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Review article

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Heterotrophic respiration by soil microbes in a changing climate

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Abstract

Soil microbes strongly influence the soil organic carbon (SOC) pool, which globally stores ~2,000 PgC. Specifically, the balance between microbial heterotrophic respiration (R_H), which degrades SOC, and plant–microbe interactions that stabilize SOC determines whether terrestrial ecosystems are a net source or sink of CO_2 to the atmosphere. In this Review, we evaluate how climate change alters these competing processes. R_H is approximately half of total soil respiration, at ~50 PgC yr^{-1}, with 70% occurring in topsoils. Warming accelerates microbial metabolism, with a 10 °C temperature increase estimated to raise R_H by ~50%, an effect that is particularly strong in Arctic soils. Warming also reduces soil moisture, further modulating R_H, which responds nonlinearly to soil moisture, being limited by saturation and desiccation and meeting a maximum at intermediate levels. Consequently, R_H is highly sensitive to future precipitation changes and drought. However, soil management strategies could enhance SOC stocks and persistence under climate change. Bacterial and fungal inoculants can promote SOC production and stabilization, while deep-rooting plants increase SOC inputs to deeper layers that experience lower R_H. Agricultural practices and biochar amendments can also enhance SOC and reduce R_H. Expanding field trials across regions, climates and soil types would improve empirical understanding of these responses and support better representation of R_H in predictive models, enabling more accurate assessments of climate impacts on SOC storage.

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Introduction

The balance of terrestrial photosynthesis and respiration determines whether the terrestrial environment acts as a source or sink of CO_2 to the atmosphere[1]. Each year, terrestrial plants take up roughly 115–130 petagrams (Pg; 10^{18} g) of carbon as CO_2 (refs. 2,3), corresponding to approximately a fifth of the carbon in the atmosphere[3]. Of this, about half is respired by plants back into the atmosphere (autotrophic respiration, R_A), and much of the remainder (~50 PgC yr^{-1}) is returned to the atmosphere by heterotrophic respiration (R_H) by soil microorganisms[4]. Today, the global terrestrial biosphere is a net CO_2 sink that offsets roughly a third of annual anthropogenic emissions, absorbing ~3 PgC yr^{-1} compared with ~10 PgC yr^{-1} of CO_2-equivalent emissions[3,5]. Whether this land sink will strengthen or weaken in the future depends, in part, on how soil microorganisms respond to a changing climate.

In soils, microbial heterotrophs perform respiratory metabolism, converting soil organic carbon (SOC), mostly deposited by plants, into atmospheric CO_2. These organic deposits include leaf litter, woody debris, root exudates, and microbial structures (for example fungal mycelia) fed by interactions with plants. Some of this carbon is quickly degraded, but other fractions persist for thousands of years, especially in cold climates[6]. Like most biological phenomena, R_H is strongly affected by environmental variables including temperature, water availability and the amount of organic carbon available in the soil[7]. Furthermore, elevated atmospheric CO_2 can fertilize plant growth, potentially resulting in increased photosynthetic output[8–11]. The resulting plant-derived carbon is stored in a variety of living and non-living forms, in plant, animal and microbial biomass, and as plant detritus. SOC is subsequently respired back to CO_2 over timescales ranging from years to millennia[12].

Atmospheric carbon dioxide (CO_2) levels have been increasing owing to anthropogenic emissions and other activities, driving a steady rise in mean global temperatures[1]. The planet reached a 1.5 °C increase above pre-industrial average global temperature for the first time in 2024 (ref. 13), with the NOAA Global Monitoring Laboratory recording unprecedented atmospheric CO_2 concentrations exceeding 430 ppm in May 2025. These atmospheric CO_2 levels are equivalent to a stock of ~1,000 Pg of carbon[3] and roughly half the global SOC stock (~2,000 Pg)[3]. The response of soil microbes to this and future global warming will strongly influence the terrestrial biosphere's status as a net CO_2 sink or source. On the one hand, warming tends to accelerate microbial respiration in soils, increasing CO_2 efflux[7]. On the other hand, soil microorganisms might also form symbioses with plants and stabilizing interactions with SOC that enhance the land sink[7]. It is therefore crucial to understand the spatial and temporal heterogeneity of these microbial effects and accurately predict whether they will intensify or attenuate the land sink.

In this Review, we synthesize diverse observational and experimental data on soil R_H (Fig. 1). First, we discuss the role of R_H in the global carbon cycle, before exploring how R_H is influenced by soil carbon chemistry and climate change. Next, we discuss interventions that might help soils lower R_H and retain soil carbon in the future. Finally, we outline priorities for future work, including expanding observational networks and using artificial intelligence (AI) to support the development of evolving microbial trait evolution in Earth system models (ESMs).

Role in the global carbon cycle

The amount of SOC contained in Earth's soils is approximately 2,000 PgC (refs. 14,15). Globally, total soil respiration estimates (R_S), including autotrophic respiration from plant roots (R_A) and R_H, range from ~90 to 130 PgC yr^{-1}, which is roughly tenfold greater than anthropogenic CO_2 emissions[2,4,16]. The highest R_S values are found in tropical regions[4]. Specifically, the highest predicted annual R_S is in evergreen broadleaf forests (~1,300 gC m^{-2} yr^{-1}), followed by savannas (~930 gC m^{-2} yr^{-1}) and deciduous broadleaf forests (~880 gC m^{-2} yr^{-1}) (Fig. 2). In addition, machine-learning predictions indicate that R_S is significantly higher in high-income regions owing to differences in the vegetation index in those regions[17]. Furthermore, simulations suggest that R_H from the topsoil layer (0–10 cm) represents ~70% of total estimated R_H, or ~282 gC m^{-2} yr^{-1} (ref. 18).

Total soil respiration is often not directly measured but estimated by scaling up site-level measurements[4,19] or by carbon balance[20] (Fig. 1). Subtracting respiration and wildfire from total photosynthesis gives the quantity of organic carbon retained by the biological land sink for carbon[7]. Both R_S and R_H are typically measured as CO_2 efflux from soil, which results from a composite of several biotic and abiotic processes[7]. Data compilations are then used to estimate global quantities[21] based on the Soil Respiration Database (SRDB)[22]. The mean R_H value in SRDB is 480 gC m^{-2} yr^{-1} (ref. 22). There are, however, substantial uncertainties in these global estimates (10–30%; refs. 4,21), and estimated respiration rates are sometimes inconsistent with other measured ecosystem properties[23]. What remains clear is that the R_H flux is large (tens of PgC yr^{-1}) and sensitive to Earth's changing climate, which affects R_H through changing temperatures[24–26], water availability[27–30] and organic carbon inputs[29,31,32], among other factors.

By applying estimates of the R_H/R_S ratio from sites where both values were measured[33,34], soil heterotrophic respiration is estimated at $R_H \approx 50$ PgC yr^{-1}, or approximately half of R_S (refs. 4,35). Although R_H is uncertain, sensitive to climate and a key source of uncertainty in climate projections[36–39], most climate model estimates indicate that R_H has been steadily increasing[18]. Extrapolating available model estimates into the future predicts a 40% global increase in heterotrophic respiration by the end of the century, driven largely by declines in soil moisture in the Arctic[18].

Soil carbon chemistry and respiration

SOC consists of different types of molecules, including organic and inorganic forms. This section discusses the influence of SOC chemistry on microbial respiration.

Carbon forms in soil

The inorganic part of soils is formed by chemical and physical weathering of minerals, and so the dry mass of soils is ~90% mineral: rocks, sand, silt and clays[40]. Most of the remainder (~10%) is soil organic matter (SOM), of which approximately 50% is carbon by mass[40], which includes all organic components of soil, such as decomposing plant and animal residues, exudates from roots and mycorrhizal fungi, living and dead microorganisms, and various substances synthesized by soil organisms[41].

Soil organics primarily originate from plants[42] and are subsequently transformed and respired by diverse microbes[43,44] yielding microbial biomass, CO_2, and other terminal products such as methane (CH_4) (Box 1). Like all organic materials, SOM contains carbon bonded to other elements such as nitrogen (N), phosphorus (P) and oxygen (O_2). SOC refers specifically to the carbon in SOM and is often measured to assess the amount of carbon stored in soils and to evaluate soil health. Generally, SOM constitutes ~50% carbon by mass, and so SOC ≈ SOM/2 (ref. 40). Globally, SOC stocks are likely to be growing[12].

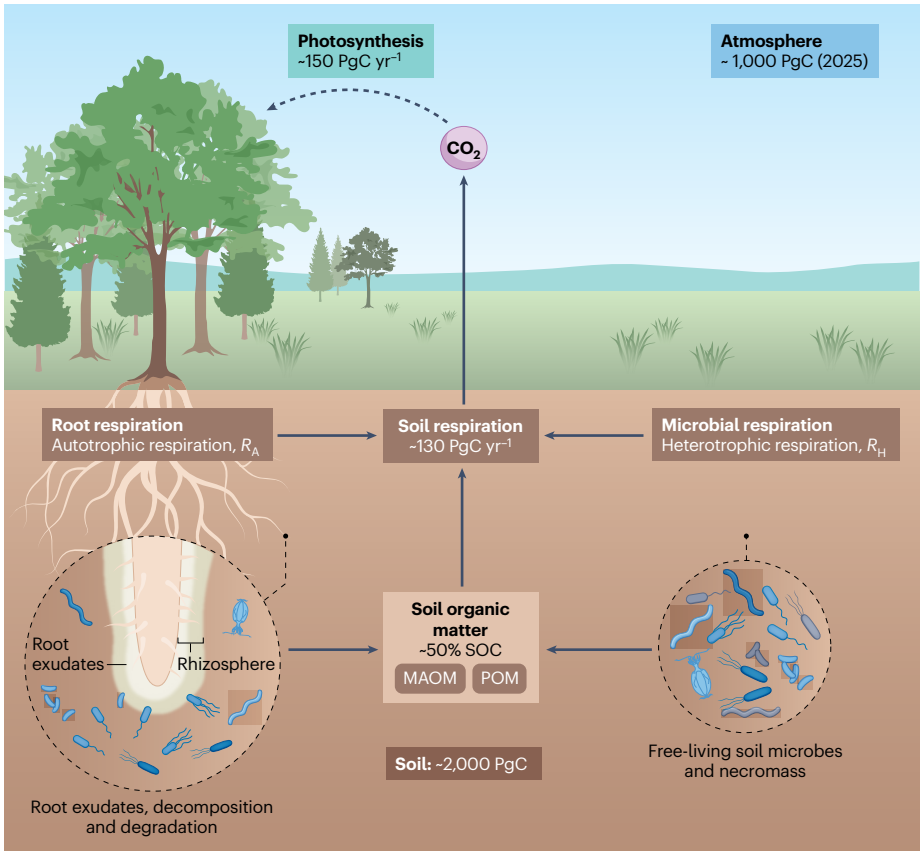


Fig. 1 | Soil carbon cycle. Plants take up carbon dioxide (CO_2) from the atmosphere by photosynthesis. Some of the plant-incorporated carbon is deposited into the soil through root exudates and decomposing plant material in the rhizosphere (area of soil influenced by the root). Soil carbon is returned as CO_2 to the atmosphere via soil respiration, including both microbial respiration (heterotrophic respiration, R_H) by free-living soil and rhizosphere microorganisms, and root respiration (autotrophic respiration, R_A). Soil organic matter contains ~50% soil organic carbon (SOC) and consists of particulate organic matter (POM) and mineral-associated organic matter (MAOM). Both free-living microbes and necromass can contribute to the soil organic matter pool, with necromass more often stabilized by association to minerals as MAOM. Black arrows represent the flow of carbon from the soil to the atmosphere. Dashed arrow represents flow of carbon from the atmosphere to plants via photosynthesis. In summary, soil respiration processes have an important role in the flow of carbon from the atmosphere to and from the soil.

SOM is traditionally subdivided into operationally defined categories that display characteristic differences in chemistry and stability[41,45]. For example, water-soluble organics are extractable with water and pass a filter. Particulate organic matter (POM), which does not pass the filter, consists mainly of highly structured and chemically complex organics[41,45]. POM is formed from the fragmentation and aggregation of plant and microbially derived materials. The structural complexity of POM means that microbes must secrete enzymes to break it down extracellularly, producing smaller molecules for uptake and intracellular metabolism[41,45]. Mineral-associated organic matter (MAOM) is formed from the sorption of SOC to soil mineral surfaces that act as a barrier to microbial access. Indeed, mean estimates of MAOM turnover times, ~130 years in the top metre of soil[46], are notably longer than the typical mean turnover time of ~23 years for POM[41,46–48]. Meta-analyses of soil fractions indicate that MAOM represents >50% of SOC in surface and deeper soil layers[49,50]. As such, the prevalence of MAOM in global soils motivates a thoughtful consideration of the factors affecting microbial access to organic substrates.

Plant and microbial inputs to soil carbon

The various plant tissues forming SOC have different physical structures and distinct chemical compositions that affect their ability to be respired by soil microorganisms[51,52]. For example, woody plant tissues are mostly composed of sugar polymers (cellulose, hemicellulose and pectin) and lignin (a cross-linked network of aromatic monolignols)[51]. Microbes secrete enzymes, which use metals (such as Mn, Cu) and reactive oxygen species (for example H_2O_2, •OH), to attack these polymer networks and generate monomers suitable for intracellular catabolism[53]. Further, woody tissues contain little protein, nucleic acid or lipids, and, consequently, far less N than leaves, microbial biomass or animal excreta. A resulting elemental imbalance is generated that makes woody tissues poor substrates for microbial growth[54]. By contrast, root exudates from perennial grasses are a mixture of smaller polar and semipolar compounds that are more readily degraded and respired[55].

In addition to plant inputs, soil microorganisms can contribute directly to the SOC pool. The microbial carbon pump concept suggests that microbial necromass (the biomass of dead microbes) is a relatively stable SOC pool[56]. Indeed, microbial necromass is potentially prone to mineral association, as the small size of microbial cells could promote association with minerals[56,57]. If microbes convert organics into biomass efficiently and then die in close association with minerals, this would form a microbial pump that contributes to MAOM formation and soil carbon stabilization[56,58,59]. Meta-analyses of proxies for microbial biomass estimate that microbial fractions of SOC[60,61] and MAOM[62] are of the order of 10–30%, even exceeding 50% in some cases. These estimates are consistent with the concept of a microbial carbon pump in soils.

Historically, it was presumed that some organic molecules are intrinsically recalcitrant to decomposition. Recalcitrant SOM was thought to be composed of highly cross-linked polymers formed by a humification process[63]. Yet these polymers have proven challenging to identify[64,65]. More broadly, the term 'recalcitrance' accommodates a range of definitions, limiting its conceptual usefulness[64,66]. A more

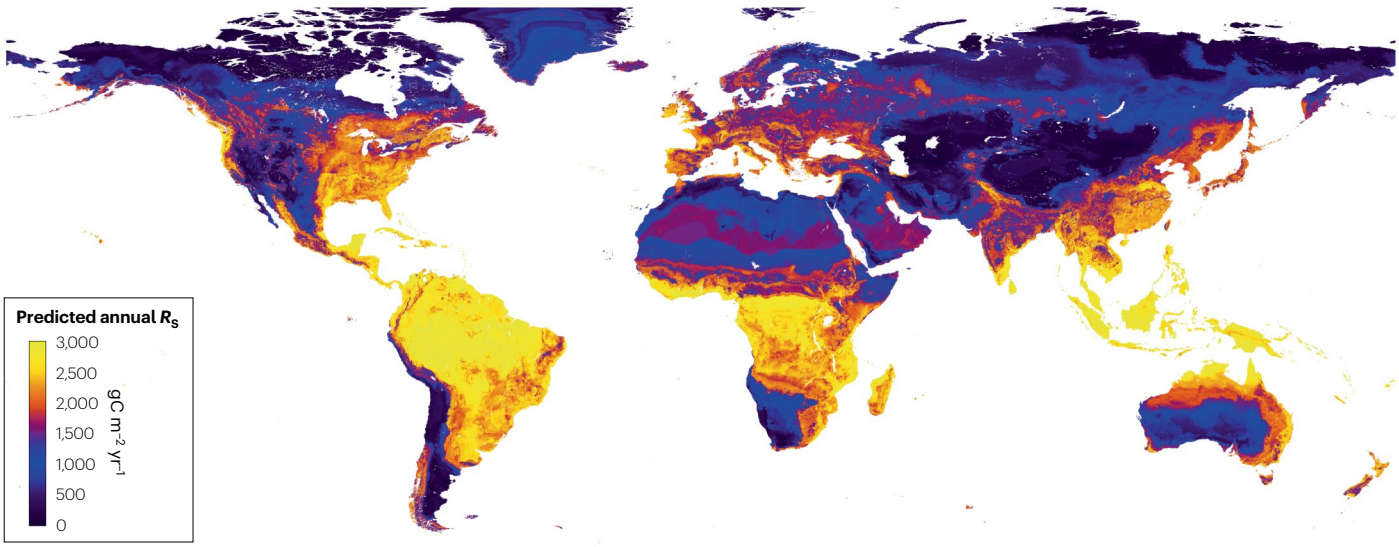


Fig. 2 | Predicted total soil respiration. Global annual estimated total soil respiration (R_S, gC m^{-2} yr^{-1}) at 1-km spatial resolution (modified from ref. 4). On a global scale, soil respiration is predicted to be higher in tropical regions.

nuanced contemporary framework posits that the rate of organic carbon degradation is an ecosystem property[65,67], meaning that SOC decomposition depends on a range of intrinsic and environmental factors. Such factors include molecular structure (for example polymerization), chemistry (for example aromaticity) and the local environment, which is itself characterized by a host of factors such as pH, O_2 tension, water potential, mineral protection, clay content, porosity and microbial community composition, as discussed in the next section. Anaerobic processes can also decompose SOC into CO_2, but aerobic processes are generally faster (Box 1).

Key factors influencing microbial respiration

Compiled evidence for key chemical features of organic molecules that affect microbial respiration is now discussed, acknowledging the highly complex chemistry of SOC. This synthesis includes organic carbon in sediments in addition to soils, given the large conceptual overlap between soils and sediments. For example, mineral association protects organics in both sediments and soils[68–71].

Evidence from sediment studies highlights that O_2 exposure time is a major factor determining microbial respiration capacity[72]. In the presence of O_2 it is both thermodynamically favourable and biochemically feasible for microbes to attack polymers, and degrade and respire all common soluble organics[53,73–75]. When O_2 is absent, however, the initial steps of SOC oxidation are less thermodynamically favourable, especially when the carbon is reduced (electron rich), as in lipids and aromatics[74–77]. As a result, lipids and waxes tend to be retained in floodplain sediments as well as wetter and deeper soils[76,78,79]. Similarly, lignified plant tissues degrade much more rapidly in oxic settings[80], partly owing to the many enzymes involved in microbial lignin degradation that rely on O_2 and reactive oxygen species[53,81,82].

Descriptors of SOC impacts on respiration

Apparent respiration rates, based on measured CO_2 efflux from the soil surface, are influenced by certain descriptors of soils and SOC. These include the redox state of carbon, its physical accessibility to microbes, the availability of key nutrients such as N and P, and the presence of high-potential electron acceptors, specifically O_2 and NO_3 (refs. 71–79). The character of the soil, its texture, lithology, chemistry and resident plants, also determines the nature of organic inputs, the penetrance of O_2, the forms of mineral association, and the physicochemical environment that microorganisms encounter[83].

Together, these descriptors determine both the rate of R_H and the spectrum of organics that microbes can profitably oxidize. In well-drained, mesic mineral soils — such as temperate agricultural fields, grasslands and tropical upland forests — air-filled pores keep O_2 replenished[84,85], aerobic heterotrophs dominate, and R_H can consume nearly the full range of plant inputs. Such inputs include labile sugars, amino acids and organic acids within hours to days[86,87]; structural polysaccharides such as cellulose and hemicellulose over weeks to months[88]; and even lignin and other aromatic polymers, given the O_2-dependent oxidative enzymes (peroxidases, laccases, mono-oxygenases and dioxygenases) needed to attack them[89,90]. Under these conditions, R_H commonly accounts for 50–70% of total soil respiration and can exceed 500 gC m^{-2} yr^{-1} in productive tropical and temperate systems[91,92].

By contrast, R_H is effectively switched off where O_2 supply collapses, most obviously following inundation or flooding: for example in peatlands, rice paddies, floodplain sediments, the active layer of thawing permafrost, and deep horizons below the water table. Because O_2 diffuses roughly four orders of magnitude more slowly through water than through air, aerobic demand quickly outstrips supply, and microbes shift down the thermodynamic ladder of alternative electron acceptors ($NO_3^- \rightarrow Mn(IV) \rightarrow Fe(III) \rightarrow SO_4^{2-} \rightarrow CO_2$; Box 1), each yielding progressively less energy[93]. The accessible substrate spectrum narrows accordingly, whereby relatively oxidized, low-molecular-weight compounds (sugars, organic acids, some amino acids) continue to be respired or fermented, and reduced or polymeric compounds (such as lipids, waxes, lignin and other aromatics), accumulate because their initial oxidation is no longer thermodynamically or enzymatically feasible. The net effect is that R_H in waterlogged peats and wetlands is often

one to two orders of magnitude slower than in adjacent aerobic soils, which is a central reason that these ecosystems store a disproportionate share of global SOC despite their limited areal extent[94,95]. Even within a single profile, millimetre-scale anoxic microsites can coexist with oxic pores, sustaining aerobic and anaerobic metabolisms in parallel and producing the heterogeneous R_H signal observed at the soil surface[84].

Small monomers that are redox neutral (sugars) or oxidized (organic acids) are more readily degraded than more complex compounds because they can be transported directly into microbial cells without prior extracellular hydrolysis, and their partially oxidized carbon requires few enzymatic steps to reach central metabolism and yield a favourable energy return[86,96]. By contrast, polymeric and reduced molecules are preferentially preserved in wet and deep soils (as outlined above), where the O_2 needed to make their oxidation thermodynamically favourable is scarce[96] (Box 1). Indeed, deeper soil layers (~3 m) are enriched in reduced molecules compared with surface soils[79]. Notably, as fractionation and detailed chemical characterization of SOM are technically challenging, the residence times of different carbon forms in different soil types, depths and climate zones merit further study.

Carbon-use efficiency and respiration

SOC can be respired by soil microorganisms to CO_2, excreted in various forms, or converted into biomass[97]. The ratio of respiratory CO_2 production to total carbon uptake (R/U) determines the fraction of total microbial carbon uptake (flux U) that becomes CO_2 (respiration flux R) and can be estimated from measurements[97]. One way to estimate the respired fraction is through its inverse, the carbon-use efficiency (CUE), which equals $1 - R/U$. CUE is a carbon yield whose value reflects the fraction of microbial SOC uptake that is not respired to CO_2 but instead retained in soil[97].

Given this definition, soils with high CUE might be expected to have high SOC stocks[59,98]. However, CUE values are usually derived from measuring the incorporation of labelled substrates, such as ^{13}C glucose, into microbial biomass over hours or days[98,99], whereas SOC is often hundreds or thousands of years old and its stocks result from processes occurring over much longer timescales[100]. Thus, to observe a correspondence between CUE and SOC stocks across sites, CUE values would need to be relatively consistent over decades and centuries, which is not at all obvious. Further challenges arise from noting that efficient carbon utilization produces microbial biomass, which can catalyse additional respiration, and microbial anabolism requires many nutrients in addition to carbon, including N and P (refs. 98,101). In addition, although CUE is widely used to understand[98,102,103] and estimate microbial respiration in global soils[36], a profound disconnect remains between physiological understanding of the CUE of laboratory cultures[104,105] and the carbon utilization that occurs in complex microbial communities in soils[97]. Thus, several confounding variables could influence the relationship between CUE and SOC stocks.

Despite these material caveats, there is a significant and positive correlation between SOC and CUE[98]. A meta-analysis of 132 sites found

Box 1 | Soil microbial respiration and greenhouse gas production

Soil microorganisms use respiration to generate energy by extracting electrons (e^-) from available e^- donors and donating them to e^- acceptors.

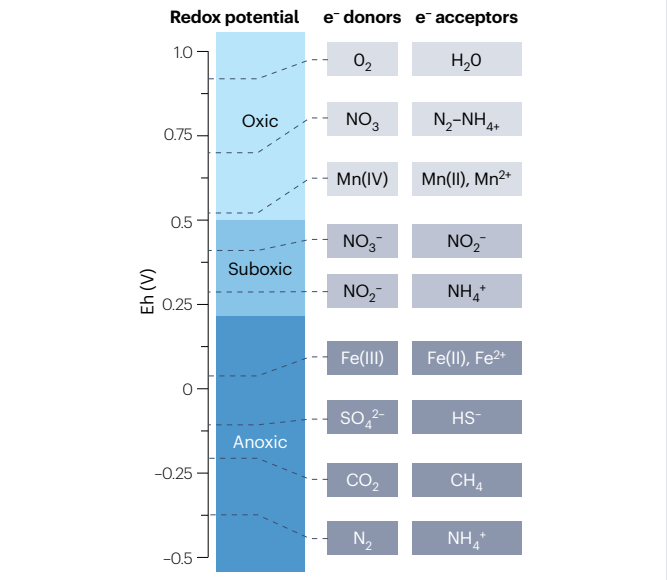
Heterotrophic respiration (R_H) generates biological energy by coupling the oxidation of organic matter to the reduction of an e^- acceptor, such as O_2 or nitrate (NO_3^-). Although the most thermodynamically favourable and vigorous process — aerobic respiration — uses O_2, microbes can use a wide range of e^- acceptors. The order of preference of e^- acceptors is O_2, then NO_3^- and then Fe^{3+}.

Denitrification is a respiratory process that uses NO_3^- as an e^- acceptor in low O_2 settings. The sequential oxidation of NO_3^- to N_2 passes through an intermediate, nitrous oxide (N_2O), the third most potent greenhouse gas (GHG) after CO_2 and methane (CH_4). N_2O and CH_4 production are strongly associated with low O_2 concentrations typical of waterlogged, suboxic or anoxic soils.

Respiration can draw e^- from other sources than organics. For example, some methanogens use molecular hydrogen (H_2) as an e^- donor to sequentially reduce CO_2 to CH_4. As CO_2 is a very poor e^- acceptor, methanogenesis typically occurs when other e^- acceptors have been exhausted, such as in anoxic and waterlogged environments.

However, moisture levels and redox conditions can fluctuate. Under these fluctuations, a substantial fraction of soil microbes can enter dormancy, later reactivating. Upon reactivation, short-term pulses of R_H are generated as intracellular reserves, and labile substrates are rapidly respired.

Therefore, applying thermodynamic concepts to natural environments requires nuance. Heterogeneous O_2 concentrations — driven by spatiotemporal variation in local microbial production and consumption — permit the coexistence of aerobic and anaerobic metabolisms at sites that seem oxic based on bulk concentrations. Thus, concentrations are imperfect proxies for fluxes. From a climate perspective, a forcing-weighted average of GHG fluxes is most important, focusing attention on rapid aerobic respirations and anaerobic metabolisms producing potent GHGs, such as N_2O and CH_4.



that CUE is more informative than other factors in explaining variation in SOC stocks[98], highlighting the usefulness of CUE in understanding the persistence of SOC.

Climate-change impacts on respiration

Climate change is associated with increasing atmospheric CO_2 and soil warming, as well as changes in the frequency and intensity of precipitation, flood and fire[106]. These changes can affect R_H in myriad ways[106] due to their impacts on microbial activity, community dynamics and substrate availability (Fig. 3). This section focuses primarily on temperature and moisture as key climate variables that influence heterotrophic respiration by soil microorganisms. Although temperature and moisture effects on respiration are linked, these two factors are discussed separately below.

Impacts on soil microbes

Climate change can affect microbial communities and their ability to respire SOC directly, through effects on microbial growth and survival; and indirectly, through changes in moisture, nutrient availability and vegetation dynamics. One way to predict temperature responses is to experiment with isolated microbes and microbial communities in the laboratory[105,107,108]. Other approaches involve soil incubations[109,110], field warming experiments[111–113] and meta-analyses of environmental datasets[114]. Unfortunately, rigorous quantitative connections between laboratory measurements, incubations and field studies remain elusive.

Characterizations of microbial community and functional diversity and composition offer insights into the responses of microbial communities to climate change[114–116]. For instance, sequencing data indicate the abundances of microbial taxa by counting ribosomal marker genes associated with particular lineages[117]. Similarly, chemical analysis of phospholipid fatty acid content reports on the relative abundance of lipids associated with certain taxa[118,119]. Other types of analyses offer insight into the functional response of soil microbes to climate change. Sequencing of total RNA (metatranscriptomics) or quantification of proteins (metaproteomics) can provide detail about how soil microorganisms respond to changes in environmental conditions by making different RNAs and proteins[120]. For example, this combination of approaches was used to document a shift from heterotrophic respiration to methanogenesis in response to permafrost thaw[121].

These approaches have been used to show that soil warming leads to a simplified microbial community structure, as opportunistic taxa increase in abundance and vulnerable taxa decline[122]. Meta-analyses across warming gradients revealed that increasing temperature reduces the species diversity of soil microbial communities[123]. Across wetland and dryland ecosystems, more than one-third of microbial taxa displayed either opportunistic (increasing) or vulnerable

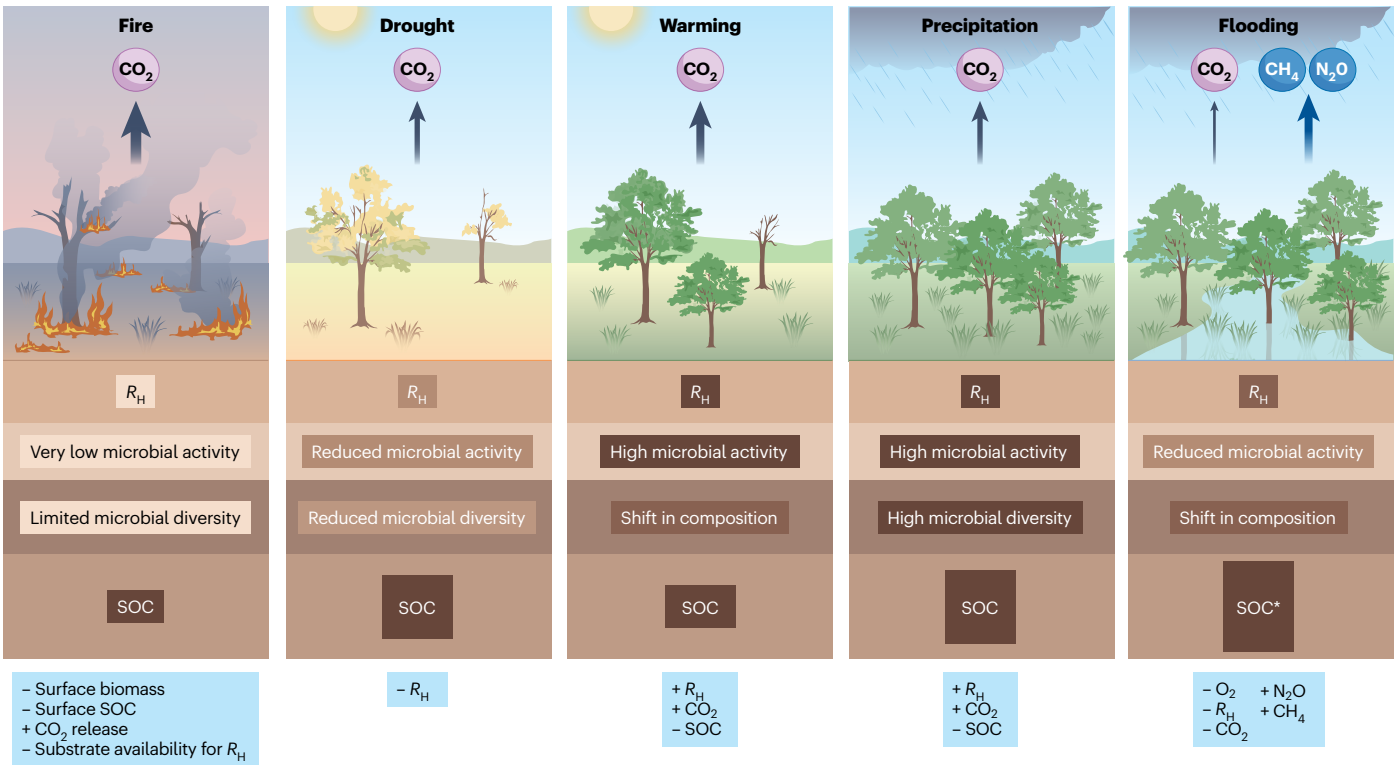


Fig. 3 | Influence of climate drivers on soil carbon stocks and heterotrophic respiration. From left to right: fire, drought, warming, precipitation and flooding are shown on individual panels that represent climate impacts on heterotrophic respiration (R_H). Grey-black arrows represent carbon dioxide (CO_2) efflux, with width proportional to flux; the blue arrow represents methane (CH_4) and nitrous oxide (N_2O) effluxes. The beige-to-brown boxes represent heterotrophic microbial respiration (R_H), microbial activity, microbial composition and the soil organic carbon (SOC) pool. The relative darkness and/or size of each box reflects the magnitude of the response. SOC* indicates that this representation is an estimate, as SOC under prolonged saturation might increase, decrease or remain stable depending on oxygen availability, dissolved organic carbon export, plant inputs, sedimentation and anaerobic mineralization. The blue boxes represent cumulative changes in soil properties as a result of different climate-change scenarios. In summary, different aspects of climate change can have different impacts on soil microorganisms and their activity, R_H and SOC pools.

(decreasing) responses to elevated temperatures[122]. However, inconsistent responses even within the same phylum highlight the limitations of predicting microbial sensitivity to climate change based solely on taxonomic affiliation. In addition, reductions in photosynthetic cover correlate with declines in vulnerable microbial taxa and increases in opportunistic ones, underscoring strong linkages between aboveground and belowground, and suggesting reduced SOC inputs[122]. Meta-analyses indicate that wetland ecosystems are particularly sensitive to warming and experience the most pronounced microbial shifts towards simplified and thermotolerant communities[123].

Both fungal and bacterial taxa are affected by climate warming. Laboratory-based incubations revealed measurable shifts in both bacterial and fungal taxa relative abundances over multiyear periods[116]. In another study, fungal taxa that responded opportunistically were positively associated with elevated R_S, implying that warming could intensify microbial-driven nutrient cycling[122]. In this analysis, drylands exhibited the highest fraction of responsive taxa, particularly among fungi[122]. In soil warming experiments[116], the ratio of fungi to bacteria[124–126] was correlated to changes in CUE and R_H, suggesting that this ratio might offer a simple descriptor that could be useful at the regional or global scale.

Influence on heterotrophic metabolism

Climate change not only influences respiration through altered microbial community composition; it also affects R_H through changes in temperature, precipitation and/or CO_2 levels[127]. In general, warming tends to accelerate microbial metabolism, whereas changing precipitation and CO_2 levels either slow or accelerate respiration, so that the global impact of climate change is more nuanced and difficult to predict[128] (Fig. 3).

Influence of CO_2. Elevated CO_2 has potential direct effects on R_H. Several long-term field experiments have used free-air CO_2 enrichment (FACE) to mimic future atmospheric CO_2 levels[129,130]. CO_2 enrichment increases plant productivity, which tends to increase carbon inputs to soil[9–11,130]. Globally, those additional inputs are partially retained as soil carbon, but some soils retain carbon and others do not[12]. In one experiment, soil respiration rates increased ~30% during the first two years of CO_2 enrichment, roughly matching the increase in plant photosynthesis[129]. The stimulatory effect declined over seven years, probably owing to changing nutrient status, in this case the loss of soil nitrogen[129,130]. Although CO_2 has some direct effects on microbial metabolism[131,132], CO_2 effects on R_H are generally considered to be the time-integrated result of increased plant productivity and therefore are mostly indirect[130].

Temperature impacts on respiration. Field and laboratory incubations are often used to characterize the temperature and water dependence of R_H. For example, extended laboratory incubations measuring R_H at a variety of temperatures[110,133] or with manipulated water content[28,134] enabled mathematical modelling of the isolated effects of temperature and water. Depending on the timescale of interest and the soil in question, manipulating water and temperature can have positive or negative effects on respiration rates. Therefore, more long-term field studies are needed to gain a better understanding of the combined impacts of water and temperature on R_H.

Generally, elevated temperatures increase respiration rates on relatively short timescales (months to years)[109,110,135]. Warming enhances R_H across spatial scales from microsites to the global biosphere, by accelerating enzymatic reactions and diffusive transport[136]. In the long term, increased R_H will deplete SOC, ultimately reducing observed respiration rates[109,137]. An early meta-analysis of R_S data in the SRDB indicated that warming does indeed accelerate total soil respiration, with an apparent temperature coefficient $Q_{10} \approx 1.5$ between 1989 and 2008 (ref. 19). This Q_{10} value indicates that a 10 °C temperature increase would increase R_S by 50%. Subsequent analyses updated these estimates and worked to resolve Q_{10} values for R_S and R_H separately, finding global Q_{10} values ranging from 2 to 3 with substantial geographic and climatological variation[109,138].

In situ soil warming is another strategy for determining temperature effects on R_H. A long-term warming experiment in a temperate hardwood forest revealed that there are four phases of respiration: an initial increase, acclimation, a second increase, and acclimation[135]. These different phases might reflect a shifting microbiome, including reductions in total microbial biomass and shifts in the community composition[135]. Therefore, the soil microbial communities adapt to changing temperatures, but their collective respiration is due to multiple complex factors including the metabolic preferences of individual taxa, the nutrient status of the soil and the composition of SOC[122,139–141].

The 'quality–availability' statistical model encapsulates a common understanding of temperature effects on soil heterotrophic respiration[109]. In this model, soil microbes preferentially consume high-quality substrates, so that the average quality and quantity of SOC decrease in time in the absence of new inputs. The model posits that low-quality, recalcitrant SOC has a greater kinetic barrier to respiration (smaller Q_{10} or larger activation energy), and that temperature increases affect R_H more when SOC is abundant. As such, it predicts a mixed temperature response in which modest increases in temperature increase R_H in the short term but the amount and quality of SOC is reduced in the longer term[109]. The quality–availability model accurately captures nearly all the variation in the temperature responses of respiration in a meta-analysis of ~700 soil incubations[109].

Temperature increases are likely to affect respiration directly and indirectly. For example, increased temperature can also reduce soil water content and provide more direct routes for gaseous O_2 to reach soil microbes. As a result of both direct and indirect effects, substantial increases in soil heterotrophic respiration are predicted in by 2100 (ref. 18). A 40% increase in global R_H is predicted by the end of the twenty-first century in high-emission scenarios, with particularly pronounced effects in the Arctic[136,142]. Arctic permafrost holds vast amounts of SOC, with estimates that it contains over 50% of the total SOC pool[143]. As global temperatures increase and permafrost thaws, previously frozen SOC can be respired. CH_4 can also be produced at wetter locations[142]. Microbial decomposition of older carbon previously locked in permafrost represents potent feedback of warming on CO_2 and CH_4 release[144,145]. However, the increase in respiration in boreal ecosystems undergoing permafrost transition is partly offset by increased photosynthetic productivity due to greening of the Arctic[146].

Comparisons of different climate models, such as the Coupled Model Intercomparison Project, show large variations in predictions of R_S and R_H with differences spanning hundreds of PgC over 50 years[38,39]. This variation is due to various factors, including limited global data on SOC stocks and changes[147], limited data on the physical and chemical status of soils[148], different models for predicting R_H (ref. 37), and sparse data regarding permafrost carbon dynamics[38]. The application of Q_{10} and Arrhenius equations to respiration poses yet another challenge. Both are widely used temperature-dependence formulations: that is, Q_{10} expresses the fold-change in respiration per 10 °C of warming, and the Arrhenius equation describes the same temperature sensitivity

through an activation energy term. This formalism has a fundamental justification rooted in the assumption of a single rate-limiting reaction step[137]. In soils, however, heterogenous organics are metabolized by a tremendous diversity of soil microbes, suggesting that more than a single barrier is justified[105]. Indeed, the quality–availability model also considers a single time-varying barrier determined via the changing SOC quality[109]. Applying statistical approaches that allow for heterogeneous or disordered kinetic barriers (a distribution of SOC quality) can overcome these single-barrier limitations[149–152].

Moisture impacts on respiration. Soil moisture shifts owing to climate change have strong influences on soil respiration, with complex interactions that amplify or constrain temperature effects[153]. Importantly, the response of R_H to soil moisture often follows a nonlinear relationship, with maximum R_H occurring at intermediate moisture levels[27,28]. Measured CO_2 efflux is generally highest at the soil optimal moisture content and decreases at lower and higher moisture levels[154,155]. One emerging theme is the importance of microscale conditions in determining the observed respiration rate, particularly under varying moisture conditions[30]. The impact of change in soil moisture on R_H is determined by several factors, including soil porosity, which governs the amount of aeration, and the availability of SOC accessible to microorganisms[156]. Pore-scale models suggest that SOC is metabolized rapidly once it becomes available[30]. However, different variables, including clay content, can restrict SOC availability[29,30]. Thus, it remains challenging to extrapolate from pore-scale models to the field scale. In addition, uncertainties in soil water estimates present a challenge for making accurate predictions of R_H (ref. 18).

Many areas of the globe are experiencing more frequent and intense precipitation events, owing to climate change[157]. An increase in soil moisture can result in saturation of soil pores, which decreases O_2 availability because the diffusion constant for O_2 is several orders of magnitude smaller in water than in air[18,134,158]. In the absence of O_2 (Box 1), anaerobic microbial processes can dominate, producing other greenhouse gases such as nitrous oxide (N_2O) and CH_4.

Other areas of the globe are experiencing decreased precipitation and, consequently, soil desiccation[157]. Arid soils limit microbial metabolism via osmotic stress and reduced mobility of organic substrates[159]. Satellite gravity observations indicate that climate warming is shifting the balance of Earth's hydrological cycle, with a loss of approximately 1.6 Gt of available soil water between 2000 and 2002 (ref. 160). Soil desiccation is further accelerated by poor landscape management and increased frequencies of fire (itself a source of CO_2)[161]. Fire alters soil structure, microbial communities and SOC reserves[162] with short and long-term impacts on R_H. Fire can also result in permafrost thaw with an immediate release of CO_2 from surface soils, although the long-term impacts of fire on permafrost are uncertain[162].

Sensitivity to drought is particularly acute in semiarid ecosystems where reduced precipitation lowers SOM content and constrains R_H, thereby reducing microbial carbon cycling capacity[163]. By contrast, the thawing of the Arctic permafrost is resulting in an increase in SOC availability for microbial respiration[164]. Higher, drier Arctic locations are more aerobic and therefore prone to respiration, whereas lower, wetter regions are prime locations for methanogenesis[164] (Box 1). Although the amount of SOC becoming available is a concern, SOC composition can also influence R_H in thawing permafrost, and SOC speciation varies substantially between different sites and with depth and is determined by the prevailing organic or mineral nature of the local soil[165].

The Birch effect is a phenomenon where apparent respiration rates increase following wetting of dry soils[166–169]. Real-time monitoring of dry soils incubated with ^{13}C-labelled glucose showed immediate CO_2 production following rewetting that was mostly derived from the native ^{12}C, with the ^{13}C label only after 15 min (ref. 170). These results suggest that rewetting promotes the consumption of intracellular ^{12}C before extracellular ^{13}C glucose, consistent with the notion that SOC pools differ in their accessibility to microbes[170]. The resident CO_2 might also be inorganic because hydration of minerals releases CO_2 (ref. 170).

Mitigating respiration and SOC loss

Climate-smart soil management practices are proposed to reduce R_H and loss of SOC stocks by promoting accumulation of stable forms of SOC, depressing R_H directly, or both[171]. These strategies must be evaluated for their ability to increase SOC stocks, as well as their performance under projected climate stressors that can accelerate R_H and SOC loss. Therefore, understanding how mitigation approaches interact with stressors, such as warming, altered precipitation, drought and extreme weather events, is essential for developing resilient, climate-smart management.

Microbiome-based interventions

As microbial metabolism is the direct catalyst of most SOC cycling, some proposed manipulations target the microbial community directly[172]. Other agricultural management practices target the broader soil environment in which microbes live and respire[172]. Microbiome stewardship is the science-based management, conservation and manipulation of microbial communities to maintain or restore the health or organisms and ecosystems[173]. Microbial interventions, whether direct, through microbial inoculants[174], or indirect, through the use of organic amendments or environmental manipulation[172], are emerging as potential tools for regenerative agricultural practices (Fig. 4). Although not directly related to soil respiration, N-fixing microbial inoculants are already widely deployed, showing the potential for harnessing microbial metabolism to support agricultural productivity and sustainability[175]. For example, N-fixing inoculants applied to Brazilian soybeans generated US$15 billion in savings and avoided 183 Mg of CO_2-equivalent emissions from 2019 to 2020, demonstrating both economic and climate benefits[176].

One microbial inoculation strategy involves the application of plant-growth-promoting bacteria[177]. These have been used in agriculture (single species and consortia) as alternatives to chemical fertilizers and pesticides[177]. Some of these inocula seem to increase SOC over the short term, potentially by accumulating microbial necromass or by supporting plant growth[178]. For example, Actinomycetes are often used as plant-growth-promoting microbes and might stabilize SOC via formation of filamentous structures[178].

The tendency of microbial necromass to mineral association and aggregate formation offers a potential mechanism of SOC stabilization[56]. If specific taxa preferentially form stabilized forms of SOC, like MAOM, one management strategy could be to add microbial inoculants that capture plant-derived SOC, die, and form necromass that becomes associated with MAOM. Although the idea of promoting the formation of MAOM-associated necromass has received substantial attention[56–58], there is still a need to better understand microbial necromass contributions to SOC and MAOM. Studies indicate that microbial residues make up a large fraction of SOC, even exceeding 50% in some cases[60,61,179], yet these measurements rely on many untested assumptions. Better characterization of necromass content and stability, especially in fluctuating conditions, is sorely needed to support the microbial carbon pump concept that underlies some inoculants[44,56,57,59,60].

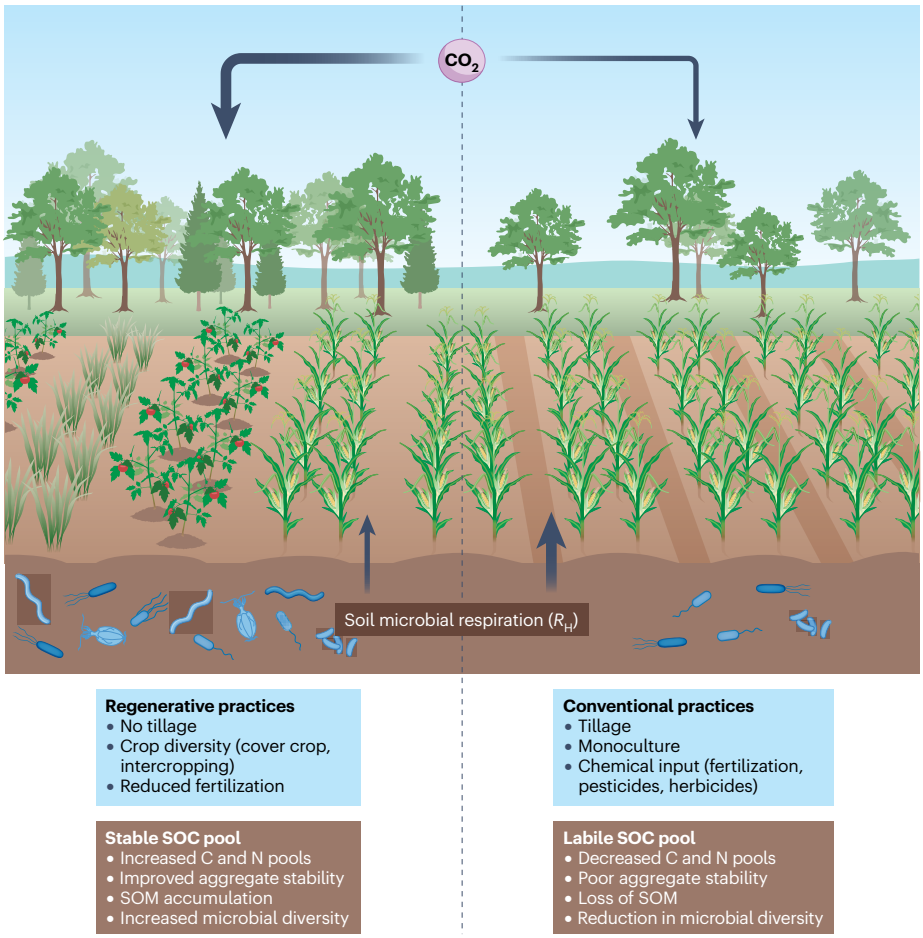


Fig. 4 | Influence of agricultural practices on soil microbial respiration. Carbon dioxide (CO_2) fluxes are represented by arrows: downward arrows represent uptake and upward arrows represent efflux. In summary, regenerative practices are better than conventional agriculture at reducing soil carbon loss through soil microbial respiration (R_H). SOC, soil organic carbon; SOM, soil organic matter.

There are several uncertainties for deployment of microbial inoculants and other strategies to reduce R_H. Despite their widespread use, microbial inoculants — whether as single species or communities — face competition from the native soil microbiome[180]. Inoculants with higher diversity tend to be less successful at establishing themselves[180–182]. Additionally, even if these introductions fail initially, they can trigger strong secondary successions, potentially shifting communities to alternative, stable functional states[183,184]. The variability in performance across field conditions, along with the ecological risks linked to the legacy of microbial inoculants, must be carefully considered when implementing these approaches.

Many uncertainties also stem from shifting climatic conditions. For example, temperature-driven metabolic acceleration, altered moisture, and nutrient availability can all change the function and persistence of inocula[177]. A key underlying assumption is that microbes have defined, manipulable roles in stabilizing or destabilizing soil carbon. However, microbes are often facultative (perform different roles in different settings), the environment is variable, and SOC is heterogeneous[185]. A gram of soil typically contains 10^7–10^9 individual bacteria representing 10^3–10^4 bacterial taxa, suggesting that the specific habits of individual species can average out even at small scales[186,187].

There are also uncertainties surrounding the extent to which microbial groups perform concrete functions owing to limitations in culturing or characterizing the full diversity of soil microbes. So, despite promising laboratory and field studies, deployment of microbial inocula is stymied by competition with native microbial populations, environmental variability, and challenges in predicting microbial persistence and function under field conditions[172,188]. Addressing these uncertainties requires a deeper understanding of the genetic or ecological mechanisms by which interventions influence communal respiration, and how these changes translate into long-term carbon stabilization[172,189].

Plant-based strategies to increase SOC

Plant-based strategies that promote root development offer a promising indirect route to enhance SOC sequestration and reduce R_H. For example, larger and deeper root systems can deposit more durable SOC into deep soil layers where it is less accessible to microbial respiration[190]. Importantly, root biomass contributes disproportionately to SOC formation relative to aboveground litter, and deeper root inputs can persist for centuries owing to mineral protection and reduced disturbance[191–193]. Deploying soil-carbon-enhanced cultivars with deeper and more massive root systems could therefore increase SOC at scale without expanding agricultural land. For example, deployment of such cultivars across ~190 Mha (~13% of global agricultural land), focused on the four major commodity crops (soybean, maize, cotton and canola) in the five countries that lead today's genetically modified

crop market, could lead to a rapid ramp-up of carbon removal that peaks at ~1 $GtCO_2$ yr^{-1} within ~13 years of first deployment, subsequently stabilizing as soils approach saturation[190]. This strategy could optimistically amount to ~7 times more CO_2 removal than all existing offsets supplied today to the global voluntary offsets market. Models of the depth-dependent age of SOC indicate that subsoil carbon can exhibit turnover times that are orders of magnitude slower than topsoil, consistent with carbon inputs below the active rhizosphere contributing disproportionately to long-term SOC persistence[194].

Enhanced crops also present a complementary approach to microbial inoculants. Instead of altering the microbial community directly, plant inputs alter the structure of the microbial environment[190]. These plant inputs provide substrates for microbial growth and necromass production, thereby driving stable SOC accumulation belowground[190–192]. However, responses of carbon-enhanced cultivars to combined warming, CO_2 enrichment, and variable precipitation regimes remains unclear.

Fungal strategies to increase SOC

Fungi are also promising inoculants for enhancing SOC storage. Fungal endophytes form different types of associations with plant roots, exchange nutrients with plants[195,196], and could increase plant carbon assimilation[197]. Fungi can also enhance plant water uptake and protect roots against thermal and osmotic stress[198,199]. Therefore, fungal symbioses could be especially important as droughts intensify and soils experience more frequent wet–dry cycles. For example, addition of endophytic fungi increased SOC by 17% over 14 weeks in a greenhouse experiment[200]. In addition, some mycorrhizal fungi produce a compound, glomalin, that is promising as a resilient carbon reservoir[200]. Certain fungi also release plant-derived carbon as exudates, with a distinct chemical profile from those released by plants[201].

The presence of fungi can alter microbial food webs, resulting in interactions with bacteria that positively affect plant growth[202]. As plants produce SOC, positive fungal interactions could potentially boost SOC as well. Indeed, certain fungi seem to transfer exudates to deeper soil horizons[203], which could result in longer-term carbon storage. In addition, some fungi produce sclerotia — resting structures containing lipids and glycogen — and hold promise for long-term retention of SOC[204]. Soil aggregation by fungi is another mechanism to stabilize SOC[205,206]. Hyphal density is an important contributor to soil aggregation, with Ascomycota fungi being the most efficient soil aggregators[206]. Although mycorrhizal fungi stabilize SOC, how they respond to warming, elevated CO_2 and moisture regimes remains unstudied. These knowledge gaps limit understanding of the potential of mycorrhizal fungi to mitigate increased R_H under climate change.

Indirect strategies for SOC storage

Manipulations of the soil environment can also influence microbial metabolism[171,189,207]. Soil management practices that reduce disturbance and increase cover can buffer R_H increases caused by warming and erratic rainfall, while enhancing water retention and thermal stability. For example, practices such as no-till agriculture, cover cropping, crop rotation and biochar amendment, especially when combined, have demonstrated the capacity to enhance carbon storage and reduce R_H (ref. 208) (Fig. 4). Meta-analyses of cover-cropping experiments indicated increased SOC content of surface soils (top 30 cm SOC increased by ~15%) and an increased rate of SOC accumulation in surface soils of 30–60 gC m^{-2} yr^{-1} (refs. 209,210). Estimated cover-cropping-associated SOC accruals therefore amount to a substantial fraction (5–15%) of the typical R_H values (~420 g m^{-2}). However, SOC increases are only evident in surface soils (depth <30 cm) and diminish with time[209,210]. Moreover, the methods of these analyses have been called into question, producing more conservative revised estimates that are 10–20-fold smaller (~3 gC m^{-2} yr^{-1})[211]. Solving this disagreement is critical because the larger values focus attention on cover cropping as a key tool for carbon sequestration, whereas the smaller values do not[211,212].

Nutrient amendments offer another indirect approach to manipulating R_H. For example, in temperate forests, N addition reduced R_H by ~15% on average[213,214], suggesting that restoring C:N balance increased microbial carbon use efficiency. However, individual sites varied from ~60% reduction to ~60% stimulation of R_H (ref. 214), emphasizing the complexity and context dependence of collective microbial respiration. Results from P addition are similarly variable, indicating that the scientific community lacks the predictive understanding of R_H that is needed to apply nutrient amendments reliably[215]. Moreover, nutrients can interact strongly with temperature and moisture[216], highlighting the need for climate-conditioned field trials.

Application of pyrolysed organic material, called biochar, has received particular attention for its potential to stabilize SOC, alter microbial metabolism, and reduce CO_2 efflux from soils[217]. Biochar is rich in carbon but relatively slow to decay[218]. Meta-analyses found increases in SOC following biochar amendments, particularly in soils with a fine texture and alkaline pH (ref. 219). However, the success and longevity of these effects are highly site specific, with environmental variables modulating microbiomes and, in turn, being modulated by microbial dynamics[220].

Emission of other microbially produced greenhouse gases, including N_2O produced via denitrification (Box 1), can also be mitigated via management strategies. Co-application of synthetic nitrification inhibitors with N-bearing nutrients can reduce N_2O emissions from agricultural soils[221,222]. Inhibition of biological nitrification limits the production of soil-borne nitrate (NO_3^-), which is a substrate of respiratory denitrification[223,224]. The reduction of N_2O emissions varies with fertilizer and soil types, as well as soil water content[225]. Meta-analyses found a consistent 30–60% reduction in N_2O efflux[223,226,227], indicating that soil microbial processes can be influenced by chemical treatment. Although nitrification inhibitors have existed since the 1960s, their deployment has been limited because cheap nitrogen fertilizers reduced the economic incentive to conserve N (refs. 228,229). As major dairy supply chains now seek lower climate footprints, inhibitors might see broader adoption owing to their ability to curb N_2O emissions[230,231]. However, their broader biogeochemical effects, including impacts on soil respiration and CO_2 fluxes, remain poorly quantified[232,233].

Although the practices reviewed offer some short-term benefits, their long-term (>10-year) effects are generally unknown. In cases in which longitudinal observations are available, they are often variable and context dependent, highlighting the need for site-specific assessments and long-term monitoring of SOC. For example, for experiments studying the effects of tillage, multidecade time series are available[234,235]. Yet these experiments can only interrogate specific sites, leaving substantial uncertainty regarding the scalability of interventions across climate zones and soil types. Analysis of long-term field data from the Rothamsted research site in England suggested that conversion of agricultural land to forest or grassland had the greatest benefit with respect to increase in SOC[236]. For example, from 1880 to 2000 there were measurable increases in SOC in soils that transitioned from agriculture to forests. However, the 4 per 1,000 initiative that aims to increase SOC by 0.4% per year was considered unrealistic, owing

to insufficient resources and economic incentives for farmers[237]. As climate change takes place over decades and centuries, it is important to determine the long-term effects of intervention. Yet, for most proposed interventions, there are quite limited long-term data.

Decision-making should consider microbiome-based and plant-based mitigation approaches, accounting for their mechanisms, climate relevance, scalability and uncertainties (Table 1). Although microbial inoculants can rapidly modify SOC dynamics, plant-based strategies provide longer-term, climate-resilient carbon inputs. Co-deployment, which optimizes microbial consortia for specific plant genotypes and climate regimes, represents a promising frontier for reduction of R_H and increasing C storage in a changing climate.

Summary and future perspectives

Soil R_H represents one of the largest and most temperature-sensitive carbon fluxes in the Earth system. It is shaped by nonlinear and synergistic interactions between temperature, moisture, substrate quality and microbial physiology. For instance, SOC persistence reflects chemical recalcitrance, mineral association and spatial protection, whilst microbial traits such as CUE, enzyme kinetics and thermal adaptation can modulate these fluxes[27,65,67,97,98,137]. Field experiments show that management interventions, such as microbial inoculants, biochar and crop diversification, can modify SOC stocks and R_H (refs. 98,172,177,209,219,238).

Microbially explicit models help to constrain uncertainty in SOC projections[238]. However, incorporating microbial traits into Earth system models (ESMs) is a major challenge as microbial responses to temperature, moisture and substrate quality are context dependent and exhibit pronounced spatial heterogeneity, sometimes shifting within centimetres and diverging further across ecosystems[239,240]. Learning how to properly average this fine-scale variability across space and time to produce responsible and generalizable models applicable at regional or global scales is a priority[238,241].

A core challenge is that microbial trait measurements do not directly map onto R_H even at the local scales. CUE, growth rates and enzyme activities are only indirect indicators of microbial processes, whereas R_H emerges from complex interactions between microbes, minerals, soil physics and hydrology. As a result, trait data often provide only partial observability of the underlying drivers of CO_2 release. This limitation is compounded because measurements of common microbial traits are typically derived from laboratory or small-plot experiments, which do not capture all of the processes at play and do not directly scale to the spatial extent of ecosystems or ESMs[242]. Moreover, microbial traits vary dynamically with environmental conditions, such as local resource supply, redox conditions and disturbance history[243,244]. Consequently, different combinations of microbial traits and soil properties can yield similar CO_2 fluxes, leading to persistent issues with parameter identifiability and equifinality[245,246].

Table 1 | Strategies to mitigate soil heterotrophic respiration and soil organic carbon loss

	Microbiome-based interventions	Plant-based interventions	Co-deployment potential
Mechanism	Directly manipulate microbial communities to alter SOC turnover, enhance necromass formation and shift CUE under changing temperature and moisture	Enhance plant root inputs (carbon quantity and depth) to increase SOC stabilization and reduce labile substrate exposure to R_H	Combined strategies couple root-driven carbon inputs with microbially mediated stabilization (for example deep-rooted plants+carbon-sequestering inoculants)
Climate-change relevance	Target microbial responses to warming, drought and redox fluctuations — drivers of accelerated R_H. Effective under scenarios in which microbial respiration dominates SOC loss	Build resilience to elevated CO_2, temperature and drought by promoting deep rooting, improved water-use efficiency and persistent subsoil carbon deposition	Integration enhances resilience of both biological components — root inputs sustain microbial communities that stabilize C under stress
Interventions	Deploy microbial inoculants, microbial necromass builders and/or engineered consortia (SynComs)	Breed or engineer carbon-enhanced crops (for example deep-rooted perennials); use crop rotations and cover crops	Bioengineer co-optimized plant–microbe pairs (for example plant genotypes matched with drought-resilient microbes)
SOC effects	Moderate short-term SOC gains through necromass accumulation and reduced R_H rates; highly context dependent	Larger, longer-term SOC gains via increased carbon inputs and protection in deeper, cooler and moister soil layers	Potential for synergistic SOC stabilization when necromass formation complements deep carbon input
Timescale of impact	Months to years (rapid microbial turnover; short feedback cycles)	Years to decades (root system development and deep C accrual)	Multidecadal persistence if co-adapted plant–microbe systems are maintained
Feasibility	Moderate: requires site-specific microbial selection, containment protocols, and long-term persistence testing	High for existing crops; moderate for engineered varieties (regulatory and adoption hurdles)	Moderate–high if co-development pipelines (breeding+inoculant) are aligned
Scalability and deployment potential	High near-term scalability in managed systems (for example continental-scale deployment of inoculants in Brazil and China), but limited predictability in the field	Very high scalability through seed-based deployment, but slower owing to breeding cycles and regional adaptation	High if integrated into regenerative agriculture frameworks or carbon-credit MRV systems
Data and monitoring needs	Requires molecular tracking and necromass quantification	Requires plant trait phenotyping, root biomass/depth mapping, and belowground SOC tracking	Joint monitoring networks combining omics, isotopic tracing, and remote sensing
Main uncertainties	Longevity, ecological displacement and functional persistence of introduced microbes under future climate extremes	Trade-offs between productivity, stress tolerance and carbon allocation; uncertain deep-root growth under different scenarios	Interaction stability: will plant–microbe mutualisms persist under long-term warming, CO_2 enrichment and altered hydrology?

CUE, carbon-use efficiency; MRV, measurement, reporting and verification; R_H, heterotrophic respiration; SOC, soil organic carbon.

Progress therefore requires more than simply expanding parameter sets, but depends on upscaling strategies that treat traits as distributions rather than single values. It also relies on observations jointly constraining traits and fluxes, and model–data integration frameworks that assess when trait-based formulations increase predictive skill relative to simpler empirical or pool-based models[36,238,242,245]. Four detailed recommendations for action to help guide future research and a microbiome-informed soil management strategy over the next 10–15 years are now outlined (Fig. 5).

First, more globally distributed and comparable field trials are needed to assess the efficacy of direct and indirect microbial interventions to increase SOC and reduce R_H, focusing on degraded or climate-sensitive soils[173]. Microbial inoculants to promote soil health and fertility are a growing global agribusiness, with >800 patents for microbial inoculants in China and >200 million doses applied in Brazil[177]. Priority biomes should include tundra and boreal zones (permafrost thaw gradients), tropical oxisols and ultisols (Amazonia, Cerrado), semiarid rangelands (Sahel, US Southwest) and temperate croplands (mollisols, alfisols). Each site should use standardized measurement, reporting and verification (MRV) protocols. Standardized approaches should include using soil CO_2 flux chambers and eddy covariance partitioning for R_H and R_A; isotopic labelling ($^{13}C/^{14}C$) for turnover constraints; metagenomic, metatranscriptomic and metabolomic profiling for microbial trait dynamics; and inoculant tracking via strain-specific quantitative PCR or barcodes. Safety, durability and function persistence should also be evaluated over multiyear intervals under realistic management and climate scenarios. Pre-registration of trial protocols and open-access data sharing will enhance comparability and replication.

Second, long-term, moisture-explicit observing systems and harmonized datasets for model calibration and validation should be developed. Most existing R_H estimates rely on short-term data, yet soil processes unfold over decades[4,7,19,34]. A network of long-term field sites co-located with infrastructures, such as NEON[247], ICOS[248], FLUXNET[249] and LTER[250], spanning diverse ecozones should be established. These sites should integrate automated soil temperature and moisture sensors, oxygen microelectrodes and repeated SOC coring at depth intervals (0–100 cm) for MAOM and POM fractions. Standardized metadata and harmonized protocols should feed into global repositories such as SoilGrids 2.0 (ref. 192), WoSIS[251] and SRDB[252]. Annual resampling and radiocarbon dating will reduce geographic bias and enable recalibration of statistical and process-based models[147]. The goal is to produce benchmark datasets that constrain and validate machine-learning and process-based models predicting R_H responses to moisture, temperature and management.

Third, microbial metabolic traits should be linked to carbon fluxes through laboratory-to-model pipelines. Controlled laboratory experiments quantifying microbial physiological traits and processes across soil types and climate treatments could help reduce uncertainty in R_H-related CO_2 fluxes. Upscaling these insights to scale could be supported by AI platforms that leverage genomics, soil chemistry and environmental metadata[253]. Large AI models can summarize omics data into useful trait inputs for ESMs by estimating likely ranges of microbial physiological parameters. Instead of assuming fixed values, these traits (such as CUE, enzyme kinetics, biomass turnover) are quantitatively represented as probability distributions learned from many different data sources[253]. AI models can also mine and combine data from scientific literature, genomic databases and environmental measurements to estimate likely trait ranges across different soil types and climates.

These trait range estimates can then be used as flexible starting assumptions in Bayesian data-assimilation pipelines, allowing traits in microbially explicit submodules (such as MESDM[242], MEND[254], CORPSE[255]) in ESMs to be continuously updated as more field observations become available. In the long term, global experimental networks could maintain priors that evolve as soils, climates and management regimes change, analogous to seasonal reanalysis frameworks used in numerical weather prediction. To improve predictive performance, improving transparency and reproducibility, standardized models should report identifiable parameters and trait uncertainty.

Finally, water-oxygen controls of R_H need to be quantified across scales. Moisture and oxygen availability are first-order regulators of R_H (refs. 27,76), yet are underrepresented in most ESMs[27]. Future

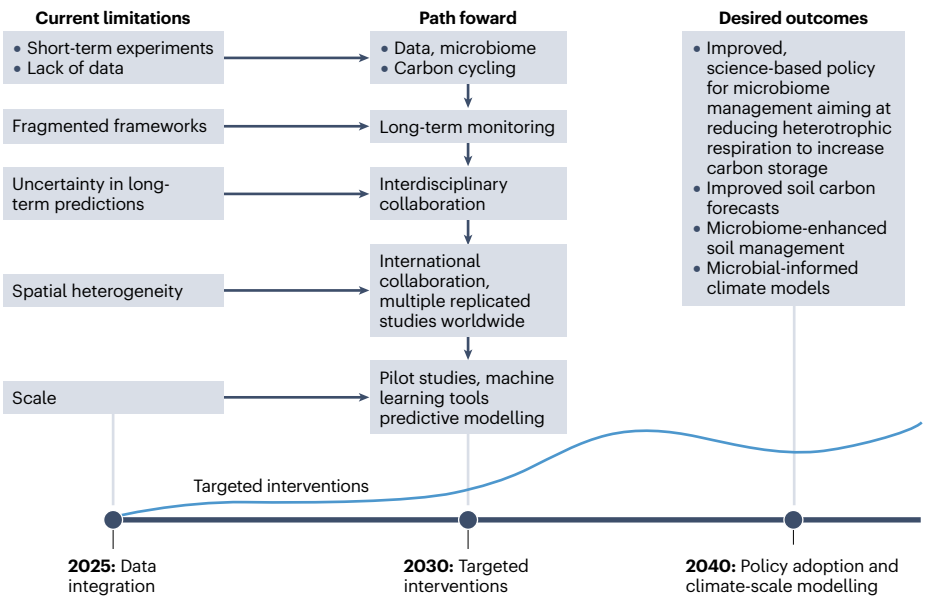


Fig. 5 | A roadmap towards microbiome-informed soil respiration management. Existing limitations in microbiome-informed soil respiration management can be overcome by specific steps towards a path forward (horizontal arrows). Vertical arrows represent successive steps under the path forward to achieve targeted interventions by the year 2030. Desired outcomes by 2040 are shown at the right. The blue line illustrates the relative increase over time in targeted interventions. To achieve desired outcomes at the policy level and for climate-scale modelling by the year 2040, it is necessary to perform specific steps via targeted interventions by the year 2030.

research should couple microscale (micro-computed tomography (μCT)-derived pore structure, diffusion modelling) and macroscale (distributed soil moisture and temperature sensing) approaches to map oxygen limitation thresholds and anaerobic transitions. Field programmes should set up instruments in thawing permafrost, post-fire boreal soils and drought-prone rangelands to capture R_H, CH_4 and N_2O fluxes alongside microbial trait adaptation. Radiocarbon and stable isotope tracing can partition fast versus slow carbon pools, and metatranscriptomics and metabolomics reveal microbial acclimation. Policy-relevant frameworks should integrate these data into MRV protocols for soil carbon markets, ensuring durability and additionality through moisture-explicit and oxygen-explicit verification[76,171].

Although not exhaustive, these coordinated empirical and modelling efforts would transform soil respiration from one of the least well-constrained to one of the best-constrained biospheric fluxes. These advances would enable mechanistically grounded and practically verifiable climate projections and mitigation strategies.

Data availability

The data supporting Fig. 2 are available from the cited primary research article[4].

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