We thank the Associate Editor and two referees for their providing constructive comments to this manuscript. Below we detail how we have revised the manuscript following their suggestions.

1. The problem of more degrees of freedom with more details models is equifinality: several combinations of parameters match the data similarly well. That needs to be incorporated in forward simulations, which usually become more uncertain with equifinality.

Response: Thanks for the comments. To address the impacts of "equifinality" on our quantifications associated with parameters, we have conducted ensemble simulations for both 20th and 21st centuries with respect to uncertain parameters. These ensemble simulations shall cover the "equifinality" set of parameters in our model. In other words, these simulations shall have included the "equifinality" impacts. We presented the simulations results in Figure 11 and Figure 12 in this revision.

2. Fig 3: It is not clearly stated, how many parameters were calibrated and Fig. 3 is barely readable because of display quality. Are there only 3 out of the 6 sites displayed?

Response: Thanks for the comments. We have revised Figure 3. Now six sites are shown andthe figure shall be more readable.

3. Cost function (17): Why did you not consider uncertainty of observed NEE? Usually, you need this to determine, which parameter sets are viable. If you have larger NEE confidence bounds, also more different parameter sets will generate predictions that are still compatible with the calibration NEE. For my main concern above it is important to keep also the slightly less optimal but compatible parameter sets.

Response: The error or uncertainty of the NEE data we used have not been provided by field experimentalists. Thus, in this study, the model parameters are only constrained by the observed magnitudes and temporal variabilities of NEE at those sites.

Microbial dormancy and its impacts on Arctic terrestrial ecosystem carbon budget

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Abstract

A large amount of soil carbon in the Arctic terrestrial ecosystems could be emitted as greenhouse gases in a warming future. However, lacking detailed microbial processes such as microbial dormancy in current biogeochemistry models might have biased the quantification of the regional carbon dynamics. Here the effect of microbial dormancy was incorporated into a biogeochemistry model to improve the quantification for the last and this century. Compared with the previous model without considering the microbial dormancy, the new model estimated the regional soils stored 75.9 Pg more C in the terrestrial ecosystems during the last century, and will store 50.4 Pg and 125.2 Pg more C under the RCP 8.5 and RCP 2.6 scenarios, respectively, in this century. This study highlights the importance of the representation of microbial dormancy in earth system models to adequately quantify the carbon dynamics in the Arctic.

1. Introduction

The land ecosystems in northern high latitudes (>45 ~~°~~ N) occupy 22% of the global surface and store over 40% of the global soil organic carbon (SOC) (McGuire & Hobbie, 1997; Melillo et al., 1993; Tarnocai et al., 2009; Hugelius et al., 2014). During the past decades, a greening accompanying a warming in the region has been documented (Zhou et al., 2001; Lloyd et al., 2002; Stow et al., 2004; Callaghan et al., 2005; Tape et al., 2006). The regional carbon dynamics are expected to loom large in the global carbon cycle and exert large feedbacks to the global climate system (McGuire et al., 2009; Davidson & Janssens, 2006; Bond-Lamberty & Thomson, 2010).

To date, numerous ecosystem models have been developed to project the feedbacks between terrestrial ecosystem carbon cycling and climate (Raich et al., 1991; Zhuang et al., 2001, 2002, 2015; Parton et al., 1993; Knorr et al., 2005; Running & Coughlan, 1988), but they can bias their quantifications due to missing detailed microbial mechanisms in these models (Schmidt et al., 2011; Todd-Brown et al., 2013; Conant et al., 2011; Treseder et al., 2011). Microorganisms play a central role in decomposition of litter and soil organic carbon, which further governs the global carbon cycling and climate change (Xu et al., 2014; Treseder et al., 2011; Wang et al., 2015). An emerging field of research has begun to incorporate microbial ecology into existing process-based models ~~to remedy the~~ to represent decomposition in ways that include important microbial processes that were previously ignored~~inadequate representation of soil decomposition process~~ (Zha & Zhuang, 2018; Schimel & Weintraub, 2003; Allison et al., 2010; German et al., 2012). These microbial-based models tend to better reproduce field and satellite observations than traditional ones that treat soil decomposition as a first-order decay process without considering microbial activities (Treseder et al., 2011; Wieder et al., 2013;

Todd-Brown et al., 2011; Lawrence et al., 2009; Moorhead et al., 2006). However, some vital microbial traits such as microbial dormancy and community shifts are still rarely explicitly considered in large-scale ecosystem models (Wieder et al., 2015), and this may introduce notable uncertainties (Graham et al., 2014, 2016; Wang et al., 2015; Bouskill et al., 2012; Kaiser et al., 2014).

Dormancy is broadly recognized as a strategy for microorganisms to cope with periodical environmental stresses (Harder & Dijkhuizen, 1983). When environmental conditions are unfavorable for growth, microbes switch to a dormant state, which is a reversible state of low to zero metabolic activity (Stolpovsky et al., 2011; Lennon & Jones, 2011). In this state, biogeochemical processes such as soil decomposition are slow (Blagodatskaya et al., 2013). At any given time, there is only a fraction of~~-~~, likely below 50%, ~~of~~ metabolically active microbes ~~in natural soilsnumber of microbes, likely below 50% of live microbes,~~ in natural soils (Wang et al., 2015; Stolpovsky et al., 2011). Soil decomposition and nutrient cycling mainly depend on these active microbes because only active ones can consume organic matter and replicate themselves (Wang et al., 2015; Blagodatskaya et al., 2014). To date, most existing biogeochemistry models use total rather than active microbial biomass as an indicator of microbial activities (Wieder et al., 2015)~~used total microbial biomass as indicator of microbial activities, rather than the active portion of microbial biomass~~, which could bias the estimates of soil decomposition and ecosystem carbon budget (Hagerty et al., 2014; He et al., 2015). Especially, the Arctic terrestrial ecosystems are nitrogen-limited, neglecting microbial dormancy will lead to incorrect estimates of nitrogen availability through soil decomposition, failing to capture nitrogen feedbacks to carbon dynamics (Wang et al., 2015; Stolpovsky et al., 2011; Thullner et al., 2005). Furthermore, the Arctic ~~Besides, it is also important because of~~has

experienced a ~~the~~ marked seasonality of ~~(i.e.~~ active ~~ity~~and ~~/~~dormant ~~cy~~microbial cycles~~)~~ and the above-global-average warming, ~~happening in those latitudes (~~which might ~~could~~ have increased the proportion of active microbes in soil~~s)~~ (He et al., 2015). Thus, incorporating dormancy effects will improve model realism to ~~and show the important role of microbial dormancy provide a betterin~~ provide a better ~~the~~ projection of the Arctic carbon dynamics.

This study incorporated the effects of microbial dormancy trait into an extant process-based biogeochemistry model (MIC-TEM) (Zha & Zhuang, 2018; He et al., 2015). The dormant and active microbial physiology has been considered explicitly in the new version of model (MIC-TEM-dormancy). The revised model was parameterized, validated, and then applied to evaluate the carbon dynamics during the last and this centuries in the Arctic terrestrial ecosystems (north 45 ~~°~~°N above). By comparing the results of MIC-TEM-dormancy and MIC-TEM, we can show that incorporating microbial dormancy may produce a much different prediction in historical and future carbon budget.

~~and demonstrate the essential role of microbial dormancy.~~

2. Methods

2.1 Overview

Due to the importance of microbial dormancy, some recent work has been done to consider the metabolic activation and deactivation of microbes in soil and its effects on soil carbon (C) dynamics and climate feedbacks ~~(Wang et al., 2015; Salazar et al., 2018)~~. For example, Wang et al.~~,~~ (2015) has incorporated transformation processes between active and dormant states to develop~~ed~~ two versions of MEND, that is, MEND with and without dormancy. The two versions of the model have been applied to quantify ~~model~~ the carbon decomposition in ~~of~~ laboratory

incubations of four soils. Salazar et al. (, 2018) have also taken ~~ook~~ microbial dormancy into account to compare their predictions of microbial biomass and soil heterotrophic respiration (R_H) under simulated cycles of stressful (dryness) and favorable (wet pulses) conditions. Our study extend those modeling studies to the whole Arctic region by developing a more detailed biogeochemistry model considering the dormancy impacts. ~~In~~ Below, ~~this paper, fFirst,~~ we first describe how we developed~~d~~ the new model (MIC-TEM-dormancy) by incorporating the microbial dormancy trait into an existing microbial-based biogeochemistry model (MIC-TEM). Second, we discuss how ~~conduct the~~ parameterization and validation of MIC-TEM-dormancy model were conducted using observed net ecosystem exchange data, and heterotrophic respiration data at representative sites ~~have been shown~~. Third, we presented how ~~apply~~ied ~~the~~ model was applied to ~~to~~ northern high latitudes (above 45 ~~o~~°N) for the 20th and 21st centuries and , discussed ~~to demonstrate~~ the dormancy effects on regional carbon budget.

2.2 Model description.

A non-dormancy version of biogeochemistry model (MIC-TEM) has been developed by incorporating a microbial module (Allison et al., 2010) into an extant large-scale biogeochemical model (TEM) to explicitly (Zhuang et al., ~~2001, 2002,~~ 2003) consider the effects of microbial dynamics and enzyme kinetics on carbon dynamics (Zha & Zhuang, 2018). Here we further advanced the MIC-TEM by incorporating algorithms that describe the effects of microbial dormancy dynamics based on He et al. (2015). Different from He et al. (2015), in which microbial module was driven with existing data of carbon stocks and fluxes, our study incorporated the microbial module into an extant MIC-TEM that simulates carbon data dynamically. This coupling enables us to extrapolate our model to whole northern high-latitudes

region, rather than only for temperate forest region in He et al. (2015). In our new model (MIC-TEM-dormancy), microbial biomass pool was divided into two fractions, including the dormant and active microbial biomass pools. The two microbial biomass pools and the reversible transition between them have been considered explicitly in the new model (Figure 1), which was ignored in MIC-TEM ~~(Figure 1)~~.

In previous MIC-TEM, heterotrophic respiration (R_H) is calculated as:

$$R_H = ASSIM*(1-CUE) \quad (1)$$

Where ASSIM and CUE represent microbial assimilation and carbon use efficiency, respectively. For detailed carbon dynamics in MIC-TEM, see Zha & Zhuang (2018).

Here we revised MIC-TEM by incorporating microbial dormancy dynamics according to He et al. (2015). In ~~the new model (~~MIC-TEM-dormancy~~)~~, the soil heterotrophic respiration R_H is comprised of three parts: the maintenance respiration from the active and dormant microorganisms and the CO_2 production through the process of microbial assimilation (He et al., 2015):

$$R_H = m_R Q_{10mic}^{\frac{temp-15}{10}} B_a + \beta m_R Q_{10mic}^{\frac{temp-15}{10}} B_d + CO_2 \quad (2)$$

where the first two terms are maintenance respiration from the active and dormant microorganisms, respectively. The last term is the CO_2 produced during the process of microbial assimilation.

For first two terms, B_a and B_d represents the active and dormant microbial biomass pool, respectively. The parameter m_R denotes the specific maintenance rate at active state (h^{-1}), and β is the ratio of dormant maintenance rate to active maintenance rate. Thus, βm_R denotes the maximum specific maintenance rate at dormant state. Temperature sensitivity was expressed as the Q_{10} function ($Q_{10}^{\frac{temp-15}{10}}$), where temp is soil temperature at top 20 cm (units: °C).

For the third term, the CO_2 produced through microbial assimilation is calculated as in He et al. (2015) and Allison et al. (2010):

$$CO_2=ASSIM*(1-Y_g) \quad (3)$$

Where ASSIM represents the ~~variable of~~ microbial assimilation and the parameter Y_g represents carbon use efficiency. Microbial assimilation (ASSIM) is calculated as in He et al. (2015):

$$ASSIM = \frac{1}{Y_g}\frac{\Phi}{\alpha} m_R Q_{10enz}^{\frac{temp-15}{10}} Ba \left(\frac{CN_{soil}}{CN_{mic}}\right)^{0.6} \quad (4)$$

Here parameter α is ~~called the~~ maintenance weight (h^{-1}), CN_{soil} and CN_{mic} denotes the C:N ratios of soil and that of microbial biomass ~~to consider substrate quality~~. Besides, Φ is the ~~called~~ substrate saturation level and defined as in He et al. (2015) and Wang et al. (2014):

$$\Phi = \frac{S}{K_s+S} \quad (5)$$

Where K_s is the half saturation constant for substrate uptake as indicated by the Michaelis–Menten kinetic, and S is soluble C substrates that are directly accessible for microbial assimilation (Wang et al., 2014). Here we quantified concentration of soluble C substrates that are directly accessible for microbial assimilation by using conceptual framework from Davidson et al. (2012):

$$S = Soluble\ C * D_{liq} * \theta^3 \quad (6)$$

The term 'Soluble C' denotes the state variable of soluble carbon pool. D_{liq} is the diffusion coefficient of the substrate in the liquid phase, and is formulated as:

$$D_{liq} = 1/(1-BD/PD)^3 \quad (7)$$

Where BD is the bulk density and PD is the soil particle density. θ is the volumetric soil moisture. Different from MIC-TEM, the transitions between active and dormant microbial biomass are included in MIC-TEM-dormancy. ~~We used $B_{a\to d}$ and $B_{d\to a}$ denotes the transition from the active~~

~~to dormant microbe and from the dormant to active microbe, respectively (He et al., 2015; Wang et al., 2014):~~

$$B_{a\to d} = (1-\Phi)m_R Q_{10mic}^{\frac{temp-15}{10}} B_a \quad (8\text{~~7~~})$$

$$B_{d\to a} = \Phi m_R Q_{10mic}^{\frac{temp-15}{10}} B_d \quad (9\text{~~8~~})$$

Where $B_{a\to d}$ and $B_{d\to a}$ denote the transition from the active to dormant microbe and from the dormant to active microbe, respectively (He et al., 2015; Wang et al., 2014).

Thus, d~~D~~ormancy rate is affected by active and dormant biomass, ~~substrate availability (B_a, B_d),~~ soil temperature (temp) and soil moisture (θ in Φ).

The active microbial biomass (B_a) is modeled as (He et al., 2015; Wang et al., 2014):

$$\frac{dBa}{dt} = ASSIM * Y_g - m_R Q_{10mic}^{\frac{temp-15}{10}} B_a - B_{a\to d} + B_{d\to a} - DEATH - EPROD \quad (10\text{~~9~~})$$

Where DEATH and EPROD denotes microbial biomass death and enzyme production, which are modeled as proportional to active microbial biomass with constant rates r_{death} and $r_{EnzProd}$ (Allison et al., 2010):

$$DEATH = r_{death} * Ba \quad (11\text{~~0~~})$$

$$EPROD = r_{EnzProd} * Ba \quad (12\text{~~1~~})$$

Where r_{death} and $r_{EnzProd}$ are the rate constants of microbial death and enzyme production, respectively.

The dormant microbial biomass (B_d) is modeled as (He et al., 2015; Wang et al., 2014):

$$\frac{dB_d}{dt} = -\beta m_R Q_{10mic}^{\frac{temp-15}{10}} B_d + B_{a\to d} - B_{d\to a} \quad (13\text{~~2~~})$$

The Soluble C pool is modeled as (He et al., 2015; Allison et al., 2010):

$$\frac{d\ Soluble\ C}{dt} = DECAY - ASSIM + ELOSS + DEATH \quad (14\text{~~3~~})$$

Where DECAY represents the enzymatic decay of soil organic carbon (SOC), and ELOSS represents the loss of enzyme.

DECAY is regulated by enzyme biomass (ENZ), soil organic carbon (SOC), soil temperature, and substrate quality (He et al., 2015):

$$DECAY = V_{max} * Q_{10enz}^{\frac{temp-15}{10}} * ENZ * \frac{SOC}{Km_{uptake}+SOC} * (120 - CN_{soil}) \quad (154)$$

Where V_{max} is the maximum SOC decay rate, Km_{uptake} is half saturation constant for enzymatic decay.

ELOSS is modeled as a first-order process (Allison et al., 2010) to represent enzyme turnover:

$$ELOSS = r_{enzloss} * ENZ \quad (165)$$

Where $r_{enzloss}$ is the rate constant of enzyme loss.

The soil organic carbon pool (SOC) is modeled as:

$$\frac{dSOC}{dt} = Litterfall - DECAY \quad (176)$$

Where Litterfall is estimated as a function of vegetation carbon (Zhuang et al., 2010).

Last, enzyme pool (ENZ) is modeled as:

$$\frac{dENZ}{dt} = EPROD - ELOSS \quad (187)$$

With the modification of microbial carbon dynamics by considering microbial life-history trait, soil decomposition is changed since it is controlled by microbes. When microbial dormancy is considered, the number of active microbes that participate in soil decomposition is much less ~~than that we considered before~~ ~~different~~. The changes in soil decomposition directly influence the amount of soil respiration, and further influence soil nitrogen (N) mineralization that determines soil N availability for plants, affecting gross primary production (GPP). Since both GPP and ~~soil~~

~~respiration (~~R_H~~)~~ can be affected by microbial dormancy, net ecosystem production (NEP) will also be affected.

2.3 Model parameterization and validation

The detailed description of parameters that are related to microbial dormancy can be found in He et al. (2015) (Table 1). Here we calibrated the MIC-TEM-dormancy at six representative sites with gap-filled monthly net ecosystem productivity (NEP, $gCm^{-2}mon^{-1}$) data in northern high latitudes (Table 2). Site-level climatic data and soil texture data were organized for driving model. All sites information can be found on AmeriFlux network (Davidson et al., 2000). The results for model parameterization were presented in Figure 2. We conducted the parameterization using a global optimization algorithm known as SCE-UA (Shuffled complex evolution) method (Duan et al., 1994). An ensemble of 50 independent sets of parameters were performed based on prior ranges from literature (Table 1) to minimize the difference between the monthly simulated and measured NEP at the chosen sites. The cost function of the minimization is:

$$\mathrm{Obj} = \sum_{i=1}^{k}(\mathrm{NEP}_{obs,i} - \mathrm{NEP}_{sim,i})^2 \quad (17)$$

Where $\mathrm{NEP}_{obs,i}$ and $\mathrm{NEP}_{sim,i}$ are the observed and simulated NEP, respectively. k is the number of data pairs for comparison. Except for the parameters of microbial dormancy, other parameters are derived directly from MIC-TEM (Zha & Zhuang, 2018). The optimized parameters were used for model validation and regional simulations.

For model validation, we chose another six sites that containing monthly NEP data from AmeriFlux network (Table 3). Moreover, we also conducted site-level validations with monthly soil respiration data from AmeriFlux network and Fluxnet dataset. The site information was provided in Table 4. For these sites, we assumed 50% of soil respiration was heterotrophic

respiration (R_H) for forest (Hanson et al., 2000), 60% and 70% of that was R_H for grassland (Wang et al., 2009) and tundra (Billings et al., 1977). Because there is a ~~of~~ limited ~~ations in the~~ amount of available RH data~~there is a limited amount of measured data of heterotrophic respiration~~, we could not conduct a regional validation for all pixels in northern high latitudes. Instead, we extracted 61 sites providing data of average annual heterotrophic respiration from ORNL global Soil Respiration Dataset (https://daac.ornl.gov/SOILS/guides/SRDB_V4.html, Bond-Lamberty et al., 2018) for model validation. The site-level observed average annual R_H was used to compare with simulated annual R_H by MIC-TEM-dormancy and MIC-TEM. The ~~new model (~~MIC-TEM-dormancy~~)~~ was run at monthly time step to keep consistent with the time step of MIC-TEM. Although microbial dynamics occur at fine temporal scales (Tang & Riley, 2014), we can still quantify the cumulative impacts of microbial dynamics on carbon and nitrogen cycling at monthly time by not changing the model structure.

2.4 Spatial extrapolation

For historical simulations during the 20th century, two sets of regional simulations using MIC-TEM-dormancy and MIC-TEM at a spatial resolution of 0.5° latitude × 0.5° longitude were conducted. Our model simulation contains two parts: spin-up and transient simulation. A typical spin-up was conducted to get the model to a steady state for each spatial location, which will be used as initial conditions for transient simulations (McGuire et al., 1992). During spin-up procedure, cyclic forcing data was used to force the model run, and repeated continuously until dynamic equilibrium was achieved at which the modeled state variables show a cyclic pattern or become constant. Specifically, this study used the monthly historical climate data from 1900 to 1940 to repeatedly drive the model for the spin-up. Before spin-up procedure, the model was

initialized with default built-in carbon stocks (Raich et al., 1991). During transient simulations, the calibrated ecosystem-specific parameters were used for regional simulations. The previous dynamic equilibrium was used as initial value for transient simulation. The historical climatic forcing data, including the monthly air temperature, precipitation, cloudiness, and atmospheric CO_2 concentrations, were organized from the Climatic Research Unit (CRU TS3.1) from the University of East Anglia (Harris et al., 2014). We also used g~~G~~ridded data of soil texture (Zhuang et al., 2003), elevation (Zhuang et al., 2015), and potential natural vegetation (Melillo et al., 1993) from literatures ~~were also used~~. In our model, we assumed that soil texture, elevation, and potential natural vegetation data only vary spatially, not vary over time (Zhuang et al., 2015).

In addition, regional simulations over the 21st century were conducted under two Intergovernmental Panel on Climate Change (IPCC) climate scenarios (RCP 2.6 and RCP 8.5). The future climatic forcing data under these two climate change scenarios were derived from the HadGEM2-ESmodel, which is a member of CMIP5project213 (https://esgf-node.llnl.gov/search/cmip5/). Then the regional estimations were obtained by summing up the gridded outputs for our study region. The positive simulated NEP represents a CO_2 sink from the atmosphere to terrestrial ecosystems, while a negative value represents a source of CO_2 from terrestrial ecosystems to the atmosphere.

2.5 Parameter equifinality effects ~~uncertainty~~

Our previous studies using TEM has demonstrated that equifinality derived from site-level parameterization will affect the uncertainty in the estimation of regional carbon dynamics (Tang and Zhuang, 2008, 2009). Here equifinality refers to that a number of sets of parameters result in model simulations that all match the data similarly well. To quantify this ~~e~~ effect on our simulation uncertainty, ~~parameter uncertainty in our model,~~ we conducted ensemble regional simulations with

50 sets of parameters for both historical and future studies. The 50 sets of parameters were obtained according to the method in Tang and Zhuang (2008).

3. Results

3.1 Inversed Model Parameters and model validation

Using SCE-UA ensemble method, 50 independent sets of parameters were converged to minimize the objective function. Then the optimized parameters are calculated as the mean of these 50 sets of inversed parameters. The boxplot of parameter posterior distributions reflects different ecosystem properties at these sites (Figure 3). For instance, growth yield~~carbon use efficiency (CUE)~~ was ~~much~~ higher in tundra types than in forests, meaning microorganisms in environment with higher energy limitation tend to enhance the efficiency of energy transportation. Besides, alpha, the maintenance weight, was also ~~much~~ higher in tundra types than in forests. F~~The opposite can be seen f~~rom the plot for parameter beta, the ratio of dormant maintenance rate to specific maintenance rate for active biomass in tundra types is lower than that~~it~~ in forest types. Other microbial related parameters did not differentiate much among different vegetation types.

After parameterization, the MIC-TEM-dormancy was validated with monthly NEP data for six representative ecosystems, and the comparisons between monthly observed NEP and simulated NEP were presented in Figure 4. With the optimized parameters, the dormancy-based model was used to reproduce NEP to compare with the measured NEP (Table 5). The ~~statistical analysis shows that~~ R^2 ranges from 0.67 for Atqasuk to 0.93 for Bartlett Experimental Forest (Table 5). Generally, our new model performs better for forest ecosystems than for tundra ecosystems. Compared with MIC-TEM~~, which is no dormancy-based~~, dormancy model performs better for alpine tundra, temperate coniferous forest, and grassland. For other sites, both~~two~~ models show similar performance (Table 5). Besides, a~~Another~~ set of ~~sites with~~ monthly soil

respiration data were selected to evaluate ~~validate the ability of~~ the estimated ~~ing~~ R_H ~~of our model~~~~conduct model validation~~. The comparisons between monthly observed R_H and simulated R_H from two contrasting models were conducted (Figure 5). MIC-TEM-dormancy has higher R^2 and lower root mean square error (RMSE) (Table 6). Sixty-one sites with average annual R_H in northern high-latitude regions were used to further evaluate the new model performance. The dormancy model has lower intercept and slope with R^2 of 0.45, while R^2 of MIC-TEM is 0.3 (Figure 6). These analyses indicate that new model is more realistic in representing ~~heterotrophic respiration (~~R_H~~)~~ by considering microbial dormancy. This difference in R_H further affects soil available nitrogen dynamics, influencing nitrogen uptake by plants, the rate of photosynthesis and NPP (Zhuang et al., 2015; Zha et al., 2018; Thullner et al., 2005).

3.2 Regional carbon dynamics during the 20th century

Regional extrapolation with both models estimated a regional carbon sink but with different magnitudes (Figure 7c). ~~Here positive values of NEP represent sinks of CO_2 into terrestrial ecosystems, while negative values represent sources of CO_2 to the atmosphere.~~ With optimized parameters, MIC-TEM estimated a regional carbon sink of 77.6 Pg with the interannual standard deviation of 0.21 Pg C yr^{-1} during the 20th century. However, MIC-TEM-dormancy nearly doubles the sink at 153.5 Pg with the interannual standard deviation of 0.12 Pg C yr^{-1} during the last century~~, which estimates 75.9 Pg more carbon sink than MIC-TEM does but with less interannual variation~~ (Figure 7c). At the end of the century, MIC-TEM estimated that NEP reaches 1.0 Pg C yr^{-1} in comparison with MIC-TEM-dormancy estimates of 1.5 Pg C yr^{-1} (Figure 7c). Both models simulated similar trends for regional NPP, R_H and NEP (Figure 7). Generally, they show an increasing trend in the 20th century~~ except a slight decrease during the 1960s~~ (Figure 7).

Meanwhile, with optimized parameters, MIC-TEM-dormancy estimated NPP and R_H at 7.94 Pg C yr^{-1} and 6.4 Pg C yr^{-1}, which are 5.8% and 16.3% less than the estimations from MIC-TEM, respectively (Figures 7a and 7b). This pronounced difference of NEP between two models comes from the disparity between the simulated NPP and R_H with them since NEP is calculated as the difference between NPP and R_H. Without considering dormancy, MIC-TEM estimates more active microbial biomass since it assumes the whole microbial biomass pool will participate in soil decomposition. The fact is only active part of microbial biomass can affect ~~decompose~~ organic matter decomposition~~work for soil decomposition~~, meaning MIC-TEM overestimates R_H. On the other hand, o~~O~~verestimation of R_H can induce higher nitrogen uptake by plants, which will accelerate rate of photosynthesis and further enhance NPP projection. Although MIC-TEM estimates higher NPP and R_H than MIC-TEM-dormancy does, NEP estimated from MIC-TEM is actually lower.

The average annual seasonal patterns of NPP, R_H and NEP during the 1990s were also organized from regional simulations with two models (Figure 8). Temporally, both ~~two~~ models projected higher NPP and R_H in summer than in winter (Figures 8a and 8b) due to higher soil temperature and moisture (McGuire et al., 1992). Setting the R_H projection from MIC-TEM as a baseline, MIC-TEM-dormancy averagely projected 33% less R_H in summer (May to September), and 30% more in winter (other months)~~MIC-TEM produced less R_H in winter but higher R_H in summer than MIC-TEM-dormancy~~ (Figure 8b), which indicates that without dormancy, model tends to estimate lower soil respiration compared to dormancy model due to ignorance of dormant respiration in winter but estimate higher soil respiration due to higher estimation of active biomass in summer. In the meantime, seasonal cycle of NPP with MIC-TEM-dormancy shows a relative flattening pattern compared with MIC-TEM, which is similar to seasonal cycle

of R_H (Figure 8a). ~~This is because higher R_H can cause higher NPP due to the reasons we have mentioned above.~~ Though R_H and NPP show the similar seasonal patterns, NEP can still show different pattern ~~since it's the difference between NPP and R_H~~. Here seasonal cycles of NEP with models are close to each other (Figure 8c), but dormancy model projected slightly higher NEP in summer. ~~Besides, setting the R_H projection from MIC-TEM as baseline, MIC-TEM-dormancy averagely projected 33% less R_H in summer (May to September), and 30% more in winter (other months). This suggested that relative difference of R_H between two models in summer was higher than in winter.~~

3.3 Regional carbon dynamics during the 21st century

Under the RCP 8.5 scenario, both models estimated the region acts as a carbon sink (Figure 9). The MIC-TEM-dormancy predicted~~ed~~~~d~~ a ~~net~~ C accumulation ~~sequestration~~ of 129.9 Pg by the end of this century. ~~that the sink is 129.9 Pg~~ with the interannual standard deviation of 0.13 Pg C yr^{-1}, whereas MIC-TEM estimates a ~~net~~ C accumulation ~~sequestration~~ of 79.5 Pg ~~the sink is 79.5 Pg~~ with the interannual standard deviation of 0.37 Pg C yr^{-1} during the 21st century (Figure 9). Thus, MIC-TEM-dormancy estimates an increase of 50.4 Pg regional carbon sequestration relative to MIC-TEM, ~~but~~ with less interannual variation (Figure 9). Under this scenario, b~~B~~oth models predict similar temporal trends for NEP, namely increasing from the 2000s and then decreasing from the 2070s onward (Figure 9). MIC-TEM-dormancy predicts that carbon sink reaches 1.36 Pg C yr^{-1} in the 2090s, which is 0.26 Pg C yr^{-1} more than projection of MIC-TEM. Moreover, MIC-TEM-dormancy estimated NPP and R_H at 10.2 Pg C yr^{-1} and 8.9 Pg C yr^{-1}, which are 1.3 Pg C yr^{-1} and 1.8 Pg C yr^{-1} less than the estimations from MIC-TEM, respectively (Figure 9).

Under the RCP 2.6 scenario, the cumulative NEP from two models diverged by 125.2 Pg C by 2100. The trajectory of inter-annual NEP estimated with the two models also diverged. The MIC-TEM predicted the region fluctuates between carbon sinks and sources, and totally acts as a carbon source of 1.6 Pg C with the interannual standard deviation of 0.24 Pg C yr^{-1} during the 21st century. In contrast, MIC-TEM-dormancy projected the region acts as a carbon sink of 123.6 Pg C with an~~the~~ interannual standard deviation of 0.1 Pg C yr^{-1} (Figure 9). MIC-TEM-dormancy estimates NPP and R_H at 9.9 Pg C yr^{-1} and 8.7 Pg C yr^{-1}, which are 0.5 Pg C yr^{-1} and 1.7 Pg C yr^{-1} less than the estimations from MIC-TEM, respectively (Figure 9). Moreover, simulations under the two contrasting climate scenarios (RCP 2.6 and RCP 8.5) exhibit a large difference of 81.1 Pg C of cumulative NEP during the 21st century by MIC-TEM, but only 6.3 Pg C of that by MIC-TEM-dormancy. This difference indicates microbes provide a resistant response to climate change due to dormancy to some extent (Treseder et al., 2011).

The average annual seasonal patterns of NPP, R_H and NEP during the 2990s by two models were also presented (Figure 10). MIC-TEM-dormancy estimated higher R_H in winter, but lower R_H in summer under both future scenarios (Figure 10). NPP is the same in winter with or without dormancy, and in the late summer is higher ~~with~~ than that without dormancy ~~(i.e. opposite to RH)~~, especially in the RCP 8.5 scenario. ~~Similar seasonal cycle pattern appears for NPP projection.~~ The combined flattening patterns of NPP and R_H result in different patterns for NEP. Under the RCP 2.6 scenario, MIC-TEM-dormancy predicts higher NEP from June to October, but lower NEP from January to April compared ~~similar NEP in other months~~ to MIC-TEM (Figure 10). Under the RCP 8.5 scenario, MIC-TEM-dormancy predicts higher NEP from June to September, but much lower NEP in other months than MIC-TEM (Figure 10).

3.4 Regional uncertainty considering equifinality effects ~~Ensemble simulations~~ during ~~for~~ 20th and 21st centuries

The ensemble simulations for the 20th century is shown in Figure 11. Given the uncertainty in parameters, MIC-TEM-dormancy predicted that the regional cumulative carbon ranges from a carbon loss of 28.2 Pg to a carbon sink of 362.1 Pg by different ensemble members, with a mean of 71.2±54.8 Pg (Figure 11). For the 21st century, MIC-TEM-dormancy predicted that the region acts from a carbon source of 49.3 Pg C to a carbon sink of 296.5 Pg C, with a mean of 112.7±116.5 Pg under the RCP 2.6 scenario (Figure 12). Under the RCP 8.5 scenario, MIC-TEM-dormancy predicted that the region acts from a carbon source of 27.1 Pg C to a carbon sink of 401.3 Pg C, with a mean of 143.1±162.5 Pg (Figure 12).

4. Discussion

Soils are the largest carbon repository in the terrestrial biosphere and hold 2.5 times more carbon than the atmosphere (Frey et al., 2013; Schlesinger & Andrews, 2000). Especially, a significant portion of soil organic carbon ~~currently~~ stored in northern high latitudes ~~region~~ (Tarnocai et al., 2009). Besides, the magnitude of the warming in these regions is larger, almost twice, that of the global average ~~climate over this region has warmed in recent decades~~ (Serreze & Francis, 2006) and the changing climate is expected to alter the carbon cycle through influencing the activities of microorganisms in controlling soil decomposition (Manzoni et al., 2012; Melillo et al., 2011). Therefore, explicit consideration of microbial traits and functions in large-scale biogeochemistry models is necessary for better quantification of carbon-climate feedbacks (Thullner et al., 2005; Wang et al., 2015). Our regional simulations with two contrasting models (MIC-TEM, MIC-TEM-dormancy) indicate the region was a carbon sink in past decades, which is consistent with results from other process-based models (White et al.,

2000; Houghton et al., 2007; McGuire et al., 2009; Schimel, 2013). However, the magnitudes of this sink are quite different in two models. Moreover, MIC-TEM-dormancy predicts the sink will decrease under both RCP 8.5 and RCP 2.6 scenarios during the 21st century, while MIC-TEM projects that the sink will increase under the RCP 8.5 but change to carbon source under the RCP 2.6 scenario. Estimations based on models without dormancy could fit observations of R_H as well as estimations with dormancy, but at the cost of underestimating microbial biomass (Wang et al., 2014). Differences in predicted R_H with and without dormancy increase with temperature and with the length of the dry periods between wetting events (Salazar et al., 2018). The large difference in two models suggests the importance of incorporating microbial dormancy effects.

The large bias between dormancy and non-dormancy models mainly comes from two parts. First, many ~~most~~ important microbial activities such as soil organic carbon decomposition and nutrient cycling largely depend on the active fraction of microbial communities, not total microbial biomass (Wang et al., 2014; Blagodatsky et al., 2000). However, only a small part (about 0.1-2%, seldom exceed 5%) of the total soil microbial biomass is recognized to be active under natural conditions (Blagodatsky et al., 2011; Werf & Verstraete, 1987). Thus, dormancy could be a prominent feature in soil systems (Wang et al., 2014). Without considering dormancy, the "effective" microbial biomass for soil decomposition could be overestimated, resulting in overestimation of heterotrophic respiration (He et al., 2015). ~~Our regional estimate of R_H is 6.4 Pg C yr^{-1} during the 20th century by MIC-TEM-dormancy, while 7.7 Pg C yr^{-1} by MIC-TEM. No dormancy model simulated 20.3% higher respiration than dormancy model. For future simulations, MIC-TEM-dormancy predicted 8.7 Pg C yr^{-1} and 9.0 Pg C yr^{-1} of R_H under RCP 2.6 and RCP 8.5 scenarios during the 21st century, respectively. Nevertheless, no dormancy model simulated 19.5% and 21.2% higher respiration than dormancy model under RCP 2.6 and RCP 8.5~~

~~scenarios, respectively.~~ He et al. (2015) predicted total soil R_H of all temperate forests (25°N-50°N) from the dormancy model amounted to 7.28 Pg C yr^{-1} and 8.83 Pg C yr^{-1} from a no-dormancy model, which is 21.3% higher than the dormancy model. Although their study region and simulation period are different from our study, the results can still be comparable. Both studies indicated that the magnitude of R_H ~~and proportion~~ from no-dormancy model are higher than dormancy models. Second, high soil respiration stimulates N mineralization in soils (Zhuang et al., 2001, 2002), making more nutrients for photosynthesis of plants (Raich et al., 1991; McGuire et al., 1995). Therefore, NPP will be higher due to the N enrichment from higher R_H. However, how NEP will change is still unclear. ~~Our regional estimate of NEP during the 20th century by MIC-TEM-dormancy is 1.54 Pg C yr^{-1}, and is 0.78 Pg C yr^{-1} by MIC-TEM.~~ Our estimates of the northern extratropical NEP in the 1980s (1.61 Pg C yr^{-1} with MIC-TEM-dormancy and 0.84 Pg C yr^{-1} with MIC-TEM) are within ranges (0.6 to 2.3 PgC yr^{-1}) reported in the literature for northern regions (Schimel et al., ~~(~~2001). ~~reported that a range of estimates of the northern extratropical NEP is from 0.6 to 2.3 PgC yr^{-1} in the 1980s. In comparison with our estimates of 1.61 Pg C yr^{-1} with MIC-TEM-dormancy and 0.84 Pg C yr^{-1} with MIC-TEM, our regional estimates of NEP are in reasonable range.~~ Moreover, our predicted time trajectory ~~trend~~ of NEP in the 21st century under the RCP 2.6 scenario is very similar to the finding of White et al. (2000), indicating that NEP increases from the 2000s to the 2070s, and then decreases in the 2090s. ~~Moreover, future simulations under two contrasting climate scenarios (RCP 2.6 and RCP 8.5) exhibit a large difference of 81.1 Pg C of cumulative NEP during the 21st century by MIC-TEM, but only 6.3 Pg C of that by MIC-TEM-dormancy. This difference indicates microbes provide a resistant response to climate change due to dormancy to some extent (Treseder et al., 2011).~~

Although our dormancy model can project reasonable carbon fluxes and indicate the importance of incorporating microbial dormancy when compared with MIC-TEM~~no dormancy model~~ (~~MIC-TEM;~~ Zha & Zhuang et al., 2018), there are some other microbial traits have not yet been considered in our model. For instance, one vital common evolutionary trait of microbe is the community shift (Wang et al., 2015) with changing environment, including warming, N fertilization and precipitation (Treseder et al., 2011; Frey et al., 2013; Allison et al., 2009; Evans & Wallenstein, 2011). Community shift will influence microbial physiology, temperature sensitivity and growth rates (Classen et al., 2015), which will further affect the rate of soil decomposition and other carbon dynamics (Treseder et al., 2011; Schimel & Schaeffer, 2012; Todd-Brown et al., 2011). ~~Moreover, microbial acclimation is another important trait to affect soil decomposition. Recent studies have found the capacity of the microbial community to maintain the warming-induced elevated respiration could decrease over time because of acclimation (Melillo et al. 1993; Todd-Brown et al., 2011). This mechanism of adaption to a new temperature regime shall be factored into future soil decomposition analysis.~~ Besides, microbial community composition was ignored in our model. We didn't separate among functional microbial groups, but gather microbes into one "box". However, microbial community composition could influence ecosystem functioning, and their variance in responses to environmental conditions could alter the prediction of the rates of decomposition of organic material (Balser et al. 2002; Fierer et al. 2007). Especially, some narrowly-distributed functions can be more sensitive to microbial community composition, and these might benefit most from explicit consideration of distinguishing functional groups in ecosystem models (McGuire & Treseder, 2010; Schimel 1995). Thus, functional dissimilarity in microbial communities can be considered in next step for model development (Strickland et al., 2009; Moorhead et al., 2006).

Moreover, microbial acclimation, a mechanism of adaption to a new temperature regime, is another important trait to affect soil decomposition. Recent studies have found that the warming-induced elevated respiration of the microbial community could decrease over time because of acclimation (Melillo et al. 1993; Todd-Brown et al., 2011). This mechanism shall be factored into future soil decomposition analysis.

Except for model limitations mentioned above~~above model limitations~~, additional uncertainties may come from inadequate model parameterization and model assumptions. For example, a critical microbial parameter, carbon use efficiency (CUE), is a primary control to soil CO_2 efflux. Higher CUE indicates more microbial growth and more carbon uptake by plants, while lower CUE indicates higher soil decomposition (Manzoni et al., 2012). Theoretical and empirical studies have suggested that CUE depends on both temperature and substrate quality (Frey et al., 2013) and decreases as temperature increases and nutrient availability decreases (Manzoni et al., 2012). Our study considered the CUE sensitivity to temperature, but not nutrient availability. On the other hand, some model assumptions can also cause uncertainties. For example, we assumed that vegetation will not change during the transient simulation. However, over the past few decades in northern high latitudes, temperature increases have led to vegetation shift from one type to another (Hansen et al., 2006; White et al., 2000). The vegetation changes will affect carbon cycling in these ecosystems.

5. Conclusions

This study incorporated microbial dormancy into a detailed microbial-based soil decomposition biogeochemistry model to examine the fate of large Arctic soil carbon under changing climate conditions. Regional simulations using MIC-TEM-dormancy indicated that,

over the 20th century, the region is a carbon sink of 153.5 Pg. This sink could decrease to 129.9 Pg under the RCP 8.5 scenario or 123.6 Pg under the RCP 2.6 scenario during the 21st century. Whether considering microbial dormancy or not can cause large differences in soil decomposition estimation between two models. Meanwhile, due to available nitrogen affected by soil decomposition, net primary production is consequently influenced in these two centuries. The combined changes in soil decomposition and net primary production led to large differences in carbon budget estimation between two models. Compared with MIC-TEM, MIC-TEM-dormancy projected 75.9 Pg more C stored in the terrestrial ecosystems over the last century, 50.4 Pg and 125.2 Pg more C under the RCP 8.5 and RCP 2.6 scenarios, respectively. This study highlights the importance of the representation of microbial dormancy in earth system models in order to adequately quantify the carbon dynamics in northern high latitudes.

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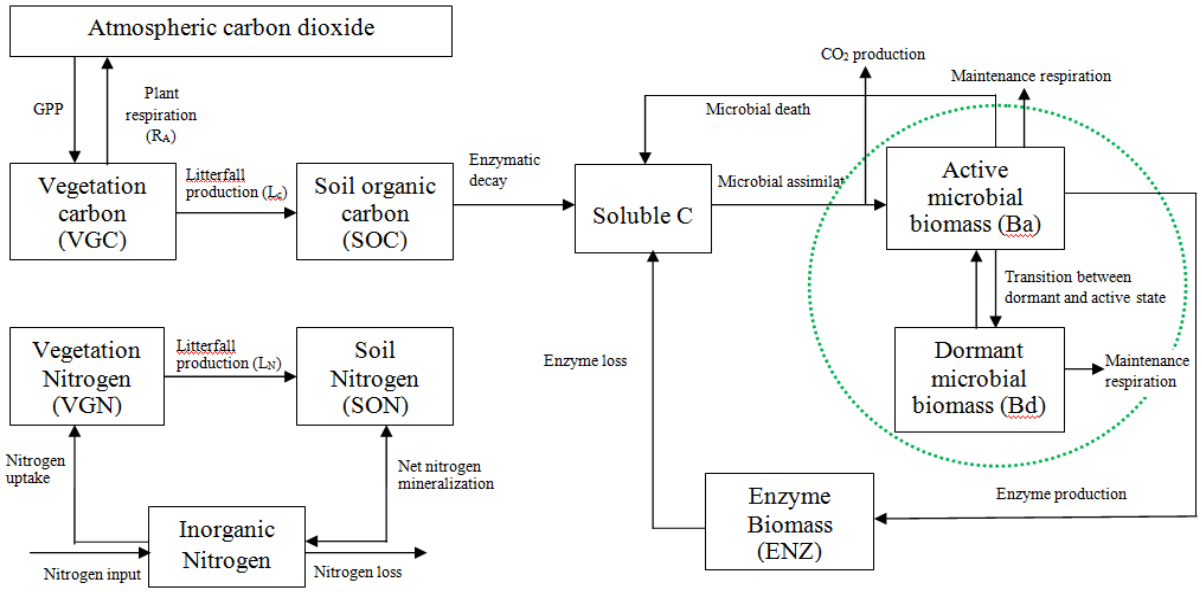


Figure 1. Framework of the dormancy model: microbial biomass is split into two parts, active microbial biomass and dormant microbial biomass (shown in the green dashed circle). Maintenance respiration from these two parts, and the CO_2 production through microbial assimilation contributes to heterotrophic respiration. The model was revised based on Zha & Zhuang (2018).

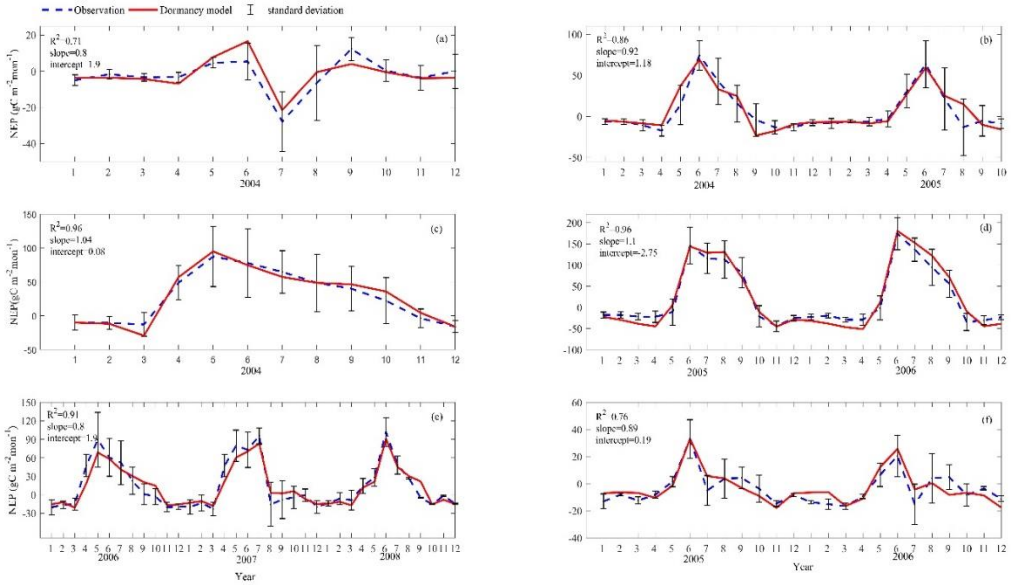


Figure 2. Comparison between observed and simulated NEP (gC $m^{-2}mon^{-1}$) at: (a) Ivotuk (alpine tundra), (b) UCI-1964 burn site (boreal forest), (c) Howland Forest (main tower) (temperate coniferous forest), (d) Univ. of Mich. Biological Station (Temperate deciduous forest), (e) KUOM Turfgrass Field (Grassland), and (f) Atqasuk (Wet tundra). Note: scales are different. Error bars represent standard errors among daily measure data in one month.

Figure 3. Boxplot of parameter posterior distribution that are obtained after ensemble inverse modeling for MIC-TEM-dormancy all six sites: US-Ivo: Ivotuk (alpine tundra), CA-NS3: UCI-1964 burn site (boreal forest), US-Ho1: Howland Forest (temperate coniferous forest), US-UMB: Univ. of Mich. Biological Station (temperate deciduous forest), US-KUT: KUOM Turfgrass Field (grassland), US-Atq: Atqasuk (wet tundra).

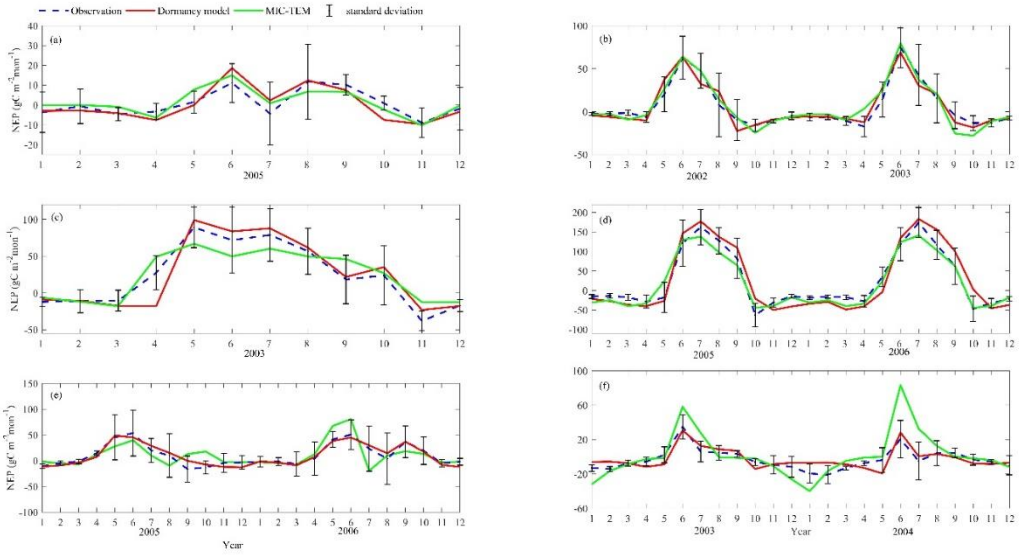


Figure 4. Comparison between observed and simulated NEP (gC $m^{-2}mon^{-1}$) at: (a) Ivotuk (alpine tundra), (b) UCI-1964 burn site (boreal forest), (c) Howland Forest (main tower) (temperate coniferous forest), (d) Bartlett Experimental Forest (Temperate deciduous forest), (e) Brookings (Grassland), and (f) Atqasuk (Wet tundra). Note: scales are different.

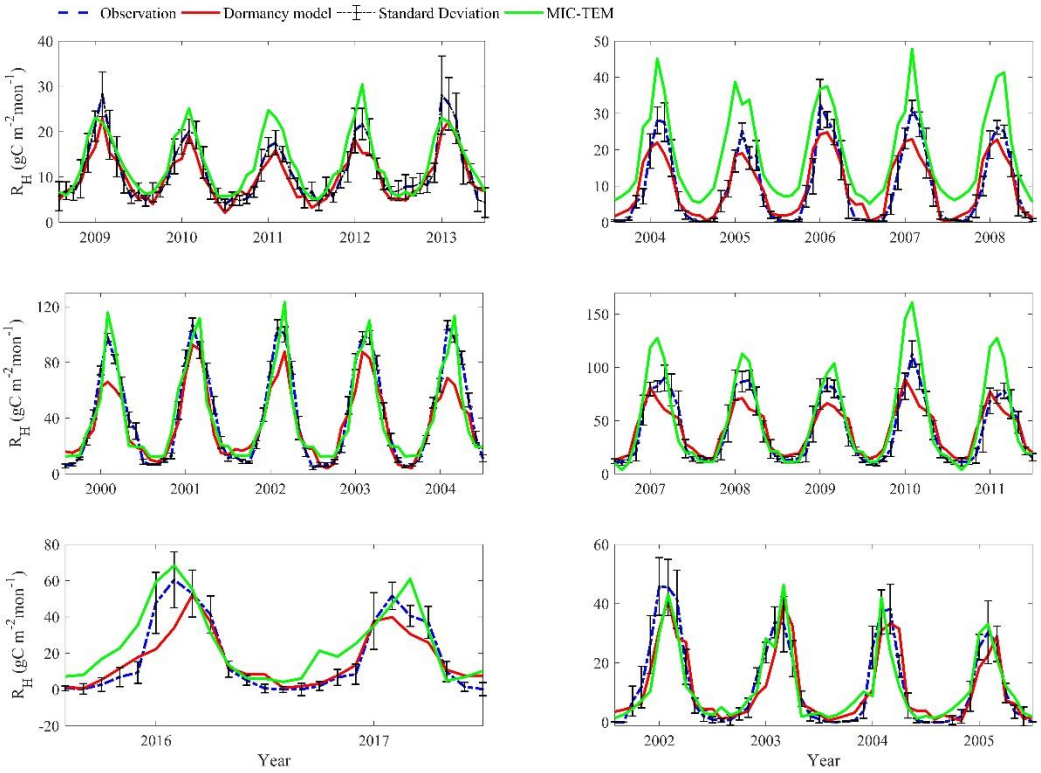
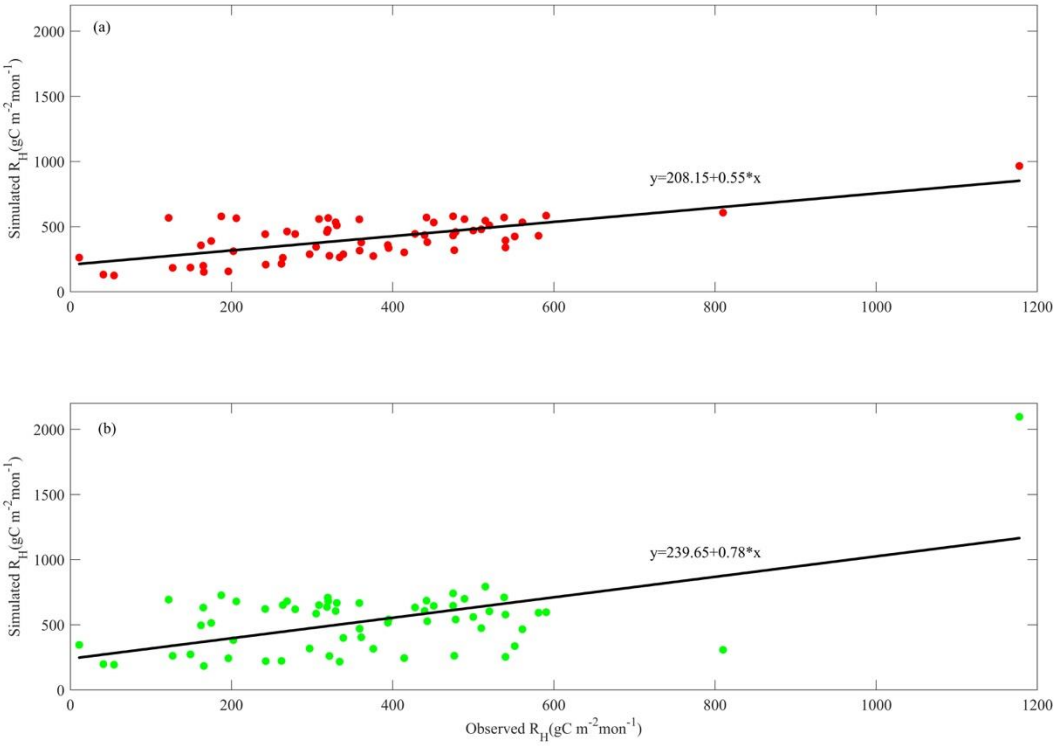


Figure 5. Comparison between observed and simulated R_H (gC $m^{-2}mon^{-1}$) at: (a) US-EML (alpine tundra), (b) CA-SJ2 (boreal forest), (c) US-Ho2 (temperate coniferous forest), (d) US-UMB (Temperate deciduous forest), (e) US-Ro4 (Grassland), and (f) RU-Che (Wet tundra). Note: scales are different.



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940 Figure 6. Linear regression between simulated and observed annual R_H (gC $m^{-2}yr^{-1}$) for: (a) MIC-
941 TEM-dormancy, and (b) MIC-TEM.
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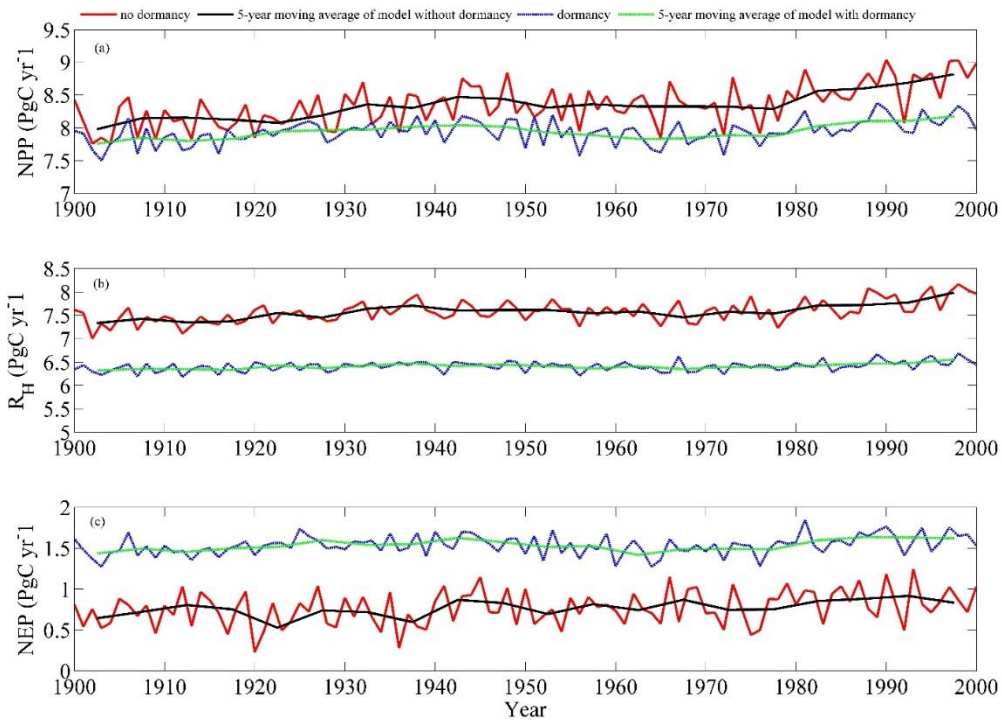

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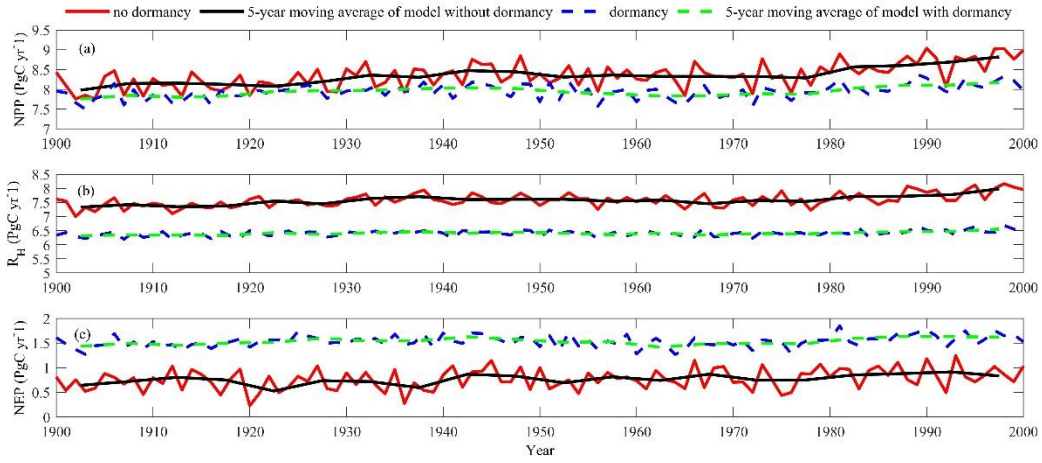

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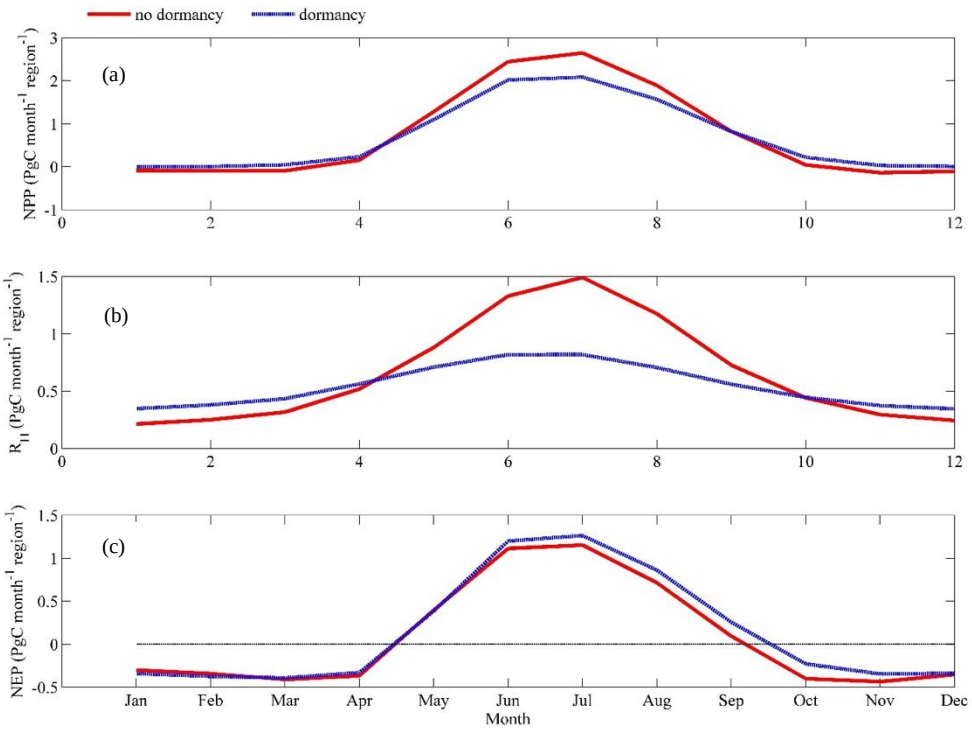
945 Figure 7. Simulated annual net primary production (NPP, top panel), heterotrophic respiration (R_H,
946 center panel) and net ecosystem production (NEP, bottom panel) during the 20th century by
947 dormancy model and MIC-TEM, respectively.



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949 Figure 8. Annual seasonal pattern of simulated (a) net primary production (NPP, top panel), (b)
950 heterotrophic respiration (R_H, center panel) and (c) net ecosystem production (NEP, bottom
951 panel) during the 1990s from dormancy model and MIC-TEM.

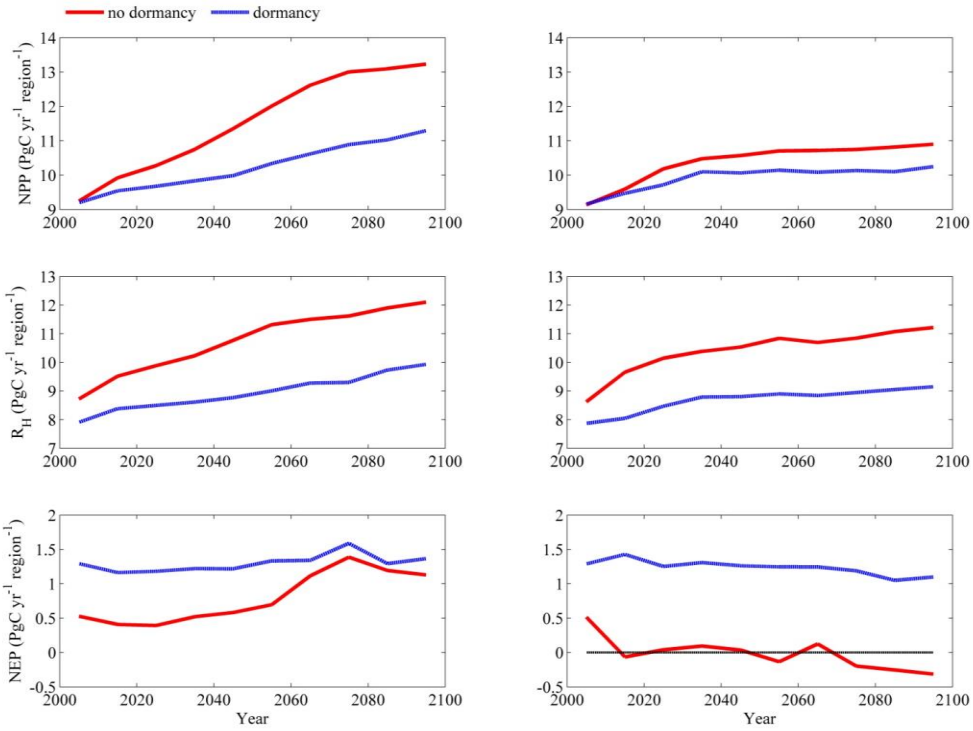
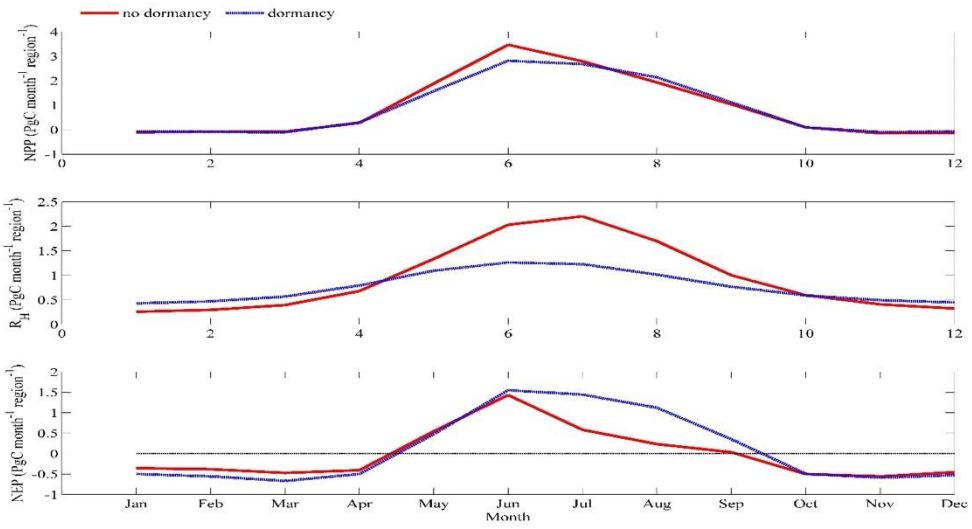


Figure 9. Predicted changes in carbon fluxes: (i) NPP, (ii) R_H, and (iii) NEP for all land areas north of 45 °N in response to transient climate change under the RCP 8.5 scenario (left panel) and RCP 2.6 scenario (right panel) with dormancy model and MIC-TEM, respectively. The decadal running mean is applied.

968 (a)



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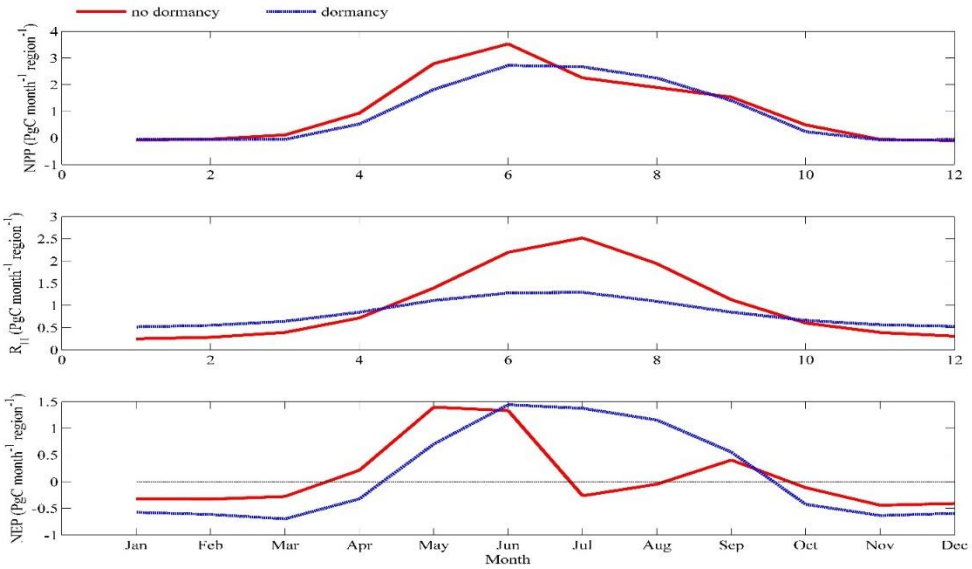
970 (b)



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972 Figure 10. Annual seasonal pattern of simulated net primary production (NPP, top panel),
973 heterotrophic respiration (R_H, center panel) and net ecosystem production (NEP, bottom panel)
974 during the 2090s from dormancy model and MIC-TEM under: (a) RCP 2.6 scenario (top panel)
975 and (b) RCP 8.5 scenario (bottom panel).
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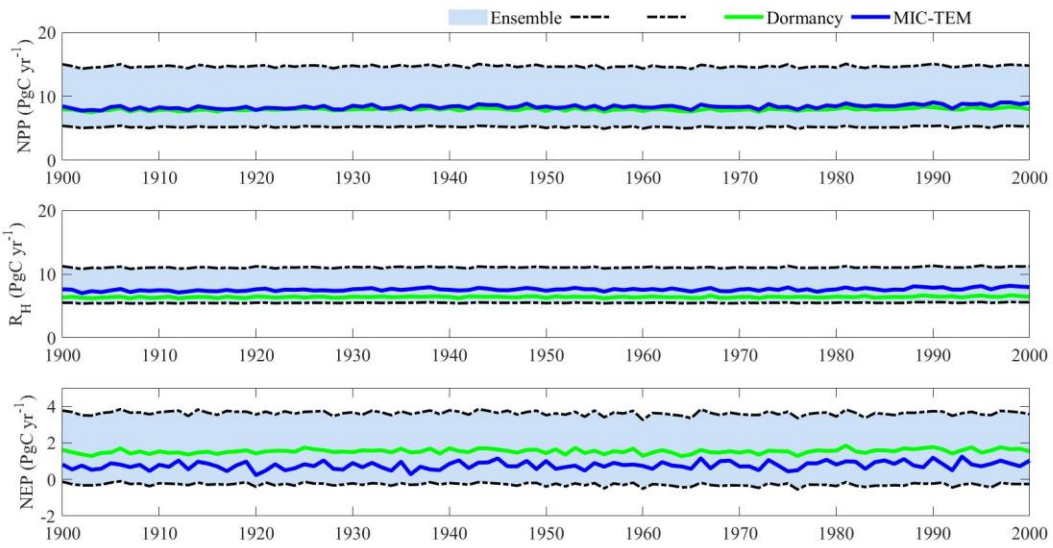

Figure 11. Simulated annual net primary production (NPP, top panel), heterotrophic respiration (R_H, center panel) and net ecosystem production (NEP, bottom panel) by MIC-TEM-dormancy with ensemble of parameters.

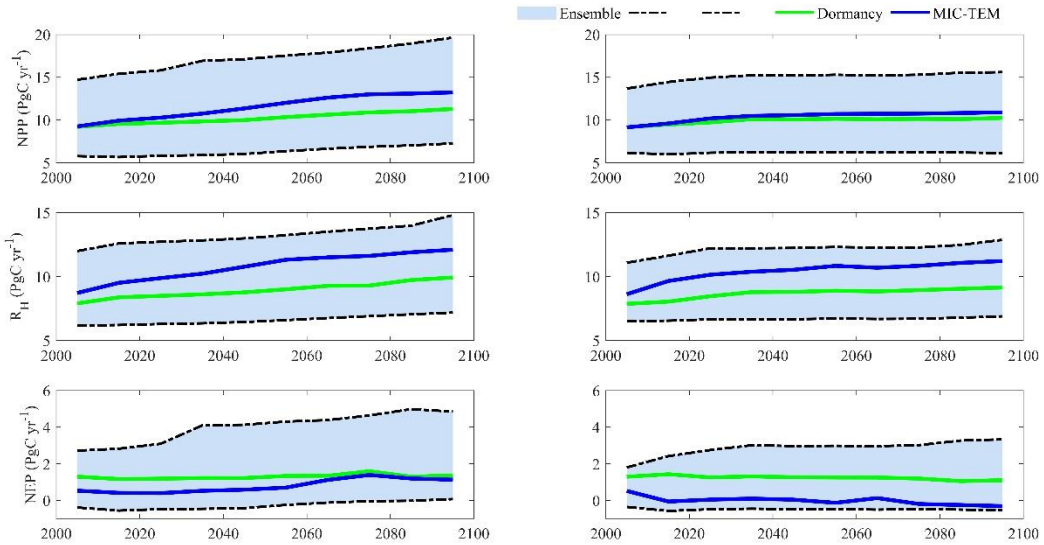

Figure 12. Simulated annual net primary production (NPP, top panel), heterotrophic respiration (R_H, center panel) and net ecosystem production (NEP, bottom panel) under RCP 8.5 scenario (left panel) and RCP 2.6 scenario (right panel) by MIC-TEM-dormancy with ensemble of parameters. The decadal running mean is applied. The grey area represents the upper and lower bounds of simulations.

Table 1. Parameters associated with detailed microbial dormancy in MIC-TEM-dormancy

parameter	unit	description	Parameter range	references
m_R	h^{-1}	Specific maintenance rate at active state	[0.001, 0.08]	Wang et al. (2014)
Q_{10mic}	-	Temperature effects on microbial metabolic activity (rate change per 10 °C increase in temperature). Based on 0.65 eV activation energy for soils	[1.5, 3.5]	He et al. (2015)
Q_{10enz}	-	Temperature effects on enzyme activity (rate change per 10 °C increase in temperature). Based on 6% rate increase per degree Celsius	1.79	He et al. (2015)
α	-	the ratio of m_R to the sum of maximum specific growth rate	[0.01, 0.5]	Wang et al. (2014)
β	-	Ratio of dormant microbial maintenance rate to m_R	[0.0005, 0.005]	Wang et al. (2014)
Y_g	-	carbon use efficiency	[0.3, 0.7]	He et al. (2015)
K_s	mgC cm^{-2}	Half-saturation constant for directly accessible substrate	[0.01, 10]	Wang et al. (2014)
Km_{uptake}	mgC cm^{-2}	Half-saturation constant for enzymatic decay of SOC	[200, 1000]	He et al. (2015)
r_{death}	h^{-1}	Potential rate of microbial death	[$2e^{-4}$, $2e^{-3}$]	Allison et al. (2010)
$r_{EnzProd}$	h^{-1}	Enzyme production rate of microbe	[$1e^{-4}$, $8e^{-4}$]	He et al. (2015)
$r_{enzloss}$	h^{-1}	Enzyme loss rate	[0.0005, 0.002]	Allison et al. (2010)
V_{max}	mgC cm^{-2} h^{-1}	Maximum SOC decay rate	[$1e^{-4}$, $5e^{-3}$]	He et al. (2015)

1025 **Table 2. Site description and measured NEP data used to calibrate MIC-TEM-dormancy**

Site Name	Location (Longitude (degrees) /Latitude (degrees))	Elevation (m)	Vegetation type	Description	Data range	Citations
Univ. of Mich. Biological Station	84.71W 45.56 N	234	Temperate deciduous forest	Located within a protected forest owned by the University of Michigan. Mean annual temperature is 5.83°C with mean annual precipitation of 803mm	01/2005-12/2006	Gough et al. (2013)
Howland Forest (main tower)	68.74W 45.20N	60	Temperate coniferous forest	Closed coniferous forest, minimal disturbance.	01/2004-12/2004	Davidson et al. (2006)
UCI-1964 burn site	98.38W 55.91N	260	Boreal forest	Located in a continental boreal forest, dominated by black spruce trees, within the BOREAS northern study area in central Manitoba, Canada.	01/2004-10/2005	Goulden et al. (2006)
KUOM Turfgrass Field	93.19W 45.0N	301	Grassland	A low-maintenance lawn consisting of cool-season turfgrasses.	01/2006-12/2008	Hiller et al. (2011)
Atqasuk	157.41W 70.47N	15	Wet tundra	100 km south of Barrow, Alaska. Variety of moist-wet coastal sedge tundra, and moist-tussock tundra surfaces in the more well-drained upland.	01/2005-12/2006	Oechel et al. (2014);
Ivotuk	155.75W 68.49N	568	Alpine tundra	300 km south of Barrow and is located at the foothill of the Brooks Range and is classified as tussock sedge, dwarf-shrub, moss tundra.	01/2004-12/2004	McEwing et al. (2015)

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1030 **Table 3. Site description and measured NEP data used to validate MIC-TEM-dormancy**

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Site Name	Location (Longitude (degrees) /Latitude (degrees))	Elevation (m)	Vegetation type	Description	Data range	Citations
Bartlett Experimental Forest	71.29W/ 44.06N	272	Temperate deciduous forest	Located within the White Mountains National Forest in north-central New Hampshire, USA, with mean annual temperature of 5.61 °C and mean annual precipitation of 1246mm.	01/2005-12/2006	Jenkins et al. (2007); Richardson et al. (2007);
Howland Forest (main tower)	68.74W/ 45.20N	60	Temperate coniferous forest	Closed coniferous forest, minimal disturbance.	01/2003-12/2003	Davidson et al. (2006)
UCI-1964 burn site	98.38W/ 55.91N	260	Boreal forest	Located in a continental boreal forest, dominated by black spruce trees, within the BOREAS northern study area in central Manitoba, Canada.	01/2002-12/2003	Goulden et al. (2006)
Brookings	96.84W/ 44.35N	510	Grassland	Located in a private pasture, belonging to the Northern Great Plains Rangelands, the grassland is representative of many in the north central United States, with seasonal winter conditions and a wet growing season.	01/2005-12/2006	Gilmanov et al. (2005)
Atqasuk	157.41W/ 70.47N	15	Wet tundra	100 km south of Barrow, Alaska. Variety of moist-wet coastal sedge tundra, and moist-tussock tundra surfaces in the more well-drained upland.	01/2003-12/2004	Oechel et al. (2014);
Ivotuk	155.75W/ 68.49N	568	Alpine tundra	300 km south of Barrow and is located at the foothill of the Brooks Range and is classified as tussock sedge, dwarf-shrub, moss tundra.	01/2005-12/2005	McEwing et al. (2015)

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Table 4. Site description and measured R_H data used to validate MIC-TEM-dormancy model

Site	Location (Longitude (degrees) /Latitude (degrees))	Elevation (m)	Vegetation type	Data range	Citations
US-EML	149.25W/ 63.88N	700	Alpine tundra	01/2009-12/2013	Belshe et al. (2012)
CA-SJ2	104.65W/ 53.95N	580	Boreal forest	01/2004-12/2008	Coursolle et al. (2006)
US-Ho2	68.75W/ 45.21N	91	Temperate coniferous forest	01/2000-12/2004	Davidson et al. (2006)
US-UMB	84.71W/ 45.56N	234	Temperate deciduous forest	01/2005-12/2006	Gough et al. (2013)
US-Ro4	93.07W/ 44.68N	274	Grasslands	01/2016-12/2017	Griffis et al. (2011)
RU-Che	161.34E/ 68.61N	6	Wet tundra	01/2002-12/2005	Merbold et al. (2009)

Table 5. Model validation statistics for Dormancy model and MIC-TEM at six sites with NEP data

Site Name	Vegetation type	Models	Intercept	Slope	R-square	Adjusted R-square	p-value
Ivotuk	Alpine tundra	MIC-TEM	0.85	0.83	0.70	0.67	<0.001
		Dormancy	-0.51	1.09	0.75	0.73	<0.001
UCI-1964 burn site	Boreal forest	MIC-TEM	0.18	1.03	0.912	0.9080	<0.001
		Dormancy	-0.21	0.96	0.90	0.894	<0.001
Howland Forest (main tower)	Temperate coniferous forest	MIC-TEM	7.29	0.72	0.85	0.83	<0.001
		Dormancy	0.27	1.05	0.89	0.88	<0.001
Bartlett Experimental Forest	Temperate deciduous forest	MIC-TEM	-6.05	0.91	0.944	0.941	<0.001
		Dormancy	-2.34	1.13	0.93	0.924	<0.001
Brookings	Grassland	MIC-TEM	3.05	0.71	0.84	0.83	<0.001
		Dormancy	0.17	0.95	0.90	0.898	<0.001
Atqasuk	Wet tundra	MIC-TEM	7.22	1.85	0.71	0.70	<0.001
		Dormancy	0.19	0.82	0.67	0.66	<0.001

1063 **Table 6. Model validation statistics for Dormancy model and MIC-TEM at six sites with R_H data**
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Site ID	Vegetation type	Models	Intercept	Slope	R-square	Adjusted R-square	RMSE	p-value
US-EML	Alpine tundra	MIC-TEM	2.90	0.91	0.79	0.78	3.55	<0.001
		Dormancy	1.81	0.74	0.87	0.85	2.69	<0.001
CA-SJ2	Boreal forest	MIC-TEM	7.59	1.12	0.84	0.83	9.8	<0.001
		Dormancy	2.6	0.74	0.86	0.85	3.97	<0.001
US-Ho2	Temperate coniferous forest	MIC-TEM	4.07	0.89	0.86	0.84	12.39	<0.001
		Dormancy	6.59	0.71	0.91	0.89	11.83	<0.001
US-UMB	Temperate deciduous forest	MIC-TEM	-4.73	1.32	0.81	0.8	20.05	<0.001
		Dormancy	13.6	0.67	0.85	0.84	12.94	<0.001
US-Ro4	Grassland	MIC-TEM	9.34	0.87	0.81	0.79	11.25	<0.001
		Dormancy	4.81	0.65	0.86	0.84	9.21	<0.001
RU-Che	Wet tundra	MIC-TEM	2.5	0.67	0.72	0.71	6.24	<0.001
		Dormancy	1.96	0.77	0.81	0.79	5.95	<0.001