

Supplementary Online Materials

for

**Historical dynamics of terrestrial carbon during 1901-2016 as simulated
by the CLM-Microbe model**

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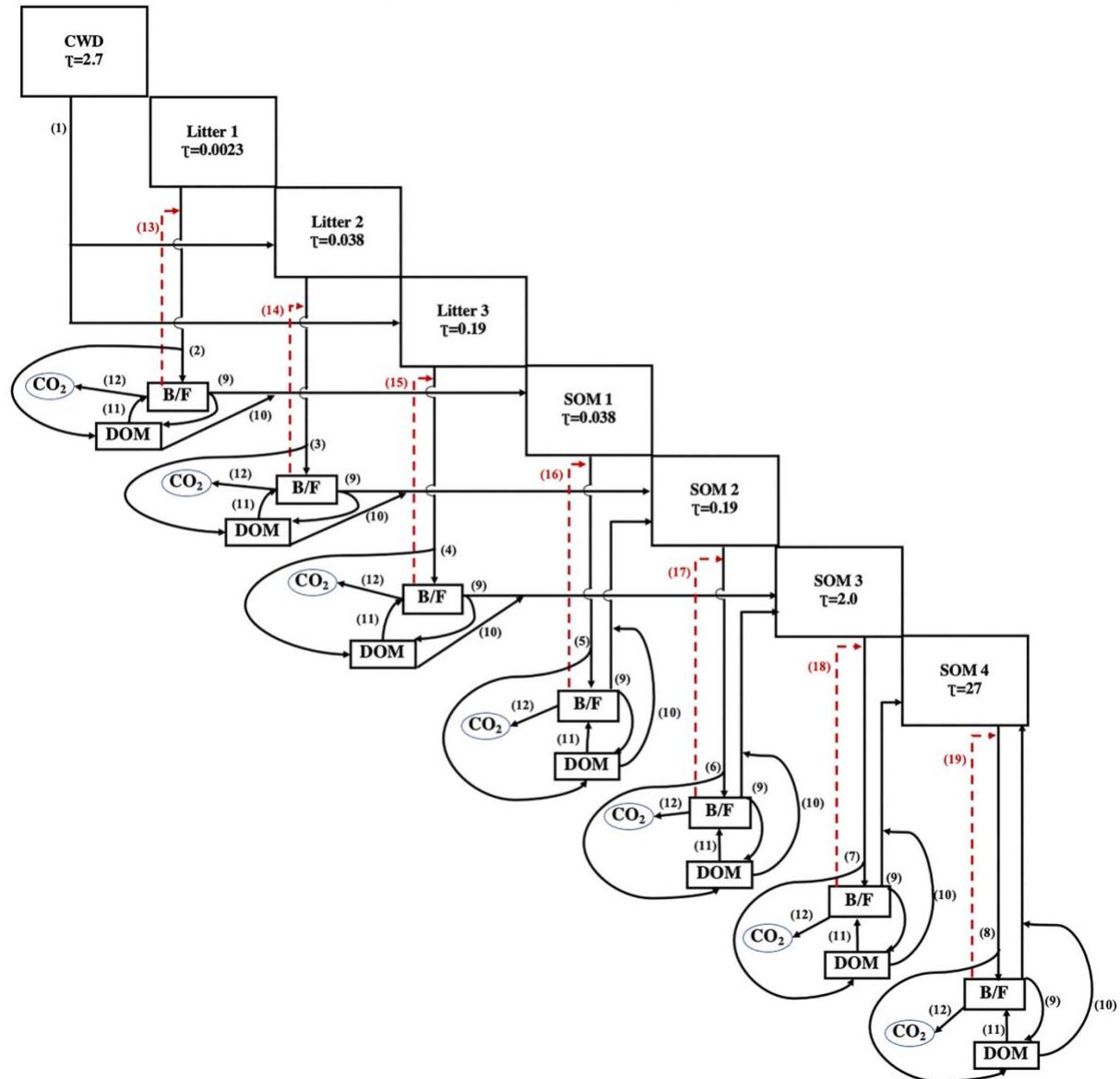


Fig. S1. Conceptual diagram showing the key processes and the roles of fungi and bacteria in the CLM-Microbe model. CWD, coarse woody debris; SOM, soil organic matter; B, bacteria; F, fungi; DOM, dissolved organic matter. In the CLM-Microbe model, number in the box means turnover time of each pool. Black solid lines indicate transitions in the CLM-Microbe model, which generally represents processes such as 1) decomposition of coarse woody debris, 2) litter 1 decomposition, 3) litter 2 decomposition, 4) litter 3 decomposition, 5) soil organic matter 1 decomposition, 6) soil organic matter 2 decomposition, 7) soil organic matter 3 decomposition, 8) soil organic matter 4 decomposition, 9) fungal and bacterial lysis, 10) dissolved organic matter adsorption, 11) dissolved organic matter uptake by fungal and bacterial, and 12) fungal and bacterial respiration. Red dash lines represent regulatory role of fungi and bacteria on the process, including fungi and bacteria regulation on 13) litter 1, 14) litter 2, 15) litter 3, 16) soil organic matter 1, 17) soil organic matter 2, 18) soil organic matter 3, and 19) soil organic matter 4 decomposition (He et al., 2021).

Table S1. Key model parameters in processes involving fungal and bacterial biomass

| Symbol | Range ^a | Unit | Description | Reference |
|-------------|--------------------|-----------------|--|--|
| k_dom | 0.0025-0.5 | d ⁻¹ | decomposition rate constant of DOM | (Wheeler et al., 1996; Kirchman et al., 1991; Cherrier et al., 1996) |
| k_bacteria | 0.00143-2 | d ⁻¹ | lysis rate constant of bacteria | (Rousk and Bååth, 2007, 2011; Moore et al., 2005; Schippers et al., 2005) |
| k_fungi | 0.00027-0.05 | d ⁻¹ | lysis rate constant of fungi | (Thornton and Rosenbloom, 2005; Rousk and Bååth, 2011; Moore et al., 2005; Wallander et al., 2004) |
| m_rf_s1m | 0-1 | | fraction factor quantifying carbon from SOM1 to microbes | Calibrated |
| m_rf_s2m | 0-1 | | fraction factor quantifying carbon from SOM2 to microbes | Calibrated |
| m_rf_s3m | 0-1 | | fraction factor quantifying carbon from SOM3 to microbes | Calibrated |
| m_rf_s4m | 0-1 | | fraction factor quantifying carbon from SOM4 to microbes | Calibrated |
| m_batm_f | 0-1 | | fraction factor quantifying carbon respired by bacteria | Calibrated |
| m_bdom_f | 0-1 | | fraction factor quantifying carbon from DOM to bacteria | Calibrated |
| m_bs1_f | 0-1 | | fraction factor quantifying carbon from bacteria to SOM1 | Calibrated |
| m_bs2_f | 0-1 | | fraction factor quantifying carbon from bacteria to SOM2 | Calibrated |
| m_bs3_f | 0-1 | | fraction factor quantifying carbon from bacteria to SOM3 | Calibrated |
| m_fatm_f | 0-1 | | fraction factor quantifying carbon respired by fungi | Calibrated |
| m_fdom_f | 0-1 | | fraction factor quantifying carbon from DOM to fungi | Calibrated |
| m_fs1_f | 0-1 | | fraction factor quantifying carbon from fungi to SOM1 | Calibrated |
| m_fs2_f | 0-1 | | fraction factor quantifying carbon from fungi to SOM2 | Calibrated |
| m_fs3_f | 0-1 | | fraction factor quantifying carbon from fungi to SOM3 | Calibrated |
| m_domb_f | 0-1 | | fraction factor quantifying carbon from DOM to bacteria | Calibrated |
| m_domf_f | 0-1 | | fraction factor quantifying carbon from DOM to fungi | Calibrated |
| m_doms1_f | 0-1 | | fraction factor quantifying carbon from DOM to SOM1 | Calibrated |
| m_doms2_f | 0-1 | | fraction factor quantifying carbon from DOM to SOM2 | Calibrated |
| m_doms3_f | 0-1 | | fraction factor quantifying carbon from DOM to SOM3 | Calibrated |
| cn_bacteria | 3-12 | | C:N ratio of bacteria | (Strickland and Rousk, 2010) |
| cn_fungi | 3-60 | | C:N ratio of fungi | (Strickland and Rousk, 2010) |
| cn_dom | 4.2-185 | | C:N ratio of DOM | (Sinsabaugh et al., 2016) |
| CUEmax | 0.46-0.9 | | maximum carbon use efficiency of microbes | (Gommers et al., 1988; Sinsabaugh et al., 2013; Sinsabaugh et al., 2016) |

^aThe values may not be the same as those from literature sources due to unit conversion.

Table S2. Validation and atmospheric forcing datasets used in this study

| Variables | Dataset | Source |
|---|---|----------------------|
| Gross and net primary productivity | MODIS gridded datasets | Zhao et al. (2005) |
| Heterotrophic and soil respiration | Global Gridded 1-km Annual Soil Respiration Database | Warner et al. (2019) |
| Soil organic carbon (0-1 m) | Harmonized World Soil Database | Wieder (2014) |
| Soil organic carbon (0-30 cm) | Global Soil Organic Carbon Map | Fao (2018) |
| Fungal and bacterial biomass carbon (0-30 cm) | Global Topsoil Fungal and Bacterial Biomass Carbon Dataset | He et al. (2020) |
| Microbial biomass carbon (0-1 m) | Global Soil Microbial Biomass Carbon, Nitrogen, and Phosphorus Dataset | Xu et al. (2013) |
| Dissolved organic carbon (0-30 cm & 0-1 m) | Global Dissolved Organic Carbon Dataset | Guo et al. (2020) |
| Meteorological Forcing | CRUNCEP Version 7 - Atmospheric Forcing Data for the Community Land Model | Viovy (2018) |

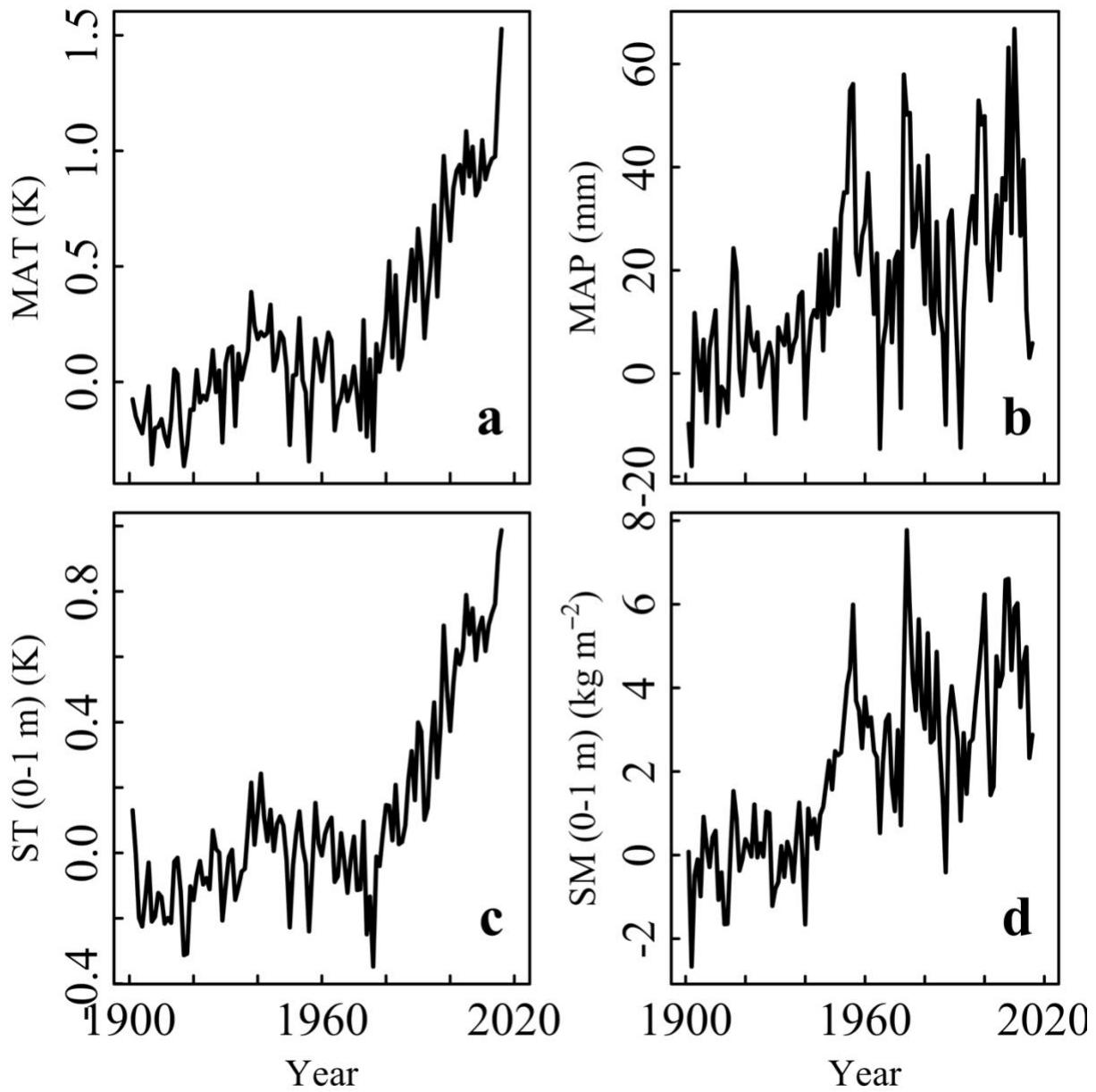


Fig. S2 Temporal variations of annual deviations in (a) MAT, (b) MAP, (c) ST of top 1m, and (d) SM of top 1m weighted by area in the CLM-Microbe model from 1901-1910. The baseline was the ten-year average of corresponding variables during 1901-1910. MAT, mean annual temperature; MAP, mean annual precipitation; ST, soil temperature; SM, soil moisture.

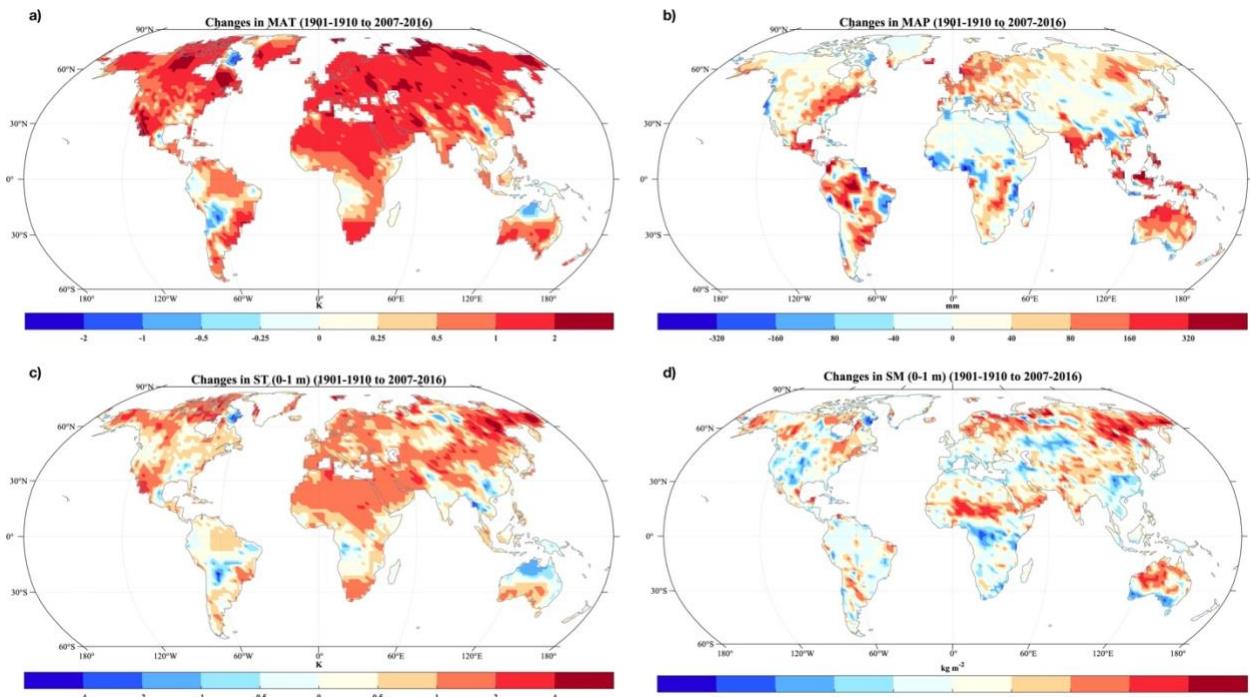


Fig. S3 Changes of (a) MAT, (b) MAP, (c) ST (0-1 m), and (d) SM (0-1 m) in 2007-2016 vs. 1901-1910. MAT, mean annual temperature; MAP, mean annual precipitation; ST, soil temperature; SM, soil moisture.

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