



Supplementary Materials

Analysis platform and primers

Sequencing data were analyzed in cloud-based platform powered by Shanghai Majorbio Bio-pharm Technology Co., Ltd

Table S1. Software and Databases

Software and databases	version	usage	Official site or url
Flash	1.2.11	pair-end sequencing joint	https://ccb.jhu.edu/software/FLASH/index.shtml
Qiime	1.9.1	Calculating taxonomy profile	http://qiime.org/install/index.html
Uparse	11	OTU clustering	http://www.drive5.com/uparse/
RDP Classifier	2.13	Taxonomy assignment	https://sourceforge.net/projects/rdp-classifier/
Usearch	11	OTU statics	http://www.drive5.com/usearch/
Mothur	1.30.2	Alpha diversity	https://www.mothur.org/wiki/Download_mothur
PICRUSt	1.1.0	Functionality prediction for 16S sequencing data	http://picrust.github.io/picrust/
Mega	7	Cladogram analysis	https://www.megasoftware.net/
SILVA	138	Taxonomy database for rRNA	https://www.arb-silva.de/
UNITE	8	ITS database for fungi	https://unite.ut.ee/
RDP	11.5	Taxonomy database for rRNA	http://rdp.cme.msu.edu/
GreenGenes	135	Taxonomy database for rRNA	http://greengenes.secondgenome.com/
FunGene	9.6	Functional database for 16S	http://www.fungene-db.fr/
MaarjAM	81	Taxonomy database for 18SrRNA	https://www.maarjam.botany.ut.ee/
PR2	1	Taxonomy database for 18SrRNA	https://github.com/vaulot/pr2_database https://figshare.com/articles/PR2_rRNA_gene_database/3803709
Funguild	1	Functional database for 18SrRNA	http://www.funguild.org/
Tax4fun	0.3.1	Functional prediction	http://tax4fun.gobics.de/
MAFFT	7.2	Multi-Sequencing alignment	https://mafft.cbrc.jp/alignment/software/
IQ-TREE	1.6.8	For cladogram tree Build	http://www.iqtree.org/
Fastp	0.19.6	Quality control	https://github.com/OpenGene/fastp
PICRUSt2	2.2.0	Functional prediction for database like KEGG orthologs (KO), EC, COG and MetaCyc	https://github.com/picrust/picrust2/
Unoise3	11	OTU clustering	https://www.drive5.com/usearch/manual/unoise_algo.html/

Table S2. Primers

3NDF	GGCAAGTCTGGTGCCAG
V4EUKR2R	ACGGTATCTRATCRTCTTCG
338F	ACTCCTACGGGAGGCAGCAG
806R	GGACTACHVGGGTWTCTAAT

Table S3. Adsorption of Nutrients by Charcoal

Day	TAN				NO ₂ - N				NO ₃ - N				PO ₄ -P				pH			
	0.5%	1.0%	2.0%	4.0%	0.5%	1.0%	2.0%	4.0%	0.5%	1.0%	2.0%	4.0%	0.5%	1.0%	2.0%	4.0%	0.5%	1.0%	2.0%	4.0%
0	91.3	91.3	91.3	91.3	0.13	0.13	0.13	0.13	1.5	1.5	1.5	1.5	25.6	25.6	25.6	25.6	7.42	7.46	7.46	7.5
1	76.5	72.7	64.1	56.2	0.10	0.10	0.16	0.06	1.5	0.9	1.3	0.9	21.3	21.4	21.9	19.7	8.04	8.03	7.88	7.74
2	64.3	72.2	55.2	55.3	0.10	0.11	0.09	0.12	1.1	1.6	1.2	1.1	20.6	21.4	22.4	22.2	8.01	7.96	7.91	7.78
4	76.0	72.9	65.4	51.9	0.11	0.12	0.12	0.14	0.8	0.8	0.8	1.3	25.5	23.2	22.6	24.1	7.98	7.95	7.91	7.81
6	74.9	64.5	61.8	50.2	0.12	0.11	0.11	0.14	0.6	0.5	0.5	0.7	19.9	19.9	21.2	19.8	8.03	7.98	7.96	7.96
8	73.1	67.1	58.9	45.8	0.14	0.11	0.11	0.13	0.5	0.7	0.6	0.6	23.8	23.2	23.4	22.0	8.04	8.01	8.01	7.96
10	62.5	65.6	58.6	48.5	0.10	0.08	0.12	0.10	0.5	0.5	0.7	0.5	23.1	24.7	23.5	22.5	7.98	7.94	7.96	7.93

* This table provides raw data for the adsorption of nutrient by charcoal over a period of time without addition or inoculation of microalgae-bacteria.

Table S4. Nutrients Adsorption by Charcoal at Equilibrium

Charcoal	TAN		PO ₄ - P	
	C _e (mg/L)	q _e (mg/g)	C _e (mg/L)	q _e (mg/g)
0.5%	13.8	2.8	4.3	0.86
1.0%	17.6	1.8	4.2	0.42
2.0%	26.2	1.3	3.7	0.19
4.0%	34.1	0.9	3.9	0.10

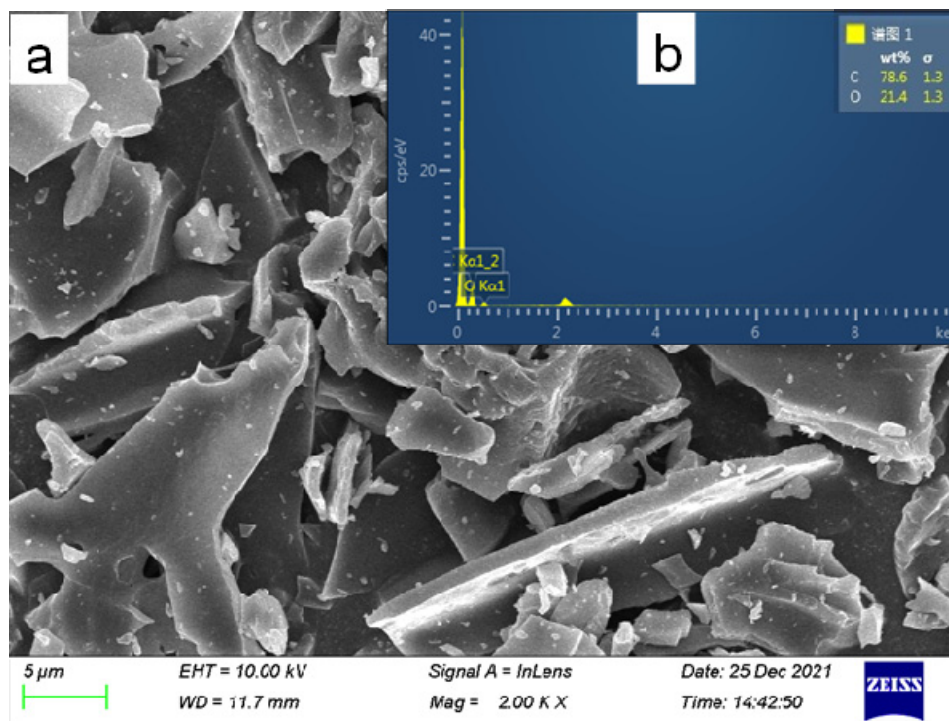


Fig. S1. (a) SEM micrograph and (b) EDX spectra of charcoal.

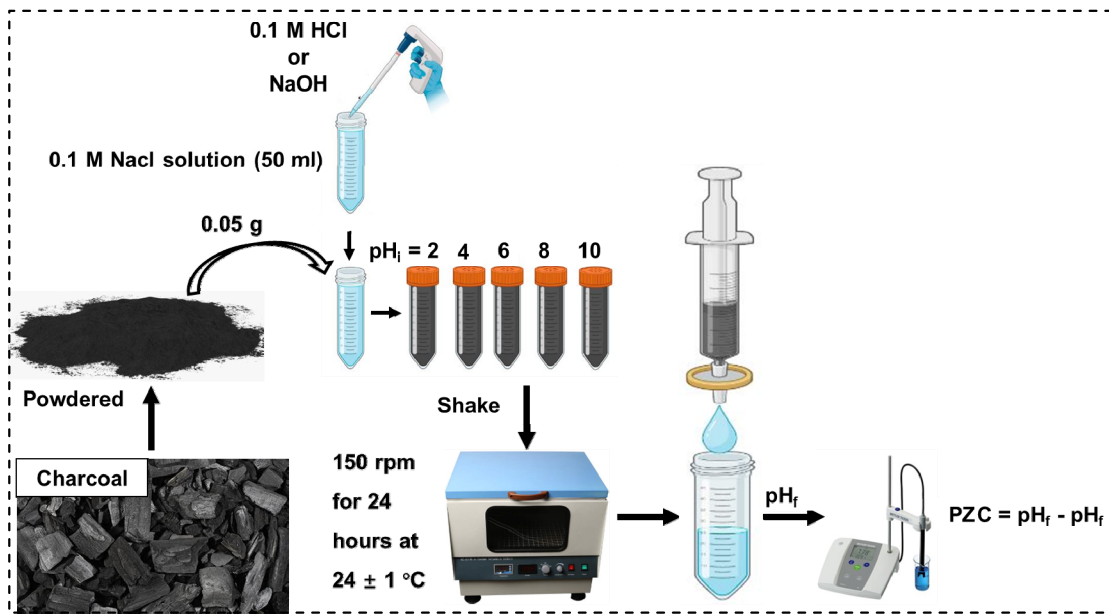


Fig. S2. Measurements of point of zero charges (PZC).

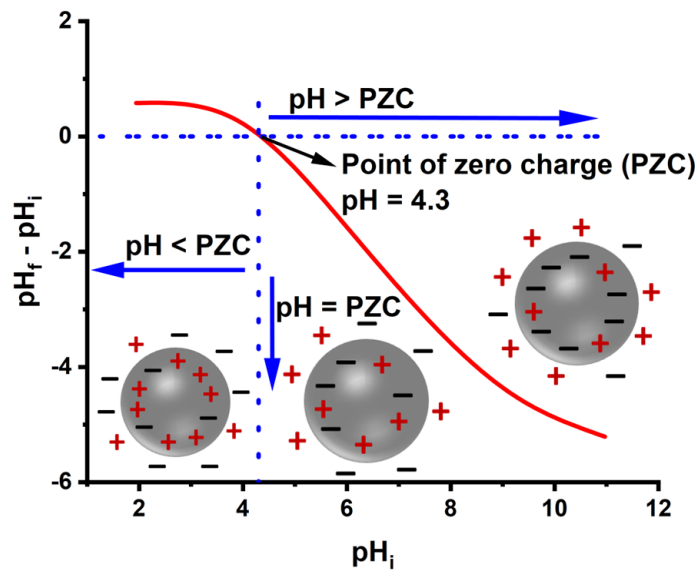


Fig. S3. Point of zero charges of charcoal.

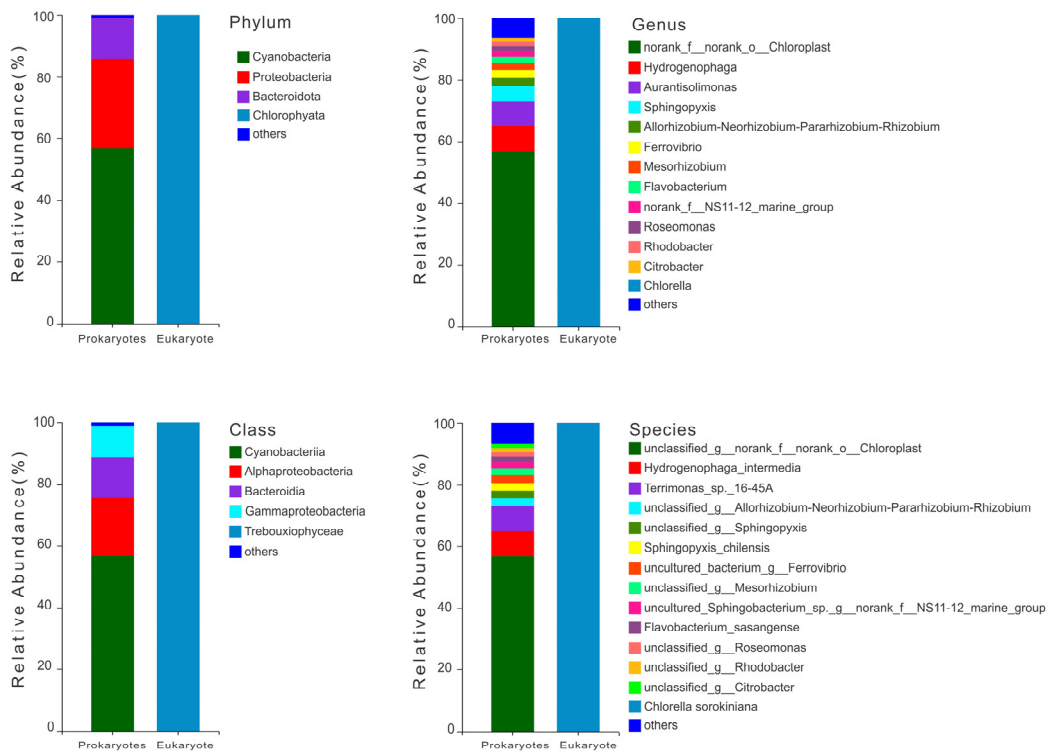


Fig. S4. *Chlorella sorokiniana* and associate bacterial communities.