

**Electronic Supplementary Material to:
The Synergism between Methanogens and Methanotrophs and
the Nature of their Contributions to the Seasonal Variation
of Methane Fluxes in a Wetland: The Case of
Dajiuju Subalpine Peatland***

Luwen WANG^{1,2,3}, Jiwen GE^{1,2,3}, Liang FENG^{2,3}, Yaoya LIU^{1,2,3}, Yu LI^{1,2,3}, Jiumei WANG^{1,2,3},
Xiang XIAO^{1,2,3}, and Zhiqi ZHANG⁴

¹*Laboratory of Basin Hydrology and Wetland Eco-Restoration, China University of Geosciences, Wuhan 430074, China*

²*Hubei Key Laboratory of Wetland Evolution and Ecological Restoration,
China University of Geosciences, Wuhan 430074, China*

³*Institution of Ecology and Environmental Sciences, China University of Geosciences, Wuhan 430074, China*

⁴*Shennongjia National Park Administration Bureau, Shennongjia Forestry District 442417, China*

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Table S1. The major topological parameters of the methanogenic and methanotrophic networks.

Network	Total nodes	Total edges	Positive connections	Negative connections	Average clustering coefficient (avgCC)	Average degree (avgK)	Diameter	Average path length (GD ^a)	Density	Modularity (Modules)
methanogen	Winter	401	4567	3215	1352	0.270	22.778	12	3.088	0.057
	Spring	621	32159	8600	23,559	0.249	103.539	9	2.286	0.167
	Summer	512	8030	4241	3789	0.277	31.367	9	3.292	0.061
	Autumn	355	11319	5588	5731	0.274	63.769	10	2.560	0.18
methanotroph	Winter	531	4945	2583	2363	0.329	18.625	10	3.218	0.035
	Spring	811	377775	348,668	29107	0.187	93.042	11	2.672	0.115
	Summer	589	2715	1950	765	0.277	9.219	14	4.580	0.016
	Autumn	741	44848	13625	31223	0.303	121.047	15	2.570	0.164

a GD, geodesic distance.

Table S2. Information of keystone species of methanogens discerned by network analysis.

Season	Topological role	OTU ID	Class	Order	Family	Genus	Species
Winter	Module hubs	otu7921	Methanomicrobia	Methanocellales	Methanocellaceae	<i>Methanocella arvoryzae</i>	
		otu28836	Methanomicrobia	Methanocellales	Methanocellaceae	<i>Methanocella paludicola</i>	
		otu12232	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	<i>Methanoregula formicina</i>	
		otu25071	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	<i>Methanoregula formicina</i>	
		otu8092	Methanomicrobia	Methanocellales	Methanocellaceae	<i>Methanocella arvoryzae</i>	
		otu28026	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	<i>Methanoregula formicina</i>	
		otu7973	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	<i>Methanoregula formicina</i>	
		otu22253	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	<i>Methanoregula formicina</i>	
		otu19105	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	<i>Methanoregula formicina</i>	
		otu28425	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	<i>Methanoregula formicina</i>	
		otu30825	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	<i>Methanolinea mesophila</i>	
		otu6322	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	<i>Methanoregula formicina</i>	
		otu9709	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	<i>Methanoregula formicina</i>	
		otu16471	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	<i>Methanoregula formicina</i>	
		otu9821	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	<i>Methanoregula formicina</i>	
Spring	Module hubs	otu881	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	<i>Methanoregula formicina</i>	
		otu20895	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	<i>Methanoregula formicina</i>	
		otu28021	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	<i>Methanoregula formicina</i>	
		otu20040	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	<i>Methanoregula formicina</i>	
		otu10443	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	<i>Methanoregula formicina</i>	
		otu4795	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	<i>Methanoregula formicina</i>	
		otu10557	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	<i>Methanoregula formicina</i>	
		otu3850	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	<i>Methanoregula formicina</i>	
		otu2115	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	<i>Methanoregula formicina</i>	
		otu3714	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	<i>Methanoregula formicina</i>	
		otu19174	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	<i>Methanoregula formicina</i>	
		otu9044	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	<i>Methanoregula formicina</i>	
		otu12523	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	<i>Methanoregula formicina</i>	
		otu20919	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	<i>Methanolinea mesophila</i>	
		otu6785	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	<i>Methanoregula formicina</i>	
		otu12968	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	<i>Methanoregula formicina</i>	
		otu2103	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	<i>Methanoregula formicina</i>	

Table S2. (Continued.)

Season	Topological role	OTU ID	Class	Order	Family	Genus	Species
Summer	Module hubs	otu29312	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	<i>Methanoregula formicica</i>	
		otu16698	Methanomicrobia	Methanocellales	Methanocellaceae	<i>Methanocella arvoryzae</i>	
		otu10110	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	<i>Methanoregula formicica</i>	
		otu5054	Methanomicrobia	Methanocellales	Methanocellaceae	<i>Methanocella arvoryzae</i>	
		otu30724	Methanomicrobia	Methanocellales	Methanocellaceae	<i>Methanoregula formicica</i>	
	Connectors	otu30856	Methanomicrobia	Methanocellales	Methanocellaceae	<i>Methanocella arvoryzae</i>	
		otu7743	Methanomicrobia	Methanocellales	Methanocellaceae	<i>Methanoregula formicica</i>	
		otu3682	Methanomicrobia	Methanocellales	Methanocellaceae	<i>Methanocella arvoryzae</i>	
		otu28026	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	<i>Methanoregula formicica</i>	
		otu19085	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	<i>Methanoregula formicica</i>	
Autumn	Module hubs	otu28628	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	<i>Methanoregula formicica</i>	

Table S3. Information of keystone species of methanotrophs discerned by network analysis.

Season	Topological role	OTU ID	Class	Order	Family	Genus	Species
Winter	Module hubs	otu19808	Alphaproteobacteria	Rhizobiales	Methyloystacae	—	type II methanotrophic bacterium
		otu30490	Gammaproteobacteria	Methyloccoccales	—	<i>Candidatus Methylophilus</i>	<i>Candidatus Methylophilus alinensis</i>
		otu6164	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	<i>Methylocapsa acidiphila</i>	
		otu14450	—	—	—	—	
		otu11307	Alphaproteobacteria	Rhizobiales	Methyloystacae	—	type II methanotrophic bacterium
	Connectors	otu3131	Alphaproteobacteria	Rhizobiales	Methyloystacae	—	type II methanotrophic bacterium
		otu22810	Alphaproteobacteria	Rhizobiales	Methyloystacae	—	type II methanotrophic bacterium
		otu763	Alphaproteobacteria	Rhizobiales	Methyloystacae	—	type II methanotrophic bacterium
		otu5335	Gammaproteobacteria	Methyloccoccales	—	<i>Candidatus Methylophilus</i>	<i>Candidatus Methylophilus alinensis</i>
		otu31869	Alphaproteobacteria	Rhizobiales	Methyloystacae	—	type II methanotrophic bacterium
Autumn	Module hubs	otu32067	Alphaproteobacteria	Rhizobiales	Methyloystacae	—	type II methanotrophic bacterium
		otu22803	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	<i>Methylocapsa</i>	<i>Methylocapsa aurea</i>
		otu32536	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	<i>Methylocapsa</i>	<i>Methylocapsa aurea</i>
		otu15588	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	<i>Methylocapsa</i>	<i>Methylocapsa aurea</i>
		otu32859	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	<i>Methylocapsa</i>	<i>Methylocapsa aurea</i>
	Connectors	otu23764	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	<i>Methylocapsa</i>	<i>Methylocapsa aurea</i>
		otu8533	Alphaproteobacteria	Rhizobiales	Methyloystacae	<i>Methylocystis</i>	<i>Methylocystis sp. M212</i>
		otu28418	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	<i>Methylocapsa</i>	<i>Methylocapsa aurea</i>
		otu35063	Alphaproteobacteria	Rhizobiales	Methyloystacae	—	type II methanotrophic bacterium

Table S3. (Continued.)

Season	Topological role	OTU ID	Class	Order	Family	Genus	Species
Spring	Module hubs	otu33237	Alphaproteobacteria	Rhizobiales	Methylocystaceae	-	type II methanotrophic bacterium
		otu29980	Alphaproteobacteria	Rhizobiales	Methylocystaceae	-	type II methanotrophic bacterium
		otu6164	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	<i>Methylcapsa acidiphila</i>	bacterium
		otu14450	-	-	-	-	type II methanotrophic bacterium
		otu13088	Alphaproteobacteria	Rhizobiales	Methylocystaceae	-	type II methanotrophic bacterium
		otu15187	Alphaproteobacteria	Rhizobiales	Methylocystaceae	-	type II methanotrophic bacterium
		otu34788	Alphaproteobacteria	Rhizobiales	Methylocystaceae	-	type II methanotrophic bacterium
		otu29565	-	-	-	-	bacterium
		otu6016	-	-	-	-	bacterium
		otu25376	-	-	-	-	bacterium
Connectors	Network hubs	otu16124	-	-	-	-	<i>Methylcystis</i> sp. M212
		otu2908	Alphaproteobacteria	Rhizobiales	Methylocystaceae	<i>Methylcystis</i>	bacterium
		otu6486	-	-	-	-	type II methanotrophic bacterium
		otu2551	Alphaproteobacteria	Rhizobiales	Methylocystaceae	-	<i>Candidatus</i> Methyloumidiphilus alinensis
		otu30490	Gammaproteobacteria	Methylococcales	-	<i>Candidatus</i> Methyloumidiphilus	
Summer	Module hubs	otu9888	Alphaproteobacteria	Rhizobiales	Methylocystaceae	-	type II methanotrophic bacterium
		otu36265	Alphaproteobacteria	Rhizobiales	Methylocystaceae	-	type II methanotrophic bacterium
		otu13088	Alphaproteobacteria	Rhizobiales	Methylocystaceae	-	type II methanotrophic bacterium
		otu514	Alphaproteobacteria	-	-	-	methanotrophic alpha proteobacterium arc2
		otu19228	Gammaproteobacteria	Methylococcales	-	<i>Candidatus</i> Methyloumidiphilus	
		otu21124	Alphaproteobacteria	Rhizobiales	Methylocystaceae	-	<i>Candidatus</i> Methyloumidiphilus alinensis
		otu31786	Alphaproteobacteria	Rhizobiales	Methylocystaceae	-	
		otu30060	-	-	-	-	
		otu18640	Alphaproteobacteria	Rhizobiales	Methylocystaceae	-	type II methanotrophic bacterium
		otu26671	-	-	-	-	bacterium
Connectors	Network hubs	otu5728	Alphaproteobacteria	Rhizobiales	Methylocystaceae	<i>Methylcystis</i>	<i>Methylcystis</i> sp. m231
		otu24589	Alphaproteobacteria	Rhizobiales	Methylocystaceae	-	type II methanotrophic bacterium
		otu37521	Alphaproteobacteria	Rhizobiales	Methylocystaceae	-	type II methanotrophic bacterium
		otu35711	Alphaproteobacteria	Rhizobiales	Methylocystaceae	-	type II methanotrophic bacterium
		otu38142	Alphaproteobacteria	Rhizobiales	Methylocystaceae	-	type II methanotrophic bacterium
		otu35267	Alphaproteobacteria	Rhizobiales	Methylocystaceae	-	type II methanotrophic bacterium
		otu1908	Alphaproteobacteria	Rhizobiales	Methylocystaceae	-	type II methanotrophic bacterium
		otu29822	Alphaproteobacteria	Rhizobiales	Methylocystaceae	-	type II methanotrophic bacterium
		otu5509	Alphaproteobacteria	Rhizobiales	Methylocystaceae	-	type II methanotrophic bacterium

Table S3. (Continued.)

Season	Topological role	OTU ID	Class	Order	Family	Genus	Species
Autumn	Module hubs	otu4659 otu21922 otu3533 otu13211 otu8689 otu15914 otu31920 otu9820 otu29080 otu19159 otu24939 otu1769 otu13210 otu24579 otu17931 otu33493 otu23063 otu675	Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria – Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria	Rhizobiales Rhizobiales Rhizobiales Rhizobiales Rhizobiales Rhizobiales – Rhizobiales Rhizobiales Rhizobiales Rhizobiales Rhizobiales Rhizobiales Rhizobiales Rhizobiales Rhizobiales Rhizobiales Rhizobiales Rhizobiales	Beijerinckiaceae Beijerinckiaceae Beijerinckiaceae Beijerinckiaceae Beijerinckiaceae Beijerinckiaceae – Beijerinckiaceae Beijerinckiaceae Beijerinckiaceae Beijerinckiaceae Beijerinckiaceae Beijerinckiaceae Beijerinckiaceae Beijerinckiaceae Beijerinckiaceae Beijerinckiaceae Beijerinckiaceae Beijerinckiaceae	<i>Methylocapsa</i> <i>Methylocapsa</i> <i>Methylocapsa</i> <i>Methylocapsa</i> <i>Methylocapsa</i> <i>Methylocapsa</i> <i>Methylocapsa</i> <i>Methylocapsa</i> <i>Methylocapsa</i> <i>Methylocapsa</i> <i>Methylocapsa</i> <i>Methylocapsa</i> <i>Methylocapsa</i> <i>Methylocapsa</i> <i>Methylocapsa</i> <i>Methylocapsa</i> <i>Methylocapsa</i> <i>Methylocapsa</i> <i>Methylocapsa</i>	<i>Methylocapsa aurea</i> <i>Methylocapsa aurea</i> <i>Methylocapsa aurea</i> <i>Methylocapsa aurea</i> <i>Methylocapsa aurea</i> <i>Methylocapsa aurea</i> <i>bacterium</i> <i>Methylocapsa aurea</i> <i>Methylocapsa aurea</i> <i>Methylocystis sp. SC2</i> <i>Methylocapsa aurea</i> <i>Methylocapsa aurea</i> <i>Methylocapsa aurea</i>

Table S4. Physicochemical soil properties in soil samples collected from the Dajiuju subalpine peatland in different seasons.

Date	Depth (cm)	pH	Eh (mV)	TN (%)	NH_4^+ -N (mg kg^{-1})	NO_3^- -N (mg kg^{-1})	NO_2^- -N (mg kg^{-1})	TOC (%)	Ts (°C)	SWC	Daily average CH_4 fluxes ($\text{nmol m}^{-2} \text{s}^{-1}$)	Water table (m)
2019.01.19	0	5.21	81.5	2.83	2.380	0.226	0.006	40.60	1.50	0.781	3.64	0.746
	10	5.79	101.3	2.67	4.396	0.261	0.006	48.37	2.47	0.654		
	30	4.84	95.5	2.28	1.485	0.200	0.004	43.74	3.55	0.636		
	50	5.05	99.5	2.17	1.666	0.170	0.002	42.58	3.78	0.597		
2019.04.26	0	4.93	110.0	2.57	3.062	0.238	0.007	40.64	16.04	0.600	4.72	0.700
	10	5.18	149.7	2.80	2.619	0.149	0.008	37.93	14.30	0.638		
	30	4.72	159.0	2.27	1.288	0.249	0.004	43.81	12.67	0.564		
	50	4.76	162.7	2.13	0.800	0.156	0.004	45.32	11.13	0.528		
2019.07.22	0	4.98	86.5	2.65	2.236	0.180	0.006	38.40	21.33	0.588	49.21	0.648
	10	4.63	90.2	2.27	1.121	0.259	0.004	35.65	20.13	0.640		
	30	4.78	85.7	2.01	0.906	0.180	0.003	47.38	18.58	0.639		
	50	5.27	93.1	2.35	0.829	0.137	0.002	41.68	16.79	0.589		
2019.10.17	0	4.47	13.4	1.87	1.205	0.154	0.003	36.18	13.73	0.786	23.78	0.781
	10	4.87	28.0	2.74	0.668	0.205	0.001	39.41	12.26	0.698		
	30	5.49	48.9	2.34	0.691	0.140	0.004	47.16	12.78	0.582		
	50	5.23	37.5	2.06	0.643	0.197	0.002	43.80	11.36	0.543		

The pH, soil temperature (Ts), and Oxidation-Reduction Potential (Eh) of soil were measured in situ. Soil water content (SWC), total organic carbon (TOC), total nitrogen (TN), ammonium (NH_4^+ -N), nitrate (NO_3^- -N), and nitrite (NO_2^- -N) were measured in the laboratory. The CH_4 fluxes were monitored by the eddy covariance (EC) system and the water table was determined by the water level monitoring instrument.

Table S5. Pearson correlation of soil physicochemical properties.

	CH_4	Water table	pH	Eh	TN	NH_4^+ -N	NO_3^- -N	NO_2^- -N	TOC	Ts	SWC
CH_4	1	-0.539**	-0.186	-0.375	-0.231	-0.425	-0.202	-0.336	-0.234	0.757**	-0.049
Water table		1	0.228	-0.528*	-0.033	-0.044	-0.050	-0.246	0.151	-0.625**	0.308
pH			1	-0.011	0.475	0.470	-0.009	0.245	0.505*	-0.401	-0.149
Eh				1	0.183	0.302	0.141	0.493	0.188	-0.032	-0.474
TN					1	0.592*	0.276	0.580*	-0.174	-0.164	0.215
NH_4^+ -N						1	0.455	0.758**	0.044	-0.331	0.207
NO_3^- -N							1	0.235	-0.005	-0.191	0.129
NO_2^- -N								1	-0.116	-0.005	0.073
TOC									1	-0.384	-0.424
Ts										1	-0.258
SWC											1

* $p \leq 0.05$, ** $p \leq 0.01$

Table S6. Correlation index between keystone species and CH_4 fluxes.

Community		P-value	Pearson's correlation coefficient
methanogen	<i>Methanoregula</i>	0.890	-0.038
	<i>Methanocella</i>	0.413	0.230
	<i>Methanolinea</i>	0.024	-0.560
	<i>Methylocapsa</i>	0.850	0.052
methanotroph	unclassified_f_Methylcystaceae	0.171	0.360
	<i>Candidatus Methyloumidiphilus</i>	0.490	-0.186
	<i>Methylocystis</i>	0.299	-0.277
	unclassified_c_Alphaproteobacteria	0.327	-0.262