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Peracetic acid disinfection kinetics for combined sewer overflows: indicator organisms, antibiotic resistance genes, and microbial community

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APPENDIX

Table S1. Primers, annealing temperatures, and amplicon lengths.

Gene	Primer sequence	Ta (°C)	Amplicon length (bp)	Source
*sul*1	CGCACCGGAAACATCGCTGCAC TGAAGTTCCGCCGCAAGGCTCG	65	163	[1]
tet(G)	GCAGAGCAGGTCGCTGG CCYGCAAGAGAAGCCAGAAG	68	134	[2]
*mex*B	GTGTTCGGCTCGCAGTACTC AACCGTCGGGATTGACCTTG	60	244	[3]
BacHum	TGA GTT CAC ATG TCC GCA TGA CGT TAC CCC GCC TAC TAT CTA ATG /56-FAM/TCC GGT AGA CGA TGG GGA TGC GTT /36-TAMSp/	60	81	[4]
16S rRNA	CCTACGGGAGGCAGCAG ATTACCGCGGCTGCTGG	65	202	[5]

Table S2. Average water quality data (±standard deviation, n=3) for source wastewater from disinfection experiments (Experiments 1 and 2) and PAA degradation experiment (Experiment 3).

	Experiment 1	**Experiment 2**	**Experiment 3**			
	WWTPa	WWTPb	WWTPa		WWTPb	
Sampling date	10/26/2015	11/16/2016	7/14/2017		7/27/2017	
Percent WW	23%	40%	23%	11.50%	40%	20%
TSS (mg/L)*	228 ±109	63 ±31	-		280	
COD (mg/L)	-	79±8	75±18	39±13	158±34	117±69
pH	-	7.7±0.01	6.88		6.59	

*TSS was measured in 100% WW samples

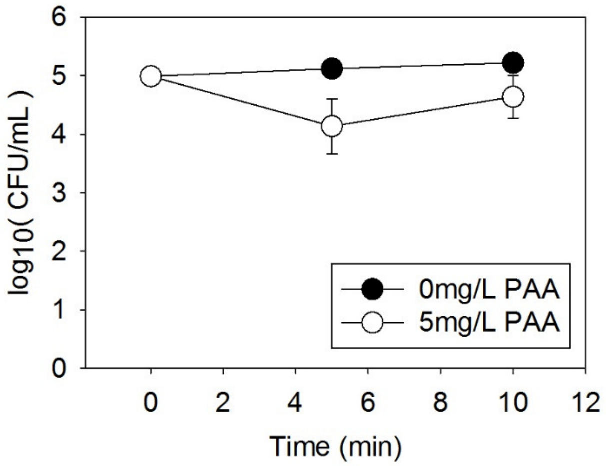

Fig. S1 Colony forming units (CFU) on LB agar from 40% WW treated with 0 mg/L or 5 mg/L PAA (n=2 or 3).

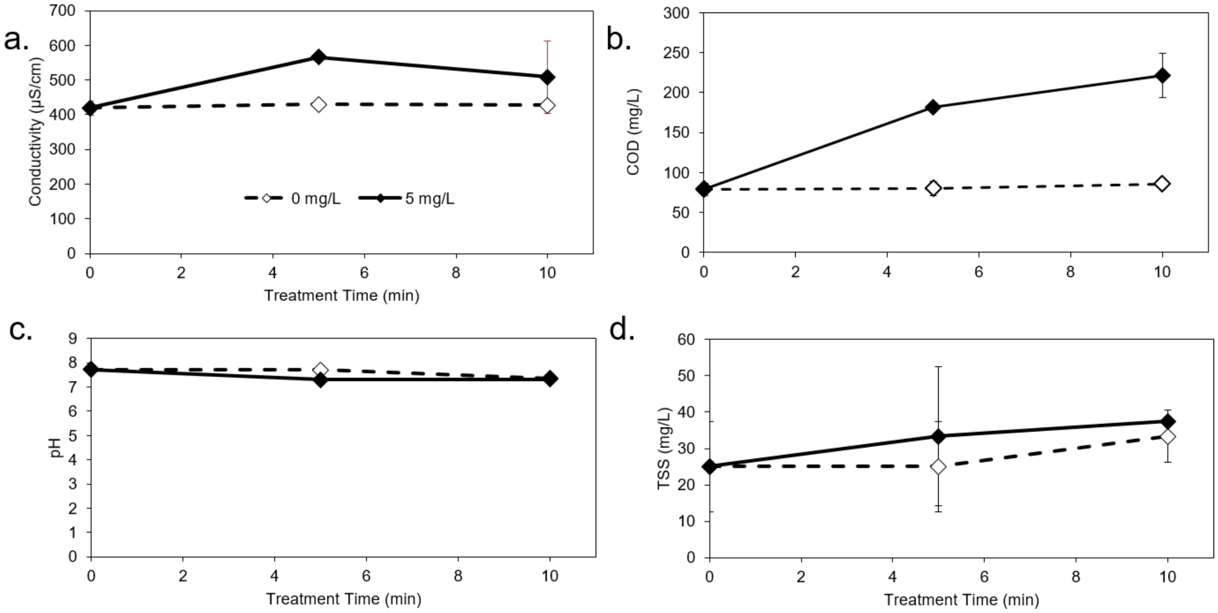

Fig. S2 Water quality parameters (a) conductivity, (b) chemical oxygen demand (COD), (c) pH and (d) total suspended solids (TSS) in 40% WW treated with 5 mg/L PAA compared to no PAA controls.

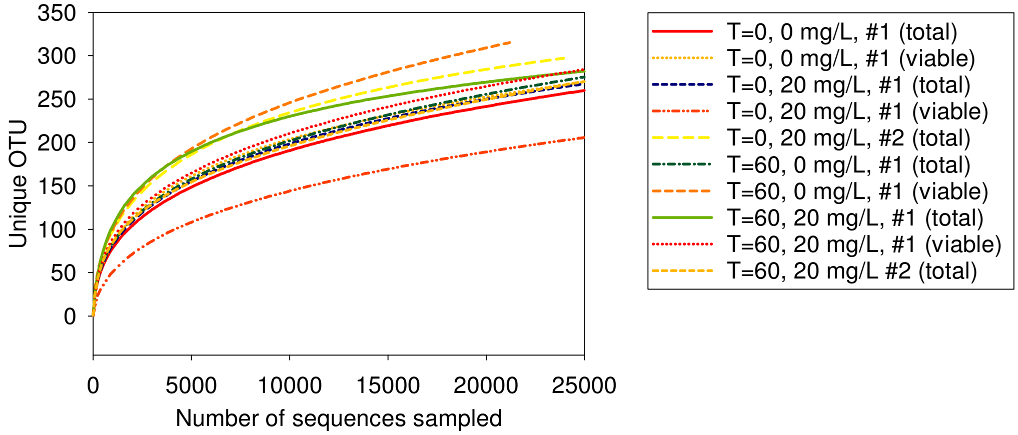

Fig. S3 Rarefaction curves for samples treated with 20mg/L PAA or no treatment controls for 0 or 60 min. Viable indicates samples treated with propidium monoazide prior to submission for sequencing. # indicates replicate number.

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