How do water table drawdown, duration of drainage and warming influence greenhouse gas emissions from drained peatlands of the Zoige Plateau?

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Abstract

As an important soil carbon pool in Qinghai-Tibet Plateau (QTP), alpine peatland are extremely sensitive to global change. Duration of drainage and water table drawdown lead to rapid soil degradation and C losses, and this may worsen under warming as the soils are no longer protected by anaerobic conditions. Hence, the objective of this study was to assess the effect of drainage on microbial characteristics, greenhouse gas (GHG) emissions and their influencing factors, and further analyze whether the the variability of GHG emissions increases with warming. The results showed that the influence of water table drawdown on microbial community structure was greater than that of duration of drainage. Both the fungal and prokaryotic community compositions varied with water table gradient, and soil microbiota may served as a biomarker to analyze the differences in GHG emissions among three different water table treatments. Intriguingly, the GHG emission decreased with the increase of drainage age, while water table drawdown reduced the CO2 and CH4 emission rates, and increased N2O emission rates. In addition, high temperature increased CO2 by 75% and N2O by 42%, but not significantly decreased the CH4 emission rates. Structural equation modeling suggested that microbial community composition was the primary factor affecting GHG emissions from drained peatlands, especially prokaryotes. Overall, our results indicate that water table plays a more important role in GHG emissions than duration of drainage, and the variability of GHG emissions increases with warming.

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Figure 1

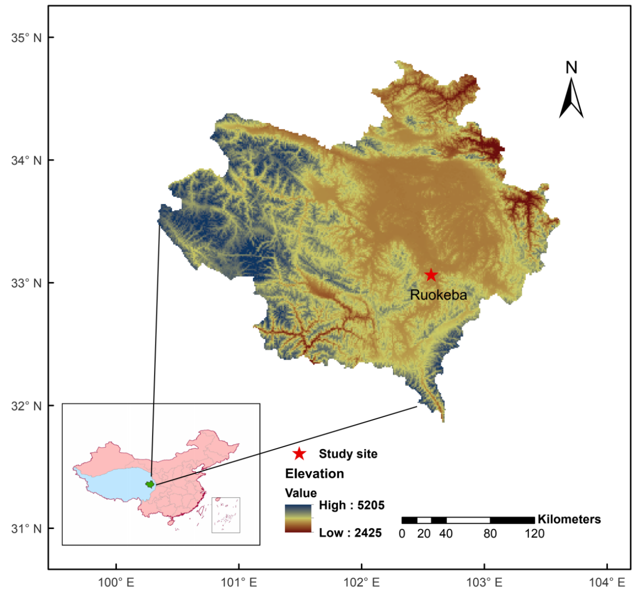


Figure 2

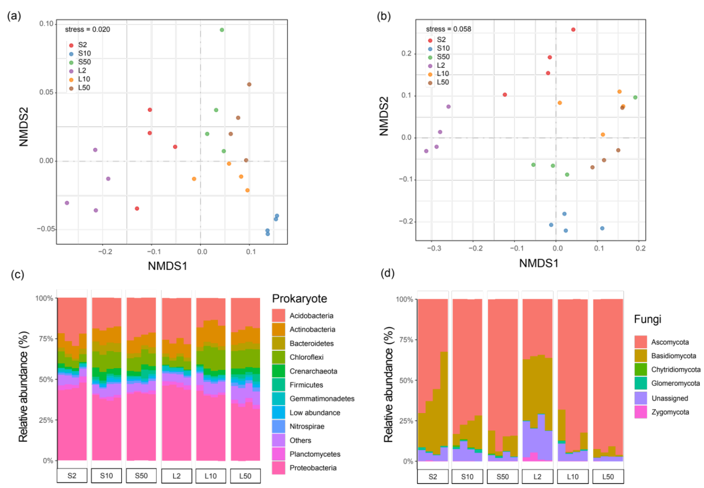


Figure 3

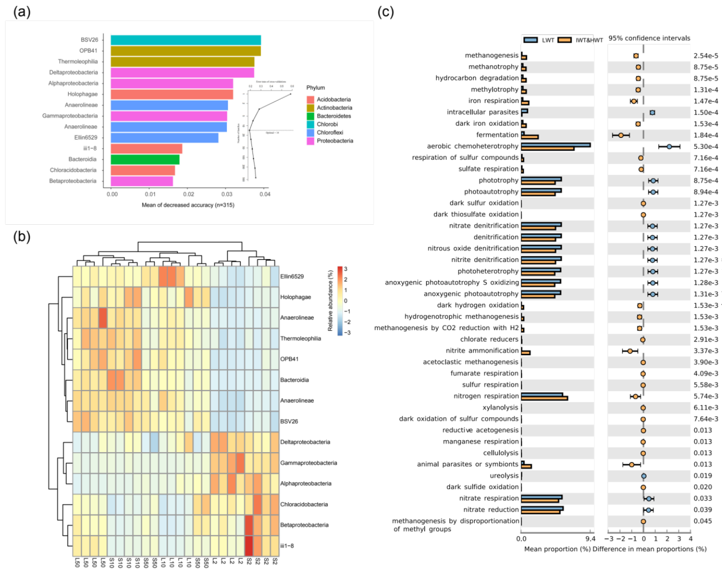
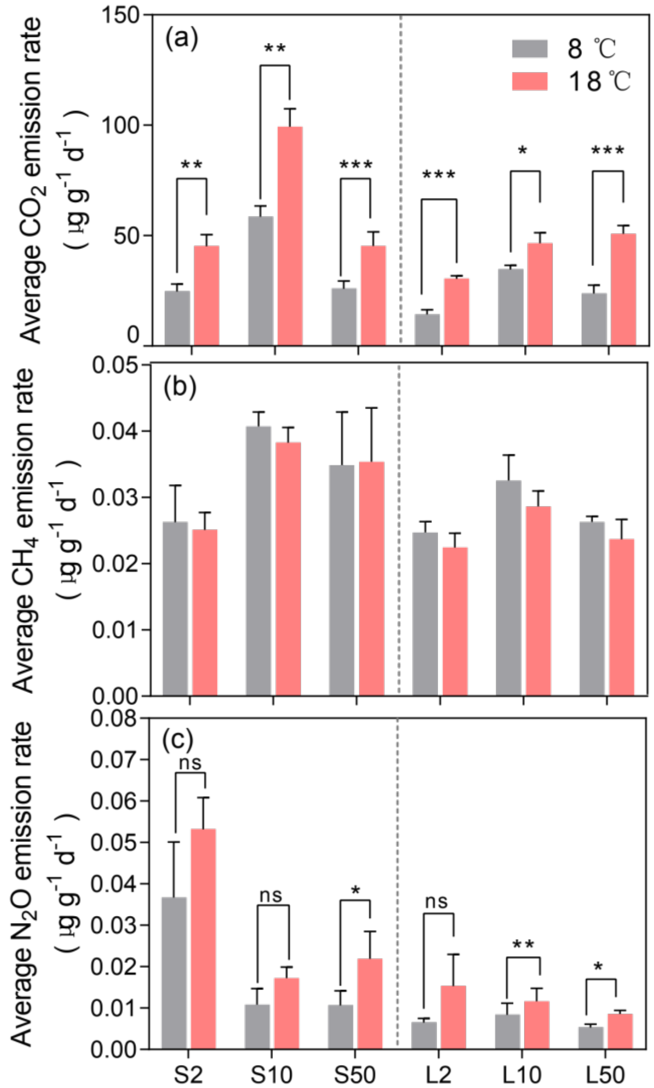
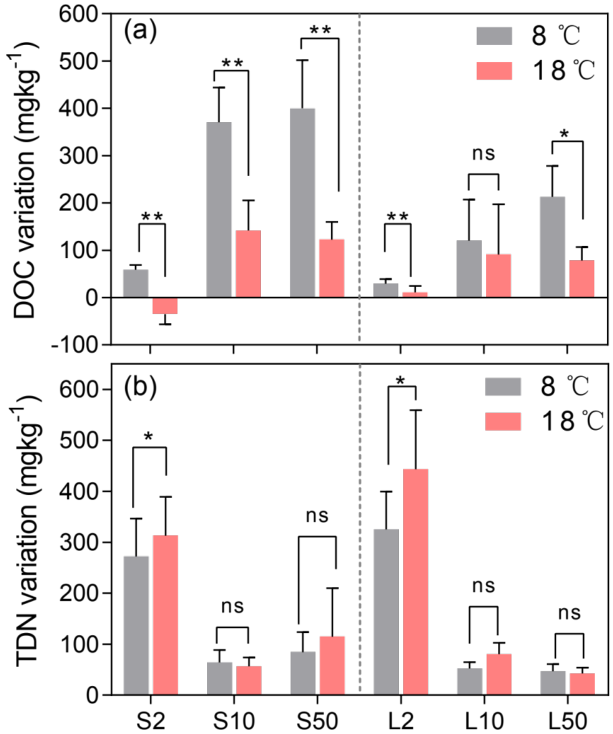

(a)
BSV26
OPB41
Thermoleophilia
Deltaproteobacteria
Alphaproteobacteria
Holophagae
Anaerolineae
Gammaproteobacteria
Anaerolineae
Ellin6529
iii1−8
Bacteroidia
Chloracidobacteria
Betaproteobacteria
Mean of decreased accuracy (n=315)
Phylum
Acidobacteria
Actinobacteria
Bacteroidetes
Chlorobi
Chloroflexi
Proteobacteria
(b)
Ellin6529
Holophagae
Anaerolineae
Thermoleophilia
OPB41
Bacteroidia
Anaerolineae
BSV26
Deltaproteobacteria
Gammaproteobacteria
Alphaproteobacteria
Chloracidobacteria
Betaproteobacteria
iii1−8
Relative abundance (%)
(c)
LWT
IWT&HWT
95% confidence intervals
methanogenesis 2.54e-5
methanotrophy 8.75e-5
hydrocarbon degradation 8.75e-5
methylotrophy 1.31e-4
iron respiration 1.47e-4
intracellular parasites 1.50e-4
dark iron oxidation 1.53e-4
fermentation 1.84e-4
aerobic chemoheterotrophy 5.30e-4
respiration of sulfur compounds 7.16e-4
sulfate respiration 7.16e-4
phototrophy 8.75e-4
photoautotrophy 8.94e-4
dark sulfur oxidation 1.27e-3
dark thiosulfate oxidation 1.27e-3
nitrate denitrification 1.27e-3
denitrification 1.27e-3
nitrous oxide denitrification 1.27e-3
nitrite denitrification 1.27e-3
photoheterotrophy 1.27e-3
anoxygenic photoautotrophy S oxidizing 1.28e-3
anoxygenic photoautotrophy 1.31e-3
dark hydrogen oxidation 1.53e-3
hydrogenotrophic methanogenesis 1.53e-3
methanogenesis by CO2 reduction with H2 1.53e-3
chlorate reducers 2.91e-3
nitrite ammonification 3.37e-3
acetoclastic methanogenesis 3.90e-3
fumarate respiration 4.09e-3
sulfur respiration 5.58e-3
nitrogen respiration 5.74e-3
xylanolysis 6.11e-3
dark oxidation of sulfur compounds 7.64e-3
reductive acetogenesis 0.013
manganese respiration 0.013
cellulolysis 0.013
animal parasites or symbionts 0.013
ureolysis 0.019
dark sulfide oxidation 0.020
nitrate respiration 0.033
nitrate reduction 0.039
methanogenesis by disproportionation of methyl groups 0.045
q-value (corrected)
0.0
9.4
Mean proportion (%)
−3 −2 −1 0 1 2 3 4
Difference in mean proportions (%)

Figure 4



(a)
(b)
(c)
8 ℃
18 ℃
Average CO_2 emission rate ($\mu g\ g^{-1}\ d^{-1}$)
Average CH_4 emission rate ($\mu g\ g^{-1}\ d^{-1}$)
Average N_2O emission rate ($\mu g\ g^{-1}\ d^{-1}$)
S2
S10
S50
L2
L10
L50

Figure 5



(a)
8 ℃
18 ℃
DOC variation (mgkg^{-1})
600
500
400
300
200
100
0
-100
**
ns
*
(b)
TDN variation (mgkg^{-1})
S2
S10
S50
L2
L10
L50

Figure 6

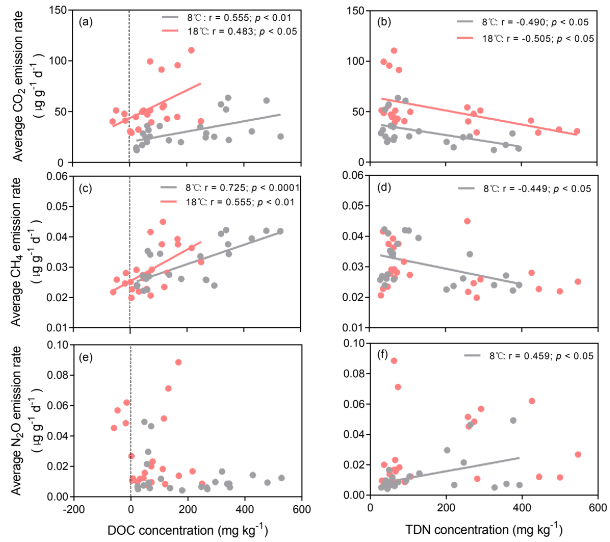


Figure 7

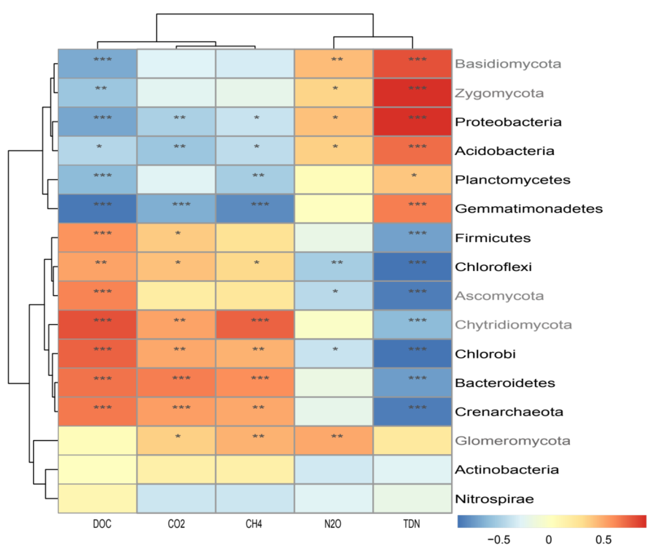
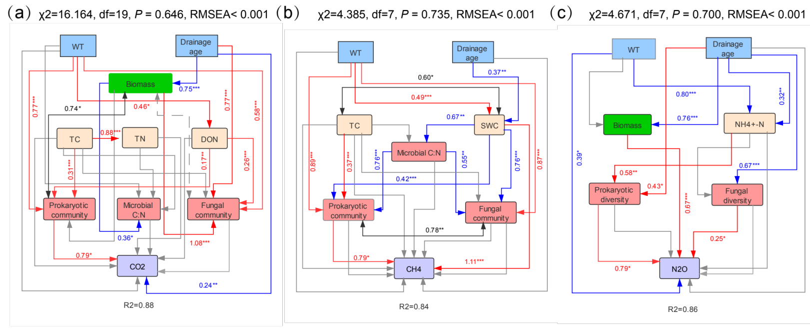


Figure 8


(a) χ2=16.164, df=19, P = 0.646, RMSEA< 0.001
WT
Drainage age
Biomass
0.75***
0.77***
0.74*
0.46*
0.77***
0.58***
TC
0.88***
TN
DON
0.31***
0.17**
0.26***
Prokaryotic community
Microbial C:N
Fungal community
0.36*
1.08***
0.79*
CO2
0.24**
R2=0.88
(b) χ2=4.385, df=7, P = 0.735, RMSEA< 0.001
WT
Drainage age
0.37**
0.60*
0.49***
TC
0.67**
SWC
Microbial C:N
0.89***
0.37***
0.76***
0.55**
0.76***
0.87***
0.42***
Prokaryotic community
Fungal community
0.78**
0.79*
CH4
1.11***
R2=0.84
(c) χ2=4.671, df=7, P = 0.700, RMSEA< 0.001
WT
Drainage age
0.80***
0.32**
Biomass
0.76***
NH4+-N
0.39*
0.58**
0.67***
0.43*
Prokaryotic diversity
0.67***
Fungal diversity
0.25*
0.79*
N2O
R2=0.86

Supplementary figure captions

Figure S1. Water table data at different distances from short- and long-term drainage ditches in recent three growing seasons (2016-2018). (a) The fluctuation of water table depth (WTD); (b) Average water table depths. S: Short-term drainage peatlands, L: Long-term drainage peatlands, S2 and L2: low water table treatment (LWT), S10 and L10: intermediate water table treatment (IWT), S50 and L50: high water table treatment (HWT).

Figure S2. Variation of GHG emission rate of soil from three different water table treatments in short- and long-term drainage peatlands under two temperatures (8 °C and 18 °C). (a) CO_2 emission rate at 8°C; (b) CH_4 emission rate at 8°C; (c) N_2O emission rate at 8°C; (d) CO_2 emission rate at 18°C; (e) CH_4 emission rate at 18°C; (f) N_2O emission rate at 18°C.

Figure S3. Temperature sensitivity (Q_{10}) value variations from three different water table treatments in short- and long-term drainage peatlands. (a) CO_2; (b) CH_4; (c) N_2O. Asterisks (*) represent significance level: *$p < 0.05$, **$p < 0.01$, or ***$p < 0.001$. S: Short-term drainage site, L: Long-term drainage site, S2 and L2: low water table treatment (LWT), S10 and L10: intermediate water table treatment (IWT), S50 and L50: high water table treatment (HWT).

Figure S4. Spearman's correlation analysis between GHG emissions and soil properties, soil prokaryotic and fungal communities. Asterisks (*) represent significance level: *$p < 0.05$, **$p < 0.01$, or ***$p < 0.001$.

Supplementary Table Captions

Table S1. The relative abundance of Prokaryote and fungi at phylum level under different water table treatments in short-term and long-term drainage peatlands.

	Phyla	S2	S10	S50	L2	L10	L50	*p*		
								drainage age	WT	drainage age×WT
Prokaryote	Proteobacteria	44.777 ± 2.157	38.42 ± 1.504	41.181 ± 0.512	45.464 ± 1.336	40.728 ± 1.721	34.064 ± 1.874	**0.05**	**<0.001**	**<0.001**
	Acidobacteria	25.055 ± 3.741	18.674 ± 1.095	23.533 ± 2.115	26.552 ± 1.761	15.486 ± 2.306	19.047 ± 1.532	**0.038**	**<0.001**	**0.039**
	Actinobacteria	8.458 ± 0.693	9.086 ± 1.01	8.402 ± 1.508	8.729 ± 0.502	12.965 ± 0.941	8.634 ± 0.885	**0.002**	**<0.001**	**0.002**
	Chloroflexi	5.736 ± 1.179	10.295 ± 0.56	8.531 ± 0.761	5.049 ± 0.901	12.233 ± 2.937	10.993 ± 0.32	**0.044**	**<0.001**	0.082
	Bacteroidetes	2.263 ± 0.867	5.696 ± 0.441	2.817 ± 0.606	2.015 ± 0.32	2.517 ± 0.098	3.191 ± 0.455	**0.005**	**<0.001**	**<0.001**
	Crenarchaeota	1.459 ± 0.882	4.666 ± 1.245	2.81 ± 0.414	0.367 ± 0.132	2.779 ± 1.099	3.513 ± 0.359	**0.032**	**<0.001**	**0.014**
	Planctomycetes	2.894 ± 0.822	1.475 ± 0.691	1.332 ± 0.676	2.62 ± 0.403	1.921 ± 0.987	2.445 ± 0.218	0.141	**0.014**	0.155
	Gemmatimonadetes	1.746 ± 0.182	1.016 ± 0.204	1.317 ± 0.151	2.262 ± 0.374	1.578 ± 0.198	1.402 ± 0.185	**0.001**	**<0.001**	0.096
	Nitrospirae	1.338 ± 0.29	0.954 ± 0.295	1.568 ± 0.27	1.278 ± 0.11	1.14 ± 0.176	2.209 ± 0.267	**0.02**	**<0.001**	**0.031**
	Firmicutes	0.411 ± 0.153	1.377 ± 0.208	2.183 ± 2.367	0.366 ± 0.06	0.544 ± 0.202	2.7 ± 1.462	0.799	**0.006**	0.508
	Chlorobi	0.529 ± 0.153	1.897 ± 0.346	1.231 ± 0.229	0.463 ± 0.056	1.119 ± 0.195	2.028 ± 0.172	0.859	**<0.001**	**<0.001**
	Others	5.335 ± 0.749	6.444 ± 1.28	5.096 ± 0.512	4.835 ± 0.165	6.992 ± 0.309	8.772 ± 0.523	**<0.001**	**<0.001**	**<0.001**
Fungi	Ascomycota	55.303 ± 16.363	76.829 ± 4.838	85.925 ± 5.59	35.701 ± 1.25	84.374 ± 12.134	93.454 ± 2.31	0.683	**<0.001**	**0.009**
	Basidiomycota	37.559 ± 15.706	13.184 ± 6.478	9.646 ± 5.278	40.737 ± 4.308	7.792 ± 8.813	3.595 ± 2.48	0.43	**<0.001**	0.482
	Chytridiomycota	0.015 ± 0.012	0.63 ± 0.459	0.293 ± 0.273	0.011 ± 0.01	0.061 ± 0.05	0.043 ± 0.024	**0.007**	**0.024**	0.058
	Glomeromycota	0.961 ± 0.433	1.176 ± 0.7	0.514 ± 0.251	0.319 ± 0.077	0.803 ± 0.716	0.048 ± 0.033	**0.017**	**0.022**	0.838
	Zygomycota	0.312 ± 0.19	0.168 ± 0.085	0.11 ± 0.032	2.376 ± 2.21	0.105 ± 0.052	0.039 ± 0.019	0.099	**0.019**	**0.046**
	Unassigned	5.849 ± 2.13	8.014 ± 3.059	3.511 ± 1.705	20.852 ± 5.692	6.861 ± 2.704	2.822 ± 0.376	**0.003**	**<0.001**	**<0.001**

Notes: All results are means (± SE) of four replicates.Significant differences are in bold ($p < 0.05$).