)	Thin	1.0~1.2 mm		Smooth	Neat	Flat	Different	Light yellow	—
T-9	<i>Pseudomonas nitroreducens</i> strain LH3 (KJ002756, 99%)	Thin	1.0~1.2 mm		Smooth	Irregular	Flat	Different	White	—

Table S3. Physiological-biochemical characteristics of isolated strains.

Title	T-1	T-2	T-3	T-4	T-5	T-6	T-7	T-8	T9	Result
Gram stain	+	-	+	-	+	-	+	-	-	-
Catalase	+	+	+	+	+	+	+	+	+	+
Nitrate reduction	+	+	+	+	+	+	+	+	+	+
Starch hydrolysis	+	+	-	-	+	+	+	-	-	-
Liquefaction of gelatin	+	+	+	-	+	+	+	+	+	+
Urease	-	+	+	+	-	+	-	-	-	-
Arginine hydrolase	-	-	+	+	-	+	-	+	+	+
Arginine decarboxylase	+	+	+	+	+	+	+	+	+	+
Citrate	+	+	+	+	+	+	+	-	-	-
45 °C growth	-	-	+	-	-	-	-	-	-	-

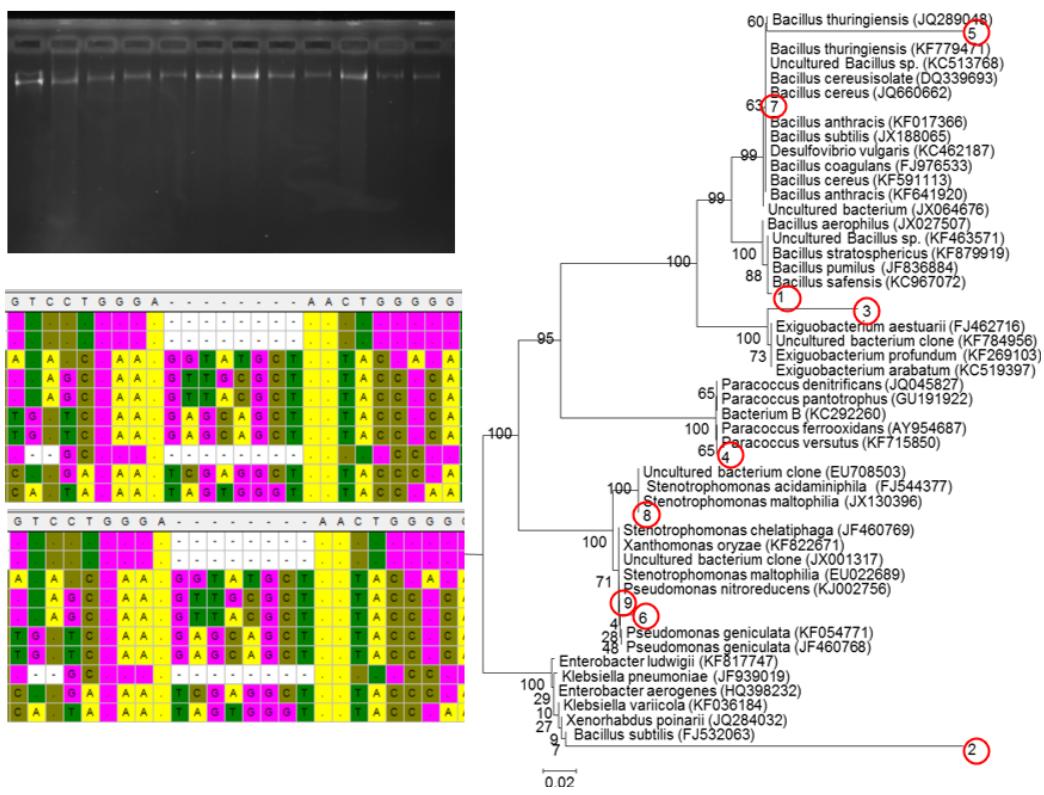


Figure S1. Molecular identification.

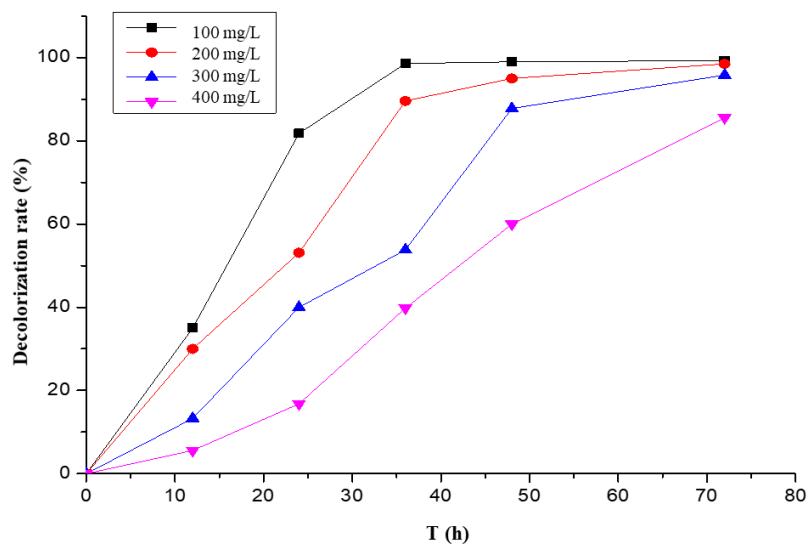


Figure S2. The concentration effect on the percentage (%) decolorization of methyl orange in the dewatered sludge.

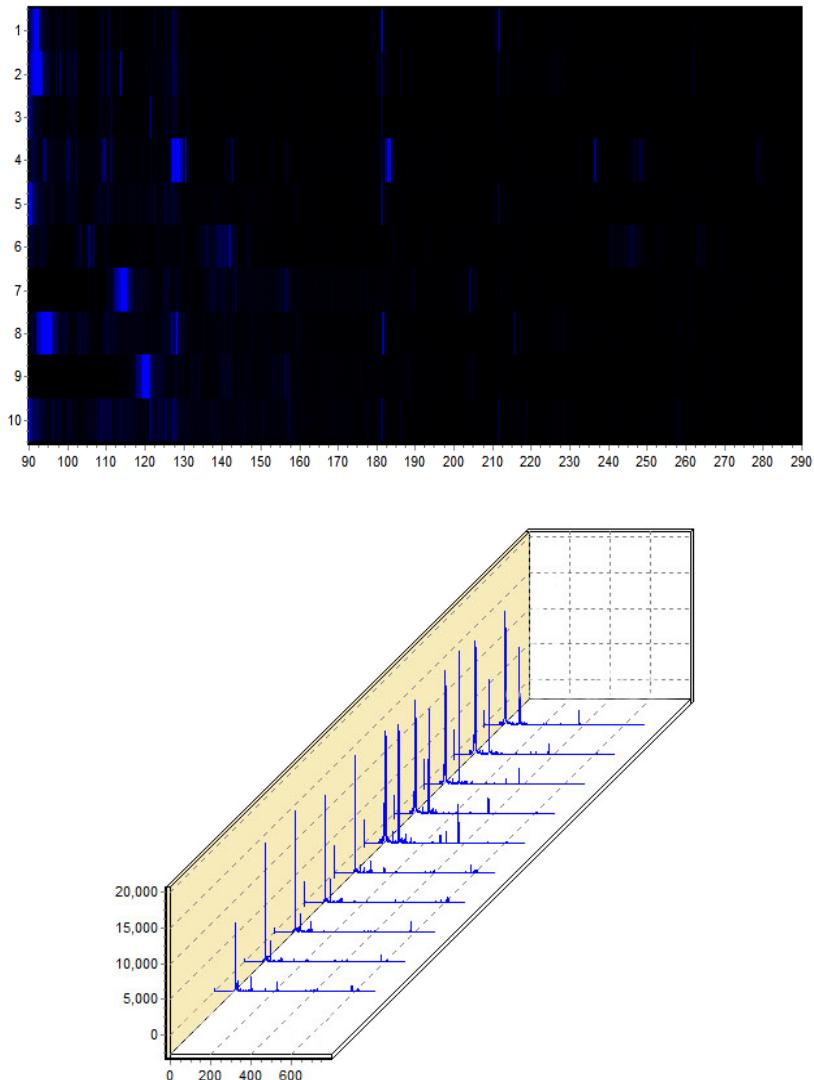


Figure S3. The metagenomic DNA gel electrophoresis patterns of different samples.

Table S4. The diversity index of the bacterial communities of different treatments.^[1]

Type	TRLFP unit*	SIMPSON(J)	SHAN-NON(H)	EVENESS	BRILLOUIN	McIntosh (Dmc)
Methyl orange	716478	0.7271	2.5951	0.6223	2.5949	0.4781
Methyl red	636292	0.5578	1.6692	0.5946	1.6692	0.3355
Orange I	651797	0.6422	1.8923	0.6761	1.7812	0.3698
Orange G	698617	0.6838	2.0092	0.7157	2.0092	0.4382
Tartrazine	714004	0.6785	2.0754	0.7393	2.0753	0.4335
Alizarin yellow R sodium salt	589331	0.6998	2.1163	0.7538	2.1162	0.4526
Azo dye mixture	659168	0.7294	2.2828	0.7609	2.2827	0.4804
Raw dewatered sludge	1271198	0.9107	3.0251	0.9125	3.2141	0.5903

* TRLFP unit is the basic potential taxa information based on the specific restriction sequence information.

Table S5. The full names of species.

Serial number	Name
Sp1	Abiotrophia
Sp2	Acidimicrobium
Sp3	Acromatium
Sp4	Aeromonas
Sp5	Alicyclobacillus
Sp6	Anaerobranca
Sp7	Aneurinibacillus
Sp8	Anhibacillus
Sp9	Arhodomonas
Sp10	Bdellovibrio
Sp11	Beggiatoa
Sp12	Brevibacillus
Sp13	Brevibacterium
Sp14	Buchnera
Sp15	Burkholderia
Sp16	Caloramator
Sp17	Capnocytophaga
Sp18	Caryophanon
Sp19	Chlorobium
Sp20	Citrobacter
Sp21	Clavibacter
Sp22	Clostridium
Sp23	Cytophaga
Sp24	Desulfitibacterium
Sp25	Dictyoglomus
Sp26	Ectothiorthodospira
Sp27	Empedobacter
Sp28	Endosymbriout
Sp29	Escherichia
Sp30	Eubacterium
Sp31	Fibrobacter
Sp32	Flavabacterium
Sp33	Flexibacter
Sp34	Francisella
Sp35	Frankia

Sp36	Fusobacterium
Sp37	Gemmata
Sp38	Geobacter
Sp39	Halobacillus
Sp40	Halomonas
Sp41	Kurthia
Sp42	Lactobacillus
Sp43	Legionella
Sp44	Leptothrix
Sp45	Leuconostoc
Sp46	Luteococcus
Sp47	Macroccoccus
Sp48	Mannheimia
Sp49	Marinobacter
Sp50	Methylocaldum
Sp51	Methylosinus
Sp52	Methlophilus
Sp53	Methylarcula(Methyoarcula)
Sp54	Microbacterium
Sp55	Microcystis
Sp56	Microscilla
Sp57	Mycoplasma
Sp58	Myxiococcus
Sp59	Oceanospirillum
Sp60	Oerskovia
Sp61	Omithobacterium
Sp62	Ornithobacterium
Sp63	Paenibacillus
Sp64	Pasteurella
Sp65	Pectinatus
Sp66	Phaeospirillum
Sp67	Phlomobacter
Sp68	Phlomobacter
Sp69	Photobacterium
Sp70	Phytoplasma
Sp71	Planococcus
Sp72	Porphyromonas
Sp73	Prevotella
Sp74	Proteus
Sp75	Psychroserpens
Sp76	Quinella
Sp77	Rathayibacter
Sp78	Rhizobium
Sp79	Rhodopila
Sp80	Rikenella
Sp81	Rubrivivax
Sp82	Rubrobacter
Sp83	Saccharococcus
Sp84	Saccharothrix
Sp85	Salmonella
Sp86	Secale
Sp87	Selenomonas

Sp88	Shewanella
Sp89	Spiroplasma
Sp90	Sporolactobacillus
Sp91	Sporosarcina
Sp92	Springomonas
Sp93	Stretomyces
Sp94	Sulfobacillus
Sp95	Synechococcus
Sp96	Telluria
Sp97	Therinomonopora
Sp98	Thermosiphon
Sp99	Treponema
Sp100	Vagococcus
Sp101	Xanthomonas
Sp102	Xylella
Sp103	Zea mays
Sp104	Zymophilus

Reference:

- 1 Barinova, S.; Tavassi, M. Study of seasonal influences on algal biodiversity in the River Yarqon (central Israel) by bio-indication and canonical correspondence analysis (CCA). *Turk. J. Botany*, **2009**, *33*, 353–372, doi:10.3906/bot-0812-12.