water

MDPI

Supplementary Information

Changes in Wastewater Treatment Performance and Microbial Community during Bioaugmentation of a Denitrifying *Pseudomonas* Strain in the Low Carbon–Nitrogen Ratio Sequencing Batch Reactor

Tianyuan Chen [1,2], Xiaoyong Yang [1], Qian Sun [1], Anyi Hu [1], Dan Qin [1], Jiangwei Li [1], Yinhan Wang [3] and Chang-Ping Yu [1,4,*]

[1] CAS Key Laboratory of Urban Pollutant Conversion, Institute of Urban Environment, Chinese Academy of Sciences, Xiamen, Fujian 361021, China
[2] University of Chinese Academy of Sciences, Beijing 100049, China
[3] Xiamen Institute of Rare Earth Materials, Haixi Institutes, Chinese Academy of Sciences
[4] Graduate Institute of Environmental Engineering, National Taiwan University, Taipei 106, Taiwan
* Correspondence: cpyu@iue.ac.cn (CP Yu.), qsun@iue.ac.cn (Q Sun)

Contents

Table S1. Primers for functional genes.

Gene name	Primer name	Primer genetic sequence
qnorB	qnorB2F	GGNCAYCARGGNTAYGA
	qnorB5R	ACCCANAGRTGNACNACCCACCA
cnorB	cnorB2F	GACAAGNNNTACTGGTGGT
	cnorB6R	GAANCCCCANACNCCNGC
nirS	cd3aF	GTSAACGTSAAGGARACSGG
	R3cd	GASTTCGGRTGSGTCTTGA
nirK	F1aCu	ATCATGGTSCTGCCGCG
	R3Cu	GCCTCGATCAGRTTGTGGTT
nosZ	nosZ2F	CGCRACGGCAASAAGGTSMSSGT
	nosZ2R	CAKRTGCAKSGCRTGGCAGAA

Note: N=A, C, G, or T; Y=C or T; R=A or G; D=G, A, or T； S=C or G

Table S2. Nitrite removal capacity of JMSTP.

Time	**TN (mg/L)**
0 h	104
12 h	2.71
24 h	0.00

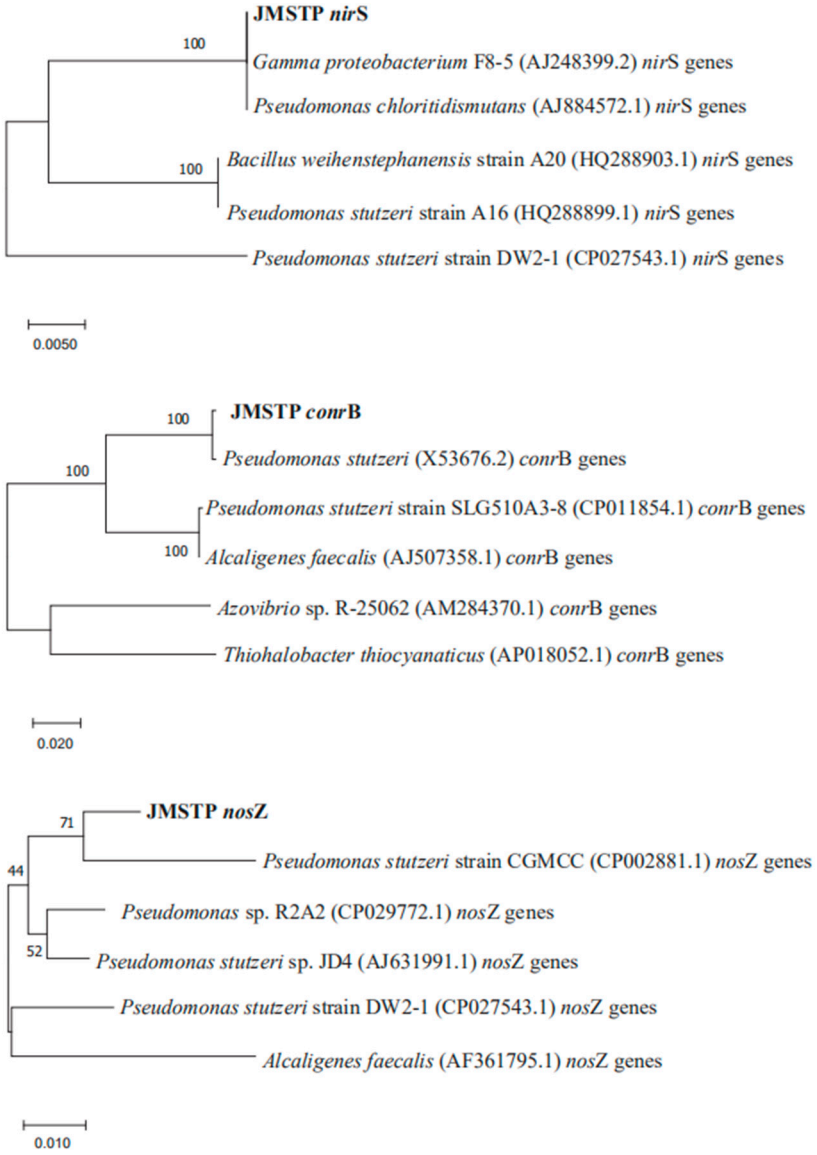

Figure S1. The result of PCR sequencing analysis of *nir*S, *nor*B, and *nos*Z.

Table S3. Community richness and diversity indices of two reactors.

SBR	Time (day)	richness	Shannon	Simpson	Pielou	chao1	ace	Goods coverage
JMSTP	B1	1196	3.180	0.884	0.449	1436.384	1468.138	0.997
	D1_1	1222	3.017	0.815	0.424	1447.822	1464.672	0.997
	D1_2	1329	3.251	0.855	0.452	1575.224	1612.856	0.997
	D1_3	1346	3.257	0.878	0.452	1587.954	1632.217	0.997
	B2	1035	2.960	0.855	0.426	1245.118	1261.835	0.997
	D2_1	872	2.342	0.770	0.346	1047.579	1097.753	0.998
	D2_2	909	2.831	0.855	0.416	1095.121	1132.869	0.998
	D2_3	1021	2.940	0.866	0.424	1244.256	1277.987	0.997
	D2_4	1059	2.993	0.879	0.430	1315.800	1377.675	0.997
	D2_5	1044	2.996	0.877	0.431	1232.894	1268.973	0.997
	D2_6	1008	2.918	0.870	0.422	1236.331	1260.837	0.997
	D2_7	905	2.664	0.838	0.391	1067.958	1120.398	0.998
Control	B1	1363	3.549	0.924	0.492	1602.963	1639.270	0.997
	D1_1	1205	3.240	0.901	0.457	1424.290	1453.056	0.997
	D1_2	1262	3.326	0.908	0.466	1485.523	1528.443	0.997
	D1_3	1255	3.363	0.909	0.471	1473.284	1491.122	0.997
	B2	1053	2.947	0.869	0.423	1252.976	1298.123	0.997
	D2_1	968	2.847	0.866	0.414	1122.214	1178.422	0.998
	D2_2	959	2.727	0.836	0.397	1149.821	1215.670	0.997
	D2_3	1012	2.906	0.876	0.420	1191.338	1237.947	0.997
	D2_4	971	2.935	0.880	0.427	1155.816	1200.821	0.998
	D2_5	1007	2.859	0.868	0.414	1226.032	1262.518	0.997
	D2_6	898	2.794	0.869	0.411	1116.765	1145.560	0.997
	D2_7	810	2.758	0.866	0.412	977.270	1001.921	0.998

Table S4. OTUs of two reactors at each sampling day during experiment.

Sample name	Number (percentage possession)		
	A	B	C
B1	384 (22.0%)	551 (31.5%)	812 (46.5%)
D1_1	430 (26.3%)	413 (25.3%)	792 (48.4%)
D1_2	495 (28.2%)	428 (24.4%)	834 (47.5%)
D1_3	496 (28.3%)	405 (23.1%)	850 (48.5%)
B2	388 (26.9%)	406 (28.2%)	647 (44.9%)
D2_1	326 (25.2%)	422 (32.6%)	546 (42.2%)
D2_2	365 (27.6%)	415 (31.3%)	544 (41.1%)
D2_3	386 (27.6%)	377 (27.0%)	635 (45.4%)
D2_4	437 (31.0%)	349 (24.8%)	622 (44.2%)
D2_5	418 (29.3%)	381 (26.7%)	626 (43.9%)
D2_6	450 (33.4%)	340 (25.2%)	558 (41.4%)
D2_7	405 (33.3%)	310 (25.5%)	500 (41.2%)

Note: Part (A) represents the unique number of OTUs in the JMSTP SBR, part (B) represents the unique number of OTUs in the control SBR, and the overlapping zone (C) represents the same OTUs in the two SBRs.

Text S1. SEM operation process.

SEM operation process:

(1) The microorganism was cleaned twice with 0.1M phosphate buffer solution (PBS), fixed with 2.5% glutaraldehyde for 4 hours, and then cleaned twice with 0.1M PBS;

(2) The samples were dehydrated by gradient with 30%, 50%, 70%, 80% and 90% ethanol solutions respectively. At last, the samples were dehydrated by 100% ethanol twice, each step lasted for 10 minutes;

(3) After adding 100% ethanol for the second time, the sample is subjected to critical point drying, which takes one day;

(4) After drying, the sample is pasted on the sample table with conductive adhesive, and then the machine is tested after spraying gold.