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S1. DGT-labile P concentration and DIFS model calculation

ZrO-AT DGT probes (Easysensor Ltd., China) were inserted vertically into sediment cores without disturbance and incubated for 24h under in-situ temperature and DO condition. The retrieved ZrO-AT DGT binding gel was sliced at 2 mm intervals using Ceramic cutter and stored in 3.0mL centrifuge tubes for DGT-labile P extraction and analysis. DGT-labile P was extracted using 0.8mL 1 mol·L⁻¹ NaOH solution, submerged the gel and elute for 16h, thus pipetted the extracting solution into 96-well microplate for photometric analysis using the molybdenum blue method (Murphy and Riley, 1962).

The DGT-labile P concentration was calculated as follows Eq. (1):

$$C_{DGT} = \frac{M\Delta_g}{DA t} \quad (1)$$

where M is the accumulated DGT-labile P on the binding gel (mg); Δ_g is the thickness of the diffusive gel layer (cm); D is the diffusion coefficient calibrated by temperature, detailed values please refer to (Wang et al., 2016); A is the exposed surface area of the DGT probe; and t is the deployment time (s).

The parameters of DGT model were calculated as follows Eq. (2) to Eq.

(5):

$$R = \frac{C_{DGT}}{C_{sol}} \quad (2)$$

$$K_d = \frac{C_s}{C_{sol}} = \frac{F_1}{C_{sol}} = \frac{k_1}{P_c k_{-1}} \quad (3)$$

$$k_{-1} = \frac{1}{T_c (P_c K_d + 1)} \quad (4)$$

$$k_1 = \frac{1}{T_c} = k_{-1} K_d P_c \quad (5)$$

where R is the ratio of DGT-measured P concentration (C_{DGT} , mg·L⁻¹) to the porewater dissolved SRP concentration (C_{sol} , $\mu\text{g}\cdot\text{L}^{-1}$), as shown in Eq. (2). The partitioning coefficient K_d (cm³·g⁻¹) between the solid and dissolved phases for each element was calculated as the ratio of the extracted exchangeable concentration (C_s , mg·g⁻¹) to dissolved concentration according to Eq. (3). The desorption rate constant K_{-1} (s⁻¹)

was determined by Eq. (4), in which the value T_c (s) was derived from DGT-induced fluxes in the sediment (DIFS) model with known values of R and K_d (Harper et al., 1998, 2000). P_c ($\text{g}\cdot\text{cm}^{-3}$) is bulk density of sediments. The adsorption constant K_1 (s^{-1}) was calculated by Eq. (5).

S2. Intact core incubation experiment

For the intact core incubation, the retrieved short sediment cores were carefully extruded into PC tubes (86mm ID and 50cm length) in an undisturbed state, then, 0.8 μm -filtered *in situ* overlying water was added dropwise along the tube wall to avoid disturbance until a water column depth of 20 cm was obtained. All cores were covered by aluminum foil to exclude light and incubated in a thermostatic incubator under *in situ* temperature. During incubation, the overlying water was continuously mixed using a magnetic stirrer, and the cores were not sealed to allow oxygen exchange. Overlying water samples were collected at 0, 12, 24, 36, 48, 60, and 72 h from 5 cm above the SWI and then filtered through 0.45 μm syringe filter for SRP analysis. Meanwhile, the same volume of the filtered *in situ* overlying water was refilled to each core immediately to maintain the water column volume. Thus, the incubated SRP fluxes can be calculated using the following Eq. (6):

$$F_{incubation} = [V(C_n - C_0 + \sum_{j=1}^n V_{j-1}(C_{j-1} - C_a))]/(S \times t) \quad (6)$$

where $F_{incubation}$ is the averaged incubated SRP flux across the SWI over three days, ($\text{mg}\cdot\text{m}^{-2}\cdot\text{d}^{-1}$); V is the volume of the water column (L^{-1}); C_n , C_0 , and C_{j-1} are the SRP concentrations at n , 0, and $j-1$ time ($\text{mg}\cdot\text{L}^{-1}$), respectively; C_a is the SRP concentration in the *in-situ* overlying water ($\text{mg}\cdot\text{L}^{-1}$); V_{j-1} is the volume of sampled overlying water samples (L^{-1}); S is the area of the SWI (m^2); t is the incubation time (d^{-1}).

S3. Sediment total microbial activity analysis

Conversion of fluorescein diacetate (FDA) to fluorescein appears to be primarily a hydrolysis followed by a dehydration reaction. This end-product absorbs strongly in the visible wavelength (490 nm) and can be measured by spectrophotometry. Generally, more than 90% of the energy flow in a soil system passes through microbial decomposers, therefore an assay which measures microbial decomposer activity will

provide a good estimate of total microbial activity (Adam and Duncan, 2001).

We subsampled ~1 g fresh wet sediments and SP in 50 mL pre-sterilized centrifuge tubes, and one control (without sample) was set up. Then, 10 mL 0.06 mol·L⁻¹ potassium phosphate buffer (pH=7.6) was added to each tube for vibration 15 min under 30°C. 0.5 mL 2 g·L⁻¹ FDA solution was then added except the control group for next 3 h static incubation under 30°C. Finally, 10 mL acetone solution was added to shut microbial activity off, and supernatant was obtained by centrifugation, and the adsorption value was detected photometrically at 490nm.

S4. Sediment alkaline phosphatase activity analysis

Alkaline phosphatase activity (APA) was measured following a modified method of (Adams et al., 2008), we subsampled ~1g wet sediment samples in 10 mL pre-sterilized centrifuge tubes, adding 6 mL 0.05 mol·L⁻¹ Tris-HCl buffer (pH=7) and 0.2 mL 10 mmol·L⁻¹ *p* nitrophenyl phosphate (*p*-NPP) as a substrate in order. All samples were incubated at 37°C and terminated the reaction using 1.5 mL 3mmol·L⁻¹ NaOH after 1h, 2h, and 3h. The concentration of produced *p* nitrophenol (*p*-NP) in the supernatant, which extracted by centrifuging at 4000 rpm for 10min, was measured by spectrophotometer at 410 nm and 500 nm. APA was calculated as μmol *p*-NPP hydrolyzed (*p*-NP or PO₄ produced) per hour per weight of sediment, using the following Eq. (7):

$$APA = \frac{A}{T \times M \times (1 - WC)} \quad (7)$$

Where A is the produced *p*-NP and PO₄ (mg·L⁻¹); M is the weight of the wet sediment (g); WC is the water content of the sediment; T is the incubation time (h).

S5. DNA Extraction and High-throughput Sequencing

Total DNA was extracted from sediment samples using Fast DNA ® SPIN Kit for Soil (MP Biomedicals, Santa Ana, CA, U.S.) according to the manufacturer's instructions. The 341F (5' -CCTAYGGGRBGCASCAG-3') and 806R (5' -GGACTACNNGGGTATCTAAT-3') primers were used to amplify the V3-V4 region of the microbial 16S rRNA gene (Walters et al., 2015). DNA samples and negative controls were amplified with the PCR reaction (20 μL) containing 4 μL of 5 × FastPfu

Buffer, 2 μ L of 2.5 mM dNTPs, 0.8 μ L of each primer (5 μ M), 0.4 μ L of FastPfu Polymerase, and 10 ng of template DNA. The final volume was adjusted to 20 μ L with sterile ddH₂O. The amplification protocol consisted of an initial denaturation step of 95 °C for 2 min, 25 cycles of denaturation at 95 °C for 30 s, annealing at 55 °C for 30 s, extension at 72 °C for 30 s, and a final extension step at 72 °C for 5 min. Then, the length and concentration of PCR products were checked by 1% agarose gel electrophoresis and purified using the AxyPrep DNA Gel Extraction Kit (Axygen Biosciences, Union City, CA, U.S.) according to the manufacturer's instructions. The sequencing library was generated using NEBNext® Ultra™ DNA Library Prep Kit for Illumina® (New England Biolabs, MA, USA) following manufacturer's protocol and index codes were added. Finally, the library was sequenced on NovaSeq PE250 platform and 250 bp paired-end sequences were generated (Shanghai BIOZERON Biotech. Co., Ltd, China). The paired-end sequences have been submitted to the NCBI Sequence Read Archive (SRA) database under the BioProject number PRJNA1455951.

Treatments	Porosity at the SWI	Infinite dilution molecular diffusion coefficients (D_0 , $\text{cm}^2\cdot\text{s}^{-1}$)			Tortuosity-correlated diffusion coefficients (D_i , $\text{cm}^2\cdot\text{s}^{-1}$)		
		PO_4^{3-}	Fe^{2+}	O_2	SRP	Fe^{2+}	O_2
0d_UDS	0.950	$4.18\cdot 10^{-6}$	$4.18\cdot 10^{-6}$	$14.63\cdot 10^{-6}$	$3.79\cdot 10^{-6}$	$3.79\cdot 10^{-6}$	$13.27\cdot 10^{-6}$
0d_D	0.798	$4.29\cdot 10^{-6}$	$4.18\cdot 10^{-6}$	$14.63\cdot 10^{-6}$	$2.95\cdot 10^{-6}$	$2.88\cdot 10^{-6}$	$10.08\cdot 10^{-6}$
60d_UDS	0.859	$5.45\cdot 10^{-6}$	$5.17\cdot 10^{-6}$	$17.54\cdot 10^{-6}$	$4.18\cdot 10^{-6}$	$3.96\cdot 10^{-6}$	$13.45\cdot 10^{-6}$
60d_DS	0.767	$5.45\cdot 10^{-6}$	$5.17\cdot 10^{-6}$	$17.54\cdot 10^{-6}$	$3.56\cdot 10^{-6}$	$3.38\cdot 10^{-6}$	$11.46\cdot 10^{-6}$
60d_D	0.712	$5.45\cdot 10^{-6}$	$5.17\cdot 10^{-6}$	$17.54\cdot 10^{-6}$	$3.25\cdot 10^{-6}$	$3.08\cdot 10^{-6}$	$10.45\cdot 10^{-6}$
120d_UDS	0.794	$7.54\cdot 10^{-6}$	$6.94\cdot 10^{-6}$	$23.34\cdot 10^{-6}$	$5.16\cdot 10^{-6}$	$4.75\cdot 10^{-6}$	$15.97\cdot 10^{-6}$
120d_DS	0.828	$7.54\cdot 10^{-6}$	$6.94\cdot 10^{-6}$	$23.34\cdot 10^{-6}$	$5.48\cdot 10^{-6}$	$5.04\cdot 10^{-6}$	$16.94\cdot 10^{-6}$
120d_D	0.729	$7.54\cdot 10^{-6}$	$6.94\cdot 10^{-6}$	$23.34\cdot 10^{-6}$	$4.62\cdot 10^{-6}$	$4.25\cdot 10^{-6}$	$14.30\cdot 10^{-6}$
180d_UDS	0.868	$8.96\cdot 10^{-6}$	$8.14\cdot 10^{-6}$	$28.41\cdot 10^{-6}$	$6.98\cdot 10^{-6}$	$6.34\cdot 10^{-6}$	$22.14\cdot 10^{-6}$
180d_DS	0.856	$8.96\cdot 10^{-6}$	$8.14\cdot 10^{-6}$	$28.41\cdot 10^{-6}$	$6.83\cdot 10^{-6}$	$6.21\cdot 10^{-6}$	$21.67\cdot 10^{-6}$
180d_D	0.796	$8.96\cdot 10^{-6}$	$8.14\cdot 10^{-6}$	$28.41\cdot 10^{-6}$	$6.15\cdot 10^{-6}$	$5.59\cdot 10^{-6}$	$19.51\cdot 10^{-6}$
240d_UDS	0.924	$8.20\cdot 10^{-6}$	$7.50\cdot 10^{-6}$	$25.46\cdot 10^{-6}$	$7.08\cdot 10^{-6}$	$6.47\cdot 10^{-6}$	$21.98\cdot 10^{-6}$
240d_DS	0.858	$8.20\cdot 10^{-6}$	$7.50\cdot 10^{-6}$	$25.46\cdot 10^{-6}$	$6.28\cdot 10^{-6}$	$5.74\cdot 10^{-6}$	$19.49\cdot 10^{-6}$
240d_D	0.824	$8.20\cdot 10^{-6}$	$7.50\cdot 10^{-6}$	$25.46\cdot 10^{-6}$	$5.91\cdot 10^{-6}$	$5.40\cdot 10^{-6}$	$18.35\cdot 10^{-6}$
300d_UDS	0.888	$6.09\cdot 10^{-6}$	$5.71\cdot 10^{-6}$	$19.22\cdot 10^{-6}$	$4.92\cdot 10^{-6}$	$4.61\cdot 10^{-6}$	$15.53\cdot 10^{-6}$
300d_DS	0.881	$6.09\cdot 10^{-6}$	$5.71\cdot 10^{-6}$	$19.22\cdot 10^{-6}$	$4.86\cdot 10^{-6}$	$4.56\cdot 10^{-6}$	$15.34\cdot 10^{-6}$
300d_D	0.822	$6.09\cdot 10^{-6}$	$5.71\cdot 10^{-6}$	$19.22\cdot 10^{-6}$	$4.38\cdot 10^{-6}$	$4.10\cdot 10^{-6}$	$13.81\cdot 10^{-6}$
360d_UDS	0.855	$4.29\cdot 10^{-6}$	$4.18\cdot 10^{-6}$	$14.63\cdot 10^{-6}$	$3.26\cdot 10^{-6}$	$3.18\cdot 10^{-6}$	$11.14\cdot 10^{-6}$
360d_DS	0.862	$4.29\cdot 10^{-6}$	$4.18\cdot 10^{-6}$	$14.63\cdot 10^{-6}$	$3.31\cdot 10^{-6}$	$3.22\cdot 10^{-6}$	$11.28\cdot 10^{-6}$
360d_D	0.823	$4.29\cdot 10^{-6}$	$4.18\cdot 10^{-6}$	$14.63\cdot 10^{-6}$	$3.08\cdot 10^{-6}$	$3.01\cdot 10^{-6}$	$10.53\cdot 10^{-6}$

Table S1. Diffusion coefficients used in fluxes at the SWI calculation. Considering sediment porosity and in-situ water temperature.

Note: The diffusion coefficient $D_i=D_0/\theta^2$ is the molecular diffusion coefficient correlated for sediment porosity ϕ using the tortuosity factor $\theta^2=1-\ln(\phi^2)$ (Boudreau, 1997); and mostly HPO_4^{2-} at the in-situ pH.

Step	Target phase	Extraction and time
Phase 1	Labile-P	NH ₄ Cl (pH = 7, 2h)
Phase 2	Fe-P	0.11M Na ₂ S ₂ O ₄ /NaHCO ₃ (pH = 7, 1h)
Wash		Deionized H ₂ O (0.5h)
Phase 3	Al-P and NaOH-TP	0.1M NaOH (16h)
Phase 4	Org-P	NaOH-TP – Al-P
Wash		Deionized H ₂ O (0.5h)
Phase 5	Ca-P	0.5M HCl (16h)
Ignition	Residue	Ignition at 550 °C (2h)
Phase 6	Res-P	1M HCl (16h)

Table S2. P sequential extraction procedure adapted from [Rydin, \(2000\)](#).

Time (d)	0d (Jan_2021)	60d (Mar_2021)	120d (May_2021)	180d (Jul_2021)	240d (Sep_2021)	300d (Nov_2021)	360d (Jan_2022)
Water temperature (°C)	5.20	12.40	24.20	32.20	27.90	16.00	5.80
pH	-	7.98	9.42	9.36	9.34	8.83	8.68
DO (mg·L ⁻¹)	-	13.27	11.72	9.14	6.95	7.99	12.85
Chl. a (µg·L ⁻¹)	-	7.59	24.06	68.47	3.35	2.86	0.22
COD _{Mn} (mg·L ⁻¹)	2.88	2.58	12.46	28.57	20.36	13.69	-
TN (mg·L ⁻¹)	1.62	2.00	1.92	1.25	1.27	1.18	0.76
NH ₄ ⁺ -N (mg·L ⁻¹)	0.47	0.12	0.21	1.17	0.16	0.21	-
NO ₃ ⁻ -N (mg·L ⁻¹)	0.91	1.74	0.41	0.40	0.43	0.67	-
TP (mg·L ⁻¹)	0.04	0.10	0.108	0.058	0.104	0.046	0.04
SRP (mg·L ⁻¹)	0.03	0.03	0.064	0.02	0.04	0.01	0.02

134 Table S3. Physicochemical parameters of the overlying water at the incubated site

135 during the experiment period.

136

Time (d)		0d	60d	120d	180d	240d	300d	360d
		Jan_2021	Mar_2021	May_2021	Jul_2021	Sep_2021	Nov_2021	Jan_2022
R	UDS	0.340	0.310	0.639	0.351	0.590	0.511	0.360
	DS	N.A.	0.280	0.310	0.504	0.539	0.543	0.342
	D	0.291	0.261	0.267	0.344	0.299	0.344	0.312
K_d (cm ³ ·g ⁻¹)	UDS	4.361	0.764	1.630	0.534	1.951	4.302	4.562
	DS	N.A.	0.783	0.533	2.500	1.359	10.383	2.349
	D	4.895	0.297	0.621	3.853	1.057	6.984	6.720
T_c (s)	UDS	$9.99 \cdot 10^6$	$9.99 \cdot 10^6$	$1.78 \cdot 10^4$	$2.09 \cdot 10^5$	$3.10 \cdot 10^4$	$6.85 \cdot 10^4$	$3.44 \cdot 10^5$
	DS	N.A.	$9.99 \cdot 10^6$	$9.62 \cdot 10^5$	$5.79 \cdot 10^4$	$3.70 \cdot 10^4$	$6.24 \cdot 10^4$	$3.60 \cdot 10^5$
	D	$9.99 \cdot 10^6$	$9.99 \cdot 10^6$	$9.99 \cdot 10^6$	$3.27 \cdot 10^5$	$1.00 \cdot 10^7$	$4.03 \cdot 10^5$	$1.00 \cdot 10^7$
k_1 (s ⁻¹)	UDS	$1.00 \cdot 10^{-7}$	$1.00 \cdot 10^{-7}$	$5.63 \cdot 10^{-5}$	$4.79 \cdot 10^{-6}$	$3.23 \cdot 10^{-5}$	$1.46 \cdot 10^{-5}$	$2.91 \cdot 10^{-6}$
	DS	N.A.	$1.00 \cdot 10^{-7}$	$1.04 \cdot 10^{-6}$	$1.73 \cdot 10^{-5}$	$2.70 \cdot 10^{-5}$	$1.60 \cdot 10^{-5}$	$6.78 \cdot 10^{-6}$
	D	$1.00 \cdot 10^{-7}$	$1.00 \cdot 10^{-7}$	$1.00 \cdot 10^{-7}$	$3.06 \cdot 10^{-6}$	$1.00 \cdot 10^{-7}$	$2.48 \cdot 10^{-6}$	$1.00 \cdot 10^{-7}$
k_{-1} (s ⁻¹)	UDS	$2.11 \cdot 10^{-8}$	$9.01 \cdot 10^{-8}$	$1.66 \cdot 10^{-5}$	$6.81 \cdot 10^{-6}$	$1.23 \cdot 10^{-5}$	$2.55 \cdot 10^{-6}$	$2.547 \cdot 10^{-6}$
	DS	N.A.	$8.62 \cdot 10^{-8}$	$1.3 \cdot 10^{-6}$	$5.22 \cdot 10^{-6}$	$1.53 \cdot 10^{-5}$	$1.14 \cdot 10^{-6}$	$2.456 \cdot 10^{-6}$
	D	$1.48 \cdot 10^{-8}$	$2 \cdot 10^{-7}$	$9.9 \cdot 10^{-8}$	$5.55 \cdot 10^{-7}$	$6.66 \cdot 10^{-8}$	$2.46 \cdot 10^{-7}$	$1.07 \cdot 10^{-8}$

138 Table S4. Parameters of DIFS model for SRP of three treatments during the incubation
 139 experiment.

Time (d)		0d	60d	120d	180d	240d	300d	360d
		Jan_21	Mar_21	May_21	Jul_21	Sep_21	Nov_21	Jan_22
Q _{max} (mg·kg ⁻¹)	UDS	990.696	904.022	763.108	1183.620	1195.635	830.2	748.7
	DS	N.A.	1407.3	1500.1	1152.2	1300.9	1167.3	962.4
	D	1526.7	1429.3	1409.2	1270.0	1407.3	1374.7	1072.7
	SP	N.A.	711.236	813.808	1051.574	1223.342	1267.6	688.371
EPC ₀ (mg·L ⁻¹)	UDS	0.097	0.102	0.118	0.087	0.093	0.088	0.064
	DS	N.A.	0.107	0.089	0.089	0.086	0.075	0.054
	D	0.085	0.080	0.070	0.075	0.083	0.078	0.053
	SP	N.A.	0.137	0.131	0.107	0.091	0.091	0.053
R ²	UDS	0.928	0.864	0.831	0.892	0.873	0.872	0.930
	DS	N.A.	0.884	0.909	0.931	0.876	0.924	0.916
	D	0.875	0.874	0.894	0.893	0.899	0.913	0.934
	SP	N.A.	0.916	0.904	0.889	0.887	0.907	0.924

140 Table S5. Langmuir isotherm parameters for P adsorption by sediments from three
141 treatments and SP over incubation period.
142

UDS		DS		D		SP	
OTU	Sequence number	OTU	Sequence number	OTU	Sequence number	OTU	Sequence number
0dUDS1	39056	0dDS	68745				
0dUDS	66945	0dDS	67208				
0dUDS	40601	0dDS	53346				
60dUD	45297	60dD	41219	60d	40567	60dS	38416
60dUD	55563	60dD	39016	60d	67362	60dS	55478
60dUD	45359	60dD	64837	60d	57653	60dS	51496
120dU	68323	120d	58324	120d	43366	120d	66089
120dU	35701	120d	68986	120d	63539	120d	54837
120dU	45655	120d	45943	120d	57658	120d	59940
180dU	45251	180d	44770	180d	57255	180d	39110
180dU	71424	180d	69564	180d	40392	180d	69197
180dU	58683	180d	64065	180d	56874	180d	45690
240dU	47092	240d	38638	240d	67282	240d	42316
240dU	51479	240d	67251	240d	57453	240d	40316
240dU	61310	240d	43804	240d	45772	240d	43857
300dU	64163	300d	67542	300d	61748	300d	71049
300dU	70199	300d	36691	300d	45348	300d	61104
300dU	49255	300d	56289	300d	54251	300d	43361
360dU	44633	360d	42208	360d	47585	360d	55304
360dU	46138	360d	46964	360d	42946	360d	45090
360dU	42465	360d	46490	360d	46832	360d	50772

Table S6. The sequence number of each sample.

143
144
145
146

Group	N	E	Pos	Neg	CC	APL	MD	AD
UDS	717	1102	87.88%	12.12%	0.30	5.779	0.679	3.074
UDS (random)	717	1102			0.003	2.525	0.058	3.074
DS	612	788	93.48%	6.52%	0.322	5.789	0.853	2.575
DS (random)	612	788			0.003	2.631	0.059	2.575
D	454	544	91.43%	8.57%	0.347	3.858	0.759	2.396
D (random)	454	544			0.002	2.124	0.057	2.396
SP	472	487	75.5%	24.5%	0.351	4.760	0.882	2.064
SP (random)	472	487			0.006	2.457	0.006	2.064

Table S7. The topological properties of microbial networks across different groups.

Note: “N” represents the number of nodes; “E” represents the number of edges; “Pos” represents the proportion of positive correlations among nodes; “Neg” represents negative correlations among nodes; “CC” represents clustering coefficient; “APL” represents average shortest path length; “MD” represents modularity; “AD” represents average degree.

Network	ASV ID	Phylum	Genus/clade	Degree	Category
UDS (36)	OTU369	Chloroflexi	SBR1031	27	Module hub
	OTU1194	Chloroflexi	Unclassified Anaerolineaceae	16	Module hub
	OTU73	Gammaproteobacteria	Unclassified Nitrosomonadaceae	26	Module hub
	OTU295	Gammaproteobacteria	Unclassified Nitrosomonadaceae	26	Module hub
	OTU187	Nitrospirota	Unclassified Thermodesulfovibrionia	33	Module hub
	OTU1447	Acidobacteriota	<i>Luteitalea</i>	5	Connector
	OTU3923	Acidobacteriota	<i>Paludibaculum</i>	6	Connector
	OTU529	Acidobacteriota	<i>Paludibaculum</i>	4	Connector
	OTU227	Acidobacteriota	Vicinamibacteria Subgroup 17	3	Connector
	OTU368	Acidobacteriota	Vicinamibacteria Subgroup 17	6	Connector
	OTU1764	Acidobacteriota	Vicinamibacteria Subgroup 17	4	Connector
	OTU672	Actinobacteriota	PeM15	6	Connector
	OTU530	Alphaproteobacteria	Unclassified Beijerinckiaceae	6	Connector
	OTU1015	Bdellovibrionota	0319-6G20	4	Connector
	OTU130	Chloroflexi	KD4-96	3	Connector
	OTU8	Chloroflexi	KD4-96	7	Connector
	OTU482	Chloroflexi	OLB14	4	Connector
	OTU1220	Chloroflexi	RBG-13-54-9	3	Connector
	OTU156	Chloroflexi	RBG-13-54-9	5	Connector
	OTU1488	Chloroflexi	Unclassified Anaerolineaceae	4	Connector
	OTU833	Chloroflexi	Unclassified Anaerolineaceae	4	Connector
	OTU72	Desulfobacterota	Unclassified Desulfosarcinaceae	4	Connector
	OTU868	Desulfobacterota	Unclassified Desulfosarcinaceae	4	Connector
	OTU302	Firmicutes	<i>Clostridium</i>	4	Connector

	OTU173	Firmicutes	<i>Clostridium</i>	6	Connector
	OTU123	Firmicutes	<i>Romboutsia</i>	6	Connector
	OTU259	Gammaproteobacteria	<i>Ferritrophicum</i>	3	Connector
	OTU1416	Gammaproteobacteria	<i>Thiobacillus</i>	6	Connector
	OTU995	Gammaproteobacteria	Unclassified Nitrosomonadaceae	8	Connector
	OTU589	Gemmatimonadota	Unclassified Gemmatimonadaceae	7	Connector
	OTU1324	Latescibacterota	Unclassified Latescibacterota	4	Connector
	OTU1591	MBNT15	MBNT15	4	Connector
	OTU580	Nitrospinota	P9X2b3D02	6	Connector
	OTU1165	Planctomycetota	WD2101	4	Connector
	OTU1458	Sva0485	Sva0485	4	Connector
	OTU1482	Verrucomicrobiota	Unclassified Pedosphaeraceae	4	Connector
DS (12)	OTU714	Acidobacteriota	Unclassified Aminicenantes	14	Module hub
	OTU624	Actinobacteriota	Unclassified Gaiellales	8	Module hub
	OTU332	Actinobacteriota	Solirubrobacterales 67-14	12	Module hub
	OTU484	Chloroflexi	SJA-15	12	Module hub
	OTU628	Gammaproteobacteria	Unclassified Hydrogenophilaceae	12	Module hub
	OTU1226	Sva0485	Sva0485	9	Module hub
	OTU106	Acidobacteriota	Subgroup 23	4	Connector
	OTU34	Actinobacteriota	Unclassified Frankiales	3	Connector
	OTU14	Actinobacteriota	Unclassified Gaiellales	5	Connector
	OTU8	Chloroflexi	KD4-96	4	Connector
	OTU701	Cyanobacteria	Unclassified Cyanobacteriia	4	Connector
	OTU273	Sva0485	Sva0485	3	Connector
D (4)	OTU2129	Nitrospirota	4-29-1	3	Connector

	OTU864	Bacteroidota	Unclassified Prolixibacteraceae	3	Connector
	OTU1793	Acidobacteriota	<i>Paludibaculum</i>	5	Connector
	OTU1358	Acetothermia	Unclassified Acetothermiia	4	Connector
	OTU145	Actinobacteriota	MB-A2-108	10	Module hub
	OTU1967	Gammaproteobacteria	Unclassified Hydrogenophilaceae	12	Module hub
	OTU23	Chloroflexi	<i>Caldilinea</i>	6	Connector
SP (7)	OTU300	Chloroflexi	KD4-96	6	Connector
	OTU78	Gammaproteobacteria	SZB7	4	Connector
	OTU278	Gammaproteobacteria	<i>Sulfurifustis</i>	4	Connector
	OTU510	Nitrospirota	Unclassified Thermodesulfovibrionia	4	Connector

154 Table S8. The keystone species in microbial networks across different groups.

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Treatments		SRP flux	O ₂ flux	O ₂ : P ratio 138:1	O ₂ : P ratio 65:1	O ₂ : P ratio 250:1
0d	UDS	-0.096	-63.778			
	D	0.128	-18.391	0.96	0.45	1.74
60d	UDS	-0.017	-18.908			
	DS	-0.156	-11.83			
	D	-0.042	-4.338			
120d	UDS	0.027	-31.623	0.12	0.06	0.21
	DS	0.168	-80.46	0.29	0.14	0.52
	D	0.068	-10.217	0.92	0.43	1.66
180d	UDS	4.669	-201.633	3.20	1.51	5.79
	DS	1.997	-31.939	8.63	4.06	15.63
	D	0.181	-7.801	3.20	1.51	5.80
240d	UDS	3.347	-49.609	9.31	4.39	16.87
	DS	2.332	-43.948	7.32	3.45	13.27
	D	0.385	-58.064	0.92	0.43	1.66
300d	UDS	0.357	-140.841	0.35	0.16	0.63
	DS	0.854	-4.588	25.69	12.10	46.53
	D	-0.196	-6.634			
360d	UDS	0.12	-22.69	0.73	0.34	1.32
	DS	0.039	-57.081	0.09	0.04	0.17
	D	0.00005	-7.32	0.00	0.00	0.00

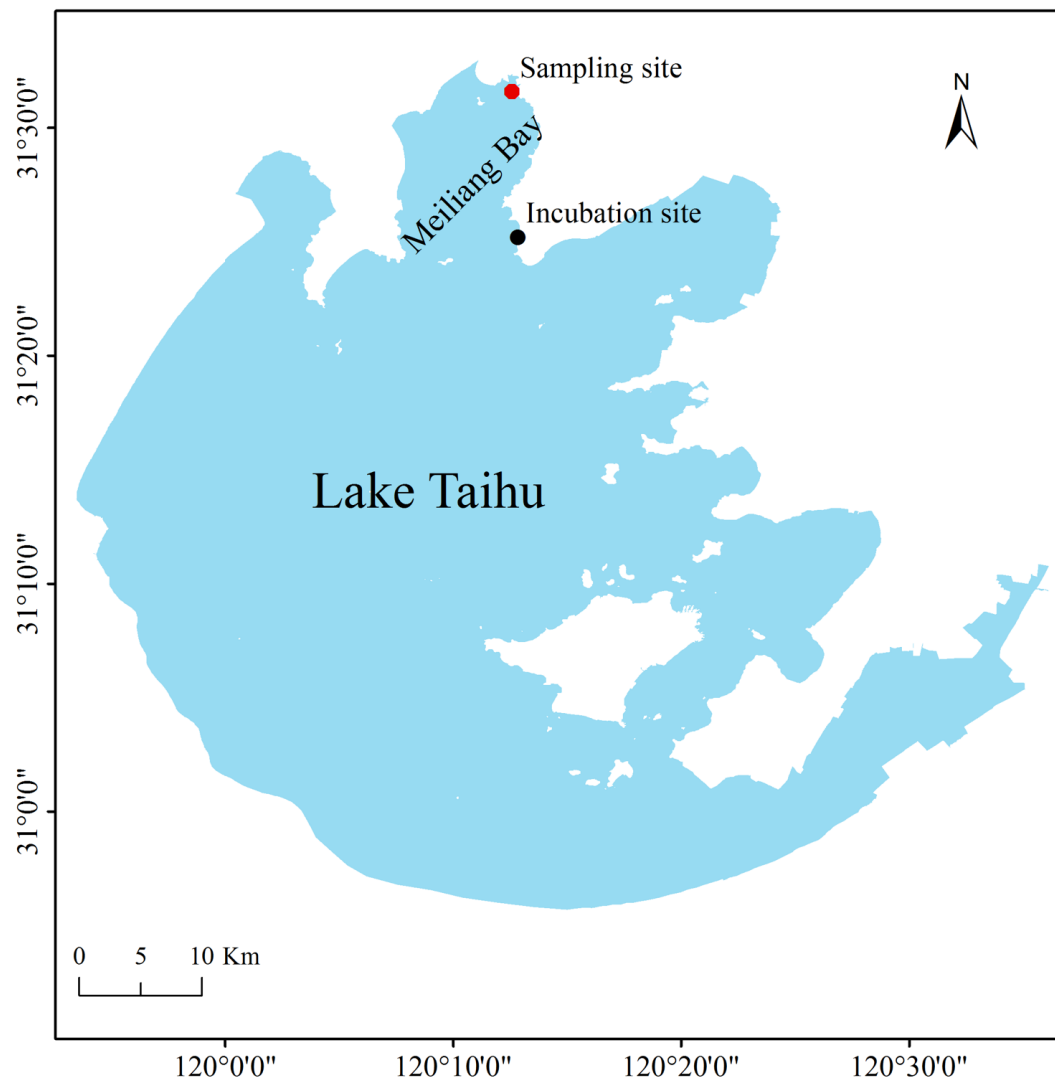
Table S9. Sensitivity analysis of the apparent P recycling ratio under different O₂:P remineralization assumptions.

Note: The apparent P recycling ratio was calculated using alternative molar O₂:P ratios of 65:1, 138:1, and 250:1, representing P-rich organic matter, Redfield-like organic matter, and P-poor/degraded organic matter remineralization scenarios, respectively.

Omitted observation	Refitted equation	Refitted exponent b	Δb from full model	R^2
None	$F_{SRP} = 0.542SOU^{0.410}$	0.410	-	0.930
180d UDS	$F_{SRP} = 0.249SOU^{0.629}$	0.629	+0.219	0.871
240d UDS	$F_{SRP} = 0.416SOU^{0.455}$	0.455	+0.045	0.999
300d DS	$F_{SRP} = 0.606SOU^{0.389}$	0.389	-0.021	0.936
180d DS	$F_{SRP} = 0.589SOU^{0.395}$	0.395	-0.015	0.937
240d DS	$F_{SRP} = 0.592SOU^{0.391}$	0.391	-0.019	0.873

Table S10. Influential-point analysis of the SOU-SRP power-law relationship using leave-one-out refitting.

Note: The power-law model was refitted after removing one observation at a time. The fitted exponent remained below 1 in all refitted models ($b = 0.389\text{--}0.629$), indicating that the sublinear form was not driven by any single observation.



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171 Fig S1. Location of sampling and incubation sites in Lake Taihu.

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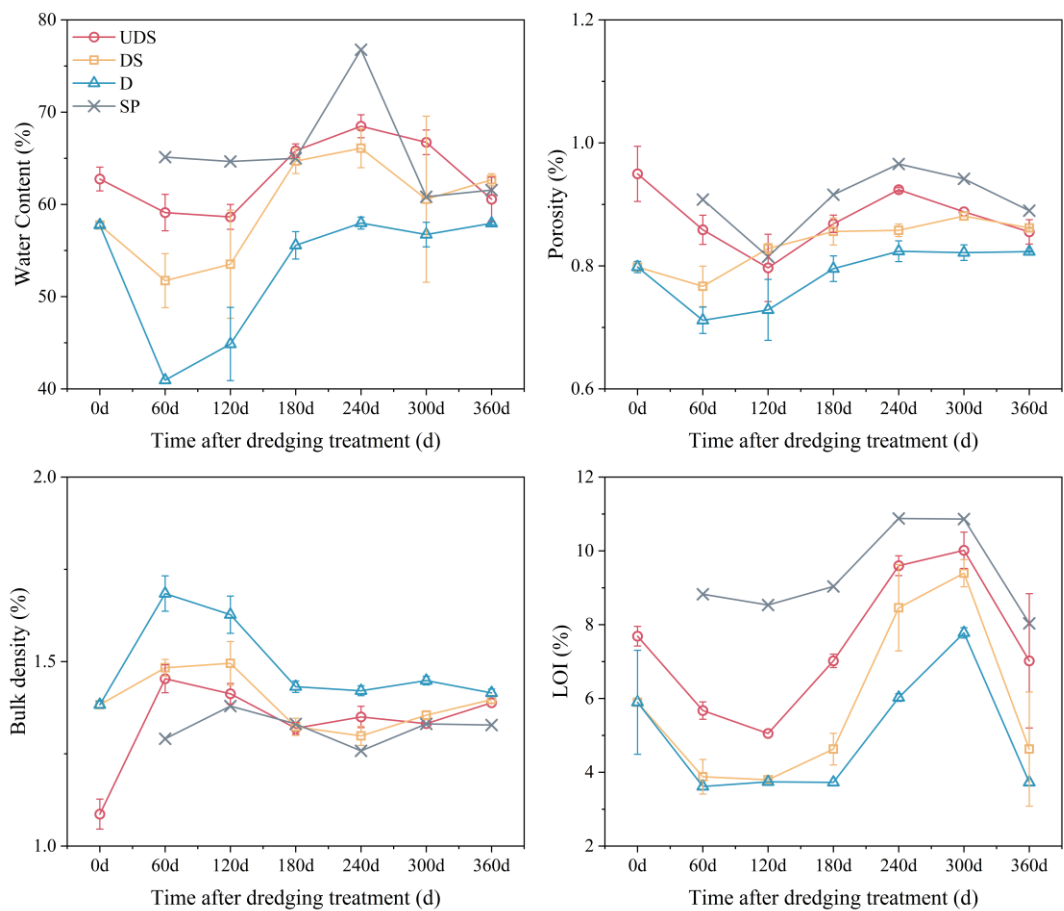
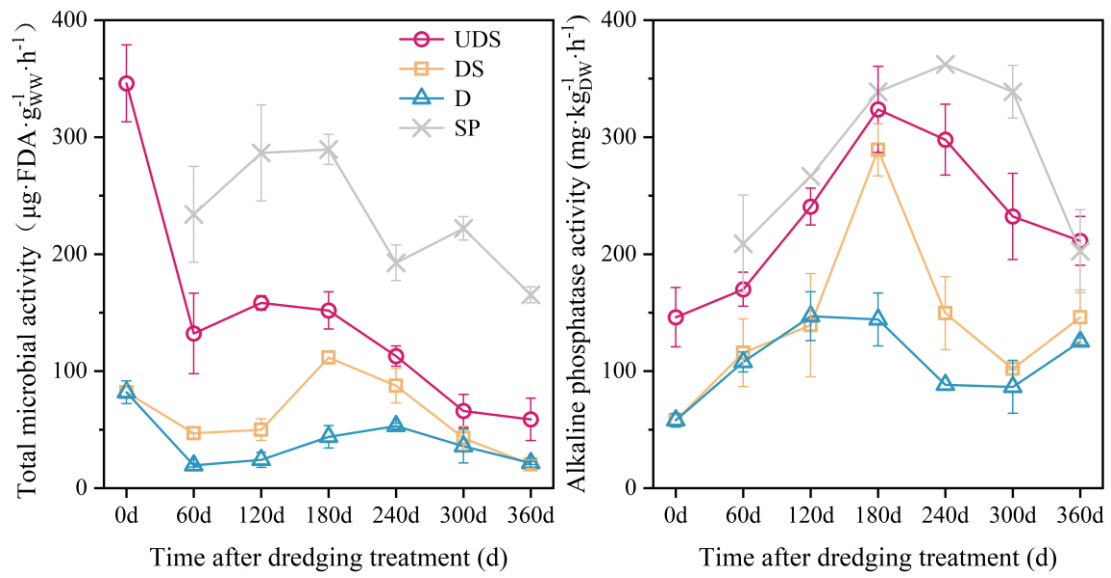


Figure S2. Variations of physicochemical parameters of the settling particle (SP) and surface sediment throughout the incubation period.

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195 Figure S3. Surface sediment (0-2cm) total microbial activity and alkaline phosphatase
 196 activity variations during the incubation period. WW and DW indicate sediment wet
 197 weight and dry weight, respectively.

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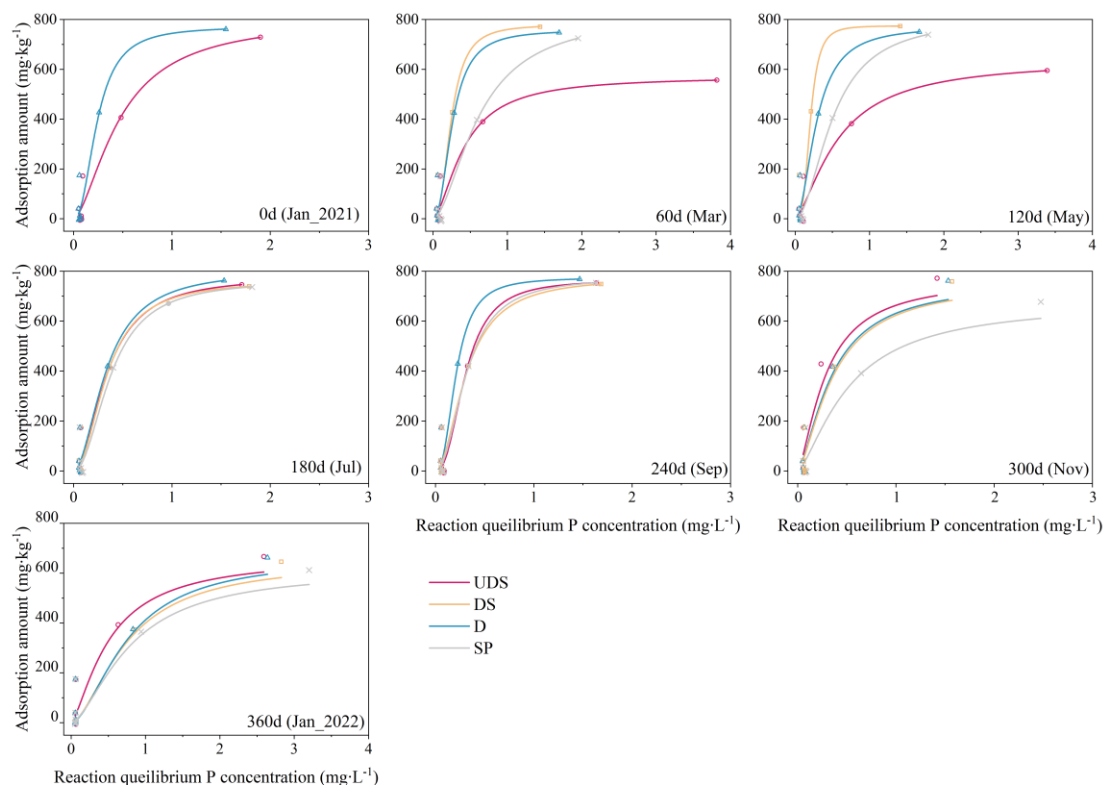


Figure S4. Phosphorus adsorption isotherm regression for UDS, DS, and D treatments, and SP using the non-linear form of the Langmuir equation.

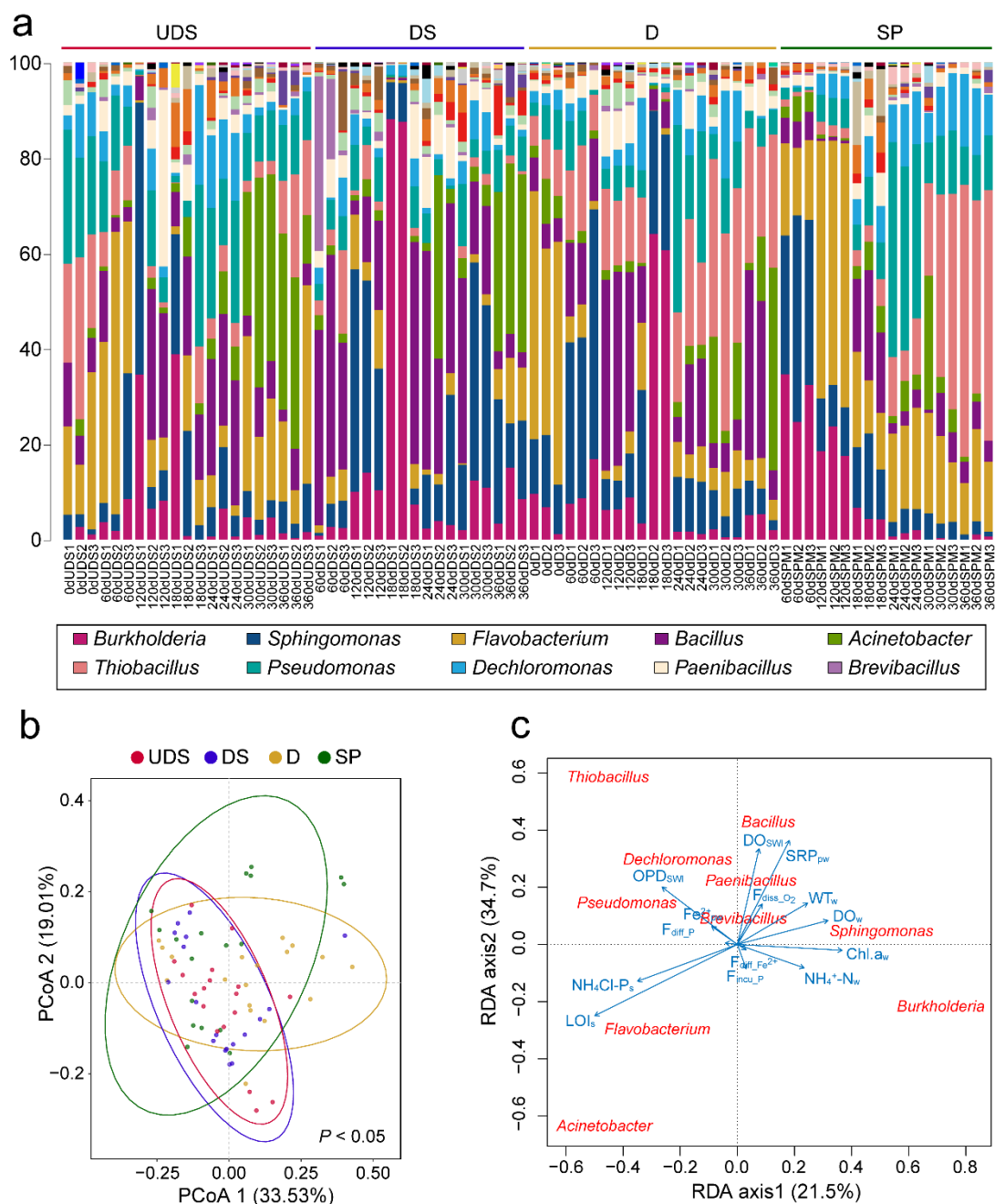


Figure S5. The diversity of phosphate solubilizing bacteria and the relationship between physicochemical properties and community composition of phosphate solubilizing bacteria. (a) The community compositions of phosphate solubilizing bacteria at genus level. The relative abundance of genus > 1% is shown. (b) PCoA of groups on the communities of phosphate solubilizing bacteria. $p < 0.05$ are considered as significant effect. (c) The RDA analysis between physicochemical properties and communities of phosphate solubilizing bacteria. The relative abundance of genus > 1% is shown.

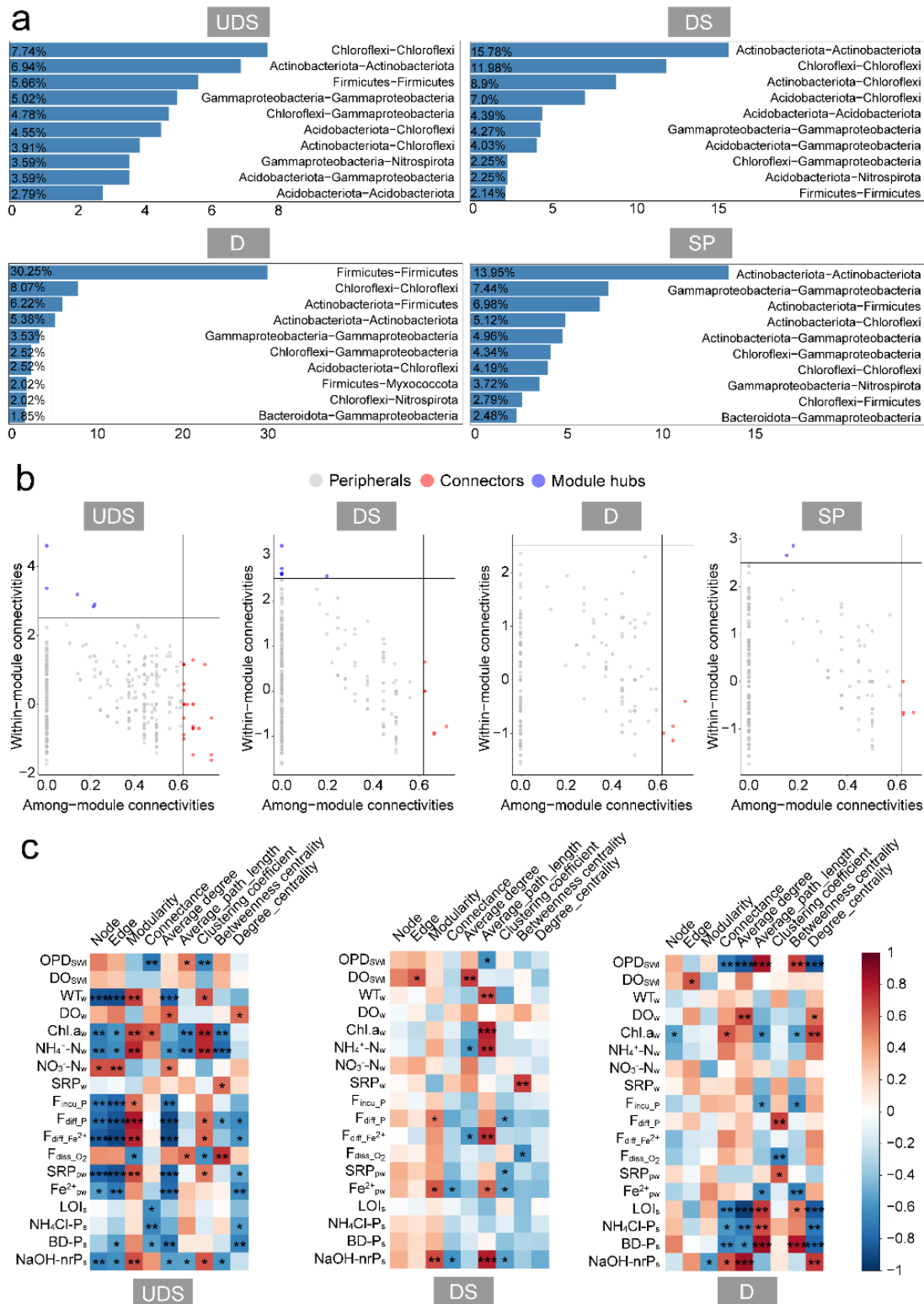


Figure S6. (a) The taxonomic correlation of microbial networks. The relative abundance of taxonomic correlation > 1% is shown. (b) The keystones of microbial networks. (c) The relationship between physicochemical properties and topological parameters of microbial networks.

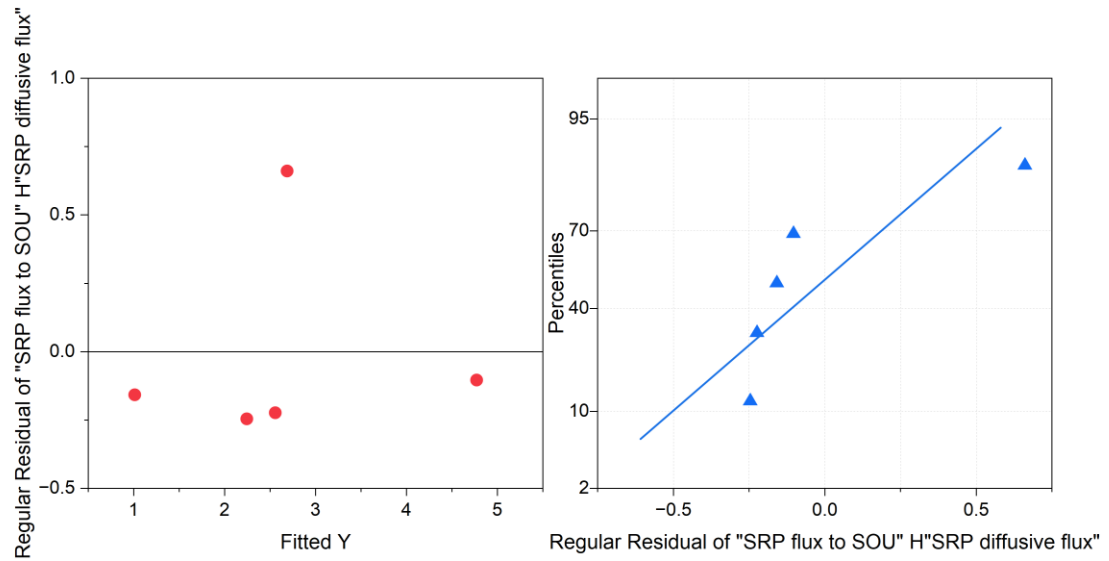


Figure S7. Residual diagnostics for the SOU-SRP power-law relationship. **(a)** Residuals versus fitted values. **(b)** Normal probability plot of residuals. These plots were used as visual diagnostics for the power-law regression based on warm-season observations ($n = 5$).

Reference

- Adam, G., Duncan, H., 2001. Development of a sensitive and rapid method for the measurement of total microbial activity using fluorescein diacetate (FDA) in a range of soils. *Soil Biology and Biochemistry* 33, 943–951. [https://doi.org/10.1016/S0038-0717\(00\)00244-3](https://doi.org/10.1016/S0038-0717(00)00244-3)
- Adams, M.M., Gómez-García, M.R., Grossman, A.R., Bhaya, D., 2008. Phosphorus deprivation responses and phosphonate utilization in a thermophilic *Synechococcus* sp. from microbial mats. *J Bacteriol* 190, 8171–8184. <https://doi.org/10.1128/JB.01011-08>
- Boudreau, B.P., 1997. *Diagenetic Models and Their Implementation: Modelling Transport and Reactions in Aquatic Sediments*. Springer.
- Murphy, J., Riley, J.P., 1962. A modified single solution method for the determination of phosphate in natural waters. *Analytica Chimica Acta* 27, 31–36. [https://doi.org/10.1016/S0003-2670\(00\)88444-5](https://doi.org/10.1016/S0003-2670(00)88444-5)
- Rydin, E., 2000. Potentially mobile phosphorus in Lake Erken sediment. *Water Res.* 34, 2037–2042.
- Walters, W., Hyde, E.R., Berg-Lyons, D., Ackermann, G., Humphrey, G., Parada, A., Gilbert, J.A., Jansson, J.K., Caporaso, J.G., Fuhrman, J.A., Apprill, A., Knight, R., 2015. Improved Bacterial 16S rRNA Gene (V4 and V4-5) and Fungal Internal Transcribed Spacer Marker Gene Primers for Microbial Community Surveys. *mSystems* 1, 10.1128/msystems.00009-15. <https://doi.org/10.1128/msystems.00009-15>