

Supporting Information

Responses of Microbial Communities to Single-Walled Carbon Nanotubes in Phenol Wastewater Treatment Systems

Yuanyuan Qu,^{†,‡,*,||} Qiao Ma,^{†,‡,||} Jie Deng,^{‡,||} Wenli Shen,[†] Xuwang Zhang,[†] Zhili He,[‡] Joy D. Van Nostrand,[‡] Jiti Zhou[†], Jizhong Zhou^{‡,§,#}

[†] Key Laboratory of Industrial Ecology and Environmental Engineering (Ministry of Education), School of Environmental Science and Technology, Dalian University of Technology, Dalian 116024, China

[‡] Institute for Environmental Genomics (IEG), Department of Microbiology and Plant Biology, University of Oklahoma, Norman, Oklahoma 73019, United States

[§] Earth Sciences Division, Lawrence Berkeley National Laboratory, Berkeley, California 94720, United States

[#] State Key Joint Laboratory of Environment Simulation and Pollution Control, School of Environment, Tsinghua University, Beijing 100084, China

There are 14 pages, containing 11 figures and 2 tables.

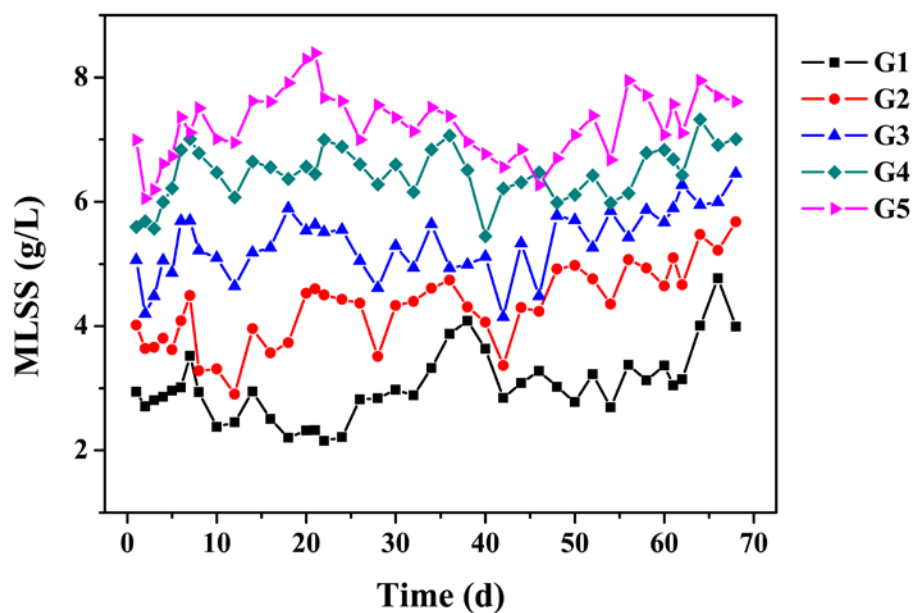


Figure S1. The mixed liquor suspended solid (MLSS) concentration of each group during the whole operation process. Two milliliter mixture from each reactor was taken for drying every other day. The data present here is the mean value of its replicates.

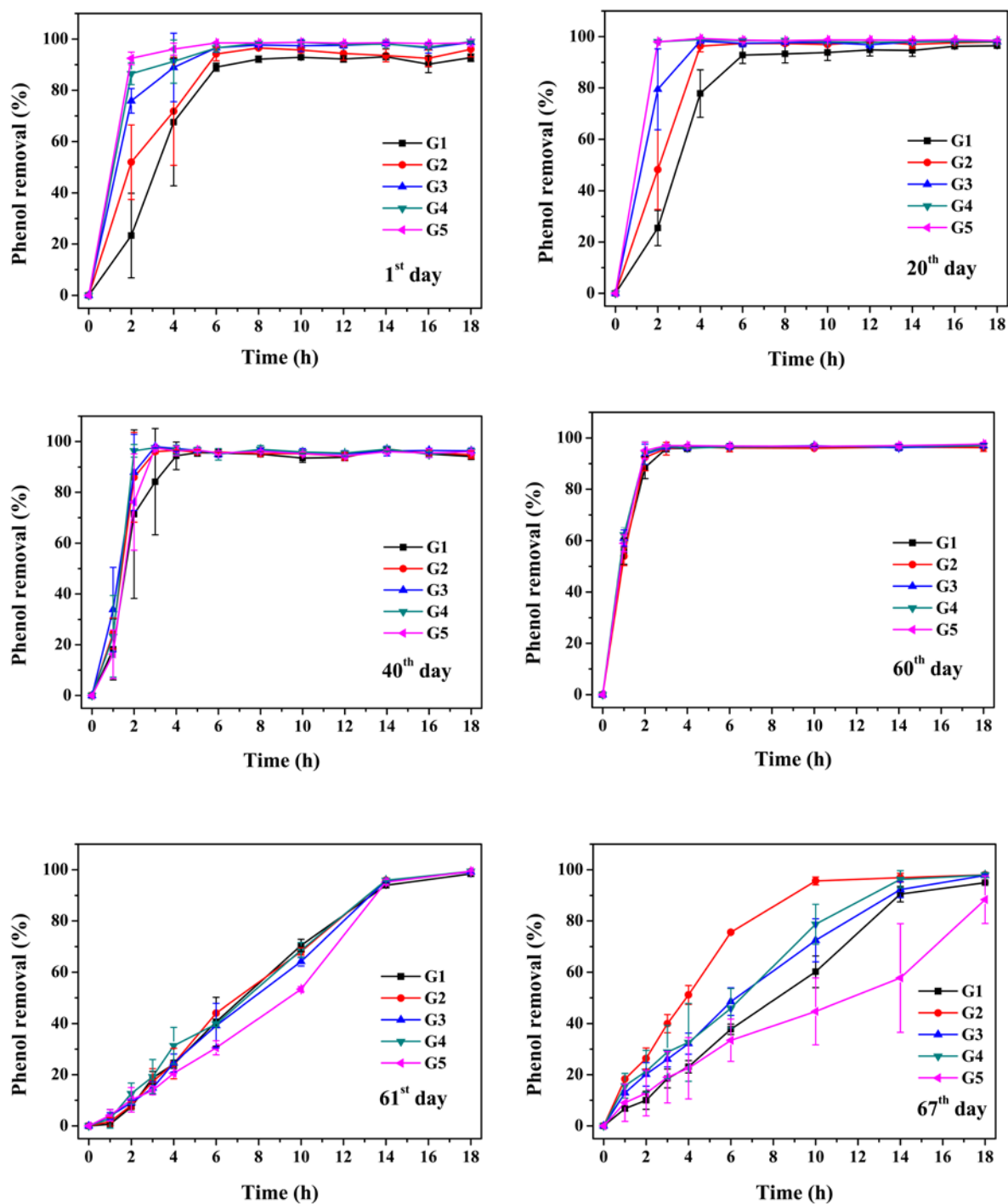


Figure S2. Phenol removal rates of each group on Day 1, 20, 40, 60, 61 and 67. Each group was performed in triplicates with different concentration of SWCNTs (g/L): 0 (G1), 0.5 (G2), 1.5 (G3), 2.5 (G4) and 3.5 (G5).

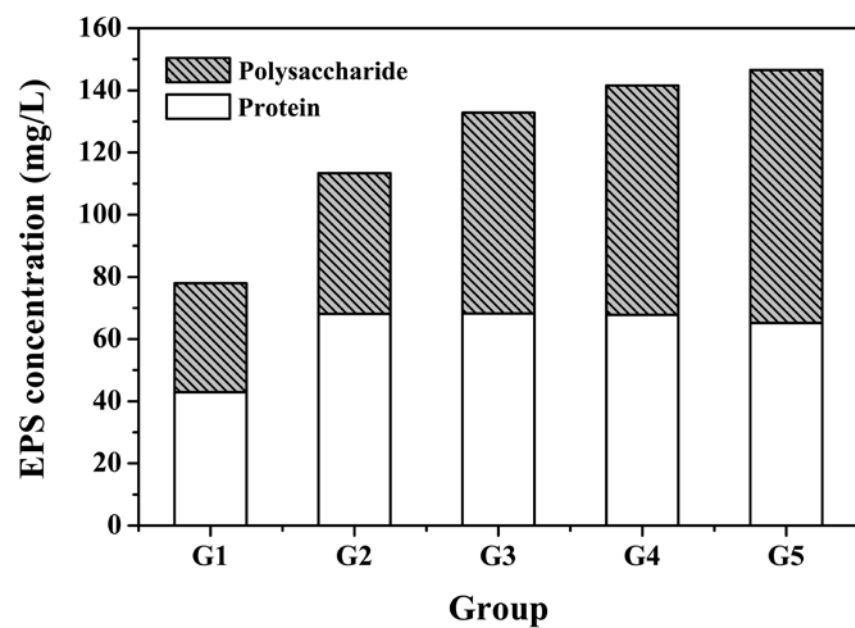


Figure S3. The concentration of bound extracellular polymeric substance in each group on Day 3.

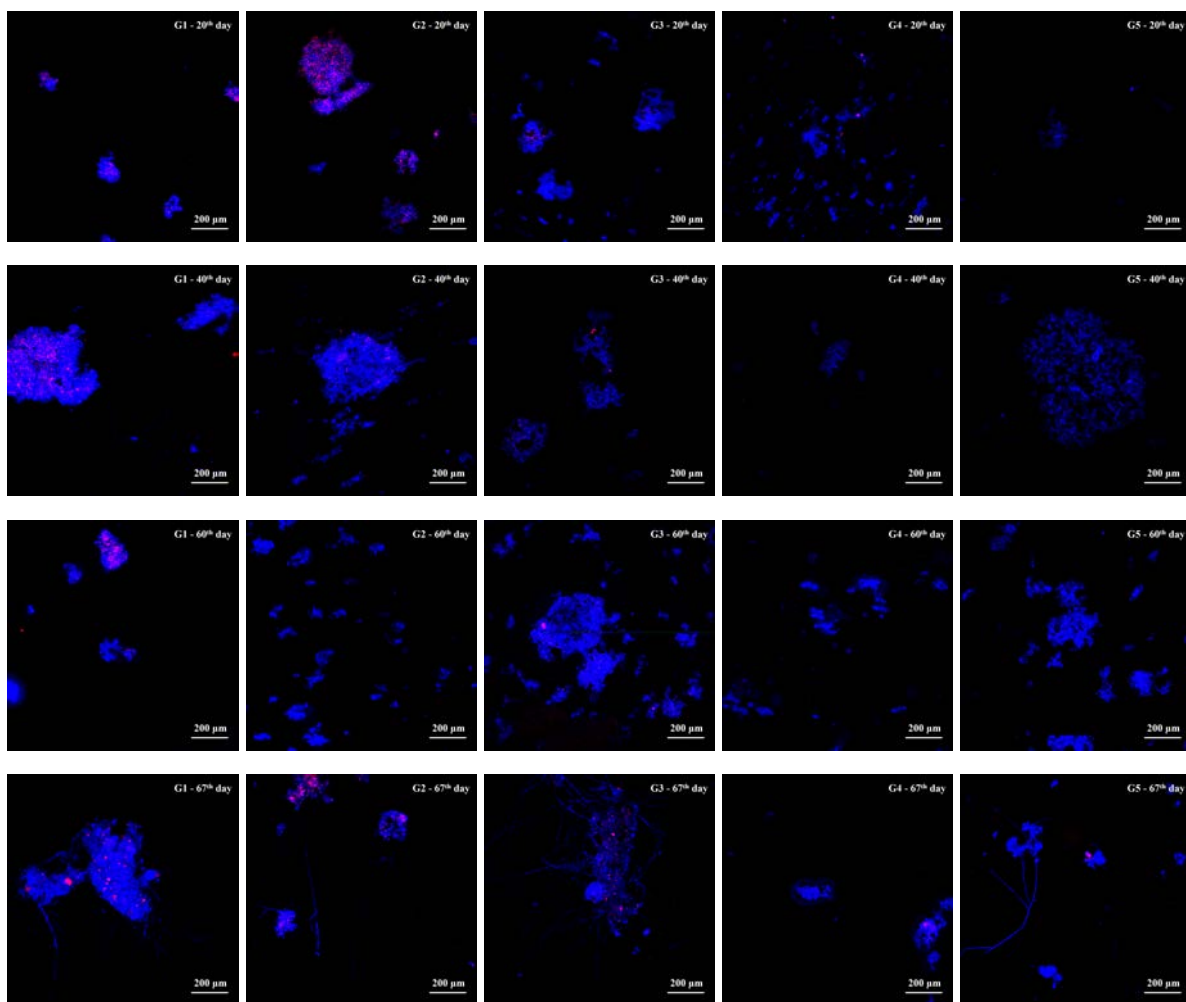


Figure S4. Fluorescence images of activated sludge on Day 20, 40, 60 and 67 (corresponding to line 1-4). Red represents dead cells and blue represents live cells.

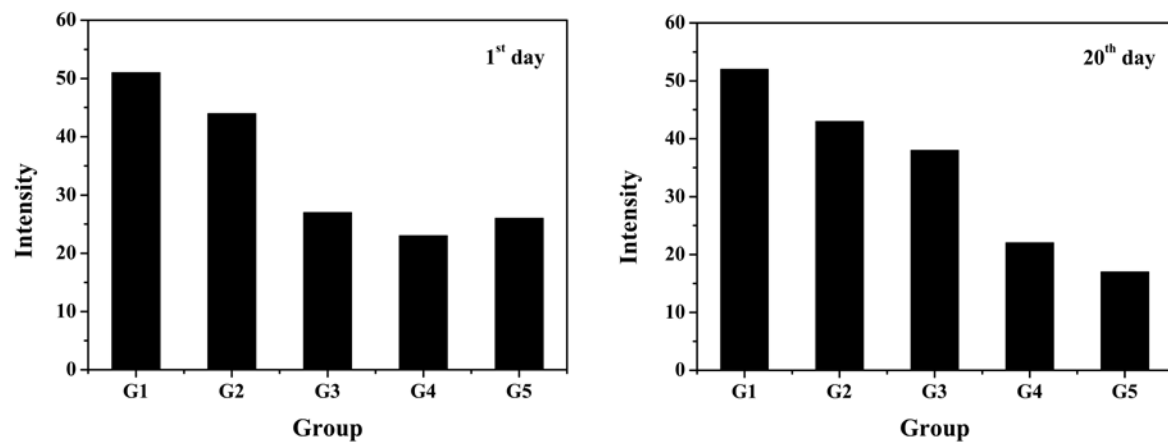


Figure S5. Cell-free DNA fluorescence of each group on Day 1 and 20.

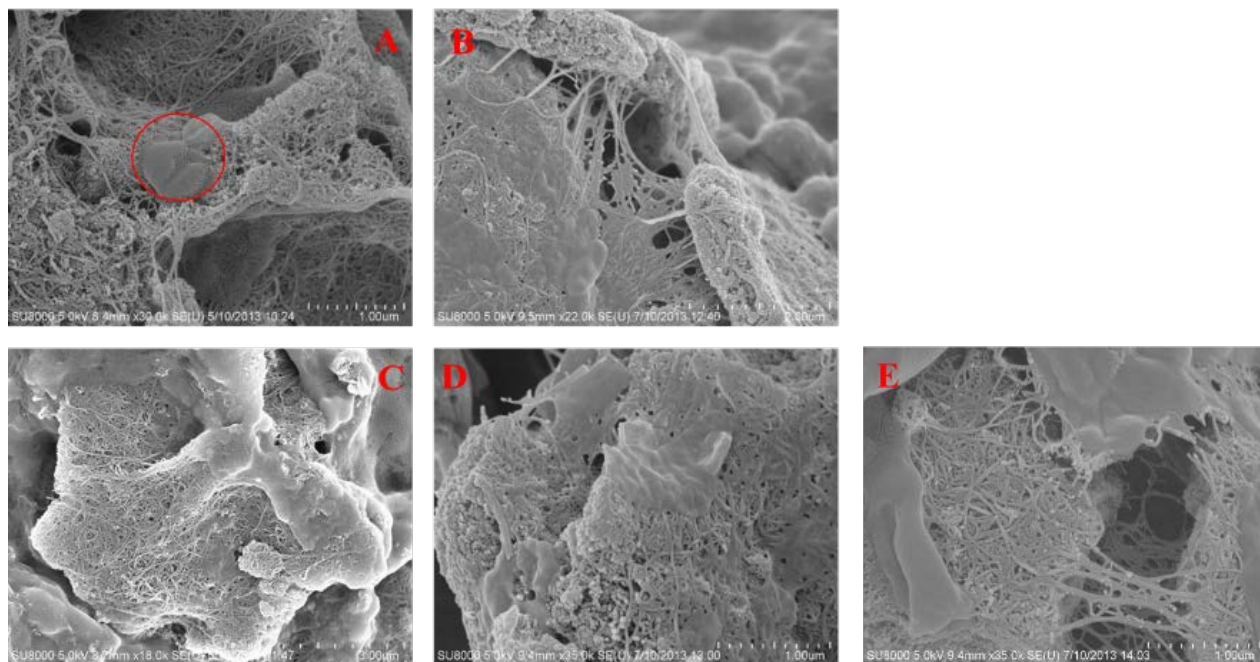


Figure S6. SEM of G2 on each sampling time. Cell in red circle is the flattened cell resulted from SWCNT toxicity. A-Day1; B-Day 20; C-Day 40; D-Day 60; E-Day 67.

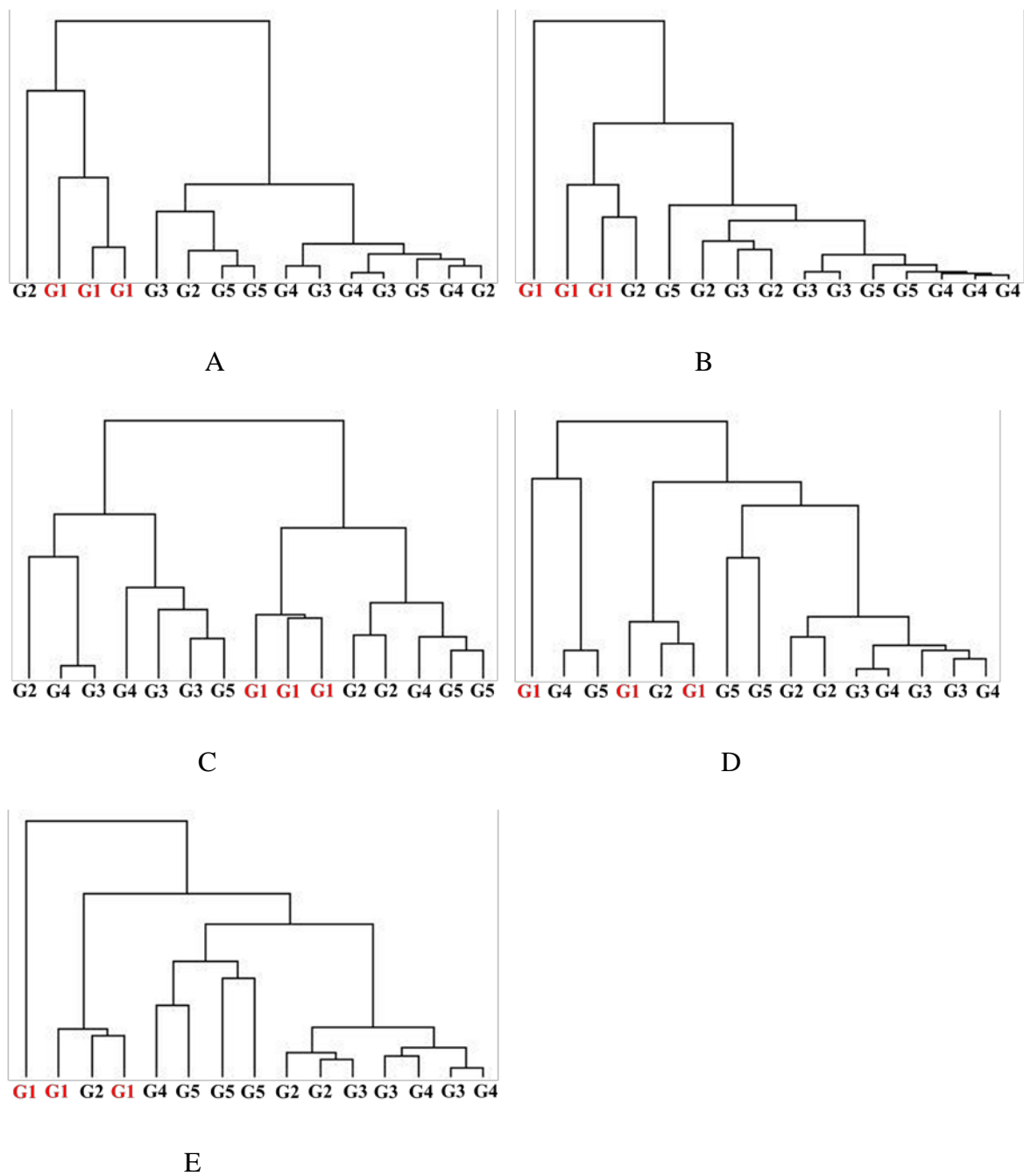


Figure S7. Hierarchical clustering analysis of all samples showing the relationships of microbial community structures among different groups at each sampling time. A-Day 1; B-Day 20; C-Day 40; D-Day 60; E-Day 67.

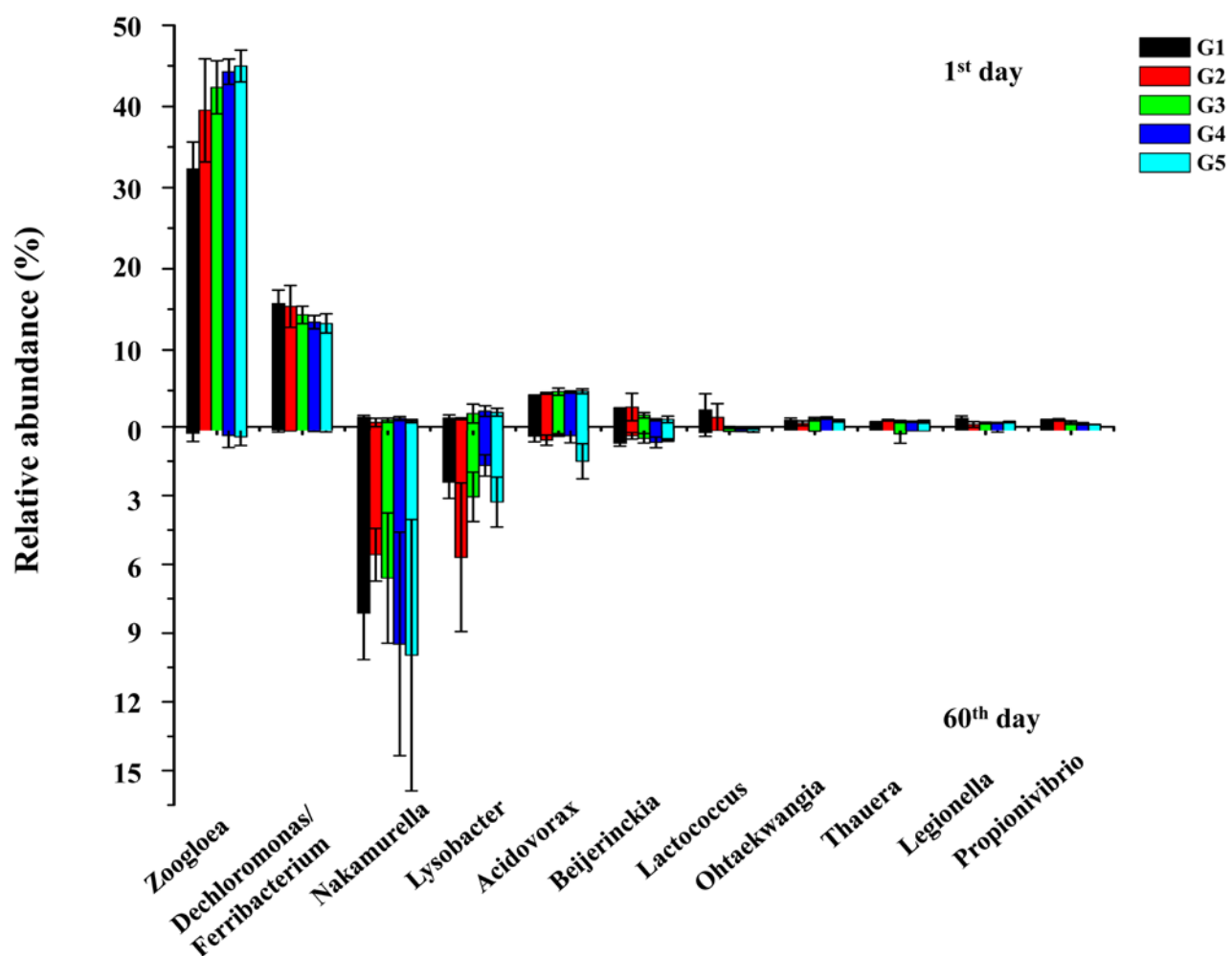


Figure S8. Relative abundances of the dominant genera in control and SWCNTs-treated groups on the initial stage (Day 1) and their corresponding relative abundances on the final stage (Day 60). Dominant means the sequence percentage is above 1% in any sample.

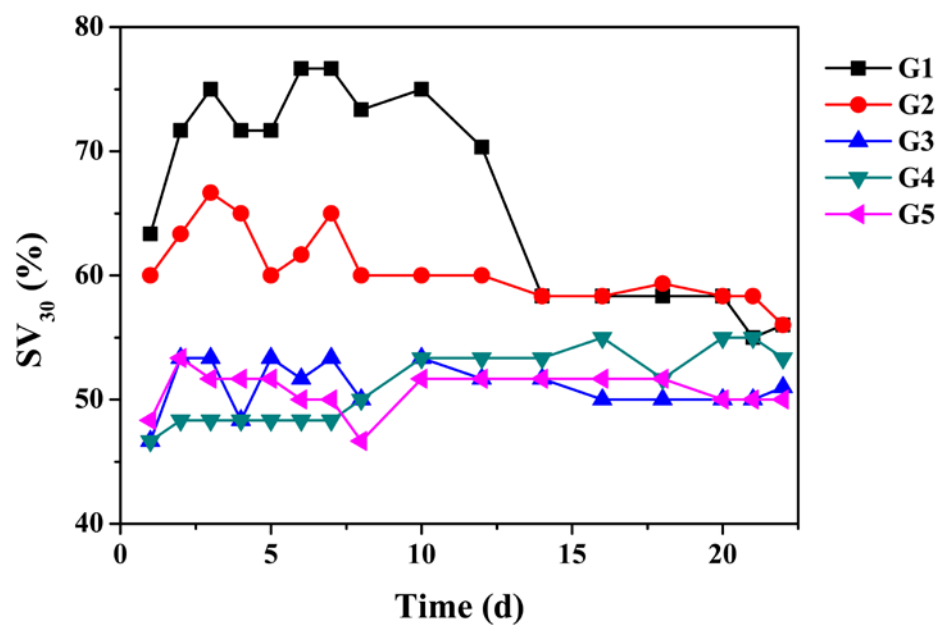


Figure S9. The SV₃₀ value of each group during the first 20 days. The data present here is the mean value of its replicates.

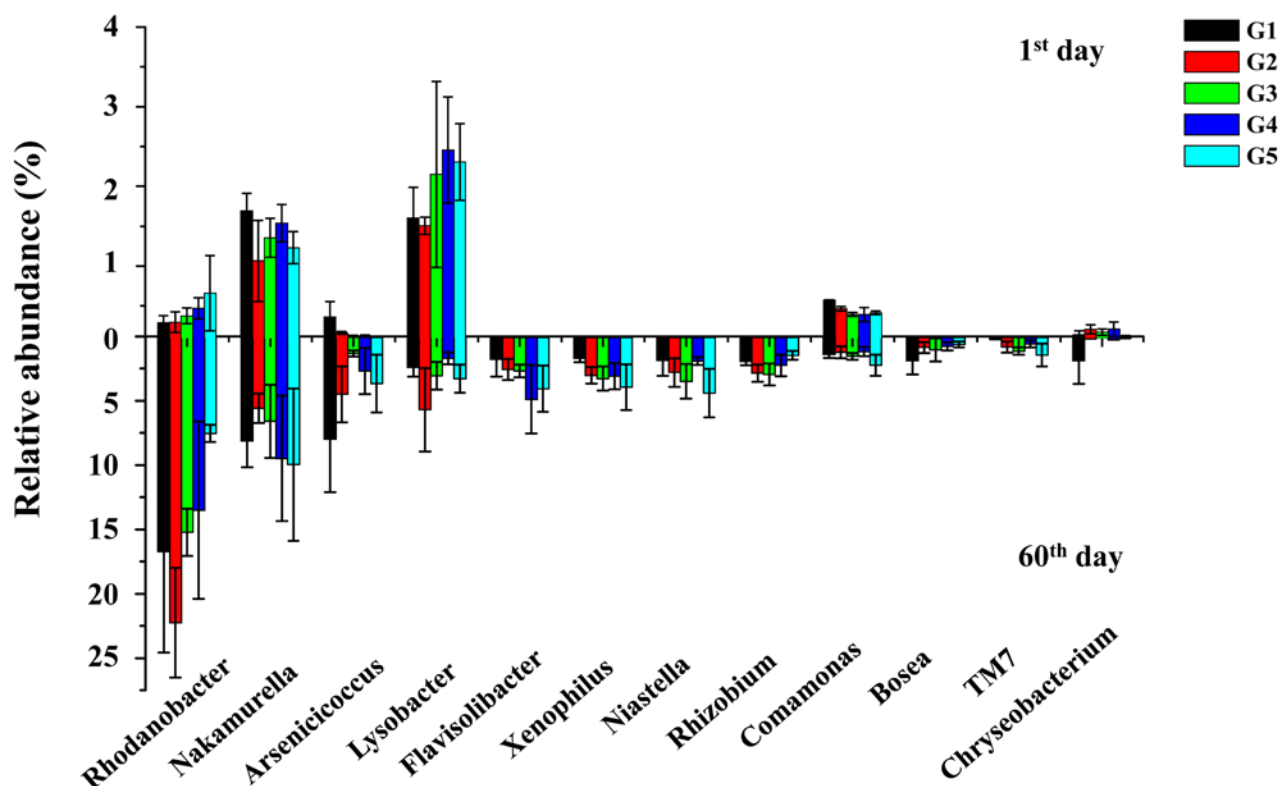


Figure S10. Relative abundances of the dominant genera in control and SWCNTs-treated groups on the final stage (Day 60) and their corresponding relative abundances on the initial stage (Day 1). Dominant means the sequence percentage is above 1% in any sample.

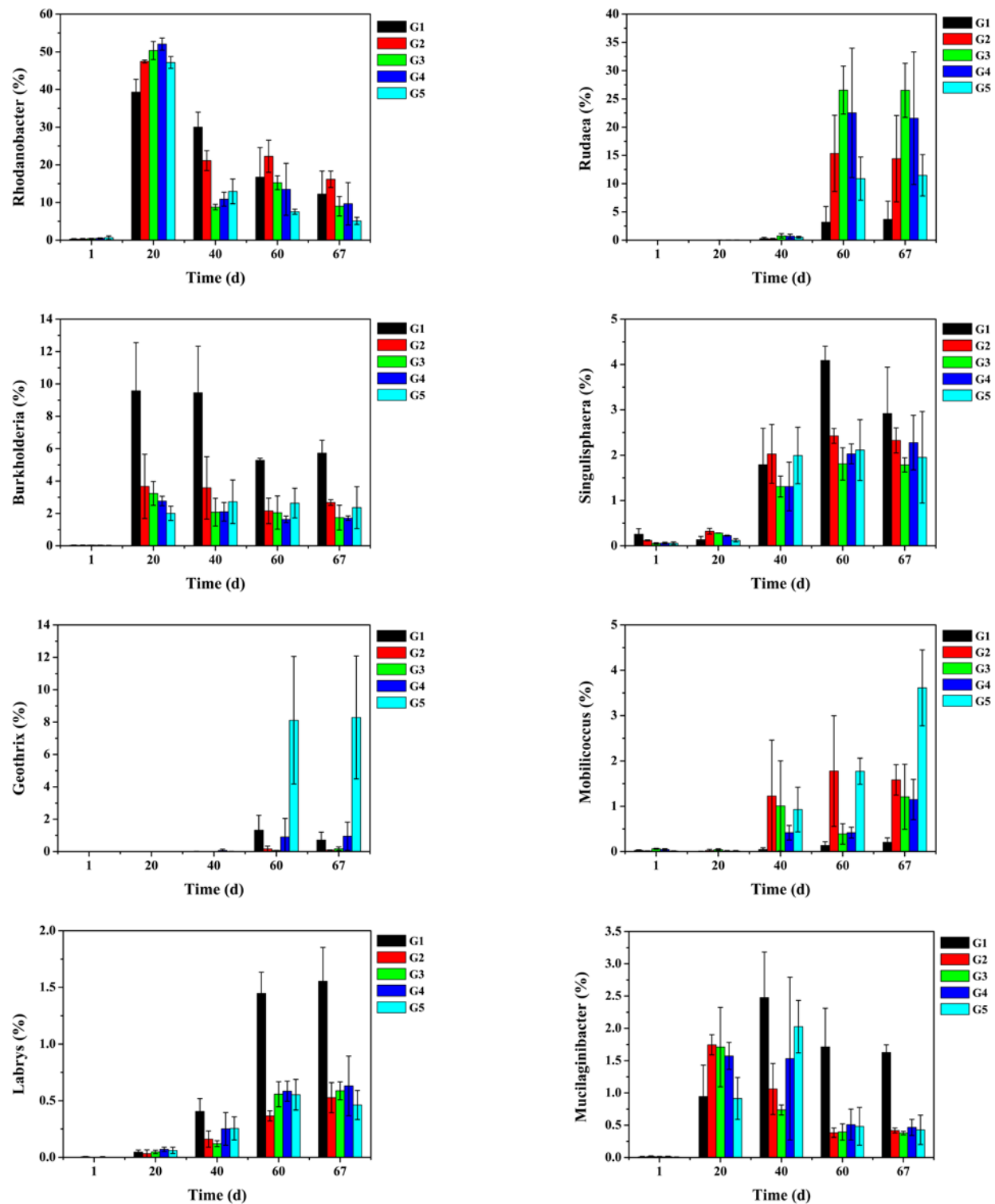


Figure S11. Relative abundances of *Rhodanobacter*, *Rudaea*, *Burkholderia*, *Singulisphaera*, *Geothrix*, *Mobilicoccus*, *Labrys* and *Mucilaginibacter* on each sampling time.

Table S1. Phenol adsorption by SWCNTs and autoclaved sludge-SWCNTs.

Group	Phenol concentration (mg/L)	
	Autoclaved sludge-SWCNTs	SWCNTs without sludge
G1	155.1 ± 2.8	174.4 ± 2.2
G2	154.7 ± 9.3	140.2 ± 13.8
G3	160.2 ± 7.0	125.9 ± 0.4
G4	155.3 ± 4.2	93.5 ± 8.0
G5	153.6 ± 3.2	74.2 ± 5.6

* The initial phenol concentration is 180 mg/L.

Table S2. Number of taxa showing significant correlations with SWCNTs.

Taxon	Day 1			Day 20			Day 40			Day 60			Day 67		
	P	N	None	P	N	None	P	N	None	P	N	None	P	N	None
Phylum	1	2	20	3	4	11	2	1	15	2	1	16	3	0	15
Class	3	7	32	7	4	26	2	2	34	2	2	34	3	4	30
Family	6	17	113	27	6	95	6	7	122	9	6	118	7	18	87
Genus	8	28	282	51	13	214	24	11	293	20	14	270	21	25	117
OTU	28	78	1315	123	32	891	66	27	1423	67	31	1249	71	55	1028

* P: positive effects ($P<0.05$), N: negative effects ($P<0.05$), None: no significant effects ($P>0.05$)