Electronic Supplementary Material (ESI) for Environmental Science: Water Research & Technology.

SUPPLEMENTARY MATERIAL

Activated sludge upon antibiotic shock loading: mechanistic description of functional stability and microbial community dynamics

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SUPPLEMENTARY TABLES

Table S1. Chao1 and Shannon indices before (day 0) and after (day 49) antibiotic shock loading

	A_0	G_0	S_0	A_{49}	G_{49}	S_{49}
Chao1	219 ± 21	248 ± 43	167 ± 11	165 ± 24	197 ± 14	208 ± 23
Shannon	2.93 ± 0.28	2.67 ± 0.34	2.45 ± 0.11	2.30 ± 0.05	2.86 ± 0.21	2.37 ± 0.18

SUPPLEMENTARY FIGURES

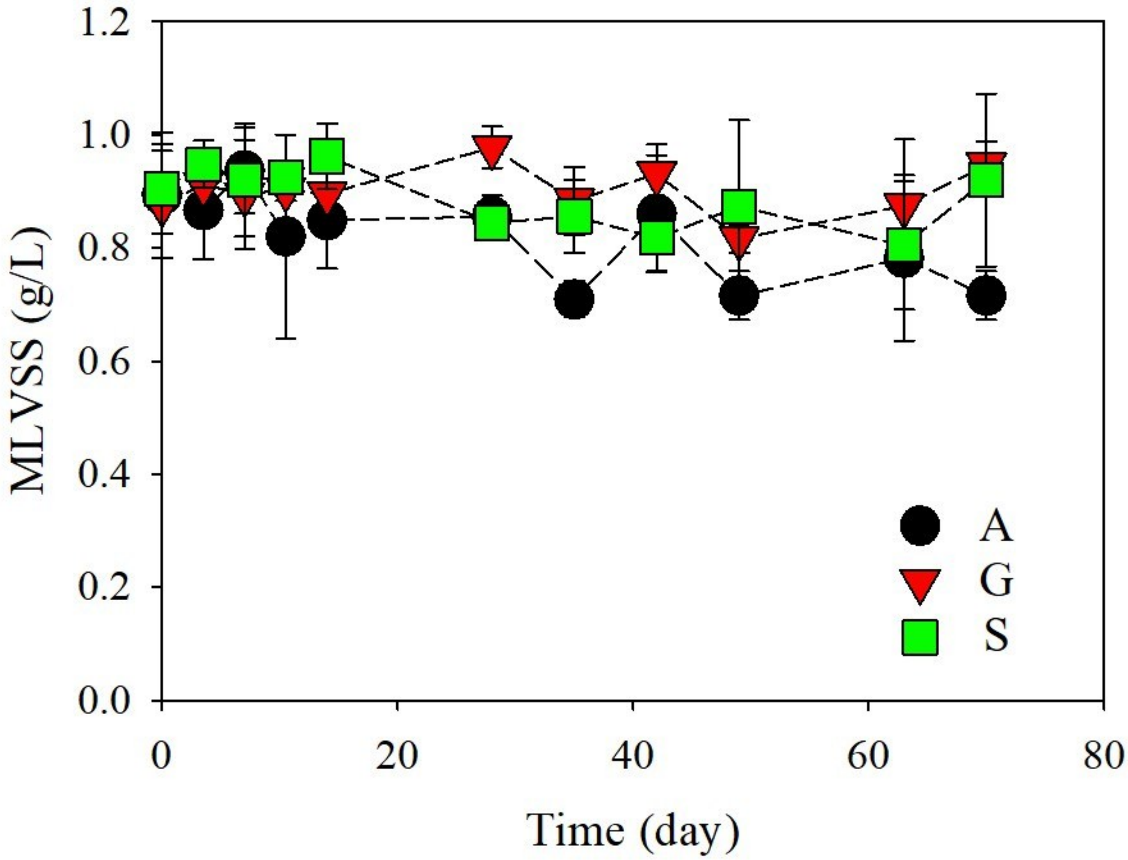

Figure S1. MLVSS of three reactors over time.

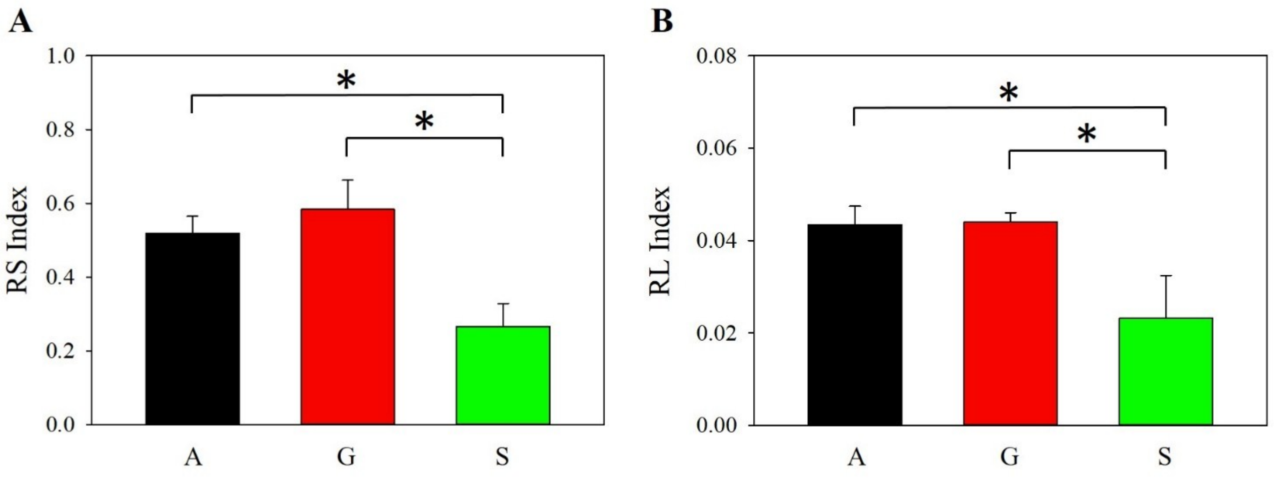

Figure S2. Resistance and resilience index upon CIP shock loadings. The RS and RL values were calculated with the COD data shown in Figure 1A using the equation (1) and (2) (See Materials and Methods), respectively. Asterisks represent statistical significance ($p < 0.05$ by Mann-Whitney U-test).

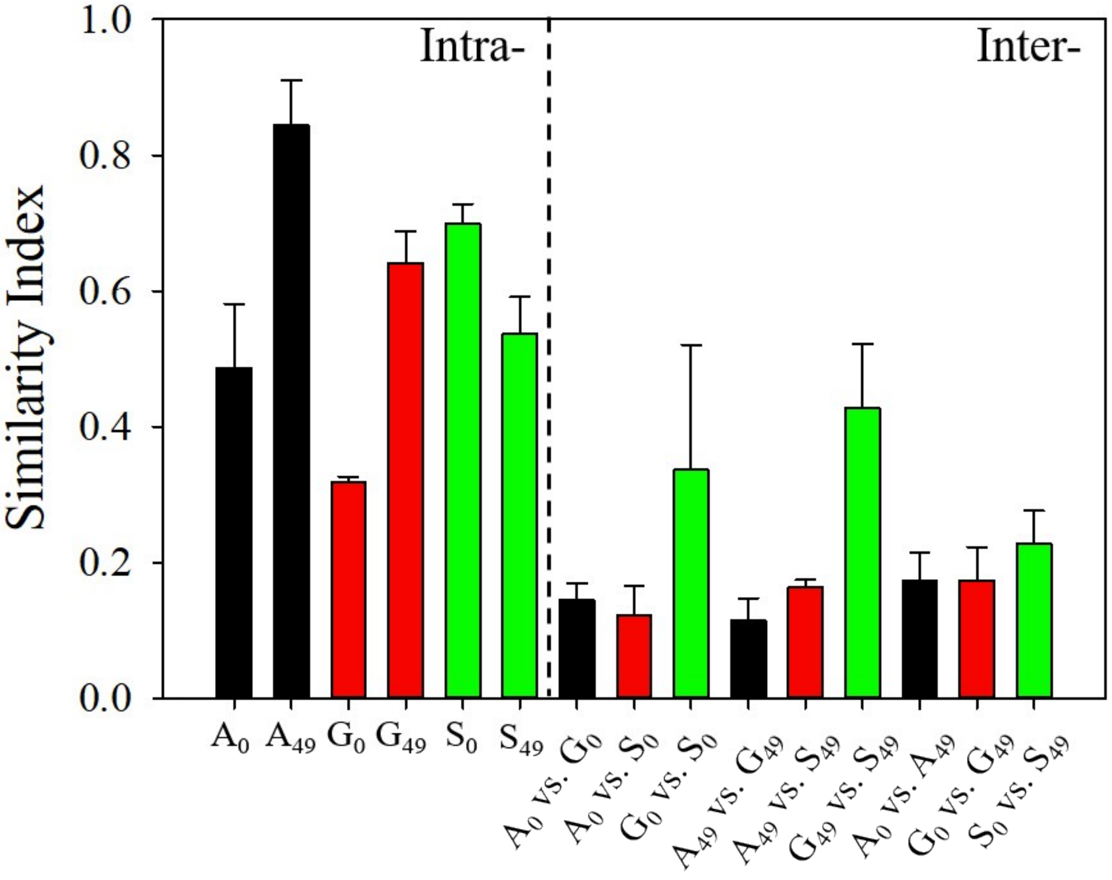

Figure S3. Similarity index of intra- and inter-groups of communities. The pairwise similarity was estimated using the Bray-Curtis distance metric.

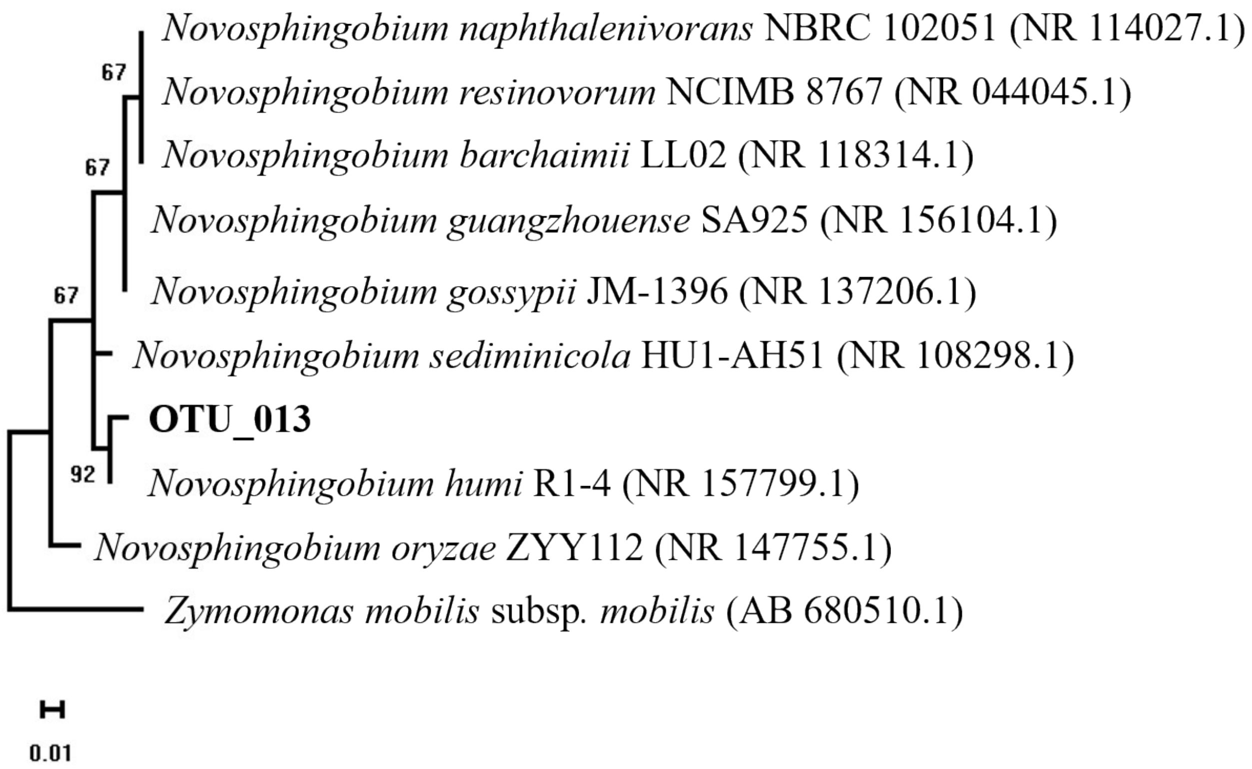

Figure S4. Phylogenetic relationship of OTU_013. The tree was constructed using MEGA X based on the maximum likelihood method with the Tamura-Nei model.[1, 2] Close relatives (e.g., *Novosphingobium* with > 97% of similarity to OTU_013) from the NCBI 16S ribosomal RNA sequence database were included for inference. Accession numbers are provided in parentheses.

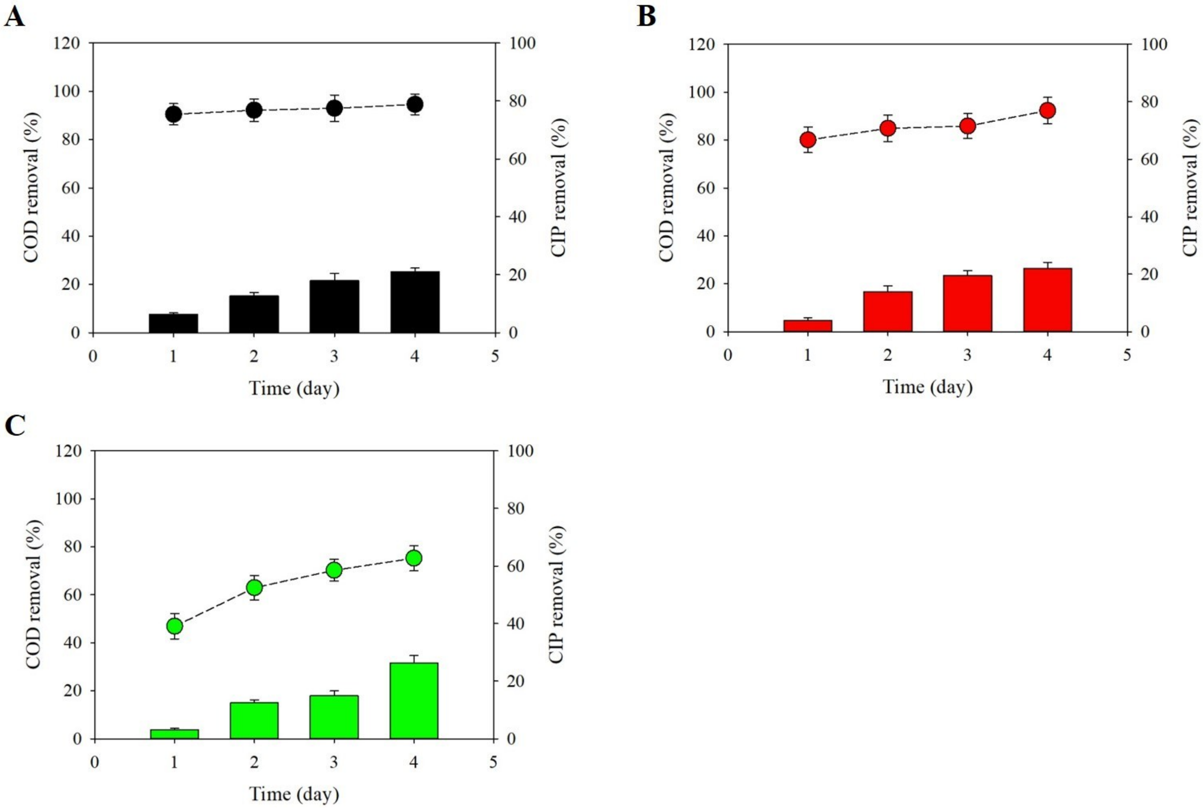

Figure S5. COD and CIP removals in three reactors occurring during a typical cycle at steady state: Acetate (A), glucose (B), and starch (C). The circle and bar indicate COD and CIP removal rate (%), respectively.

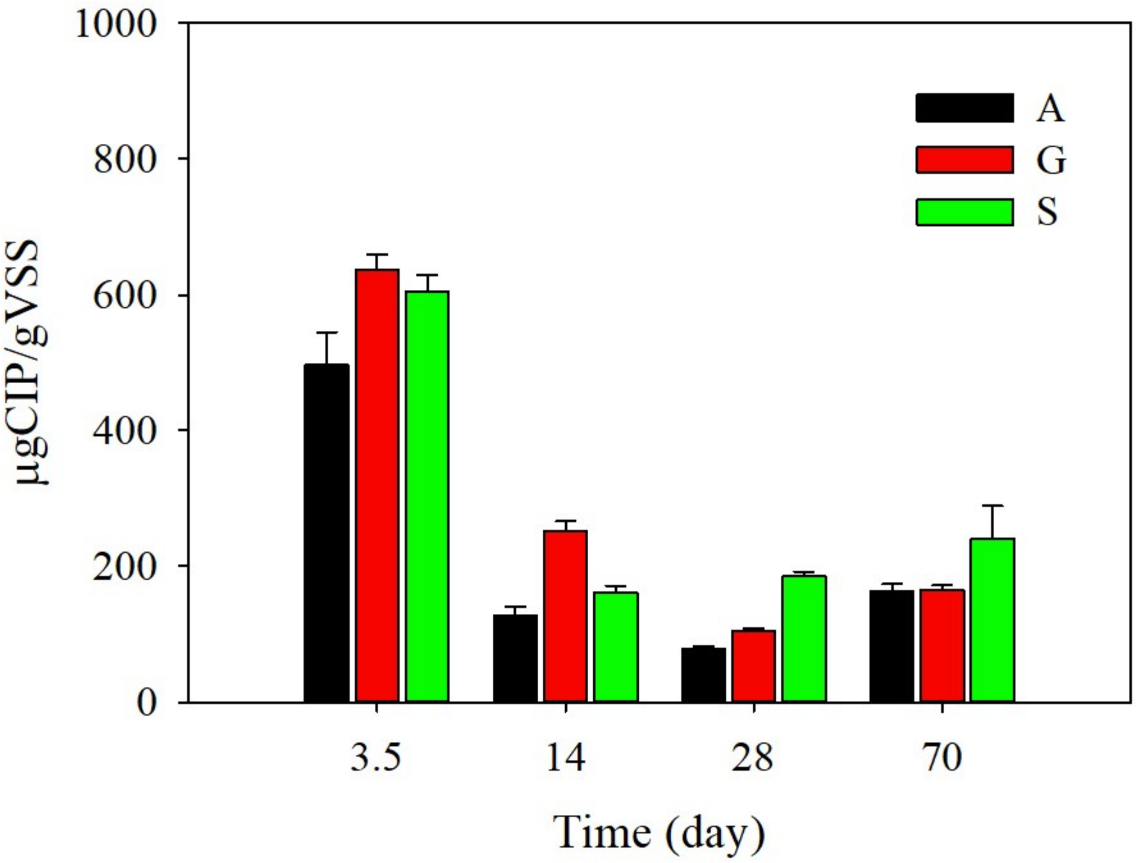

Figure S6. CIP sorbed onto biomass of three bioreactors over time.

Reference

1. K. Tamura and M. Nei, Estimation of the number of nucleotide substitutions in the control region of mitochondrial DNA in humans and chimpanzees. *Mol. Biol. Evol.*, 1993, **10**(3), 512-526.
2. S. Kumar, G. Stecher, M. Li, C. Knyaz and K. Tamura, MEGA X: Molecular Evolutionary Genetics Analysis across Computing Platforms. *Mol. Biol. Evol.*, 2018, **35**(6), 1547-1549.