

Supplementary information

Table S1. Location information and HAILS level (see Equ (1)) of land use patterns for the 16 sampling sites considered in the Yuan River basin.

Region	Water sampling site	Farmland area percentage (%)	Forest area percentage (%)	Water area percentage (%)	Residential land area percentage (%)	Other area percentage (%)	HAILS (%)
Upper reaches	Y01	11.12	84.41	0.11	1.17	3.18	28.38 (16.58) ^b
	Y02	13.80	80.89	2.81	1.26	1.23	
	Y03	40.18	45.52	0.87	11.83	1.6	
	Y04	22.58	72.14	1.34	2.04	1.9	
	Y05	34.95	58.95	0.79	2.96	2.36	
Middle reaches	Y06	18.34	69.44	0.89	8.82	2.5	33.08 (16.79) ^b
	Y07	33.15	38.04	1.50	23.85	3.45	
	Y08	32.80	60.26	1.55	4.05	1.34	
	Y09	15.97	70.19	8.13	4.68	1.09	
	Y10	10.00	78.85	8.94	1.23	0.98	
	Y11	35.47	50.02	2.04	10.11	2.35	
Lower reaches	Y12	35.18	44.69	2.03	15.90	2.2	66.09 (10.9) ^a
	Y13	44.67	33.43	2.72	16.50	2.68	
	Y14	72.25	11.75	3.31	8.20	4.49	
	Y15	63.75	21.26	3.80	6.51	4.69	
	Y16	62.26	22.60	3.33	5.21	3.59	

* HAILS is the mean of five or six sampling sites with standard errors in parentheses. Within column different letters show statistical significance at ($p < 0.05$). One-way ANOVA was performed on three regions (n=3).

Table S2. Numbers of OTUs, sequence reads, relative percentage and taxonomic groups for bacterioplanktonic communities in the Yuan River.

Taxa	OTUs	Sequences		Phylum	Class	Order	Family	Genus	Species
	Richness	Reads abu.	Percentage						
Wet season	2074	892,792	48.89%	41	90	173	314	607	1006
Dry season	3634	933,377	51.11%	46	116	209	378	816	1556
Whole	3945	1,826,169	100.00%	46	118	213	392	847	1619

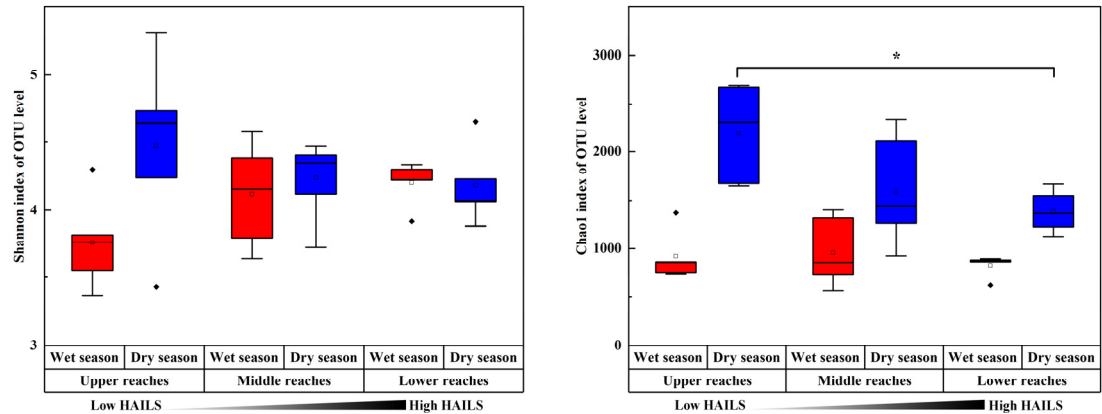
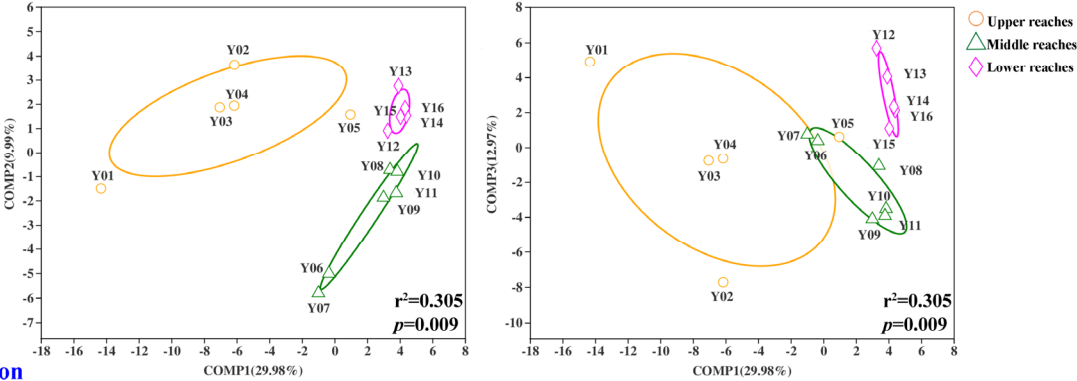


Figure S1. Comparison of Shannon diversity indices and Chao1 richness of communities from along the upper and downstream reaches of the Yuan River. Boxes show means \pm SE, while whiskers show means \pm SD. Wet season distributions are in red and dry season distributions in blue. The “*” indicates a statistically significant difference at $p < 0.05$ (one-way ANOVA).

Wet season



Dry season

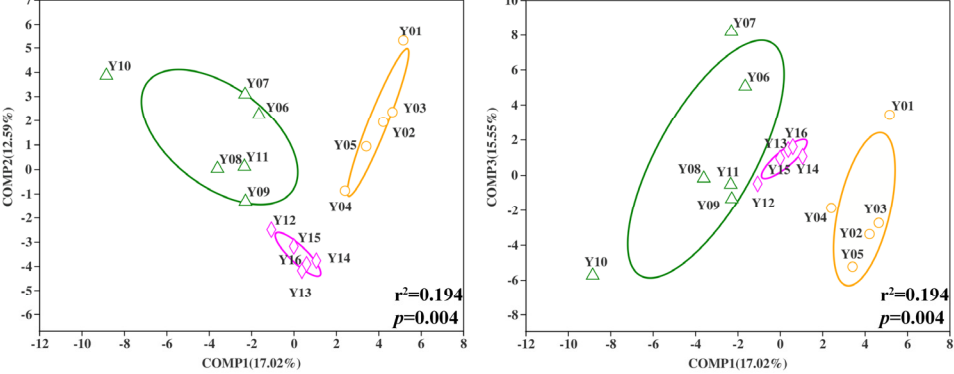


Figure S2. Partial Least Squares Discriminant Analysis score plots of bacterial communities.

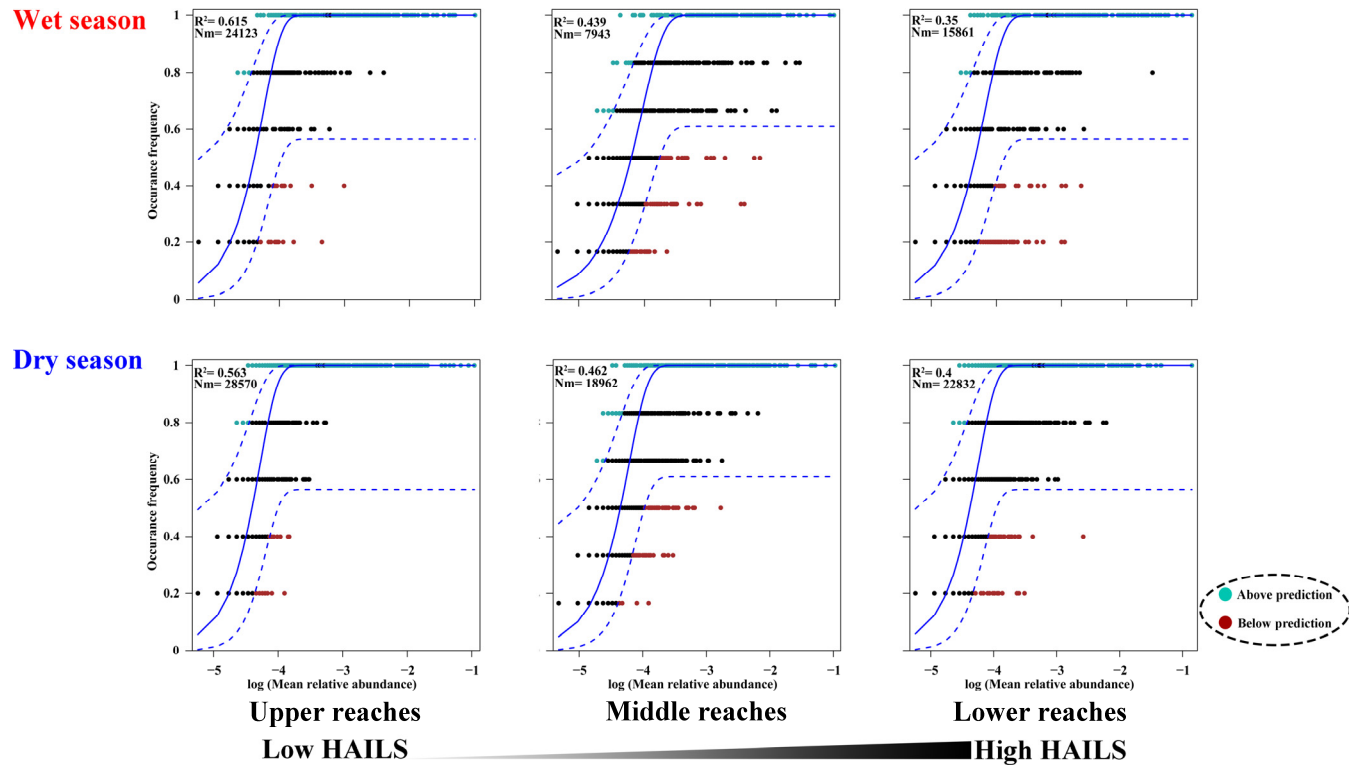


Figure S3. Fit of the neutral community model (NCM) of community assembly. The predicted occurrence frequencies for wet season, dry season, and all seasons, representing bacterioplanktonic communities in each respective time period. The solid blue lines indicate the best fit to the NCM as in Chen et al.[1], and the dashed blue lines represent 95% confidence intervals around the model prediction. OTUs that occur more or less frequently than predicted by the NCM are shown in different colors. Nm indicates the metacommunity size times immigration, R^2 indicates the fit to this model.

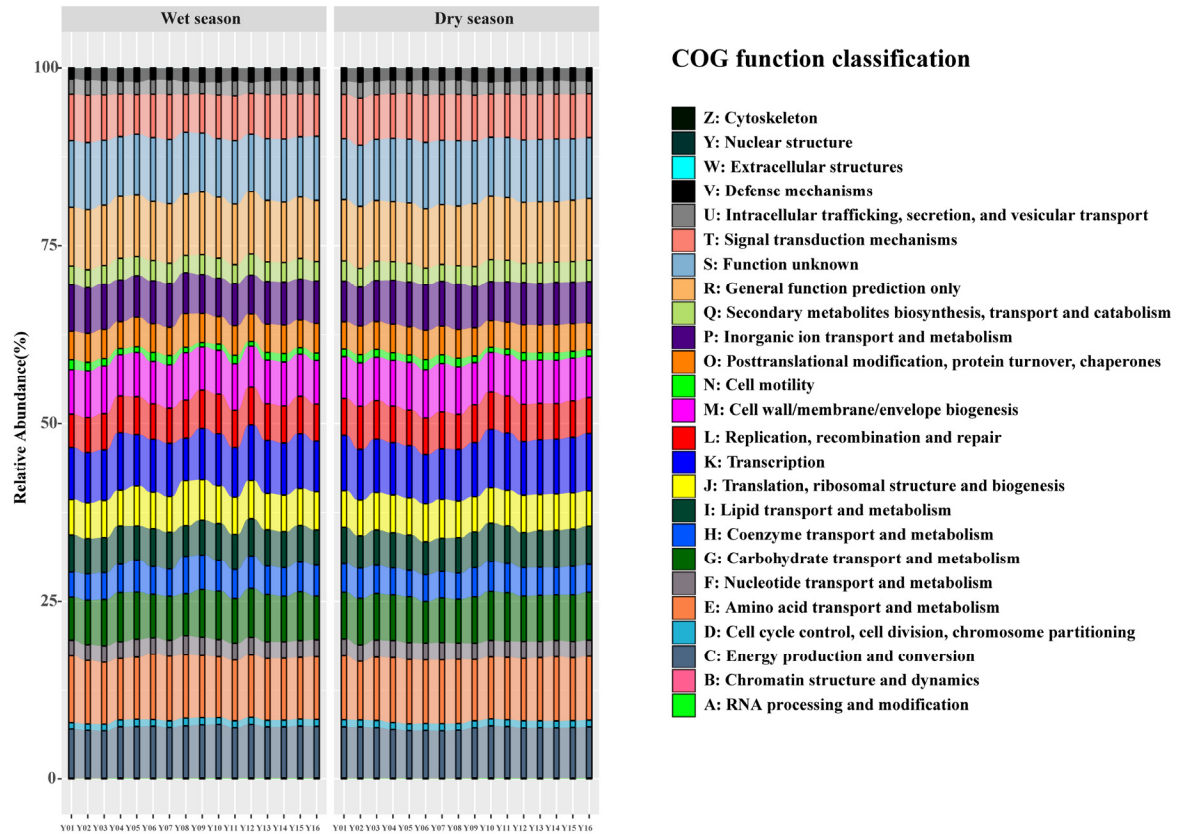


Figure S4. Relative abundance of PICRUSt inferred functions according to color shading (wet season and dry season). The relative abundances are calculated by averaging the abundances of bacteria.

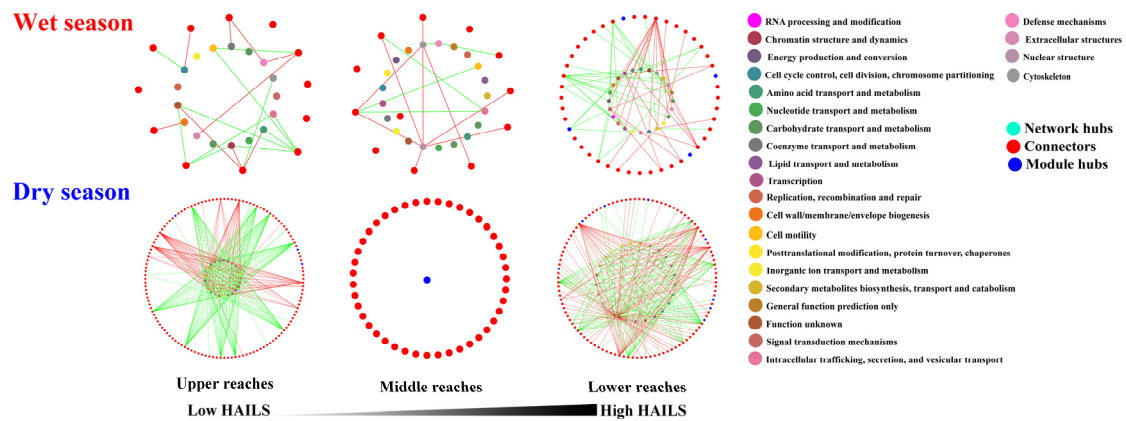


Figure S5. Mutualistic networks of interaction between keystone species community and functions during the wet and dry season in the Yuan River.

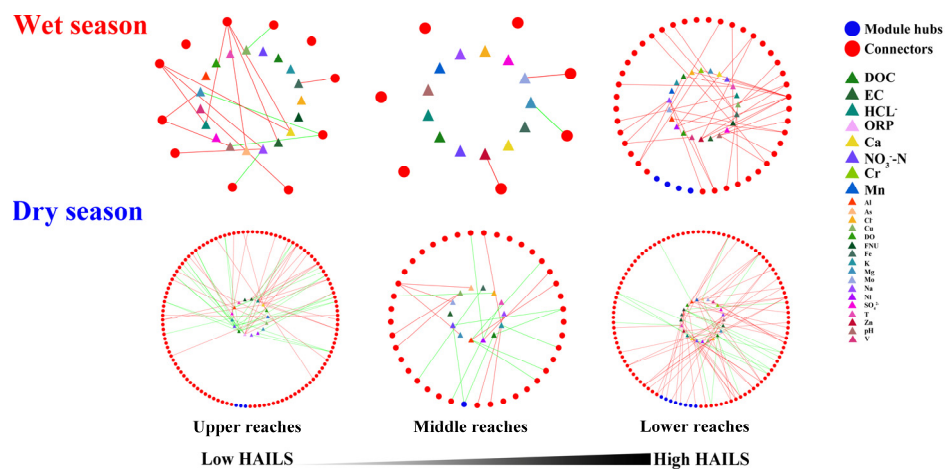


Figure S6. Mutualistic networks of interaction between keystone species community and water chemistry parameters during the wet and dry seasons in the Yuan River.

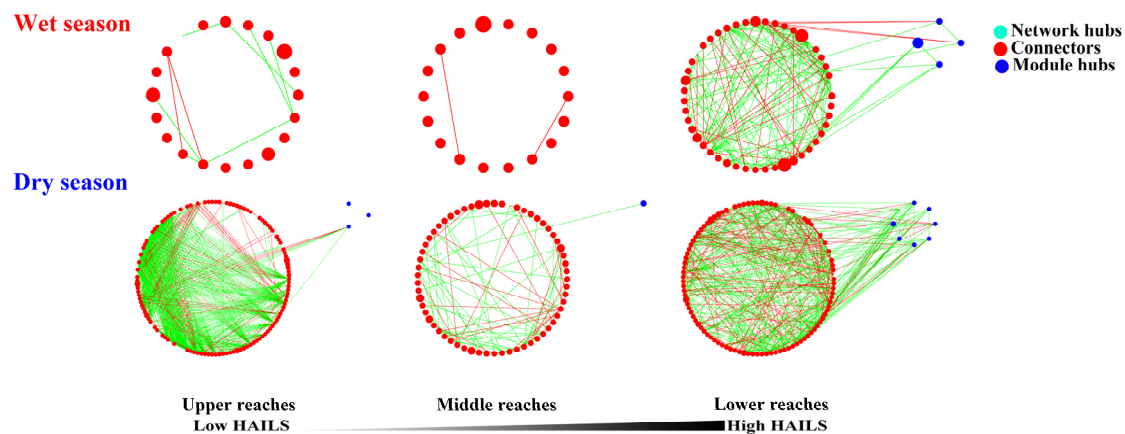


Figure S7. Mutualistic networks of interaction between keystone species community during the wet and dry seasons in the Yuan River.

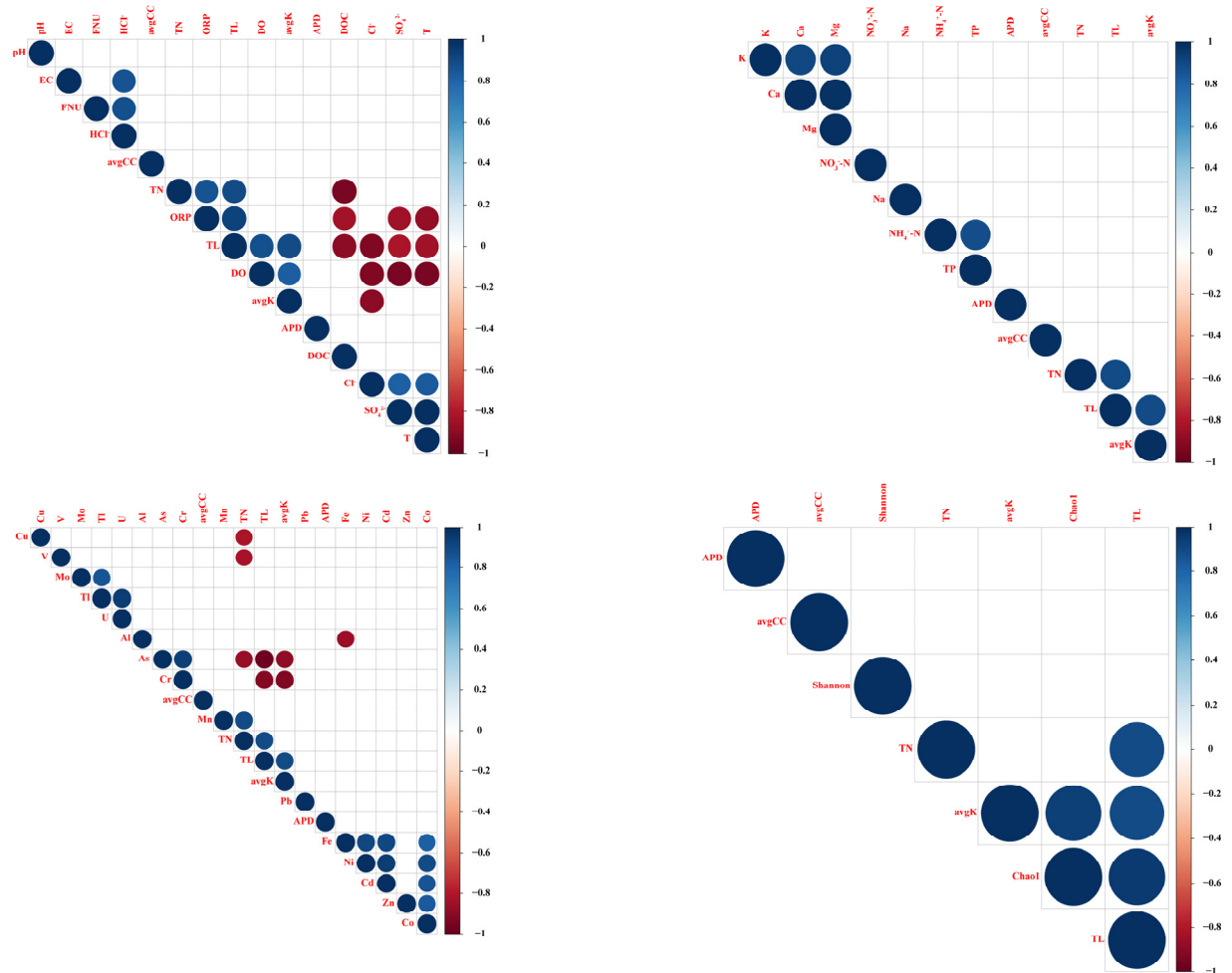


Figure S8. Pearson's correlation values between major modules network indexes (including avgK, TN, TL, avgCC and APD) with water chemistry parameter (including DO, ORP, Cl⁻, SO₄²⁻, T, DOC, pH, EC, FUN and HCl⁻), nutrient variables (including K, Ca, Mg, NO₃-N, Na, NH₄⁺-N and TP), heavy metals (including Pb, Fe, Ni, Cd, Zn, Co, Mn, Cu, V, Mo, Ti, U, As, Cr and Al) and diversity index (including Shannon index and Chao1 index), respectively

Table S3. Key topological features of the major modules in the bacterioplankton molecular ecological networks

Network indexes	Wet season		
	Upper reaches	Middle reaches	Lower reaches
Total nodes (TN)	118	35	63
Total links (TL)	713	299	221
Negative links (NL)	256	103	52
Positive links (PL)	457	196	169
Negative / Positive (NP)	0.56	0.526	0.308
Average degree (avgK)	12.085	17.086	7.016
Average clustering coefficient (avgCC)	0.559	0.545	0.682
Average path distance (APD)	3.436	1.524	3.209

Network indexes	Dry season		
	Upper reaches	Middle reaches	Lower reaches
Total nodes (TN)	275	120	182
Total links (TL)	7730	2062	1519
Negative links (NL)	1418	544	458
Positive links (PL)	6312	1518	1061
Negative / Positive (NP)	0.225	0.358	0.432
Average degree (avgK)	56.218	34.367	16.692
Average clustering coefficient (avgCC)	0.797	0.904	0.366
Average path distance (APD)	2.806	1.158	2.582

References

1. Chen, W.; Ren, K.; Isabwe, A.; Chen, H.; Liu, M.; Yang, J. Stochastic processes shape microeukaryotic community assembly in a subtropical river across wet and dry seasons. *MICROBIOME* **2019**, *7*, 138.