Supporting Information

Synergistic effect of permanganate and in situ synthesized hydrated manganese oxide for removing antibiotic resistance genes from wastewater treatment plant effluent

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This supporting information contains 11-page document, including 5 figures, 3 tables and 1 scheme as well as this cover page.

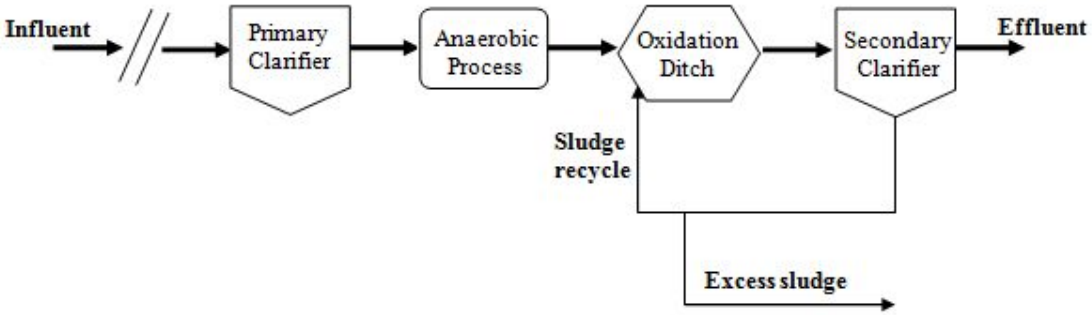


Figure S1. The treatment process of the local municipal wastewater treatment plant

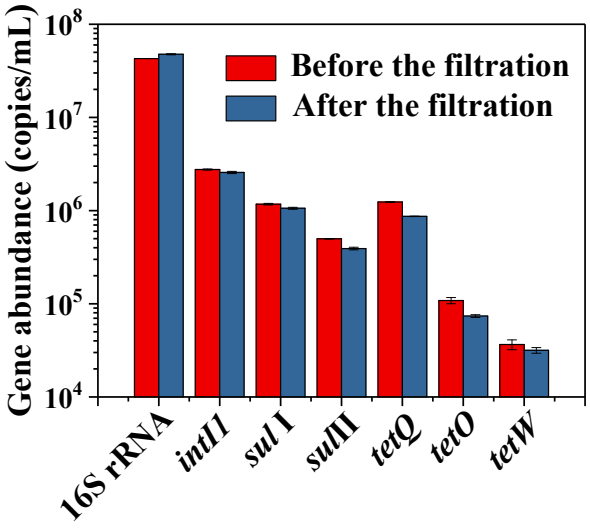
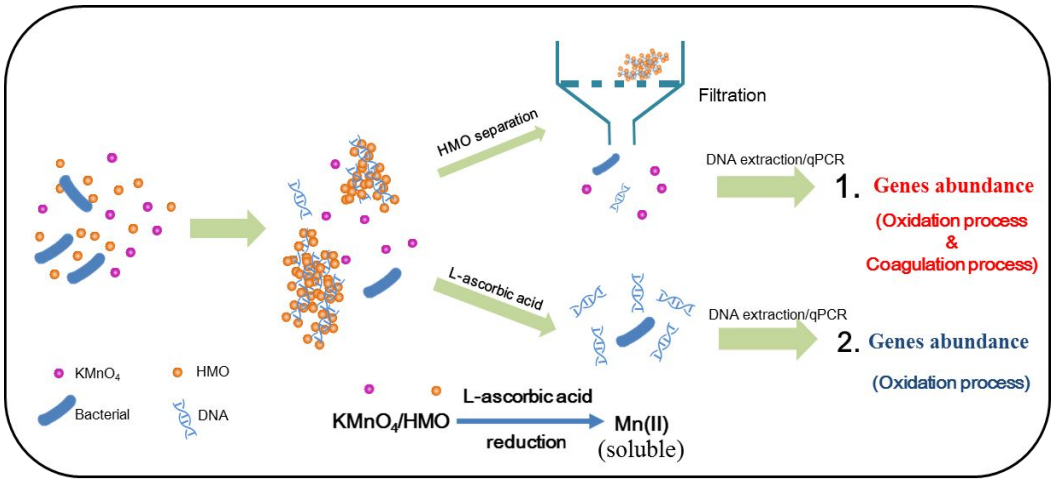


Figure S2. Gene abundances in the effluent before and after filtration using the medium speed qualitative filter paper



Scheme S1. Two kinds of quenching procedures to quantify the contributions of HMO coagulation and $KMnO_4$ oxidation to ARGs removal.

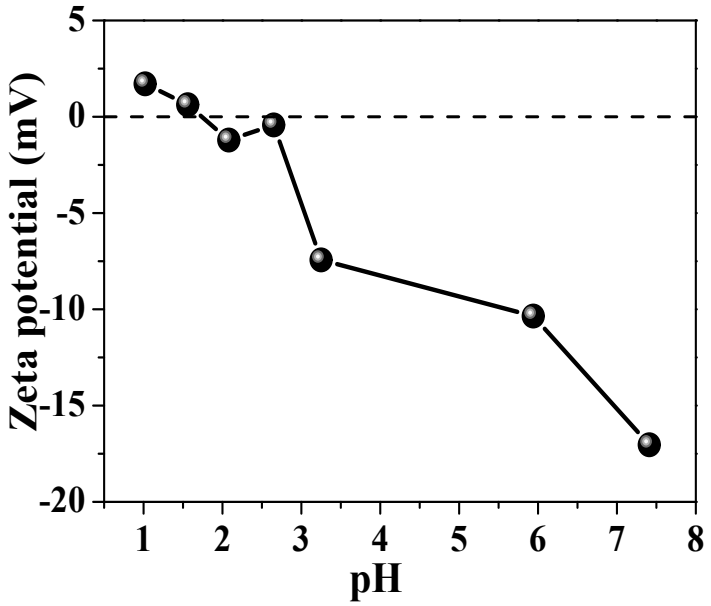


Figure S3. Zeta potentials of hydrated manganese oxide at various pHs

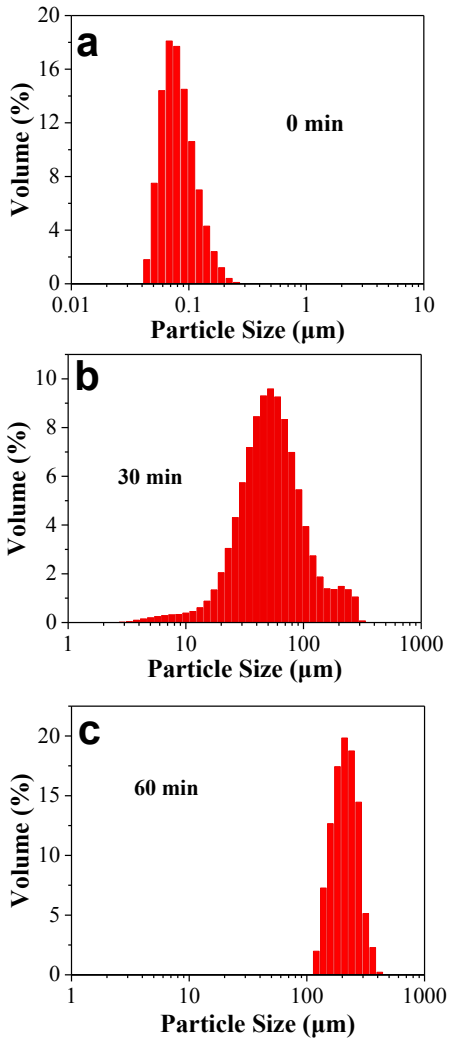


Figure S4. The initial hydrodynamic diameter of HMO in the DI water (a); the hydrodynamic diameter of HMO after 30 min (b); and 60 min (c) stirring in the secondary effluent.

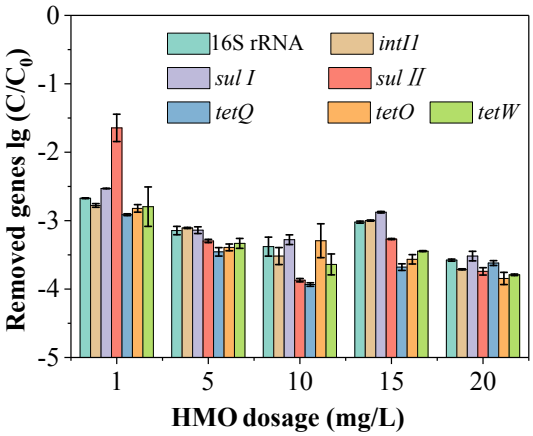


Figure S5. The effect of HMO dosage on the ARGs removal in the $KMnO_4$-HMO system. (The contact time for all treatments was 1 h, and the concentration of $KMnO_4$ was 10 mg/L)

Table S1. Characteristics of the secondary effluent

dissolved organic carbon (mg-C/L)	NH_4^+-N (mg/L)	total phosphorus (mg/L)	UV_{254}	cultivable bacteria (CFU/mL)
10.6±1.2	2.6±0.6	0.7±0.2	0.105±0.009	1400±800

Table S2. Primers and PCR conditions used in this study.

target gene	primer	sequence	annealing temp. (°C)	amplicon size (bp)	references
16S rRNA	BACT1369R	CGGTGAATACGTTCYCGG	55	143	1
	PROK1492R	GGWTACCTTGTTACGACTT			
*int*I1	*int*I1-F	CCTCCCGCACGATGATC	55	280	2
	*int*I1-R	TCCACGCATCGTCAGGC			
*sul*I	*sul*I-F	CACCGGAAACATCGCTGCA	57	158	3
	*sul*I-R	AAGTTCCGCCGCAAGGCT			
*sul*II	*sul*II-F	CTCCGATGGAGGCCGGTAT	60	190	3
	*sul*II-R	GGGAATGCCATCTGCCTTGA			
*tet*Q	*tet*Q-F	AGAATCTGCTGTTTGCCAGTG	63	169	4
	*tet*Q-R	CGGAGTGTCAATGATATTGCA			
*tet*O	*tet*O-F	GATGGCATACAGGCACAGACC	57	172	3
	*tet*O-R	GCCCAACCTTTTGCTTCACTA			
*tet*W	*tet*w-F	GAGAGCCTGCTATATGCCAGC	60	168	4
	*tet*w-R	GGGCGTATCCACAATGTTAAC			

Table S3. Standard curves and amplification efficiencies of qPCR

target gene	standard curves	amplification efficiencies	R^2	LOD (copies/μL)	LOQ (copies/μL)	Ct of NTC
16S rRNA	y = -3.7259x + 39.76	1.86	0.99	4	16	36.69 ± 0.14
*Int*I1	y = -3.4217x + 38.86	1.96	1.00	2	16	>40
*sul*I	y = -3.7349x + 41.30	1.85	0.99	4	16	36.91 ± 1.24
*sul*II	y = -3.5485x + 40.57	1.91	1.00	6	32	>40
*tet*Q	y = -3.5550x + 38.18	1.82	0.99	2	16	>40
*tet*O	y = -3.8305x + 40.44	1.86	0.99	4	16	39.00 ± 1.95
*tet*W	y = -3.5623x + 38.87	1.93	10	2	16	38.21 ± 1.14

LOD: the lowest concentration at which 95% of the positive samples are detected.[5, 6]

LOQ: the lowest concentration at which the coefficient of variation is below the arbitrary threshold of 40%.[5, 6]

Ct of NTC：the cycle number of the threshold of no template control (NTC).

References

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