
Soil Microbes as Key Drivers of Global Carbon Cycling in the Context of Climatic Change

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.Abstract

Soil microbial communities constitute the primary biological engine regulating the global **carbon** cycle, yet their responses to anthropogenic climate change remain a critical source of uncertainty in terrestrial feedback projections (Bardgett et al., 2008; Falkowski et al., 2008; Gougoulias et al., 2014). This review synthesizes findings from twenty-nine research studies to evaluate how **global change factors**, including rising temperatures and **elevated carbon dioxide**, transform microbial diversity, community architecture, and metabolic function (Classen et al., 2015; He et al., 2014; Xue et al., 2016). Research across diverse biomes indicates that chronic warming induces an "**oligotrophic transition**," characterized by a decline in total biomass and a shift toward taxa with low **ribosomal ribonucleic acid** operon copy numbers adapted to processing recalcitrant **carbon** (DeAngelis et al., 2015; Frey et al., 2008). Simultaneously, **elevated carbon dioxide** primarily influences the "underground" world indirectly by increasing plant **rhizodeposition**, which can stimulate the rhizosphere microbiome and trigger "**priming effects**" that accelerate the decomposition of stable **soil organic matter** (Drigo et al., 2008; He et al., 2014). We emphasize a fundamental paradigm shift in contemporary ecology: viewing the persistence of **soil organic matter** not as an intrinsic chemical trait of plant litter, but as an "**ecosystem property**" governed by microbial accessibility and physical protection (Schmidt et al., 2011). Furthermore, this synthesis identifies significant research gaps, particularly the mismatch between the microscopic scale of microbial activity and the macroscopic scale of **Earth system models** (Gougoulias et al., 2014; Classen et al., 2015). We conclude that integrating mechanistic microbial data—such as **carbon use efficiency** and functional gene expressions—is imperative for moving beyond "black box" modeling and accurately predicting the magnitude of global climate feedbacks in the **Anthropocene** (Wieder et al., 2015; Xue et al., 2016; Cavicchioli et al., 2019). The objective of this review is to clarify how these underground dynamics will dictate the future stability of the Earth's largest terrestrial **carbon** reservoir.

1. Introduction

Soil microbial communities represent the "unseen majority" and constitute the fundamental life-support system of the terrestrial biosphere (Bardgett et al., 2008; Falkowski et al., 2008; Gougoulias et al., 2014). As the primary drivers of biogeochemical processes, these diverse assemblages of bacteria, fungi, archaea, and protists are responsible for the essential recycling of elements such as **nitrogen**, phosphorus, and **carbon**, without which ecosystem productivity would cease (Prosser, 2007; Gougoulias et al., 2014). Soils serve as the largest terrestrial reservoir of organic **carbon**, containing approximately 1,500 to 2,000 **Gigatonnes**—a stock that is significantly larger than the combined **carbon** found in the atmosphere and global vegetation (Schmidt et al., 2011; Gougoulias et al., 2014; Patoine et al., 2022). Consequently, soil microorganisms play a disproportionate role in maintaining global ecosystem health

by regulating the flow of material and energy through these massive reservoirs (Bardgett et al., 2008; Jassey et al., 2022).

Microorganisms regulate global **carbon** cycling by balancing the accumulation of organic matter against its release through decomposition and respiration (Schmidt et al., 2011; Jassey et al., 2022). This regulation is facilitated by complex microbial enzyme systems, often described as the "engines" that drive the Earth's biogeochemical cycles (Falkowski et al., 2008; Gougoulias et al., 2014). Heterotrophic soil respiration, which releases approximately 60 **Petagrams of carbon** annually, is a dominant flux that overshadows fossil fuel emissions by tenfold (Bardgett et al., 2008; Liu et al., 2018). Recent research has shifted the paradigm of **soil organic carbon** dynamics, suggesting that the persistence of organic matter is an "**ecosystem property**" rather than a result of the molecular structure of plant inputs alone; its stability depends heavily on microbial accessibility, physical protection within soil aggregates, and environmental constraints (Schmidt et al., 2011; Gougoulias et al., 2014). Furthermore, microorganisms do not merely mineralize **soil organic carbon**; they also contribute to long-term **carbon** stabilization through the formation of necromass and metabolic byproducts that serve as precursors for stable soil organic matter (Liang et al., 2017; Liu et al., 2024).

Anthropogenic activities have driven atmospheric **carbon dioxide** concentrations to historic levels, triggering global temperature increases and altered precipitation patterns (IPCC, 2007; Cavicchioli et al., 2019). These **global change factors** influence microbial communities through both direct and indirect pathways (Classen et al., 2015). Direct effects involve the immediate response of microbial metabolic rates and enzyme kinetics to warming and moisture fluctuations (Gougoulias et al., 2014; Classen et al., 2015). Conversely, indirect effects are mediated through climate-driven shifts in plant physiology, such as increased photosynthesis and rhizodeposition under **elevated carbon dioxide**, which alters the supply of labile **carbon** to the rhizosphere (Drigo et al., 2008; He et al., 2014). Additionally, climate change can cause shifts in plant community composition, such as the transition from **Carbon-3** to **Carbon-4** species, which fundamentally alters the quality and quantity of litter inputs available to the decomposer community (Xue et al., 2016; Yu et al., 2018).

Recent studies have highlighted significant structural and functional shifts within soil microbiomes in response to these stressors (Zhou et al., 2020). Long-term field experiments indicate that chronic warming can reduce total microbial biomass and favor the growth of **oligotrophic bacteria** adapted to extracting resources from limited, recalcitrant supplies (Frey et al., 2008; DeAngelis et al., 2015). A global analysis revealed that global soil microbial biomass **carbon** stocks decreased by approximately 3.4% between 1992 and 2013, primarily driven by increasing temperatures in northern circumpolar regions (Patoine et al., 2022). Under **elevated carbon dioxide**, key functional genes involved in **carbon** fixation and degradation are generally stimulated, especially in the rhizosphere (He et al., 2014; Yu et al., 2018). However, reciprocal transplant experiments demonstrate that decomposition rates are not solely dictated by climate; instead, they depend on specific **community-by-environment interactions**, indicating that microbial communities are not functionally redundant (Glassman et al., 2018).

Understanding these microbial processes is essential for predicting **climate-carbon** feedbacks. Most current **Earth system models** treat soil microbial biomass as a "black box," assuming that biogeochemical rates remain invariant regardless of changes in microbial community size or composition

(Schmidt et al., 2011; Gougoulias et al., 2014; Wieder et al., 2015). Yet, emerging evidence suggests that microbial physiological responses—such as changes in **carbon use efficiency** and thermal adaptation—determine whether an ecosystem acts as a **carbon** sink or source (Hartley et al., 2008; Frey et al., 2013). Warming-induced acceleration of decomposition, particularly of older recalcitrant **carbon** pools, represents a powerful positive feedback that could exacerbate global warming (Schmidt et al., 2011; DeAngelis et al., 2015; Xue et al., 2016).

The objective of this review is to synthesize current research on the role of soil microbial communities in global **carbon** cycling under the pressure of climate change. It evaluates the direct and indirect impacts of warming, **elevated carbon dioxide**, and interactive environmental stressors on microbial diversity, structure, and functional gene expression. By exploring the mechanisms of community-by-environment interactions and **carbon** stabilization, this review aims to clarify how "underground" microbial dynamics will dictate the future stability of terrestrial **carbon** stocks and the magnitude of global climate feedbacks.

2. Methods

The studies synthesized in this review utilized a diverse range of experimental and analytical methodologies to investigate **microbial-climate** interactions.

- **Environmental Manipulations:** Simulation of global change was achieved through long-term field experiments, including **Free-Air Carbon dioxide Enrichment** to simulate **elevated carbon dioxide** (Drigo et al., 2008; He et al., 2014; Yu et al., 2018) and the use of buried resistance cables or infrared radiators to increase soil temperature (Frey et al., 2008; DeAngelis et al., 2015; Xue et al., 2016). **Reciprocal transplant experiments** were employed to disentangle the effects of the microbial community from those of the abiotic environment (Bond-Lamberty et al., 2016; Glassman et al., 2018).
- **Microbial Characterization:** Taxonomic and functional diversity were assessed using high-throughput sequencing of **16S and Internal Transcribed Spacer ribosomal ribonucleic acid** genes (DeAngelis et al., 2015; Glassman et al., 2018) and **functional gene microarrays (GeoChip 3.0)** (He et al., 2014; Xue et al., 2016; Yu et al., 2018). **Stable Isotope Probing** was used to track **Carbon-13** and **Carbon-14** from plants into specific microbial groups (Drigo et al., 2008; Gougoulias et al., 2014).
- **Functional Assays:** Soil respiration and methane fluxes were measured using **Infrared Gas Analyzers** and gas chromatography (Bond-Lamberty et al., 2016; Medina, 2019). Enzyme activities were quantified using fluorometric and colorimetric assays to evaluate metabolic potential (Pold et al., 2015; Albright et al., 2020).
- **Data Integration:** Large-scale trends were synthesized through global meta-analyses and machine learning models (**random forest**) to predict biomass dynamics over decades (Zhou et al., 2020; Patoine et al., 2022).

3. Results

3.1 Shifts in Microbial Community Structure and Diversity

Research indicates that **global change factors** significantly alter microbial taxonomic composition, though these changes often manifest over decades. Long-term forest soil warming (20 years) resulted in a significant reduction in total microbial biomass and a specific decline in fungal abundance (Frey et al., 2008; DeAngelis et al., 2015). This was accompanied by an "**oligotrophic transition**," where warming favored taxa with lower **ribosomal ribonucleic acid** operon copy numbers, such as Alphaproteobacteria and Acidobacteria, adapted to limited resources (DeAngelis et al., 2015). Globally, microbial biomass **carbon** stocks decreased by 3.4% from 1992 to 2013, primarily due to northern hemisphere warming (Patoine et al., 2022). While some stressors reduce diversity, **land-use changes** can surprisingly increase alpha diversity, though rare species remain highly sensitive to all **global change factors** (Zhou et al., 2020).

3.2 Elevated Carbon Dioxide and Rhizosphere Dynamics

The impact of **elevated carbon dioxide** is primarily indirect, mediated through increased plant **rhizodeposition** (Drigo et al., 2008). This influx of labile **carbon** stimulates bacterial and fungal activity in the rhizosphere but has minimal effects on bulk soil (Drigo et al., 2008; He et al., 2014). However, this stimulation often triggers a "**priming effect**," where increased microbial activity accelerates the decomposition of native **soil organic matter**, potentially turning soils from **carbon** sinks into sources (Carney et al., 2007; Drigo et al., 2008). Elevated ozone tends to counteract these effects by inhibiting **nitrogen** fixation and mineralization (He et al., 2014).

3.3 Functional Gene Expression and Metabolism

Warming and **elevated carbon dioxide** generally stimulate functional genes involved in **carbon** fixation and degradation (He et al., 2014; Yu et al., 2018). In tallgrass prairies, 9 years of warming specifically stimulated the expression of genes responsible for degrading recalcitrant **carbon** (e.g., lignin and aromatics), likely due to a plant community shift toward **Carbon-4** species (Xue et al., 2016). In semiarid grasslands, moisture constraints can inhibit **nitrogen-cycling** genes under warming, highlighting the critical interaction between temperature and water availability (Classen et al., 2015; Yu et al., 2018).

3.4 Regulation of Carbon Fluxes and Stabilization

Microbial community composition is a unique predictor of soil respiration, explaining up to 12% of variation that abiotic factors cannot account for (Liu et al., 2018). Bacterial and fungal richness were identified as robust predictors of **dissolved organic carbon** concentrations, which are vital for long-term **carbon** stabilization (Albright et al., 2020). Furthermore, reciprocal transplants show that decomposer communities are not functionally redundant; their performance depends on specific **community-by-environment interactions** (Glassman et al., 2018).

4. Discussion

4.1 Interpreting Key Findings: Beyond the "Black Box"

The evidence synthesized here strongly supports moving beyond the "black box" approach in **Earth system models** (Gougoulias et al., 2014; Wieder et al., 2015). The observation that microbial composition uniquely drives respiration suggests that models must account for microbial life strategies (e.g., copiotrophs vs. oligotrophs) to accurately predict **carbon** balance (DeAngelis et al., 2015; Liu et al., 2018). The "oligotrophic transition" observed at Harvard Forest implies that long-term warming may destabilize recalcitrant **carbon** pools that were previously protected, creating a positive climate feedback (Schmidt et al., 2011; DeAngelis et al., 2015).

4.2 Limitations and Research Gaps

Significant limitations include the **spatial and temporal scale mismatch**; microbial activity occurs at the sub-micrometre scale over minutes, yet is measured at the ecosystem scale over years (Gougoulias et al., 2014; Classen et al., 2015). Methodologically, most studies rely on **deoxyribonucleic acid-based** sequencing, which does not distinguish between active and dormant populations (DeAngelis et al., 2015). There is also a critical lack of data on **horizontal gene transfer** and **predatory protists**, both of which likely play major roles in community adaptation and **carbon** budgets (Anderson, 2011; Gougoulias et al., 2014). Furthermore, the **phenological asynchrony** between roots and microbes remains largely unquantified (Classen et al., 2015).

4.3 Future Research Directions

Future studies should prioritize:

1. **Integrated "Omics" and Stable Isotope Probing:** Combining transcriptomics with **stable isotope probing** to track **carbon** flow in situ (Drigo et al., 2008; Gougoulias et al., 2014).
2. **Model Calibration:** Using real-world data (e.g., enzyme activity, **carbon use efficiency**) rather than assumed parameters (Wieder et al., 2015; Patoine et al., 2022).
3. **Multi-Factor Interactions:** Conducting experiments that simultaneously manipulate warming, **elevated carbon dioxide**, and moisture to capture realistic ecosystem responses (Classen et al., 2015; Yu et al., 2018).

5. Conclusion

Soil microbial communities are keystone components of the global climate system. The research synthesized demonstrates that climate change induces profound structural and functional shifts in these communities, often amplifying **carbon** loss through priming effects and the degradation of stable organic matter. While microbial responses are complex and context-dependent, ignoring their role limits our ability to achieve environmental sustainability. A concerted effort to include mechanistic microbial dynamics in policy and modeling is required to navigate the challenges of the **Anthropocene**.

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