

# Selective colonization mechanism of *Shewanella putrefaciens* in dyeing wastewater outlet

Jiajie Xu,<sup>a,b</sup> Weina He,<sup>a</sup> Yanyan Li,<sup>a,c</sup> DiJun Zhang,<sup>a</sup> Jun Zhou,<sup>a</sup> Chundan Zhang,<sup>a</sup> Yi Li,<sup>a</sup> Rixin Wang<sup>a</sup>  
and Xiurong Su<sup>a\*</sup>

<sup>a</sup>. School of Marine Science, Ningbo University, Zhejiang, 315211, China

<sup>b</sup>. College of Engineering, China Agricultural University, Beijing, 100083, China

<sup>c</sup>. Department of Food Science, Cornell University, Ithaca, NY 14853, USA

Correspondence to: [suxiurong@nbu.edu.cn](mailto:suxiurong@nbu.edu.cn)

## Supplementary Information:

Tables S1-S2

Figures S1-S6

Table S1 The compositions of the waste water in Xiangshan Junxi sewage outlet

	TS (g L <sup>-1</sup> ) (n=6)	Ammonia (mg L <sup>-1</sup> ) (n=6)	TCOD (mg L <sup>-1</sup> ) (n=6)	BOD (mg L <sup>-1</sup> ) (n=6)	pH (n=6)
Wast					
e	4.49±0.05	38.59±5.66	1376.93±157.2	217.13±4.6	8.1±0.45
water					



Table S2 List of spots/proteins identified by MS analysis from *Shewanella putrefaciens* by 2-DE

Spot number	ncbi accession number	name of protein	Functional category	Theoretical MW(kDa)/PI	Mascot score/ Matched peptides	Threshold (P<0.05)	Species
1	gi 386312552	outer membrane porin, Omp35	NO Foud	37959/4.64	602/14	56	[ <i>S.putrefaciens</i> 200]
2	gi 386313291	porin	NO Foud	45685/4.53	174/13	56	[ <i>S.putrefaciens</i> 200]
3	gi 146293566	aromatic hydrocarbon degradation membrane protein	NO Foud	47545/4.71	237/5	56	[ <i>S.putrefaciens</i> CN-32]
4	gi 146292153	OmpA/MotB domain-containing protein	NO Foud	40022/4.82	110/6	56	[ <i>S.putrefaciens</i> CN-32]
5	gi 146292973	elongation factor P	NO Foud	20672/4.79	164/4	56	[ <i>S.putrefaciens</i> CN-32]
6	gi 146292505	3-ketoacyl-ACP reductase	Metabolic pathways, Fatty acid biosynthesis, Biosynthesis of unsaturated fatty acids, Fatty acid metabolism, Biotin metabolism	26645/4.72	65/4	56	[ <i>S.putrefaciens</i> CN-32]
7	gi 146293364	2-oxoglutarate dehydrogenase, E2 subunit, dihydrolipoamide succinyltransferase	Metabolic pathways, Carbon metabolism, Microbial metabolism in diverse environments, Biosynthesis of secondary metabolites, Citrate cycle (TCA cycle), Lysine degradation	43234/5.34	358/8	56	[ <i>S.putrefaciens</i> CN-32]

8	gi 146293363	succinyl-CoA synthetase subunit beta	Metabolic pathways, Carbon metabolism, Microbial metabolism in diverse environments, Biosynthesis of secondary metabolites, Citrate cycle (TCA cycle), C5-Branched dibasic acid metabolism, Propanoate metabolism	41699/5.32	352/16	56	[ <i>S.putrefaciens</i> CN-32]
9	gi 146293466	cysteine synthase A	Metabolic pathways, Carbon metabolism, Microbial metabolism in diverse environments, Cysteine and methionine metabolism, Biosynthesis of amino acids , Sulfur metabolism	34498/5.62	241/9	56	[ <i>S.putrefaciens</i> CN-32]
10	gi 146293923	polynucleotide phosphorylase/polyadenylase	RNA degradation, Pyrimidine metabolism, Purine metabolism	75520/5.09	274/20	56	[ <i>S.putrefaciens</i> CN-32]
11	gi 146293339	phosphoenolpyruvate synthase	Metabolic pathways, Carbon metabolism, Microbial metabolism in diverse environments, Pyruvate and Methane metabolism	86879/4.98	315/14	56	[ <i>S.putrefaciens</i> CN-32]
12	gi 386315234	aconitate hydratase 2	Biosynthesis of secondary metabolites and amino acids, Metabolic pathways, Propanoate metabolism, Glyoxylate and dicarboxylate metabolism, Microbial metabolism in diverse environments, Citrate cycle (TCA cycle), 2-Oxocarboxylic acid metabolism, Carbon metabolism	94116/5.09	270/20	56	[ <i>S.putrefaciens</i> 200]
13	gi 146291806	chaperonin GroEL	RNA degradation	57170/4.85	476/15	56	[ <i>S.putrefaciens</i> CN-32]
14	gi 146292589	trigger factor	NO Foud	47730/4.80	231/16	56	[ <i>S.putrefaciens</i> CN-32]

15	gi 146292616	TonB-dependent receptor	NO Foud	102004/4.55	297/11	56	[ <i>S.putrefaciens</i> CN-32]
16	gi 146293339	phosphoenolpyruvate synthase	Metabolic pathways, Carbon metabolism, Microbial metabolism in diverse environments, Pyruvate metabolism, Methane metabolism	86879/4.98	85/3	56	[ <i>S.putrefaciens</i> CN-32]
17	gi 146294855	elongation factor Tu	NO Foud	43547/5.08	407/16	56	[ <i>S.putrefaciens</i> CN-32]
18	gi 146292699	alkyl hydroperoxide reductase	NO Foud	22102/5.01	267/7	56	[ <i>S.putrefaciens</i> CN-32]
19	gi 270381546	elongation factor Tu	NO Foud	28913/4.67	333/14	56	[ <i>S.putrefaciens</i> ]
20	gi 386314796	ABC transporter	NO Foud	27193/5.87	306/12	56	[ <i>S.putrefaciens</i> 200]
21	gi 146295038	FOF1 ATP synthase subunit alpha	Metabolic pathways, Oxidative phosphorylation	55285/5.46	398/10	56	[ <i>S.putrefaciens</i> CN-32]
22	gi 146294500	dihydrolipoamide dehydrogenase	Metabolic pathways, Carbon metabolism, Microbial metabolism in diverse environments, Biosynthesis of secondary metabolites, Citrate cycle (TCA cycle) , Pyruvate metabolism, Glycine, serine and threonine metabolism, Valine, leucine and isoleucine degradation, Glycolysis / Gluconeogenesis	50708/5.56	290/8	56	[ <i>S.putrefaciens</i> CN-32]

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23	gi 386312950	chorismate mutase	Biosynthesis of secondary metabolites, Metabolic pathways, Biosynthesis of amino acids, Phenylalanine, tyrosine and tryptophan biosynthesis, Novobiocin biosynthesis	42820/5.57	123/8	56	[ <i>S.putrefaciens</i> 200]
24	gi 146293334	Glu/Leu/Phe/Val dehydrogenase	Metabolic pathways, Biosynthesis of secondary metabolites, Valine, leucine and isoleucine degradation, Valine, leucine and isoleucine biosynthesis	37279/ 5.56	387/12	56	[ <i>S.putrefaciens</i> CN-32]
25	gi 146294306	malate dehydrogenase	Metabolic pathways, Carbon metabolism, Microbial metabolism in diverse environments, Biosynthesis of secondary metabolites, Citrate cycle (TCA cycle), Pyruvate metabolism, Methane metabolism, Glyoxylate and dicarboxylate metabolism	32260/5.37	490/10	56	[ <i>S.putrefaciens</i> CN-32]
26	gi 146294298	glycine cleavage system aminomethyltransferasT	Metabolic pathways, Carbon metabolism, Glycine, serine and threonine metabolism, One carbon pool by folate	39885/5.19	108/7	56	[ <i>S.putrefaciens</i> CN-32]

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Fig. S1 Map of 10 terrestrial sewage outlets sites in coastal areas of Ningbo

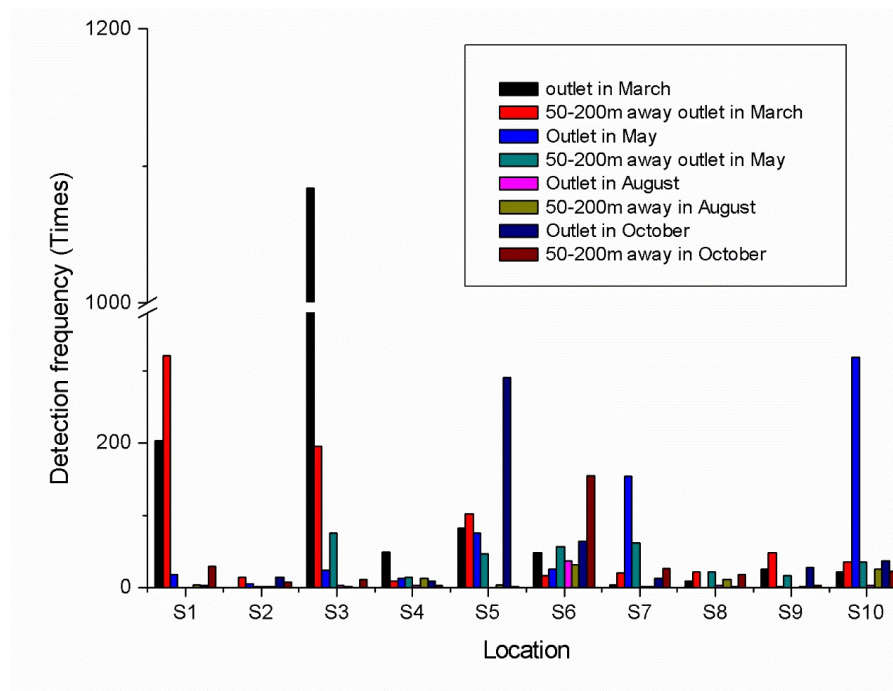


Fig. S2 The detection frequency of *S. putrefaciens* in different 10 terrestrial sewage outlets in coastal areas of Ningbo. S1: Xiangshan Junxi sewage outlet; S2: Xiangshan S.T. sewage outlet; S3: Xiangshan Shipu sewage outlet; S4: Xiangshan Xizhou sewage outlet; S5: Xiangshan Q.T. sewage outlet; S6: Beilun Sanshan sewage outlet; S7: Ninghai Xidian sewage outlet; S8: Fenghua Xiachen sewage outlet; S9: Ninghai Yangong sewage outlet; S10: Yuyao Huangjiang sewage outlet.



Fig. S3 photomicrograph of isolated *S. putrefaciens*

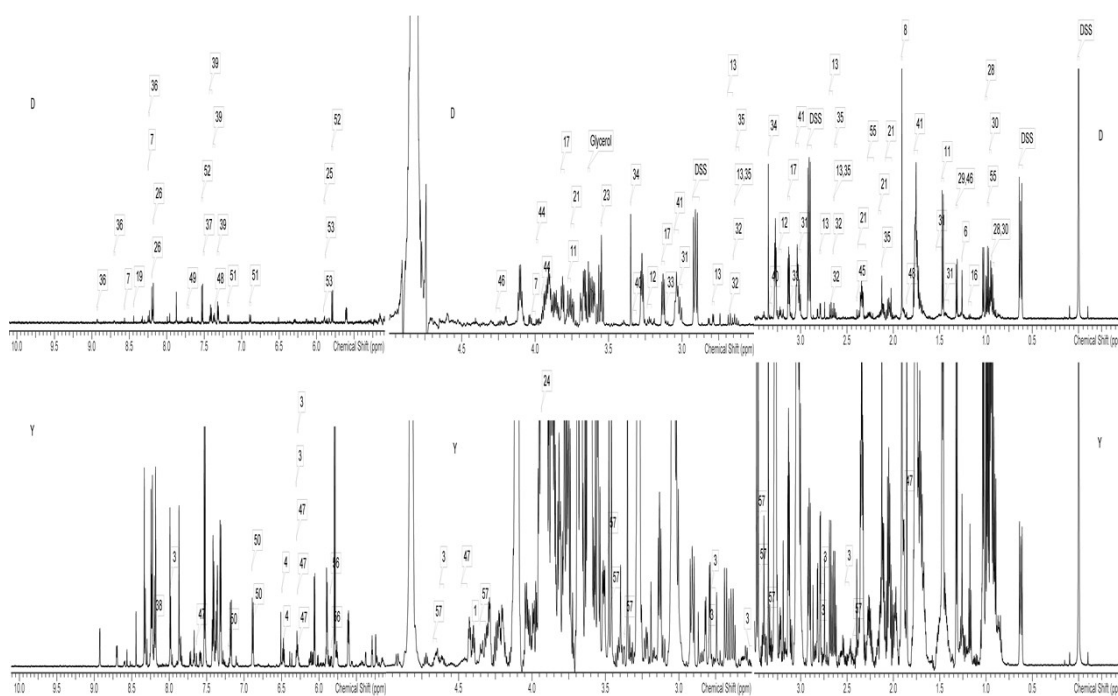


Figure S4. <sup>1</sup>H NMR ownership spectrum of intracellular metabolites from *S. putrefaciens* in fresh water and dyeing wastewater





Figure S5 Photographs of dyeing wastewater outlets

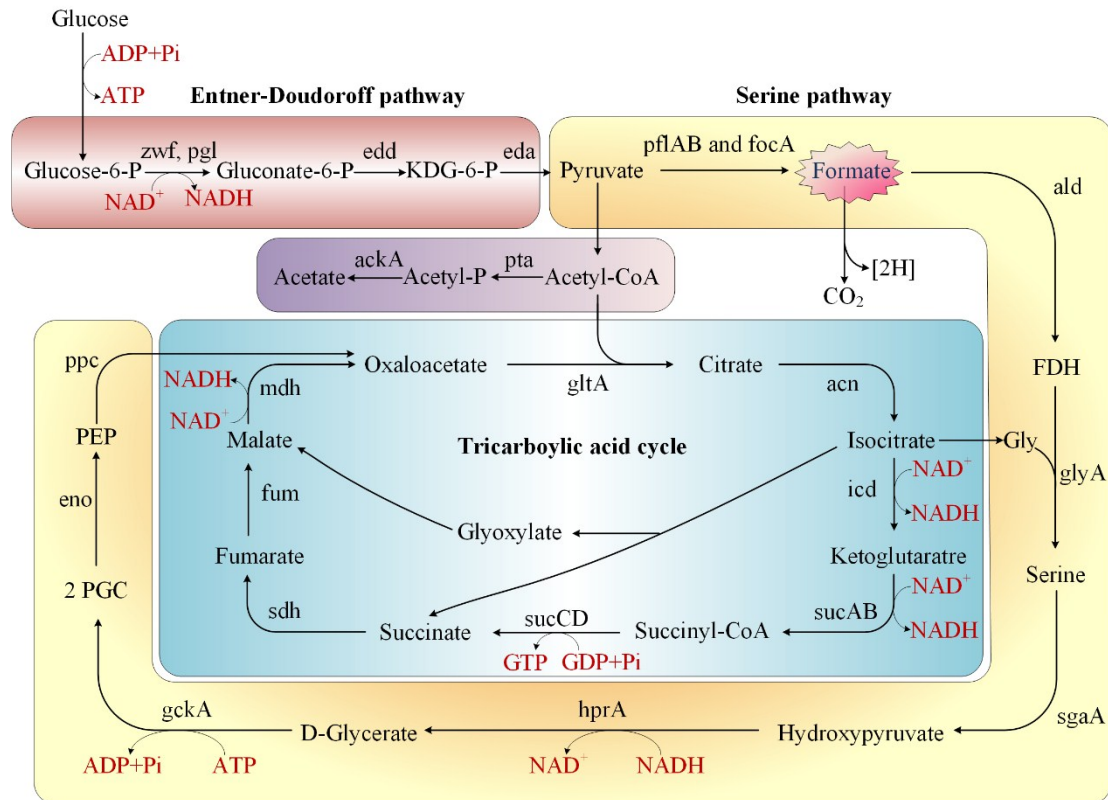


Figure S6 Transcriptional regulatory networks in the carbohydrate mechanisms of *Shewanella* according to KEGG and previous research <sup>1-3</sup>. Genes that encode the enzymes in this schematic are referred to by their commonly used names. KDG-6-P, 2-keto-3-deoxy-6-phosphogluconate; P, phosphate; FDH, Formaldehyde; 2PGC, 2 Phosphoglycerate; Gly, glycine; PEP, phosphoenolpyruvate.

## Reference

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