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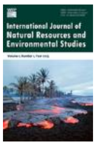

The Chemotactic Behavior of Microorganisms Plays a Critical Role in the Spatial Regulation of Carbon Emission Hotspots

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ABSTRACT

The global carbon cycle is fundamentally a biological achievement of spatial organization, yet conventional soil carbon models frequently overlook the active role of microbial motility by assuming spatial homogeneity. This review challenges that assumption by elucidating the impact of bacterial chemotaxis—mediated by the Che A/Che Y signal transduction pathway—on the formation of metabolic hotspots. We demonstrate how microorganisms navigate tortuous pore networks to sense chemical fingerprints (e.g., root exudates), generating micrometer-scale zones where metabolic activity increases by two to three orders of magnitude. The physical disruption of this spatial order, particularly through tillage, leads to a profound "decoupling" of the carbon cycle, evidenced by a 27%–34% reduction in soil respiration and a loss of carbon sink capacity. By integrating molecular ecology with microscale process dynamics, we propose a novel framework that elucidates the cascade mechanism extending from chemical fingerprint recognition to community self-organization, and ultimately to carbon flux regulation." This approach links chemotactic protein signaling to gas diffusion processes, offering a robust theoretical foundation for the precise regulation of soil carbon sinks in the pursuit of carbon neutrality.

KEYWORDS

Soil; Carbon; Metabolic hotspots.

1. INTRODUCTION

The global carbon cycle is not merely a chemical equation balanced by thermodynamics; it is a biological achievement of spatial organization[1]. Soil microorganisms, utilizing the ancient machinery of the Che A/Che Y signal transduction pathway, actively engineer their environment. They navigate tortuous pore networks, decipher chemical fingerprints, and assemble into highly structured metabolic hotspots that defy the laws of bulk chemistry[2].

Conventional soil carbon models frequently rely on assumptions of spatial homogeneity, thereby overlooking the impact of active microbial motility on the patterning of carbon fluxes, which compromises their ability to accurately explain the emergence of emission hotspots. Chemotaxis fundamentally reshapes resource competition at pore-aggregate interfaces: by sensing carbon sources such as root exudates via specialized receptors (e.g., MCPs), microorganisms generate micrometer-scale hotspots where metabolic activity varies by up to two to three orders of magnitude. Such spatial heterogeneity accelerates organic matter decomposition and reconfigures carbon release pathways through mechanisms like interspecific electron transfer, including the co-localization of methanogens and methanotrophs[2, 3]. The disruption of this spatial order—through the blunt force of tillage—leads to a profound "decoupling" of the cycle, evidenced by the 27%–34% reduction in soil respiration and the loss of carbon sink capacity. This review presents a novel integration of molecular ecology with microscale process dynamics, systematically elucidating the cascade mechanism of "chemical fingerprint recognition → community self-organization → carbon flux regulation" mediated by chemotactic behavior. By establishing a mechanistic link between chemotactic signal transduction proteins (Che A/Che Y) and gas diffusion processes in soil pore networks, this framework transcends the oversimplified representations of microbial spatial behavior in traditional models, offering a robust theoretical foundation for the precise regulation of soil carbon sink function in pursuit of carbon neutrality.

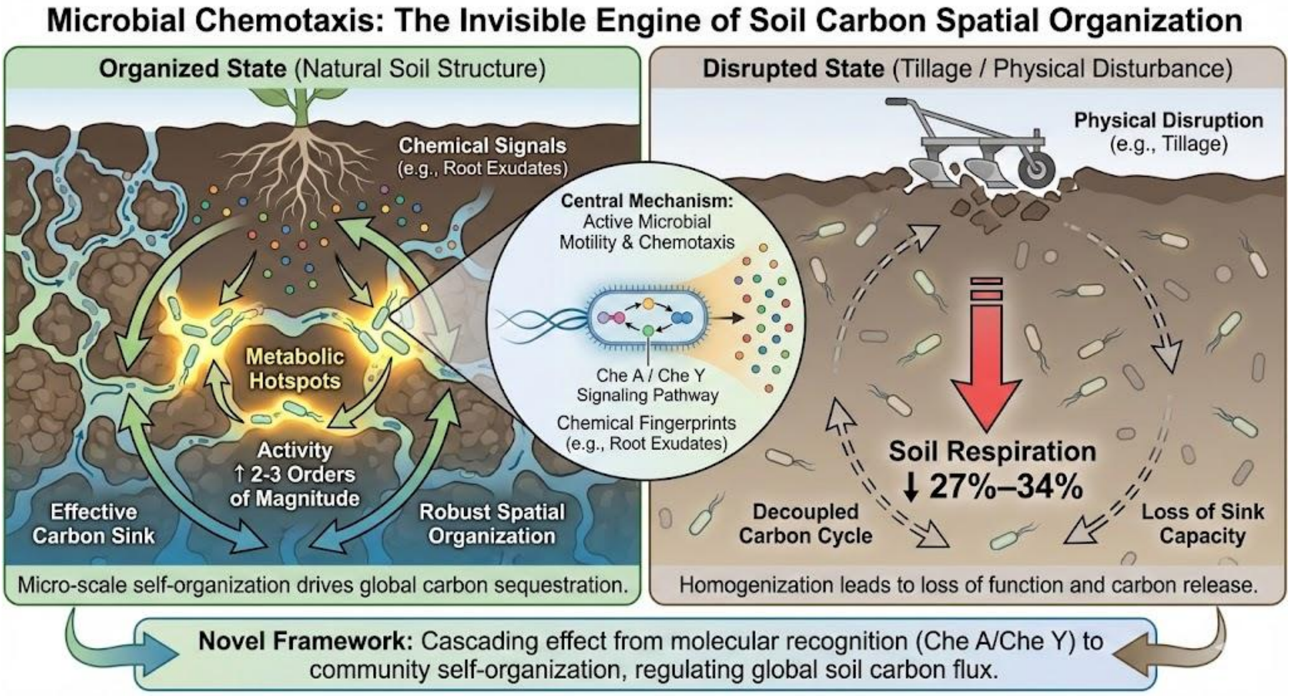

Figure 1. The mechanism diagram of the cascading effect of microbial chemotaxis in driving the spatial organization of soil carbon

2. SPATIAL REGULATION OF MICROBIAL CHEMOTAXIS BEHAVIOR ON CARBON EMISSION HOTSPOTS

2.1. Molecular and ecological mechanisms of chemotaxis signaling pathways

The signal transduction pathway of microbial chemotaxis behavior centers around a two-component regulatory system, consisting of a multilevel regulatory network composed of transmembrane receptors (such as MCPs), sensor kinases Che A, and response regulators Che Y[4]. When microorganisms perceive a carbon source gradient in the environment (such as root exudates or organic acids), MCPs receptors bind to chemical ligands, triggering CheA autophosphorylation and transferring phosphoryl groups to CheY, forming an active CheY-P complex. The phosphorylated Che Y-P regulates the direction of flagellar rotation by binding to the flagellar motor: counterclockwise rotation drives the microorganisms to move linearly along the carbon source gradient, while dephosphorylation of Che Y-P (dependent on Che Z protein) initiates clockwise flagellar rotation, causing the microorganisms to tumble and adjust their migration direction[4, 5]. At the ecological level, the dynamic regulation of chemotactic signaling pathways enables microorganisms to efficiently locate carbon-rich areas and form local metabolic hotspots. For example, the stability of the CheA-CheW complex is enhanced under high-pressure conditions (such as the CheA homolog protein of the deep-sea bacterium Thermococcus kodakaraensis, maintaining 85% activity at 40 MPa), ensuring chemotactic efficiency under extreme conditions[6]. Meanwhile, chemotactic receptor methylation modification (regulated by CheR and CheB) maintains the spatial precision of chemotactic response in carbon source fluctuations by dynamically balancing chemical signal sensitivity. This mechanism significantly enhances the activity intensity and spatial heterogeneity of carbon emission hotspots by accelerating organic matter decomposition and interspecies electron transfer[4, 6].

2.2. Diversity of chemotactic strategies and their ecological mechanisms

The diversity of microbial chemotaxis strategies is reflected in the co-evolution of movement patterns and carbon source capture efficiency. Swimming chemotaxis (such as flagellar rotation in Escherichia coli) is suitable for homogeneous carbon source environments, achieving wide-area exploration through "tumble-and-go" movement; whereas swarm chemotaxis (such as type IV pili gliding in Pseudomonas aeruginosa) forms biofilm precursors in heterogeneous environments, relying on group collaboration to accelerate local carbon source utilization[7]. In extreme environments, chemotaxis systems exhibit high-pressure adaptability, such as the CheA protein of the deep-sea bacterium Thermococcus kodakaraensis, which maintains approximately 85% activity at 40 MPa, ensuring stable signal transduction[8]. In different ecological niches, chemotactic differentiation reflects carbon source preference regulation: methanogens occupy pollution hotspots by sensing aromatic compounds through specific receptors, while methanotrophs rely on formate gradient sensing to co-locate with them, forming a carbon cycle microecology[6]. Furthermore, epigenetic regulation (such as chemotactic receptor methylation) enables microorganisms to dynamically adjust sensitivity in response to carbon source fluctuations. For example, demethylation of chemotactic receptors in saline-alkali soil enhances response to low-concentration carbon sources. Overall, these diverse chemotaxis strategies increase the decomposition rate of organic matter by 2–3 orders of magnitude by regulating community metabolic division of labor, providing a new perspective for understanding the spatial heterogeneity of soil carbon flux[4].

3. SPATIAL REGULATION OF MICROBIAL CHEMOTAXIS BEHAVIOR ON CARBON EMISSION HOTSPOTS

Microbial chemotaxis shapes the spatial heterogeneity of carbon emission hotspots in soil through chemical gradient sensing and directed migration. Microorganisms recognize carbon source signals such as root exudates and organic acids through chemotactic receptors (e.g., MCPs), triggering the CheA-CheY signaling cascade, which drives flagellar rotation and directional aggregation to areas enriched with carbon sources[9]. This local localization forms regions of high metabolic activity, where the decomposition rate of local organic matter can be increased by 2-3 orders of magnitude. Chemotaxis not only enhances the metabolic activity of individual communities but also accelerates the mineralization of organic matter through extracellular enzymes (such as cellulases and chitinases), releasing CO_2[10]. Simultaneously, interspecific chemotactic co-localization (such as between methanogens and methanotrophs) forms a coupled network of electron transfer and carbon metabolism, improving the efficiency of CH_4 production and oxidation and reducing gas diffusion losses. In nitrogen-enriched environments, microorganisms exhibit heightened sensitivity to intermediate products such as NO_3^-, and chemotaxis towards high nitrogen areas accelerates substrate decomposition and releases N_2O[11]. Furthermore, the migration pathways of microorganisms along pore networks and gas diffusion channels form spatial coupling, causing local steep gradients in CO_2 and CH_4 concentrations, which drives the concentration of carbon emission hotspots towards aggregate edges or rhizosphere interfaces[12].

In the temporal dimension, chemotactic behavior regulates carbon emission dynamics through metabolic rhythms. For instance, microbial responses to diurnal temperature variations can induce periodic changes in extracellular enzyme activity. For every 1°C increase in soil temperature, β-glucosidase activity increases by approximately 15%-20%, resulting in a 30% higher peak carbon emission during the day compared to at night[13]. Simultaneously, methylation modification of chemotactic receptors (such as CheR/CheB regulation) enables microorganisms to rapidly adjust their migration and metabolic strategies in response to fluctuations in carbon sources. Under drought conditions, they preferentially migrate to areas enriched with residual organic matter, maintaining the continuity of decomposition activities[11, 14]. Overall, microbial chemotactic behavior, through the spatiotemporal coupling mechanism of "chemical sensing-spatial aggregation-metabolic enhancement," not only forms and maintains carbon emission hotspots but also significantly enhances soil carbon transformation efficiency, providing a scientific basis for precise prediction and regulation of soil carbon flux.

4. REGULATION OF THE CHEMOTAXIS-CARBON EMISSION RELATIONSHIP BY ENVIRONMENTAL FACTORS

The interaction between physicochemical factors and human activities jointly determines the formation and distribution of carbon emission hotspots by regulating microbial chemotactic signaling and metabolic activity. The coupling of temperature and pH significantly affects chemotactic signaling: increased temperature accelerates the phosphorylation rate of CheA kinase, enhancing the response to carbon source gradients, while acidic conditions ($pH < 5.5$) inhibit CheZ activity, prolonging the duration of CheY-P signaling, and enabling stable aggregation of microorganisms in organic matter-enriched areas[15]. The synergistic effect of dissolved oxygen and salinity also reconstructs the carbon emission pathway. Low-oxygen environments induce the upregulation of the methanogen mcrA gene, promoting its migration to carbon-rich areas. High salinity enhances the chemotactic efficiency of halophilic bacteria by stabilizing the CheW-CheA complex, thereby facilitating the accumulation of methane precursors, such as acetic acid[16]. Meanwhile, water dynamics regulate pore connectivity: a continuous water film is conducive to flagellar motility, while during drought, microorganisms rely on extracellular polysaccharides to glide, maintaining migration and decomposition processes[17]. In addition, the composition of dissolved organic matter (DOM) and redox potential jointly shape the chemotactic microenvironment. Aromatic-rich DOM generates small-molecule acids under $Eh < -200$ mV conditions, activating the methanogen MCP2901 receptor and promoting its colocalization with methane-oxidizing bacteria, resulting in a 40%–60% increase in the spatial matching degree between $CH4$ generation and oxidation[18, 19].

Human activities further amplify or disrupt this mechanism. Agricultural intensification and high nitrogen fertilizer application weaken the chemotactic sensitivity of methanogens, leading to a 30%–50% decrease in CH_4 emissions from rice paddies. Deforestation and urbanization damage the pore network, weaken chemical gradient signals, and reduce the decomposition rate of organic matter by about 40%. Industrial pollutants alter the carbon emission pattern through signal toxicity inhibition. Heavy metals can bind to CheA kinase phosphorylation sites to block signal transduction, forming metabolic inert zones. Microplastics adsorb dissolved organic matter (DOM), creating "chemical traps" on the surface of aggregates, inducing chemotactic aggregation but inhibiting extracellular enzyme secretion, resulting in a 60% decrease in local carbon flux. Hydrological regulation also significantly alters the redox environment: drainage projects weaken the low-oxygen response of methanogens, eliminating CH_4 hotspots; while artificial irrigation promotes the formation of new carbon oxidation hotspots by enhancing chemotactic migration under an O_2/CH_4 dual gradient, reducing net carbon emissions by about 20%.

Overall, temperature, moisture, salinity, redox conditions, and human intervention jointly shape the chemical perception thresholds and movement paths of microbial chemotaxis, thereby determining the spatiotemporal distribution and intensity of carbon emission hotspots. This interactive regulatory mechanism reveals the sensitivity of the carbon cycle to environmental changes and human activities, providing a theoretical basis for the precise regulation of global carbon emissions.

CONFLICTS OF INTEREST

The authors declare that they have no conflict of interest.

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