Supporting Materials

Appendix A: Supporting Information

Table S1 Pore structure of the three types of GAC

GAC type	Iodine value	Micropores (D < 2 nm)	Mesopores (D = 2–50 nm)	Macropores (D > 50 nm)	Micro-level macropores (D = 0.2–10 μm)	Super-Macropores (D > 100 μm)
1# Shaanxi	650	0.1349	0.2197	0.4158	0.1535	0.1627
2# Huaqing	1050	0.2998	0.0942	0.4334	0.2265	0.1451
3# Calgon	950	0.2803	0.0854	0.6961	0.3046	0.3111

Notes: The unit of pore volume is mL/g, and the iodine value is dimensionless

Table S2 Surface functional groups (SFG) and elemental composition of GAC using X-ray photoelectron spectroscopy (XPS) analysis

GAC	SFG content (%) (Lu et al., 2020)		
	Hydroxyl groups	Carboxyl groups	Total acidic groups
1# Shaanxi	14.61	17.93	32.54
2# Huaqing	14.89	17.68	32.57
3# Calgon	17.08	15.8	32.88

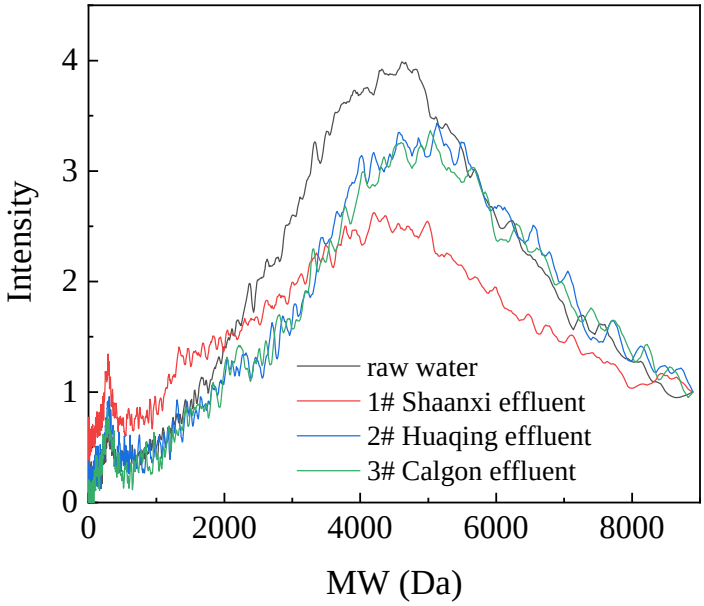


Fig. S1 MW distribution of raw water and treated water

Table S3 EEM region divided by excitation and emission wavelengths

No.	Region name	Excitation wavelength (nm)	Emission wavelength (nm)
I	Aromatic Protein I	200–250	280–330
II	Aromatic Protein II	200–250	330–380
III	Fulvic acid-like	200–250	380–500
IV	Soluble microbial by-product-like	250–340	280–380
V	Humic acid-like	250–340	380–500

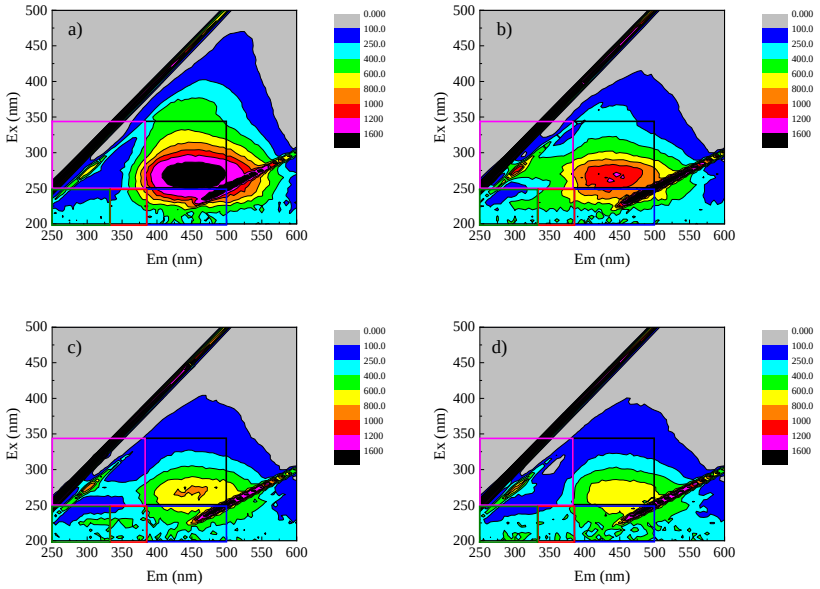


Fig. S2 EEM of (a) influent, (b) 1# BAC treated water, (c) 2# BAC treated water, (d) 3# BAC treated water

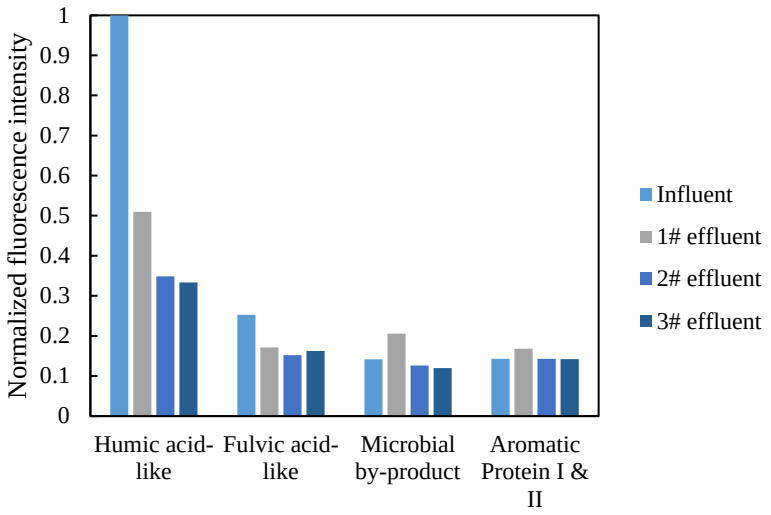
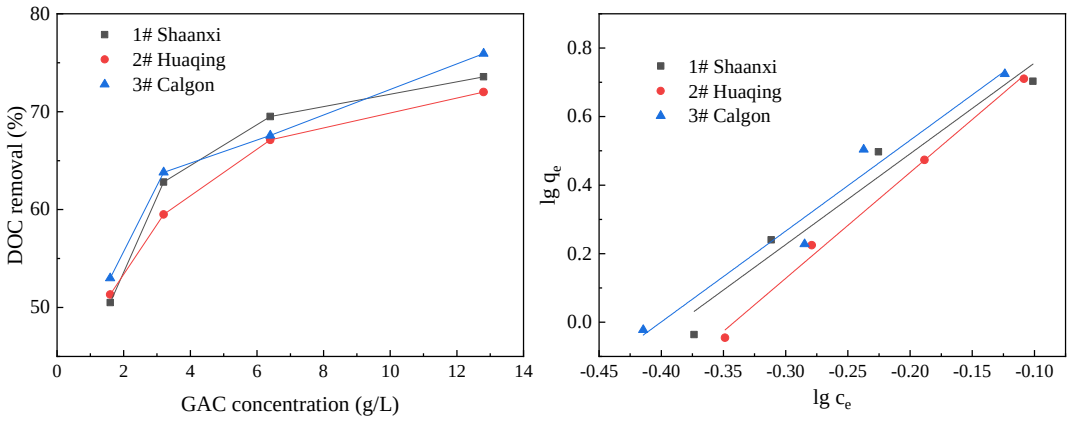


Fig. S3 Fluorescence intensity change of each fluorescence region



(a) (b)

Fig. S4 Adsorption on the different GACs by Freundlich isotherm: (a) Static DOC removal with different GAC concentration; (b) Freundlich adsorption model parameters of the 3 types of GAC

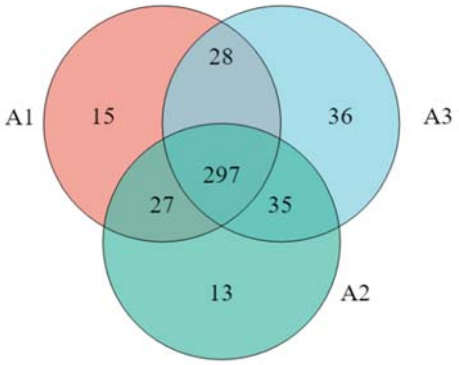


Fig. S5 Venn diagram of three types of BACs

Operational taxonomic unit (OTU) is a cluster of microorganisms with highly consistent DNA sequences. The higher the OTU, the higher the degree of biodiversity in the sample. The species diversity of each sample was judged according to the rarefaction curve (Fig. S6).

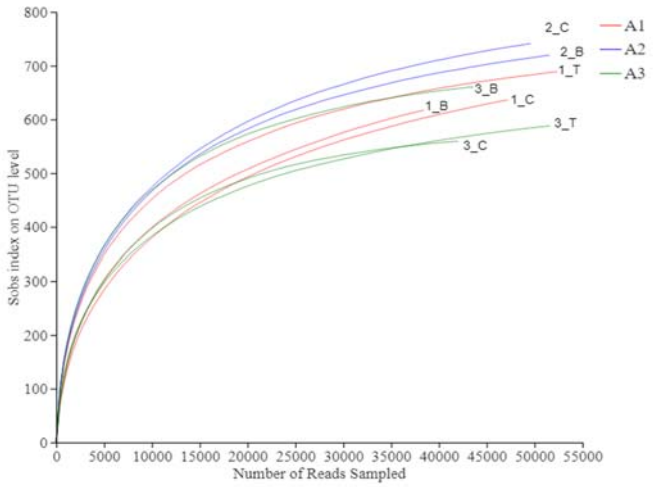


Fig. S6 Rarefaction curves of samples

In the labels beside the curves in Fig. S6, 1, 2, and 3 represent 1#, 2#, and 3# BAC, U, M, and D represent the upper (inlet), middle, and lower (outlet) ends of the carbon column, respectively.

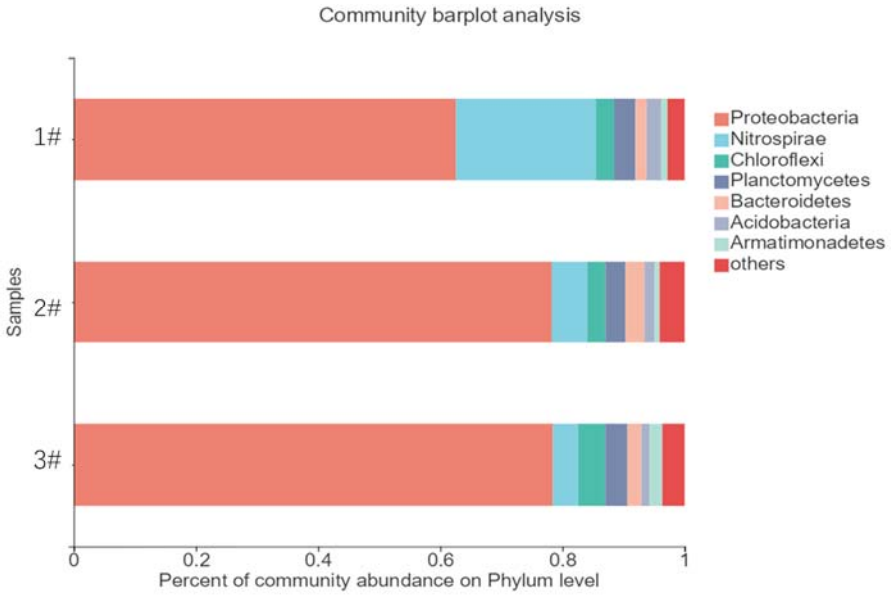


Fig. S7 Community structure of the BAC biofilm samples on phylum level

Models used to quantify the pore volume

Barret-Joyner-Halenda (BJH) model for mesopores:

$$\ln\frac{p}{p_s}=\frac{2\sigma v}{rRT} \tag{S1}$$

where p/p_s is the relative pressure of adsorbate vapor, r is the Kevin equivalent radius of the pores, σ is the surface tension of adsorbate and v is the molar volume of adsorbate.

The desorption branch of the N_2 adsorption/desorption isotherm was used to determine the filling pore volume corresponding to the effective radius of the mesopore.

HKSF model for micropores:

$$RT\ln(p/p_s)=\frac{3\pi K}{4}\left[\frac{N_a A_a+N_A A_A}{(2d_0)^4}\right]\cdot\sum\left\{\left[\frac{1}{2K+1}\left(1-\frac{2d_0}{r_p}\right)^{2K}\right]-\left[\frac{21\alpha}{32}\left(\frac{2d_0}{r_p}\right)^{10}-\beta\left(\frac{2d_0}{r_p}\right)^{4}\right]\right\} \tag{S2}$$

where p/p_s is the relative vapor pressure of the adsorbate, K is the sum index integer, r_p is the radius of cylindrical hole, α and β are calculation parameters, N_a is the number of atoms per unit surface area, N_A is the number of molecules per unit surface area, A_a and A_A are parameters of the Kirkwood-Muller equation, and d_0 is the sum of adsorbent diameter and adsorbate molecular diameter.

The pore volume corresponding to different pore sizes was obtained according to the nitrogen adsorption isotherm data and the corresponding relationship between relative pressure and pore size.